Molecular diversity and stability analysis for seed yield and its components in cluster bean [*Cyamopsis tetragonoloba* (L.)Taub.]

By

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CERTIFICATE–I

This is to certify that this dissertation entitled **“Molecular diversity and stability analysis for seed yield and its components in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]” s**ubmitted for the degree of Doctor of Philosophy, in the subject of **Genetics and Plant Breeding** to the **Chaudhary Charan Singh Haryana Agricultural University, Hisar**, is a bonafide research work carried out by **Mr. Ravish Panchta** Admission No. 2017A31D, under my supervision and that no part of this dissertation has been submitted for any other degree.

The assistance and help received during the course of investigation have been fully acknowledged.

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CERTIFICATE-II

This is to certify that this dissertation entitled **"Molecular diversity and stability analysis for seed yield and its components in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]"** submitted by **Mr. Ravish Panchta** (Admission No. 2017A31D), to the **Chaudhary Charan Singh Haryana Agricultural University, Hisar** in partial fulfillment of the requirements for the degree of **Doctor of Philosophy**, in the subject of Genetics and Plant Breeding, has been approved by the student's Advisory Committee after an oral examination on the same.

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Format for P.G. Thesis

This is to certify that the thesis submitted by Mr. Ravish Panchta, Admission no. 2017A31D, Ph.D. student of this department has been checked and found as per specification of the format circulated by the Dean, PGS vide his memo no. PGS/A-1/09/6926-90 dated 26.08.2009.

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ABBREVIATIONS

Abbreviations used	**Description**
AMMI	Additive main effect and multiplicative interaction
HS 19	Hisar summer 2019
BS 19	Bawal summer 2019
HK 19	Hisar *kharif* 2019
BK 19	Bawal *kharif* 2019
HS 20	Hisar summer 2020
BS 20	Bawal summer 2020
HK 20	Hisar *kharif* 2020
BK 20	Bawal *kharif* 2020
PH	Plant height (cm)
DFF	Days to 50% flowering
DM	Days to maturity
PMS	Pods on main stem (no.)
PPP	Pods per plant (no.)
PPC	Pods per cluster (no.)
SPP	Seeds per pod (no.)
BPP	Branches per plant (no.)
100SW	100 seed weight (g)
PL	Pod length (cm)
BMPP	Biomass per plot (kg)
HI	Harvest Index (%)
CPP	Cluster per plant (no.)
SYPP	Seed yield per plot (kg)
GC	Gum content (%)
PC	Protein content (%)
TSS	Total soluble sugar content (mg/g dry weight)
RS	Reducing sugar content (mg/g dry weight)
NRS	Non-Reducing sugar content (mg/g dry weight)
Lignin	Lignin content (% dry weight basis)
CellC	Cellulose content (% dry weight basis)
HCellC	Hemicellulose content (% dry weight basis)
Silica	Silica content (% dry weight basis)
ADF	Acid detergent fibre content (% dry weight basis)
NDF	Neutral detergent fibre content (% dry weight basis)
BLBI	Bacterial leaf blight intensity (%)
PNB	*Pusa Nav Bahar*

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CHAPTER-I

INTRODUCTION

Cluster bean (*Cyamopsis tetragonoloba* L. Taub.) is an important multipurpose crop of arid and semi-arid regions primarily grown for its seed. The genus *Cyamopsis* contains four species namely, *C. tetragonoloba, C. senegalensis, C. serrata,* and *C. dentata*belonging to *Fabaceae* family and *Papilionoideae* sub-family (Dwivedi and Bhatnagar, 2002; Chevalier, 1939). *Cyamopsis* was emphasized to be a separate genus and probably originated from Africa center of origin (Gillett, 1958). According to Vavilov (1951), India is the center of variability for cluster bean. It is believed to be originated through the process of Trans-domestication (Hymowitz, 1972). The cultivated cluster bean species, *C. tetragonoloba,* reported to be developed from a drought tolerant wild African species *C. senegalensis* (Mudgil *et al.,* 2014).

Cluster bean is a diploid (2n=14), self-pollinated, erect herb with papilionaceous flowers arranged in axillary raceme with 10 stamens in diadelphous condition and head shaped stigma. The flower can be of either purplish pink or white in colour. The seed is dicotyledonous and can be grey to white in colour containing hull (14-17%), endosperm (35-42%) and germ (43-47%). The endosperm contains 19-34% galactomannan gum, while, the guar meal (hull+germ) obtained after the gum extraction contains about 29-46% protein. The guar meal is used in poultry and cattle feeding (Kumari *et al.,* 2020). The cultivation of cluster bean has been reported back in ancient ages in Indian subcontinent as fodder, green manure and vegetable. India is the leading cluster bean producing country accounting for more than 80% of its production in the world. Apart from India it is also grown in the arid and semi-arid areas of Pakistan, U.S.A., Italy, Morocco, Germany and Spain (Jukanti *et al.,* 2015; Kumari *et al.,* 2020). In India, it is grown in the states like Rajasthan, Gujarat, Haryana, Punjab, Uttar Pradesh and Madhya Pradesh in the areas with light to medium textured soils, no water logging, rainfall range of 250 – 450 mm with 3-4 spells and temperature range of 25 to 40°C (Panchta *et al.,* 2017; Kumar *et al.,* 2019). Rajasthan is the major cluster bean producing state followed by Haryana.

Cluster bean is regarded as an Industrial crop due to versatile applications of its galactomannan gum commonly known as guar gum in various industries. The guar gum is having a straight chain of D-mannose unit linked together by β (1- 4) glycoside linkage and D-galactose units are joined to it at each alternate position by (1-6) glycosidic linkage. It forms a rod like polymeric structure with a mannose backbone linked to galactose side chains, which are randomly placed on mannose backbone with an average ratio of 1:2 galactose to mannose1, 7. The polymeric structure contains numerous hydroxyl groups, which are treated for manufacturing different derivatives used for various applications in industries (Tripathy *et al.,* 2018). Cluster bean gum has a potential in many pharmaceutical applications due to its non-toxic, biodegradable nature and viscous dispersions or gel forming ability in aqueous media. The cluster bean gum can be used in effective transdermal, colon specific and antihypertensive drug delivery systems in the form of hydrogels, nanoparticles and bead forms. In pharmacology, it is used for the treatment of hypercholesterolemia, hyperglycemia and obesity (Manjunath *et al.*, 2016). In food industry, the cluster bean gum is extensively used for the production of gluten free pasta and bread, as fat replacer in yoghurts and ice creams, as egg replacer in bakery products (Theocharidou *et al.*, 2022). In cosmetic industry it is used in the formulation of shampoo, hair conditioners, hair colours, shaving creams, face masks, tooth pastes *etc.* Apart from these, it is used in paper industry, textiles, explosives and bio remediation *etc.* During 2012-13, there was a huge demand of cluster bean gum from U.S.A. due to its extensive use in hydraulic fracturing in the shale gas extraction. Hydroxypropyl guar and carboxymethylhydroxypropyl guar are commonly used guar derivatives in fracturing fluids. Due to desirable rheological and thermal properties of these co-polymers at different degrees of grafting, temperature, time, concentration, the cluster bean gum has become a valuable material in the global market for its applications in hydraulic fracturing for oil and gas well drilling (Thombare *et al.*, 2016).India has exported 234,871.31 MT of cluster bean gum to the world for the worth of Rs. 1949.07 Crores/ 262.99 USD Millions during the year 2020-21 and U S A, Germany, Russia, China, Norway were the major export destinations (APEDA, 2020-21).

In the states like Rajasthan which covers the 80% of cluster bean production it is the backbone for the arid and semi-arid areas during *kharif* season where its cultivation is almost entirely dependent on monsoon rains. Cluster beanis highly capable to recover from drought stress exposure. Nodule number is less in guar than in other legumes due to meristematic types of nodules. Unlike any other legume the nitrogenase activity may be reversible even if water content of guar nodules is decreased by 60-70 percent. The threshold limit for nitrogenase activities had been observed to the extent of 0-2.4MPa (Rao &Venkateswarlu, 1987). Therefore, it is physiologically more efficient than the other legumes with respect to water stress. The farmers demand the cluster bean varieties which are branched, good pod bearing, high yielding, drought hardy and resistant against foliar diseases with high gum content. The phto-thermo insensitivity is another desirable character which makes its cultivation possible after the harvesting of *raya* crop during summer season in the areas where there is a provision of at least one irrigation. Erratic rainfall, long duration (100 days) and high susceptibility to the bacterial leaf blight caused by *Xanthomonas axonopodis pv. Cyamopsidis* are the major constraints in the cluster bean cultivation.

The availability, collection, maintenance, utilization and conservation of genetic diversity are essential for effective selection in any crop improvement programme for yield and quality. In order to study the variability present in the genetic stock of crop, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are measured. The characters having high GCV and PCV possess large variation. To determine the heritable proportion of variation for any character and to predict the effect of selection, heritability and genetic gain are studied together. The high heritability coupled with high genetic advance as per cent of mean (GAM) has been found effective in improvement through selection (Nguyen*et al.*, 2019). To achieve genetically pure seeds of high standards, each cultivar should be characterised with suitable descriptors called DUS (distinctness, uniformity and stability) characters to maintain its identity during seed production through field inspection and certification. This is essential to differentiate among the cultivars having different yield potential and having specific character. The characterization of cultivars is also required for their protection under PPV & FR Act 2001(Arya*et al.*, 2021).

It is imperative to have knowledge about the mutual relationship among the yield and its component characters. Correlation coefficient analysis measures the magnitude of relationship between various plant characters and determines the component character on which selection can be based for improvement of seed yield. Correlation can be exploited efficiently to frame the selection tactics for yield enhancement but it does not reveal the direct and indirect effect of individual character on a complex character like yield. Therefore, for precise selection, the relative magnitude of different characters contributing to yield has to be assessed. The path coefficient analysis enables us to estimate the direct and indirect contribution of various independent characters on yield (Sharma *et al.*, 2021).

Selection of genotypes for varietal identification based on performance in single environment is not effective as yield is a complex quantitative character which is highly influenced by environment. Therefore, it is essential to select the genotypes based on yield stability performance. In crops selection of genotypes for stability and adaptability is required prior to their recommendation for commercial cultivation in wide range of environments. Stability is suitability of a variety over a wide range of environments while, adaptability is the better survival of a genotype over any specific environment. Evaluation of genotypes at several locations provides an opportunity to the plant breeders to identify the adaptability of a genotype to a particular environment and also stability of the genotype over a range of different environments. The newly developed varieties are wished to adapt to a wide range of target environments. Effects of genotype (G), environment (E) and genotype x environment (G X E) interaction determine the phenotypic performance and its general and specific adaptation to different environments. G X E interaction effect reveals the yield changeability of genotypes over different environments which cannot be explained by individual E and G effects (Pour-Aboughadareh *et al*., 2022). Although there are several conventional methods to analyze the stability and G X E interaction which is multivariate in nature, but the additive main effect and multiplicative interaction (AMMI) model is more popular. The AMMI method which is also referred to as double centered principal component analysis presents information on main and interaction effects in addition to a biplot and is specifically efficient for illustrating adaptive responses. It is a hybrid model which involves both additive and multiplicative components. This model quantifies the G X E interaction through PCA and graphical representation and has widely been used in multi-environment cultivar trials. The AMMI model combines ANOVA for the genotype and environment main effects with principal components analysis of G X E interaction (Dwivedi *et al*., 2020). Therefore, genotype with high mean yield along with low variability in multiple environments *i.e*., with the smallest G X E interaction as a result of AMMI analysis is the best genotype for wide adaptation (Katsenios *et al*., 2021).

Variability assessment based on morphological characters sometimes fails to reflect accurate method of genetic variation as these characters are influenced by environmental factors. This many times makes the selection efforts ineffective. Hence, DNA based markers have been found suitable and accurate for the assessment of genetic diversity, molecular characterization and marker aided selection clubbed with other new techniques like development of marker based gene tags, cloning of agronomical important genes and so on. The use of molecular markers can be very useful for the development of improved varieties with quality characters in cluster bean in shorter period and with lesser efforts. DNA markers are useful in generating high density linkage maps with applications in QTL mapping and genome assembly, in identification and isolation of genes through map-based cloning, in association mapping, comparative mapping, evolutionary studies, genetic diversity studies, and plant variety and germplasm protection (Tribhuvan *et al*., 2019).

Among different class of markers available, microsatellites or SSRs (simple sequence repeats) are highly valued by geneticist and evolutionary biologist, and are commonly used due to their co-dominant inheritance, high level of polymorphism, good genome coverage, multi-allelic properties and high transferability between the populations. SSRs are repetitive DNA sequences, present abundantly in eukaryotic genome and containing generally, 2–6 bp long motifs. Depending on their locations in the genome, the SSRs can be broadly categorized into genomic SSRs and genic-SSRs. The genic-SSRs or EST-SSRs are found in the transcribed region with known functions. On the other hand, the genomic SSRs are found in both transcribed and non-transcribed areas with unknown functions (Chang *et al*., 2019; Shingane 2014). The genic-SSR markers provide several advantages over genomic SSR markers despite of being not as abundant and as polymorphic as genomic SSR. This includes higher probability of finding association with functional gene, higher degree of transferability across related species, and lower occurrence of null alleles. Therefore, genic-SSR markers have been used successfully in population genetic and evolutionary studies in many species (Arya *et al.*, 2013; Li *et al.*, 2016; Zhou *et al*., 2016). Transcriptome sequencing coupled with established bioinformatics data have been used effectively for high throughput identification of genic-SSR markers from various organisms. Some of the tools used for SSR mining include Microsatellite identification tool (MISA) (Beier*et al*., 2017), FullSSR (Metz *et al.*, 2016) and Genome-wide Microsatellite analyzing tool package (GMATA) (Wang *et al.*, 2016).

In cluster bean, molecular markers such as Allozyme, Isozyme, RAPD, AFLP, SSRs, ISSR and SCAR have been used. Simple Sequence Repeats (SSRs) in particular have been used extensively to analyze the structure of germplasm collections as these are abundant, co-dominant, multi-allelic, highly polymorphic and chromosome specific.

Keeping in view the above, research problem was formulated with the following objectives.

i. To study the genotype x environment interaction patterns
ii. To study association of yield with its component characters in various environments
iii. To study molecular diversity in cluster bean genotypes using SSR markers

CHAPTER-II

REVIEW OF LITERATURE

Genetic variability based on quantitative and qualitative characters, correlation, path coefficient analysis, genetic divergence and genetic advance have been studied by several researchers. The information generated from these studies enables the breeders to formulate their breeding programme more efficiently. The newly developed genotypes have to be evaluated under a range of different environments for the assessment of their stability and adaptability. Early analysis of multi-location trial data treated genotype and environment as confounding factor to identify a stable genotype, less affected by G X E interaction.For cultivation in large area the yield stability is desirable but for achieving maximum productivity, adaptability to best target environments that is preferred.There are several methods to study stability of characters.Additive main effects and multiplicative interaction (AMMI) model is one of latest and popular method.This method quantifies the genotype environment interaction through PCA and graphical representation and has been widely applied in the multi-environment/ multi-location varietal trials. The molecular diversity in crops has also been studied by many investigators using RAPD, AFLP, SSRs, ISSR and SCAR markers.These studies generated useful data on genetic diversity, molecular characterization, marker aided selection,and marker based gene tags and cloning of agronomical important genes*etc*. An experiment was formulated to analyse the molecular diversity and stability for seed yield and its components in cluster bean.

A number of studies on above aspects have been conducted and are being reviewed in relation to the present investigations under the following headings:

A. Characterization based on morpho-biochemical and yield contributing characters

B. Genetic variability, heritability and genetic advance as per cent of mean

C. Correlation and path coefficient analysis

D. Disease intensity studies

E. Genotype x environment interaction and stability parameters

   i. Eberhart and Russell‘s model, 1966

   ii. AMMI model by Gauch and Zobel, 1997

F. Molecular diversity using SSR markers

A. Characterization based on morpho-biochemical and yield contributing characters

Umesha *et al.* (2015) conducted a study to characterize 20 indigenous cluster bean genotypes by using morphological markers. Different morphological characters *viz.*, flower colour, seed shape, leaf pubescence, pod shape, number of pods per plant, pod length were studied in this investigation. Such characterization of genotypes may provide the valuable information for the effective plant breeding and plant variety protection programme.

Manivannan *et al.* (2016) characterized 42 genotypes for seven morphological characters across three locations. PCA analysis showed that genotypes namely PNB, T local, HG 884, RGC 471, MRSG6 were very different from each other. Cluster analysis separated genotypes into two major groups: one of vegetable genotypes and gum genotype and further gum genotypes into sub clusters possessing unbranched type and white color flowered genotypes. The genotype MRSG6 exhibiting brown seed differed from the predominant grey-seeded group. The leaflet texture (pubescence) and leaflet shape (narrow) correlated highly with gum genotypes while; glabrous broad leaflets were linked with vegetable genotypes.

Olasupo *et al.* (2016) exercised mutagenesis through gamma irradiation for creating new genetic variability in cultivar improvement. Seeds of eight cowpea accessions were irradiated with different doses of gamma radiations. The seeds were sown in pots to evaluate the treatment effects on seed germination (SG), seedling survival (SS) and growth habits which includes plant height primary leaf area, terminal leaflet area, seedling height seed testa texture, thickness and seed weight of M_1 generation. Data were analyzed using descriptive statistics. Hence, radio sensitivity of cowpea accessions to gamma irradiation *w.r.t.* morphological characters was investigated.

Arya *et al.* (2021) characterized cowpea [*Vigna unguiculata* L.Walp] genotypes for morphological characters and established distinctness among different genotypes. Less variability was recorded for the number of branches per plant, terminal leaflet length, terminal leaf breadth, number of pods per cluster, pod breadth, 100-seed weight. But for the remaining characters *viz.*, plant growth habit& pattern, flower colour, colour of immature and mature pods, seed test texture and seed colour, wide variability was observed. Likewise seed colour also exhibited a wide colour variation. The characterization of cowpea genotypes provides valuable information on the diversity of morphological and quantitative characters for strengthening the future breeding plan.

B. Genetic Variability, heritability and genetic advance

Reddy *et al.* (2017) studied variability for yield and yield attributes in 51 cluster bean genotypes. All the sixteen characters studied had shown highly significant differences. The characters evaluated recorded high estimates of genotypic and phenotypic coefficients of variation, high heritability along with high genetic advance over mean.

Kumar *et al.* (2017) evaluated to genotype of cluster bean to study variability, heritability and genetic advance for yield and its contributing characters. The coefficients of variation (GCV & PCV) were found high for most of the characters including seed yield per plant and low for days to 50% flowering. High estimates of genetic advance were reported for plant height and lowest for 100 seed weight. However, high heritability estimates was associated with high predicted genetic advance for plant height. These characters were mostly governed by additive gene action and these characters are important for the breeder to construct selection indices.

A study was conducted by Gowd *et al*. (2019) to analyze the variability and heritability in cluster bean genotypes for growth, pod yield and yield parameters showing highly significant differences among genotypes. High range of variability, high heritability coupled with high genetic advance over mean was observed for most of the yield contributing and quality characters. The results of this study suggested that selection based on number of branches per plant at maturity, number of clusters per plant, pod length, pod yield per plant, 100 seed weight and protein content might bring improvement in vegetable pod yield of cluster bean.

Ugale *et al.* (2020) studied genetic parameters in cluster bean genotypes and revealed high estimates of variation, heritability coupled with high values of genetic advance over mean (GAM) for almost all the characters including vegetable pod yield per plot. This indicates predominance of additive component for these characters and hence direct selection would be more effective in improving these characters.

In a study, cluster bean cv. *Pusa Nav bahar* was treated by Lavanya *et al.* (2021) with different level of gamma rays. The obtained M_2 population was subjected to variability estimation for yield and its attributing characters. The variance between the control and the mutants was found to be significant for yield and attributing characters. Genetic advance expressed as percentage over mean was found high for plant height and lowest for pod length. The characters like plant height, pod length, pod width, pulp to seed ratio showed sufficient variability due to induced mutation. All these characters showed medium to high heritability and high genetic advance hence selection for these characters will be effective.

The study was conducted by Depashree *et al.* (2021) on genetic parameters of cluster bean genotypes revealed, high estimates of variation and high estimates of heritability coupled with high values of genetic advance over mean (GAM) for of yield and attributing along with quality characters. These results showed prevalence of additive constituents for these characters and hence direct selection would be rewarding for improving these characters.

Thangam *et al.* (2020) evaluated twenty-nine genotypes of vegetable cowpea to estimate genetic variability, heritability, genetic advance and genetic divergence for twelve quantitative characters. High variability was observed for pod yield/plant, number of pods/plant and pod length. The GCV value was maximum for pod yield per plant (g) followed by pod weight (g) and number of pods per plant. Low values of GCV were observed for days to first flowering, days to first harvest and number of seeds per pod. These genotypes could be grouped into fourteen clusters based on genetic distance. High coefficient of variation was observed for pod yield per plant, pod weight, number of pods per plant and pod length indicating their significant contribution in determining the inter cluster distances.

Rai and Sharma (2020) conducted a study to analyze different variability parameters, correlation and path coefficient for 12 attributes in thirty cowpea genotypes. ANOVA showed significant genetic variability among the genotypes for all the characters studied. The characters like number of pods per plant, harvest index, seed yield per plant and plant height were found high in phenotypic and genotypic coefficient of variation along with heritability and genetic advance as per cent of mean. Plant height, number of pods per plant, harvest index and number of seeds per pod were significantly and positively associated with seed yield and also contributed directly towards seed yield.

Ugale *et al.* (2020) carried out a field experiment on genetic variability and genetic divergence in thirty-one genotypes ofcowpea for 12 characters. They found that GAM, GCV and PCV values were at par with one another for most of the characters, indicating that the influence of the environment on the character was very negligible. The differences between PCV and GCV values were less indicating that these characters were less influenced by environment and could be improved by following phenotypic selection. High heritability coupled with high GAM was observed for all growth, flower attributes, earliness attributes and pod attributes except days to 50% flowering and pod width indicating that these characters were less influenced by environmental effects and these characters were governed by additive genes and selection will be rewarding for improvement of such characters.

In a study carried out by Tambitkar *et al.* (2021) on 41 genotypes, which were evaluated for genetic variability studies for fourteen characters. The characters *viz.*, iron content, dry matter yield per plant and plant height at maturity showed comparatively wide variation while, the lowest variation was recorded for number of primary branches per plant. The characters like iron content, dry matter yield per plant, plant height at maturity, days to initiation of flowering and days to 50% flowering were recorded highest heritability. The lowest heritability recorded in number of seeds per pod, pod length, hundred seed weight and number of primary branches per plant.

C. Correlation and Path coefficient analysis

Sivia *et al.* (2016) evaluated 33 genotypes of clusterbean for various biometrical characters. The correlation coefficients revealed positive and significant association of gum content with 100 seed weight while days to maturity and plant height had negative association. Path coefficient analysis revealed that 100 seed weight had positive and high direct effect followed by number of seeds per pod and plant height.

Khalid *et al.* (2017) studied 12 quantitative characters to determinate ample variation and association amongst 100 cluster bean genotypes to screen out the best performing lines. Principal component analysis indicated the quantity of variation by principal components 1 to

4 viz., 38.9, 14.7, 10.6 and 8.3%, respectively. Cluster analysis based on different quantitative characters arranged 100 cluster bean accessions into eight groups using Ward clustering method to construct dendrogram based on quantitative characters of genotypes.

Panchta *et al.* (2017) evaluated cluster bean genotypes for nine characters in RBD during summer season. High PCV and GCV estimates were found for most of the characters. High heritability coupled with genetic advance as per cent of mean was observed for characters like number of branches per plant and seed yield per plant, indicating additive effect in these characters. High positive and significant correlation of seed yield per plant observed with number of pods per plant followed by seed weight, number of branches per plant, number of seeds per pod and pod length. Path coefficient study revealed very high direct positive effect on seed yield per plant by 100 seed weight, number of pods per plant and pod length. The number of branches per plant showed positive indirect effect on seed yield per plant *via* 100 seed weight and number of pods per plant.

Reddy *et al.* (2018) conducted a study with fifty one genotypes in cluster bean revealing that pod yield per plant exhibited highly significant and positive association with pod yield per hectare, pod length, pod weight, number of pods per plant, number of clusters per plant, pod girth, number of branches per plant, plant height, gum content, number of pods per cluster, number of seeds per pod, protein content and fibre content. These characters are to be given due consideration in selection for yield improvement of the crop. Path analysis revealed that maximum positive direct effect on pod yield per plant was exhibited through pod weight followed by number of pods per plant.

Patel *et al.* (2018) studied the variability, correlation and path analysis using 22 genotypes evaluated through 10 characters. Analysis of variance indicated sufficient variability present in studied material for all 10 characters. Pods per plant showed high heritability couple with high genetic advance means selection is effective through this character. Yield per plant should significant and positive correlation with primary branches per plant, clusters per plant and pods per plant whereas negative correlation with days to flowering, days to maturity and pods per cluster. Cluster per plant had maximum positive direct effects on yield per plot followed by days to 50% flowering, days to maturity, plant stand and pods per plant.

Choyal *et al.* (2018) conducted the correlation study in cluster bean. Pod yield/plant showed significant and positive correlation with plant height 45 days, number of pods/plant and days to 50% flowering at both phenotypic and genotypic level. Seed yield/plant (g) showed non-significant and positive correlation with fruit cluster/plant, pod/cluster and 100 seed weight at both phenotypic and genotypic level. The path coefficient analysis showed that pods/plant had positive direct effect on pod yield/plant. Fruit clusters/plant had direct negative effect on seed yield/plant. Seeds/pod had direct negative effect on seed yield/plant.

Kumar *et al.* (2017) conducted an experiment on cluster bean to identify the correlation among characters and direct and indirect effects of characters on seed yield per plant. Seed yield per plant was found significantly and positively correlated with the characters like number of pods per plant, number of branches per plant, number of seeds per pod, pod length and plant height. Protein content has a negative and significant correlation with the seed yield per plant. The number of pods per plant has a maximum direct effect on seed yield per plant followed by the number of seeds per pods and 100 seed weight.

Nguyen *et al.* (2019) studied the genetic variation and inter-relationships of 17 agro-morphological characters. Their results showed that GCV and PCV were high for almost all characters while plant height, harvest index, number of clusters per plant, seed yield per plant, pod yield per plant, number of branches per plant, pod weight, days to 50% flowering, 100 seed weight, number of seeds per pod, days to maturity, and pod length all had high broad sense heritability.

An experiment was conducted by Mishra *et al.* (2020) to assess the variability using 38 diverse germplasm lines of vegetable type cluster bean. The characters like number of pods per plant, pod length, pod weight, plant height, number of clusters per plant, pods per cluster showed high coefficient of variations and high heritability with high genetic gain indicating their suitability for effective selection. Analysis of phenotypic and genotypic correlation co-efficient and path analysis revealed that characters like pod length, pod diameter, pod weight and seeds per pod had significant positive correlation with pod yield.

Chaudhary *et al.* (2020) conducted a study using 30 accessions of cowpea to evaluate eleven agro-morphological characters. Significant positive correlation was found between seed yield per plant and number of pods per plant; number of seeds per pod; number of branches per plant; pod length and plant height. Whereas, negative significant correlation was observed between seed yield per plant with days to flowering and days to maturity. Days to flowering had highest negative direct effect on seed yield per plant. Pod length recorded the highest positive direct effect on seed yield per plant followed by number of branches per plant and number of pods per plant. Both correlation and path analyses indicated that number of pods per plant, number of seeds per pod, number of branches per plant and pod length were the major direct contributors to seed yield.

Under rainfed conditions, Panchta *et al.* (2020) evaluated 22 genotypes of grain cowpea for various eight morphological characters to study the main yield contributory characters. The characters like seed yield per plot and plant height, days to 50% flowering, days to maturity andnumber of pods per plant showed highly significant and positive correlation, indicating the importance of these characters for seed yield per plot. Highly significant and negative correlation was observed between seed yield per plot and 100 seed weight. The path coefficient analysis revealed that the plant height, days to maturity and number of pods per showed the highest positive and direct contribution towards seed yield per plot plant indicating that selection for these characters would improve seed yield of cowpea under rainfed condition.

D. Disease intensity studies

Suman Lata *et al.* (2016) studied the changes in structural and non-structural carbohydrate contents and their role in bacterial blight (*Xanthomonas axonopodis* pv. *cyamopsidis*) resistance in forage guar. Lesion size was observed to be in direct correlation with the disease susceptibility. Non-structural carbohydrate content decreased in inoculated leaves as compared to uninoculated one, while structural carbohydrates (NDF, ADF, hemicellulose, cellulose, lignin and silica) increased in inoculated leaves.

Gresta *et al.* (2017) studied seed yield and biochemical characters of six guar genotypes coming from India, South Africa and the USA, grown in a Mediterranean environment, both for industrial use (galactomannans) and as animal feed (guar meal). Yield ranged from 1.49 t/ha to 2.05 t/ha. Galactomannan content reached values from 28.6 g/100 g to 34.6 g/100 g with the highest significative value exhibited by Indian genotype, followed by Lewis and South African genotype. The other biochemical characters included protein & lipid content, crude fibre content, NDF, ADF, ADL and polyphenols.

Wadhwa and Joshi (2017) estimated galactomannan content and activity of enzymes involved in galactomannan metabolism in mature seeds of 17 guar genotypes. Galactomannan content was found in the range of 16.82 to 36.68 per cent. It can be inferred that the ß-D-mannosidase requires prior activity of ß-1, 4-mannanase for galactomannan catabolism while α-galactosyltransferase activity is positively correlated with galactomannan content and play a major role in guar gum synthesis and can be further used for gum improvement via genetic manipulation.

Gresta *et al*. (2018) conducted multi-character characterization of 68 guar genotypes to identify an ideotype combining desirable characters. 11 morpho-biochemical characters were evaluated and correlations between morphological characters and seed yield were applied. A lower coefficient of variation was observed for galactomannan and protein contents as compared to the morphological or productive characters. Correlation analysis showed that plant production was related to cluster number, number of pods per plant, seeds per pod, number of branches and length of crop cycle. Galactomannan content was found to be negative associated with protein content.

E. Genotype x environment interaction and stability parameters

i. Eberhart and Russell‘s model, 1966

Phenotypic stability was studied by Wankhade *et al.* (2017) for seed yield and their component characters in 55 genotypes of gum cluster bean under four environments. The environment + (genotypes x environment) was highly significant for all the characters The effects due to environments (linear) was highly significant for all the characters indicating distinct nature of environments. The linear components of G x E interaction were significant against pooled deviation for all the characters except number of dry pods per plant and seed yield per hectare while, the non-linear component (pooled deviation) was also highly significant for all the characters except number of primary branches per plant, number of seeds per dry pod and gum content in seed. Five genotypes *viz.*, IC-421834, IC-421839, IC-421815, IC-324032, and IC-421798 were stable in performance for seed yield per hectare based on stability parameters and over all mean. The genotypes IC-421830, IC-421840 and IC-298638 were most stable for the quality characters.

Nirmal Raj *et al.* (2019) identified the stable maize hybrids out of twenty-one Maize hybrids and two commercial checks over three locations in India using Eberhart and Russell stability analysis model. A significant effect of each environment on the hybrids taken, for all the ten morphological characters except the number of leaves was found. The hybrids AU-101 and AU-114 were identified as stable hybrids with high mean under less favorable and under favorable conditions respectively. None of the check hybrids showed stability in any of the environment.

Wankhade *et al.* (2021) studied stability for seed yield and their component characters in 55 genotypes of cluster bean under four environmental conditions. The variance due to genotype × environment (linear) was found to be highly significant against pooled deviation for six characters.The nonlinear component (pooled deviation) was also highly significant for three characters. The environment + (genotypes x environment) was highly significant for all the characters except two characters against pooled deviation. This indicates the distinct nature of environments and the effects due to environments (linear) was highly significant for all the characters. The genotypes viz., IC421839, IC-324032, IC-329036, IC-421816, IC-421815 and IC-421834 were stable in performance for dry pod yield per hectare and the genotypes namely IC-421834, IC-421839, IC-421815, IC-324032 and IC421798 were stable in performance for seed yield per plot.

Teja *et al.* (2022) worked out G x E interaction and stability analysis as per the model given by Eberhart and Russel (1966) for seed yield and its attributes. Twenty-five genotypes of cluster bean including one check were evaluated for this study. The environments effects linear were highly significant for all the characters, suggesting that the environments were effective in affecting the performance of all the genotypes with respect to cluster bean yield attributing characters. Genotypes IC-9052, IC-10323, IC-10333, IC103295 and IC-200680 were high yielding and stable under all environments, IC-103295, IC-10323 and IC-9077P1 for higher gum content, IC-10333, IC-28286, IC-103295 and IC-200715 for protein content and genotype IC- 9077-P1 for fibre content were considered as desirable and stable over the environments.

Shojaei *et al.* (2022) studied 12 maize hybrids to find out the stable genotypes with yield using six environments. The combined analysis results showed a significanteffect on the environment, the effects of genotype, and the interaction of genotype×environment in the studied hybrids different. In order to identify stable cultivars, six stability parameters were used. Based on Eberhart and Russell regression coefficient KSC400 and SC647 were the stable genotypes.

ii. AMMI model (Gauch and Zobel (1997)

Baraki *et al.* (2020) conducted an experiment on mung bean genotypes to study G X E interactions revealing that genotypic,environmental and the genotype x environment interaction (GIE) accounted about30.47%, 45.01% and 11.59% of the total variation, respectively. The AMMIbi-plot and GGE bi-plot depicted that, SML-668 and SML-32 were the high yielding and lowyielding genotype, respectively. E1, E2 and E6 are discriminating environments and the most representative than E3, E4 and E5. Generally, SML-668 was the idealgenotype with higher mean yield and relatively good stability; Local-2 Sheraro was the moderately good yielding and the most unstable genotype; Whereas, SML-32 was the poorly yielding and unstable genotype.

Present experiment was conducted by Jeberson *et al.* (2020) with 20 diverse urd bean genotypes over three environments. AMMI analysis revealed that environments (E), genotypes (G) and G x E interaction effects werefound significant for grain yield (GY). The environment, genotypes and their interactions accounted 46.29, 25.9and 22.23 ofthe total variation. The interaction principal components Axis 1(IPCA 1) and IPCA 2 of AMMI were founds significant ($P<0.01$) for grain yield. The IPCA1 accounted more than 89% of the G x E interactions effects for the grain yield. In GGE biplot PC1 and PC2 captured 99.3% of the total variations. Based on GGE and AMMI biplots the genotypes with wider adaptability were VBG 12-034, IPU 13-3 and COBG 13-04.

In a study, Kumar *et al.* (2020) evaluated mung bean genotypes for stability performance under different environments. Environmental indices indicated that environment E2 and E3 were most favourable for yield and majority of yield attributing characters. The environment E3 alone was important for seed yield/plant and number of seeds/ pod. Pusa Vishal, PD139, IPM2-3, IPM2057 and PML2-14 showed higher IPCA scores coupled with high population mean in E3 and the basis of AMMI models. AMMI2 analysis indicated ML2056, and K851 with high IPCA1 in E3 whereas IPM99-125, BM63 and PM2-14 with high IPCA2 in the same environment. The genotypes least effected by G x E interactions were positioned very close to centre point while the genotypes more affected by G x E interactions and hence not stable were presented away from the point of centre.

Arya *et al.* (2021) observed highly significant effects of genotypes yield during field evaluation. In AMMI analysis, 51% of total variation accounted by the environments, 32.9%

by genotype x environment interaction, and only 10.7% due to the genotypes. Adaptability measure harmonic means of relative performance of genotypes ranked HB 13-48, HB13-10 and HB13-11 as per their performance. The relative performances of genetic values were settled for HB13-48, HB13-10, and HB13-26 genotypes. ASV1 and ASV measures pointed HB13-26, HB13-15 and HB13-40 as of stable performance. Biplot analysis observed the strong bondage of arithmetic, geometric and harmonic means along with relative performance of genetic values and measure of the relative performance of the genotypic values.

Dhasarathan *et al.* (2021) made an attempt to isolate novel black gram mutants by selecting for yield-related characters derived through gamma irradiation and testing the mutant genotype's stability across the different environments. Desirable mutants were selected from M3 to M5 generations. M4 established three divergent groups in each black gram cultivar revealed by clustering analysis. G × E interactions were higher than the variation due to genotype for single plant yield. AMMI analysis revealed that there was limited environmental interaction was observed for the genotypes G24, G16, G36, G30, and G17, and the genotypes G18 and G29, as revealed by GGE. GGE biplot identified the environment-specific genotypes G13 for E1, G7 for E2 and G34 for E3.

Kindie *et al.* (2021) studied genotype by environment interaction to identify the most stable cowpea genotype(s) and the desirable environment(s) for cowpea. The grain yield was significantly affected by environments, genotypes, and GE interactions as shown by combined analysis of variance. AMMI analysis revealed the contribution of environment, genotype, and GEI for 29.79%, 15.6%, and 42.06% of variation on grain yield. The first two principal components explained 57.97% of the total GEI variance. AMMI model selected G24 as 1st and 2nd best genotype at five environments. The GGE biplot identified three mega-environments (ME1, ME2, and ME3) with winning genotypes namely, G24, G3, and G16, respectively.

Kumar *et al.* (2021) evaluated28pigeonpea genotypes for stability andadaptability across ten rainfed locations using AMMI model and GGEbiplot method.The grain yields were significantly affected by environment(56.8%) followed by genotype × environment interaction(27.6%) and genotype (18.6%) variances. Four genotypes were found best. E2, E3 and E6 were the mostdiscriminating environments. Genotypes, ICPH 2740, PRG176 and TS 3R were the best cultivars in all the environments whereas PRG 158, ICPL 87119, ICPL 20098 and ICPL 96058 were suitable across a wide range ofenvironments.

An experiment was conducted by Nitesh *et al.* (2021) to assess the stability of 48 F_1 hybrids along with 19 homozygous mung bean parents for seedyield per plant. AMMI1 biplot for seed yield per plant showed that the four hybrids and two parentshad IPCA1 score close to zero with high main effects indicating that these hybrids were less influenced byenvironments and high yielders. Four hybrids and four parents were found to be high yielders withhigh interaction with the environment. The hybrids *viz.,* PM1125 × MH1142 and PDM139 × KM2355 were foundless interacting with high seed yield per plant.

Yohane *et al.* (2021) conducted a study with objectives to quantify the GEIeffects and to determine grain yield stability among diverse pigeon pea genotypes using AMMI analysis and GGE biplot analysis. Genotype, environment, andgenotype × environment interaction (GEI) accounted for 16.4, 33.5, and 49.6%, respectively, ofthe total variation for grain yield. The AMMI and GGE analyses indicated thatthe top-yielding and stable genotypes across the test environments were MWPLR 24, ICEAP01155, MWPLR 14, TZA 5582, and MWPLR 4.

Kishore*et al.* (2022) studied the yield stability of promisingpigeon pea genotypes across six locations using AMMI analysis and GGE biplot analysis. The yield was significantly affected by genotypes,environments and genotype X environment interaction as shown by the combined analysis of variance. The first two interactions principal componentsfromthe AMMI analysis accounted for 68.48% and from GGE accounted for 64.4% of variation due to GxEinteraction. G3 and G4 were identified as most stable andG4 with the highest yieldacross six locations according to both AMMI and GGE biplots. The E1and E2fell into one mega environment (ME 1) followed by E3and E6 another (ME 2). Environments E5and E1were most representative while E1could beregarded as least representative environment.

F. Molecular diversity using SSR markers

Kuravadi *et al.* (2014) performed the mining of simple sequence repeat (SSR) sequences from 16,476 expressed sequence tags (ESTs) of guar using the microsatellite (MISA) identification tool. A total of 907 SSR-containing sequences were identified. A total of 362 pairs of primers were designed, out of which 224 were synthesized and used for assessment of amplification and polymorphism in five accessions of three *Cyamopsis* species. Out of 224 primer pairs, 187, 184, and 121 resulted in the amplification of SSR-containing sequences producing reliable and reproducible DNA bands in *C. tetragonoloba, C. serrata*, and *C. senegalensis*, respectively. The analysis of the DNA bands revealed that 44 SSR markers were monomorphic in all the five accessions. Four SSR markers showed polymorphism in all three tested varieties of *C. tetragonoloba*.

Kumar *et al.* (2015) developed 100 novel primers pairs from 16,476 expressed sequence tags (ESTs) sequence of cluster bean. A total of 50 primers pairs with function annotation of gum synthesis were selected and validated on a panel of 32 genotypes. Among the 50 primers 39 primers were amplified with a total of 45 loci. The polymorphic information content (PIC) ranged from 0.00 to 0.42 with an average of 0.13. With low polymorphic simple sequence repeats (SSRs) and narrow genetic base, most of the genotypes scattered into three clusters regardless of their geographical origin. The study showed the existence of very low genetic diversity in cluster bean genotypes used.

Boghara *et al.* (2016) Studied the genetic/diversity among 31 cluster bean genotypes using morpho-physiological, yield and SSR markers. SSR amplification with 17 primers detected 33 alleles with a mean of 1.83 alleles/SSR. The clustering revealed five distinct groups at 0.68 cut-off value. The cluster analysis showed low genetic variation among the genotypes studied. The phenotype-based cluster did not correspond with the molecular-based cluster as the correlation coefficient for the two clustering matrices was negative ($r = -0.72$). They concluded that molecular markers as a complementary tool should be used in conjunction with morphological characterization for better description of the level and pattern of genetic diversity and for crop improvement.

Kaur *et al.* (2018) used SSR marker is to analyze the genetic diversity amongst 23 genotypes of mung bean. Out of a total of 10 primers used for SSR analysis revealed generation of 15 alleles. The number of alleles per locus ranged from one to three, with an average of 1.5 allele per primer. The size of amplification products varied in case of each primer and the range was found to be 100 to 190 bp. 13 out of 15 alleles were found polymorphic. The average PIC value of SSR marker was found to be 0.205. The range of Jaccard’s similarity coefficient was from 0.28-1.00 with an average value of 0.64. The dendrogram constructed on SSR molecular marker data through UPGMA method and PCA using average linkage, had enabled grouping of the genotypes into three main clusters and indicated the narrow genetic base of mung bean genotypes.

Tribhuvan *et al.* (2018) identified 1859 genomic SSRs, from 1091 scaffolds representing 60% of the cluster bean genome and also validated 89 of these markers using 54 cultivated guar accessions and two wild relatives, *Cyamopsis serrata* and *Cyamopsis senegalensis*. 11 SSRs were polymorphic only between species with 72 being polymorphic within *C. tetragonoloba* accessions. Polymorphism information content (PIC) of the markers ranged from 0.017 to 0.62 with an average of 0.19. Genomic SSRs mined showed a high proportion of dinucleotide repeats (48.5%), while tri- and tetra nucleotide repeats were found to be more polymorphic. Genetic diversity analysis of the 56 accessions using the 82 polymorphic markers could differentiate the cultivated accessions of *C. tetragonoloba* into four major clusters, two of which had two sub-clusters while the wild accessions formed a separate cluster. Population structure analysis (PSA) using these markers revealed six subpopulations, more or less similar to the major and sub-clusters identified by the neighbor joining analysis.

Thakur and Randhawa (2018) carried out RNA-Seq analysis of the roots of two guar varieties, namely, RGC-1066 and M-83. A total of 102,479 unigenes with an average length of 1016 bp were assembled from about 30 million high quality pair-end reads generated by an IlluminaHiSeq 2500 platform. The assembled unigenes had 86.55% complete and 97.71% partially conserved eukaryotic genes (CEGs). The functional annotation of assembled unigenes using BLASTX against six databases showed that the guar unigenes were most similar to Glycine max. The screening of 102,479 unigenes with MISA and SAMtools version 1.4 softwares resulted in the identification of 25,040 high-confidence molecular markers which consisted of 18,792 SSRs, 5999 SNPs and 249 InDels. These markers tagged most of the genes involved in root development, stress tolerance and other general metabolic activities. Each of the 25,040 molecular markers was characterized, particularly with respect to its position in the unigene. For 71% of the molecular markers, we could determine the names, products and functions of the unigenes. About 80% of the markers, from a random sample of molecular markers, showed PCR amplification.

Giogia *et al.* (2019) conducted a study to determine the amount of genetic variation and the degree of relatedness among 192 selected common bean advanced cultivars using 58 simple-sequence-repeat markers (SSR) evenly distributed along the 11 linkage groups of the *Phaseolus* reference map. Population structure, principal components analyses, cluster analysis, and discriminant analysis of principal components (DAPC) were used to distinguish Andean and Mesoamerican genotypes as well as most American commercial type classes. The genetic relationship among the commercial cultivars revealed by the SSR markers was generally in agreement with known pedigree data. The Mesoamerican cultivars were separated into three major groups—black, small white, and navy accessions clustered together in a distinct group, while great northern and pinto clustered in another group, showing mixed origin. The Andean cultivars were distributed in two different groups. An overall reduction in genetic diversity was observed in both gene pools, Andean and Mesoamerican, from wild to landraces to advanced cultivars.

Molecular diversity study of 20 Indian bean genotypes was conducted by Dholakia *et al.* (2019) using molecular markers *viz*., Random Amplified Polymorphic DNA (RAPD), Inter Simple Sequence Repeats (ISSR) and Simple Sequence Repeats (SSR). 13 RAPD, 10 ISSR and 10 SSR primers produced total 78, 61 and 32 bands, respectively. RAPD and ISSR primers share 100% polymorphism, while SSR primer shares 98.33% polymorphism. Mean polymorphic content value highest for RAPD (0.72) and ISSR (0.71) as compared to SSR (0.43). SSR markers exhibit wide range of similarity (0.57-0.96) compared to RAPD and ISSR markers. SSR shows low primer index as compared to RAPD and ISSR primer. In Mental test, combined analysis of RAPD, ISSR and SSR shows r = 0.80 (good fit).

CHAPTER-III

MATERIALS AND METHODS

The present research work entitled **"Molecular diversity and stability analysis for seed yield and its components in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]"** was undertaken to study the genetic variability, association, molecular diversity and stability analysis in cluster bean.

A set of 25 diverse cluster bean genotypes were evaluated in the field experiments conducted during summer 2019 & 2020 and *kharif* 2019 & 2020 at two locations *i.e.* dry land research area, CCS Haryana Agricultural University, Hisar and research area, Regional Research Station, Bawal, CCS Haryana Agricultural University, Hisar in a Randomized Block Design (RBD) with three replications.

3.1 Experimental Material

The plant material comprised 25 diverse cluster bean genotypes. A brief description of genotypes is presented in **Table 3.1**.

Table 3.1 List of cluster bean genotypes along with their source/origin

S. No.	Genotype	Source/Origin	S. No.	Genotype	Source/Origin
1	HG 2-20	CCSHAU, Hisar	**14**	GG 2	SDAU Gujarat
2	HG 884	CCSHAU, Hisar	**15**	RGC 1017	RARI, Durgapura
3	HG 870	CCSHAU, Hisar	**16**	RGC 1038	RARI, Durgapura
4	HG 563	CCSHAU, Hisar	**17**	RGC 936	RARI, Durgapura
5	HG 365	CCSHAU, Hisar	**18**	RGC 1055	RARI, Durgapura
6	HG 3-52	CCSHAU, Hisar	**19**	RGC 1002	RARI, Durgapura
7	HG 6	CCSHAU, Hisar	**20**	RGC 1003	RARI, Durgapura
8	HVG 2-30	CCSHAU, Hisar	**21**	RGC 1066	RARI, Durgapura
9	HG 100	CCSHAU, Hisar	**22**	RGS 3	RARI, Durgapura
10	FS 277	CCSHAU, Hisar	**23**	M 83	RARI, Durgapura
11	X 10	Shaktivardhak Seeds	**24**	HG 75	CCSHAU, Hisar
12	PNB	IARI, New Delhi	**25**	RGC 1033	RARI, Durgapura
13	GG 1	SDAU Gujarat			

3.2 Environments

The field experiments were conducted at two different locations *viz*., dry land research area, CCSHAU, Hisar and RRS, Bawal comprising 8 environments. The experiments were conducted on two separate dates of sowing in two seasons *i.e*., summer and *kharif* over both the locations and years. The information of environments and dates of sowings is given in **Table 3.2**.

Table 3.2 Details of environments and code used for different environments

Season	Code	Date of sowing	Location	Year
Summer	HS 19	18/03/2019	Hisar	2019
Kharif	HK 19	28/06/2019		
Summer	BS 19	19/03/2019	Bawal	
Kharif	BK 19	07/07/2019		
Summer	HS 20	19/03/2020	Hisar	2020
Kharif	HK 20	01/07/2020		
Summer	BS 20	21/03/2020	Bawal	
Kharif	BK 20	04/07/2022		

3.3 Methods

The study was conducted to evaluate twenty five cluster bean genotypes under eight different environments for phenology, yield, yield components and related physiological characters in field conditions.

3.3.1 Layout of field experiment

The seeds were sown with hand plough under all the environments in three replications in a randomized block design (RBD). Each plot of 7.2 m^2 comprised of four rows of 4meter length each with a row to row spacing of 45 cm. The recommendedpackage of practices was followed to raise the crop. The meteorological data on maximum and minimum temperatures, relative humidity, and rainfall for the crop period (March 2019 to November 2019 and March 2020 to November 2020) of both the locations was collected from Department of Agriclutural meteorology, CCS HAU, Hisar (Annexure I).

3.4 Observations recorded

Observations were recorded on five randomly selected competitive plants per genotype per replication under all the environments. Data were recorded for the yield, yield components and physiological characters. The following observations were recorded during the period of investigation.

3.4.1 Qualitative characters

a) **Plant growth habit:** Plant growth habit was recorded at the time of maturity.

b) **Position of first trifoliate leaf from bottom:** Position of first trifoliate leaf was recorded from the base of plant to the node bearing first trifoliate leaf.

c) **Leaf Pubescence:** Based on leaf pubescence the genotypes were grouped intoglabrous and pubescent.

d) **Leaf Margin:** The genotypes were categorized as having serrated leaves and non-serrated leaves at pod formation stage.

e) **Leaf colour:** Leaf colour in genotypes was recorded at the time of pod formation.

f) **Flower colour:** The colour of the flower was visually observed in the morning hours and genotypes were grouped into white and pink.

g) **Pod pubescence:** Based on pod pubescence, the genotypes were grouped into glabrous and pubescent.

h) **Position of first cluster from bottom:** The position of first cluster was recorded from base of the plant to the first cluster bearing node at the time of maturity.

i) **Seed colour:** Seed colour of fully dried seeds was recorded after harvesting as pale yellow pink, moderate orange, medium grey, light grey and light greenish grey.

j) **Seed shape**: Seed shape was recorded after harvesting. The seed shape was grouped into flat, round and square.

3.4.2 Quantitative characters

a) **Plant Height (cm):** The plant height from the base of the plant to the top shoot of plant (cm) was measured at the time of harvesting.

b) **Days to 50% flowering:** The number of days taken to 50 per cent flowering was recorded by taking whole population in to consideration in each genotype and calculated from the date of sowing.

c) **Days to maturity:** The number of days was calculated from the date of sowing to the date on which 90% pods of a genotype got dried up.

d) **Pods on main stem (no.):** The numbers of pods per plant on the main stem were counted at the time of harvesting.

e) **Pods per cluster (no.):** The number of pods per cluster was counted at the time of harvesting.

f) **Clusters per plant (no.)**: The number of clusters per plant was counted at the time of harvest.

g) **Pods per plant (no.):** The numbers of pods per plant were counted at the time of harvesting.

h) **Seeds per pod (no.):** The ten random pods were selected from total number of pods of five plants, threshed and counted to work out average number of seeds per pod.

i) **Pod length (cm):** Randomly, ten pods from total pods of five plants were measured for average pod length in centimeters.

j) **Branches per plant (no.):** The number of branches per plant was counted at the time of harvesting.

k) **100 Seed weight (g):** One hundred seeds were counted manually from each genotype harvested and weighted in grams.

l) **Biomass per plot (kg):**The weight of all plants from each plot per replication was taken for each genotype at harvesting.

m) **Harvest Index (%):** Harvest index was calculated as a ratio of seed yield (Economicyield) to biological yield (excluding roots) for all the genotypes and is expressed in per cent.

$$\textbf{Harvest index}\ (\%) = \frac{\text{Seed yield } per \text{ plot}}{\text{Biological yield } per \text{ plot}} \times 100$$

n) **Seed yield per plot (kg):** Total seed yield harvested from each plot per replication was taken for each genotype after threshing.

3.4.2 Biochemical characters

a) Gum content (%)

The gum content was estimated by extraction of galactomannan followed by its purification, precipitation and precipitate was finally dissolved to measure spectrophotometrically using method given by Das *et al*. (1977) and further improved by Joshi (2004).

Galactomannan content estimation

i) Reagents:

1) 0.01 M $HgCl_2$
2) Absolute alcohol
3) 2% Phenol
4) Conc. H_2SO_4

ii) Procedure:

- Seed samples were ground by using Cyclone Sample Mill (0.2 mm screen, cP Cole Parmer). The 100 mg ground sample was taken in a 100 ml conical flask containing 40 ml of 0.01M $HgCl_2$.
- The mouth of the flasks was plugged with cotton plug & aluminium foils for autoclaving the samples at 15 psi for an hour. After autoclave samples were brought to room temperature and volume of the sample was made to 100 ml using distilled H_2O.
- After shaking the samples, 10 ml was taken in a centrifuge tube to centrifuge the samples at 5000 rpm for 15 min.
- 0.5 ml supernatant was taken in another centrifuge tube and 4.5 ml of absolute alcohol (ethanol) was added. The 90% alcohol solution thus obtained was refrigerated overnight at 4°C.
- Next day, the samples were again centrifuged for 15 min at 5000 rpm and supernatant was discarded.
- 0.01M $HgCl_2$was added to tubes to dissolve the residue and tubes were kept in water bath for an hour, the extracts were cooled and volume make up was done to make it 5ml using 0.01M $HgCl_2$.
- One ml of the extract was taken and 2 ml of 2 per cent phenol was added to it, followed by addition of 5 ml of conc. H_2SO_4. Samples were shaken vigorously and cooled for 30 minutes. Blank and standard was also run along with the samples.

- The galactomannan content was estimated using standard curve prepared by Galactose: Mannose (1:2) by taking the absorbance or O.D. at 490 nm.

b) Protein content (%)

Protein content was determined by multiplying nitrogen content obtained by micro Kjeldhal method (Stuart, 1936) with a factor 6.25 (Dubetz and Welis, 1968).

Estimation Procedure: Reagents

1) Concentrated sulphuric acid
2) Methyl red indicator
3) 40% Sodium hydroxide solution
4) N/100 sulphuric acid
5) K_2SO_4:$CuSO_4$mixture (9:1)
6) N/100 sodium hydroxide

i)Digestion

One hundred milligram of ground sample of each genotype was weighed and transferred to 100 ml digestion flask. Approximately 0.5 g of K_2SO_4:$CuSO_4$ mixture (9:1) and 10 ml of concentrated sulphuric acid were added to it. The flasks were heated on an electric heater in a fume hood and gradually increased the heat to keep the contents boiling until the solution is colourless/very light green. After cooling, distilled water was added and shacked carefully the flask, cooled and transferred to 100ml volumetric flask. The volume was made up to the mark with distilled water.

ii)Distillation

10 ml of N/100 sulphuric acid was taken in a 100ml conical flask containing one or two drops of methyl red indicator. 10 ml of the digested solution and 10 ml of 40% NaOH were pipetted out and put into the distilling portion of the set. It was distilled and the ammonia was collected in the flask until the volume in the flask increases by 30-40 ml.

iii)Estimation of Ammonia

N/100 sodium hydroxide was titrated with the amount of ammonia absorbed by N/100 sulphuric acid until the colour changes to light yellow and noted the titrated value. A black preparation except sample was also digested and distilled. The percent of nitrogen was calculated as the following:

$$\text{Nitrogen (\%) of the sample} = \frac{\text{Volume of N/100 } H_2SO_4 \text{ consumed} \times 0.00014 \times 100}{\text{Volume of digested material taken} \times \text{weight of sample (g)}}$$

Protein (%) =Nitrogen (%) × 6.25

c) Total soluble sugar content (mg/g dry weight)

Total soluble sugars in plant samples may be estimated by modified method of Dubios *et al.* (1956).

In hot acidic medium glucose is dehydrated to hydroxymethyl furfural. This form a golden yellow coloured complex with phenol and has absorption maxima at 490 nm.

Extraction of Sugars

Non-structural carbohydrates are those that occur either as simple sugars or that can be broken down by enzymes. These, also called as soluble carbohydrates, are soluble in 80% ethanol. It includes glucose, fructose, galactose and other monosaccharides and disaccharides.

Procedure

i. 100 mg of powdered samples was taken in 100 ml flat bottomed volumetric flask and 10 ml of 80% ethanol was added.
ii. The flask was kept in water bath, maintained at 70ºC, for 1 hour and the filtrate was collected in 25 ml volumetric flask.
iii. The extraction procedure was repeated 5 times till sample became free form sugars.
iv. The final volume was made 25-30 ml with 80% ethanol.

Reagents for TSS estimation

i. 2% phenol: Prepared by dissolving 2g phenol in 100 ml of distilled water.
ii. Conc. H_2SO_4 (G.R.)

Procedure for TSS estimation

i. 1 ml of the diluted sugar extract (1ml of sugar extract + 9 ml of distilled water) was taken in a test tube.
ii. Added 2 ml of 2% phenol solution followed by 5 ml of conc. H_2SO_4. Added acid in such a way that it directly pour on to the solution and tubes were shaked.
iii. The test tubes were allowed to cool for 30 minutes and read the absorbance of the solution at 490 nm on spectrophotometer.
iv. The concentration of total sugars was calculated from the standard curve of glucose prepared simultaneously and the data was expressed as mg/g dry weight or on percent dry weight basis.

d) Reducing sugar content (mg/g dry weight)

Nelson (1944) method further modified by Somogyi (1952) was used for the estimation of reducing sugars.

Principle

On the basis of principles, when alkaline copper tartrate is heated with reducing sugars then reduction of cupric ions to cuprous state occurs and then formation of cuprous oxide takes place. Further, reduction of molybdic acid to molybdenum blue occurs, when cuprous oxide treated with arsenomolybdic acid. At 520 nm, the coloured developed is measured spectrophotometrically.

Reagents

1) **Fehling solution A**: 2.5 g anhydrous sodium carbonate, 2g sodium hydrogen carbonate. 2.5 g potassium sodium tartrate and 20 g anhydrous sodium sulphate was dissolved in 80 mL distilled water and volume was made up to 100 ml.

2) **Fehling solution B**: Thirty milliliters of distilled water were used to dissolve 7.5 gm of copper sulphatepentahydrate and one drop of drop concentrated sulphuric acid was added. The volume was made up to 50 ml.
3) **Alkaline copper reagent**: Freshly made by combining reagents A and B in a 25:1 ratio prior to use.
4) **Arsenomolybdate reagent**: 450 ml of distilled water were used to dissolve 25 g of ammonium molybedate and then 21 ml of conc. Sulphuric acid was added while stirring continuously. In 25 ml distilled water 3.0 g sodium hydrogen arsenate dissolved was poured into the previous solution while being continuously stirred and then kept in water bath at 55o C for 25 minutes with occasional stirring. Store this reagent in a brown bottle in a dark place.

Determination of Reducing sugars

1.0 ml of each extract was diluted with distilled water to keep absorbance within calibration limits for estimating reducing sugars. After that, 1.0 ml distilled water was applied followed by a 1.0 ml alkaline copper reagent and the solution was combined before being heated in a boiling water bath for 20 minutes. The tubes were brought to room temperature before being filled with 1.0 ml of arsenomolybedate reagent. With distilled water, the contents were thoroughly mixed and the volume was increased to 10.0 ml.Using a UV spectrophotometer absorbance of the solution was measured at 520 nm against a blank prepared. The standard curve was used to measure the amount of reducing sugars found in the extracts and the results were expressed in milligram per gram.

e) Non-Reducing sugar content (mg/g dry weight)

The concentration of non-reducing sugars can be calculated by subtracting the reducingsugars from the total sugars.

f) ADF content (% dry weight basis)

Acid Detergent Fiber (ADF) is the fibrous, least digestible portion of feed. ADFconsists of lignin and cellulose. The ADF content is expressed as a percentage by masson basic of organic matter. ADF, ADL, cellulose and silica were determined by usingFoss, Fibertec^{TM} 8000.

Reagents

i. Acetone, technical grade
ii. Filtration aid, Diatomaceous earth, acid washed, Celite 545 AW, or equivalent
iii. Antifoaming agent, n-Octanol
iv. Acid Detergent Solution (ADS)

0.5 M H_2SO_4 with CTAB. 49.04 g reagent grade conc.$H_2SO_4$was weighed into a 1000 ml volumetric flask containing 400 ml H_2O. The volume was made up with distilled water at 20 ºC. 20 g CTAB (Cetyl trimethylammonium bromide), technical grade was added and dissolve.

Analytical Procedure

A blank was run through entire procedure along with each batch of samples.

ADF Extraction Step

1. The empty crucibles were dried in an oven at 105 ºC ±2 ºC for >4 h and tare weight (W_1) was recorded.
2. Pre-dried crucibles were placed on a balance and tare. To simplify the filtration, 1000±2 mg of Celite 545 was weighed into the crucible. 1 g of sample was weighed to an accuracy of ±2 mg into a pre-dried crucible and weighed (W_2).
3. Crucibles were placed in front of hot extraction unit using the crucible holder and lock into position in front of the heater ensuring the safety handle engages. The reflector was placed in front of the crucibles.
4. ADS tank was filled with ADS solution and placed in the left position (R_1) of the drawer and all connections were fixed. Antifoaming agent, n-Octanol, was added to the amber bottle inside the side door.
5. Water tap (about 2 l/min) was opened for reflux system.
6. The instrument was turned “ON” and default ADF program started by pressing "START" twice for confirmation.
7. At the end of the extraction, the reflector and crucibles were removed.
8. 25 ml acetone was added to each crucible and was allowed soak for 3-5 minutes; the solvent was filtered out by placing the valve in "vacuum" position. Repeated three times.
9. Crucibles were dried in an oven at 105 ±2 ºC for at least 5 h and cooled to room temperature in desiccators and weighed (W_3).

Calculation

% ADF, dry matter basis:

$$\%AD\ F=100\ X\ (W3-W1) - (B3-B1)/W2$$

Where

W_1 = Initial crucible weight (g)

W_2 = Sample weight (g)

W_3 = Crucible + residue weight (g) after ADF extraction

B_1 = Initial blank weight (g)

B_2 = Blank weight (g) after ADF extraction

g) Lignin content (% dry weight basis)

Acid Detergent Lignin (ADL) is a complex indigestible substance contained in the woody parts of plants, such as cobs, hulls and the fibrous portion of stems and leaves. The ADL content is expressed as a percentage by mass on basic of organic matter.

ADL Extraction Step

1. After weighing W_3 during ADF extraction 25 ml 72 % $H_2SO_4$was added in each crucible, cooled to 15 °C and stirred every hour with glass rod.
2. After 3 h, filtered as completely as possible with vacuum, and washed with hot H_2O until acid free to pH paper.Usually 5 times is needed.
3. Crucibles were driedat 105 ±2 ºC for at least 5 h.
4. Cooled to room temperature in desiccator and weighed (W_4).
5. Crucibles and fibre residue were ignited in a 525 ±15 °C furnace for at least 3 h.
6. Cooled to room temperature in desiccator and weighed (W_5).

Calculation

% ADL, dry matter basis:

$$\%ADL = 100 \text{ X } (W_4\text{-}W_5) - (B_4\text{-}B_5)/W_2$$

Where,

W_2 = Sample weight (g)
W_4 = Crucible + residue weight (g) after ADL extraction
W_5 = Crucible + residue weight (g) after ashing step
B_4 = Blank weight (g) after ADL extraction
B_5 = Blank weight (g) after ashing step

h) Cellulose content (% dry weight basis)

The concentration of cellulose can be calculated by subtracting the Acid detergent lignin content (ADL %) from the Acid detergent fiber content (ADF %).

% Cellulose = %ADF-%ADL

i) Silica content (% dry weight basis)

Reagents

i. 72% sulphuric acids (w/v) *i.e.* mix 39 ml sulphuric acid in 28 ml distilled water.
ii. Acetone

Procedure

1. After ADF extraction, cover the content of crucible with cooled 72% sulphuric acid (w/v) and stir with a glass rod to a smooth paste, break all lumps.
2. Again half fill the crucible with 72% sulphuric acid and stir regularly at an interval of 1hr and keep for 3 hours at room temperature.
3. The excess of sulphuric acid may be filtered off under the vacuum and wash the content with hot distilled water until it is free from acid, rinse the glass rods with hot distilled water.
4. Keep the crucibles in an oven at 100°C for overnight, cool in desiccator and weight it again (W3).
5. The loss in weight of crucible is expressed as cellulose content.
6. Place these crucibles in a muffle furnace and ignite at 550oC for 3hr.

7. Next day, take these crucible cool in a desiccator and weight again (W4).The loss in the weight indicate lignin content.
8. Subtract the original weight of crucible from this weight in order to calculate the Ash content.
9. Express the result on per cent dry weight basis.

Calculation

$$Silica\ (\%, dryweightbasis) = \frac{W4 - W1}{W} X\ 100$$

W = Weight of sample

j) NDF content (% dry weight basis)

NDF is an estimate of the content of hemicellulose, cellulose and lignin in samples of plant origin. The original NDF-methods of Goering and van Soest (1970) are commonly modified by the addition of heat-stable alpha amylase, to remove starch.NDF was determined by using Foss, Fibertec^{TM}8000.

Reagents

i. Acetone, technical grade
ii. Celite, Diatomaceous earth, acid washed, Celite 545 AW, or equivalent
iii. Antifoaming agent, n-Octanol
iv. EDTA (Disodium Ethylene DiamineTetraacetate), $C_{10}H_{14}N_2Na_2O_8 \cdot 2H_2O$
v. Sodium Borate decahydrate, $Na_2B_4O_7 \cdot 10H_2O$
vi. Sodium Lauryl Sulphate, $C_{12}H_{25}OSO_3Na$
vii. Triethylene glycol, $C_6H_{14}O_4$
viii. Disodium hydrogen phosphate, Na_2HPO4
ix. Sodium sulphite – 96 % (Na_2SO_3)
x. Burke's iodine solution (2 g KI, 1 g I_2 in 100 ml dH_2O).
xi. Termamyl 300 L, Type DX
xii. Neutral Detergent Solution (NDS)

18.61 g of EDTA and 6.81 g of Sodium Borate decahydrate, was placed in a beaker and some distilled water was added.Heated until dissolved.Added 30 g Sodium Lauryl Sulphate, 10 ml of Triethylene glycol and 4.56 g Disodium Hydrogen phosphate. Added water and heated until dissolved. Mixed and diluted to 1000 ml. The pH is kept between 6.95-7.05, and adjusted with conc. HCl or NaOH as required.

Analytical Procedure

A blank was run through entire procedure along with each batch of samples.

NDF Extraction Step

1. Pre-dried crucibles were placed on a balance and tare. To simplify the filtration,weighed 1000 ±2 mg of Celite 545 into the crucible. Weighed 500 ±2 mg sample into the crucible ($W1$).
2. Added 0.5 (±0.1) g of sodium sulphite to each crucible, placed in hot extraction uni tusingthe crucible holder and locked into position in front of the heater in the Fibertec^{TM} 8000ensuring that the safety handle engages. Placed the reflector in front of the crucibles.
3. Filled NDS tank with NDS solution and placed it in the left position (R_1) of the drawer. Fixed all connections.Added antifoaming agent, n-Octanol, to the amber bottle inside theside door.
5. Opened water tap (about 2 L/min) for reflux system.
6. Turned "ON" the instrument and default NDF program can be started by pressing "START" twice for confirmation.
7. At the end of the extraction, the reflector and crucibles were removed.
8. Added25 ml acetone to each crucible and allowed soak for 3-5 minutes, filtered solvent out by placing the valve in "vacuum" position. Repeated one time.
9. Removed crucible and air dried for 10-60 min to remove acetone.
10. Crucibles dried at 105 ±2 ºC for at least 5 h. Cooled to room temperature in a desiccator and weighed (W_2).
11. Crucible and fibre ignited in a 525 ±15 ºC furnace for at least 5 h or until C-free. The crucibles were allowed to cool down to below 250 ºC before moving them from the furnace. Cooled in desiccators and weighed to nearest 0.1 mg (W_3). Subtracted weight of crucible and Celite to determine ash weight.

Calculation

$$\%NDF = 100 \text{ X } (W_2 - W_3) - (B_2 - B_3)/W_1$$

Where,

W_1 = Sample weight

W_2 = Sample and crucible including filtration aid after extraction and drying, in grams

W_3 = Sample and crucible including filtration aid after ashing, in grams

B_1 = Crucible including filtration aid after extraction and drying, in grams

B_2 = Blank crucible including filtering aid after ashing, in grams

k) Hemicellulose content (% dry weight basis)

The concentration of hemicellulose can be calculated by subtracting the Acid detergent fiber content (ADF %) from the Neutral detergent fiber content (NDF %).

$$\% \text{ Hemicellulose} = \%NDF - \%ADF$$

3.4.3 Disease Scoring

a) Bacterial leaf blight intensity (%)

Observations for disease intensity of bacterial leaf blight were recorded in natural conditions using 0-9 disease scale followed by AINP on Arid legumes ICAR-IIPR.

The percent disease index was calculated as:

$$\boldsymbol{Percent\ Disease\ Intensity} = \frac{\boldsymbol{Sum\ of\ all\ Individual\ rating\ \times 100}}{\boldsymbol{Total\ no.\ of\ leaves\ assessed\ \times Maximum\ rating}}$$

Five plants from each replication selected randomly, were tagged and 6-8 leaves from each plant were selected at random for assessing the infected leaf area, according to standard method using 0-5 scale.

Grade	Percent Disease Intensity	Disease Reaction
0	0	Disease Free
1	0.1-5	Highly Resistant
2-3	5.1-10	Resistant
4-5	10.1-20	Moderately Resistant
6-7	20.1-50	Susceptible
8-9	>50	Highly Susceptible

3.5 Statistical Analysis

Analysis of variance for the design of experiment, genetic parameters like phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability broad sense (h^2 (bs) (%)) and genetic advance (GA) for all characters studied was executed using OP-Stat software (available at *http://www.hau.ac.in*) developed by CCSHAU. Association among characters was determined by correlation coefficient analysis done by OP-Stat software and path analysis, were estimated employing software $\text{GRAPES}_{1.0.0}$ (available at *http://www.https://www.kaugrapes.com/*).

3.5.3 Analysis of Variance (ANOVA)

The analysis of variance for randomized complete block design was carried out for individual characters to test the significance of difference among the genotypes following the method given by (Fisher, 1925). The software OP-Stat was used for the analysis purpose.

$$\boldsymbol{Y_{ij} = \mathrm{m} + a_j + b_j + e_{ij}}$$

$\boldsymbol{Y_{ij}}$= observation in the i^{th} treatment and j^{th} replication

$\mathbf{m}$ = general mean

$\boldsymbol{a_i}$ = i^{th} treatment effect

$\boldsymbol{b_j}$ = j^{th} replication effect

$\boldsymbol{e_{ij}}$= random error associated with the i^{th} treatment and j^{th} replication.

Table 3.3 Analysis of variance tables for all the characters under study were constructed as

Source of variation	**Degree of Freedom**	**Mean sum of square**	**Expected Mean sum of square**	**F Calculated**
Replications	**(r-1)**	**MSr**	$\sigma_e^2 + g\,\sigma_r^2$	**MSr/MSe**
Genotypes	**(g-1)**	**MSg**	$\sigma_e^2 + r\,\sigma_g^2$	**MSg/MSe**
Error	**(r-1) (g-1)**	**MSe**	σ_e^2	
Total	**rg-1**			

Where,

r = number of replications
g = number of genotypes
MSr = mean sum of squares due to replications
MSg = mean sum of squares due to genotypes
MSe = mean sum of squares due to error
σ^2g = Genotypic variance of character
σ^2r = Variance due to replications
σ^2e = Error variance of character

$$\text{Genotypic Variance } (\sigma^2 g) = \frac{MSg - MSe}{r}$$

$$\text{Phenotypic Variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

3.5.4 Parameters of variability

a) Mean (X)

The mean value of each character was worked out by dividing the total value by corresponding number of observations.

$$\bar{X} = \frac{1}{n}\sum_{i=1}^{n} X_i$$

Where,

$\bar{X}$ = Mean
X_i =ith observation
n = Total number of observations

b) Range

The lowest and the highest values for each character were recorded.

c) Standard error (SE)

Standard error of difference of two treatment means was calculated with help of error mean square from the analysis of variance table as follows:

$$\text{S.E.}_{(d)} \pm = \sqrt{\frac{2MSe}{r}}$$

Where,

MSe = Error mean sum of square

S.E.$_{(d)}$ = Standard error of difference of two mean

r = Number of replications

d) Critical difference (CD)

For all the character's critical difference was calculated to compare the treatment means. Critical difference is the difference of two means and tabulated value of 't' at 1 & 5 *per* cent level of significance and at error degree of freedom using the following formula,

C.D. = **S.E.$_{(d)}$** x "**t**"at 5% or 1% for error d.f.

Where,

S.E.$_{(d)}$ = Standard error (SE) of difference of two treatment mean

t =t distribution tabulated value for error degree of freedom at 5% or 1% significance

e) Genotypic and phenotypic coefficient of variation (CV)

Genotypic and phenotypic coefficients of variation were calculated by the formula suggested by (Burton and de Vane, 1953) given as below:

Genotypic coefficient of variation **(G.C.V.)** = $\frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$

Phenotypic coefficient of variation **(P.C.V.)** = $\frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$

Where,

$\bar{x}$ = mean for that character

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The genotypic and phenotypic coefficients of variation were categorized as *per* the method suggested by (Sivasubramanian and Madhavamenon, 1973):

0-10%= Low **10-20% = Moderate** **20% = High**

f) Heritability (h^2)

Heritability in broad sense was calculated for each character according to the formula suggested by (Johnson *et al.*, 1955)

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

h^2 = Heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The heritability was classified into three groups as suggested by (Johnson *et al.*, 1955):

0-30% = Low **30-60% = Moderate** **>60% = High**

g) Genetic advance expressed as percentage of mean

Estimates of appropriate components were substituted for the parameters to predict expected genetic gain as suggested by (Johnson *et al.*, 1955). The expected genetic advance was calculated at 5 *per* cent selection intensity for each character as

$$\text{Genetic advance (\% of mean)} = \frac{k\ \sigma p\ h^2}{\bar{X}}$$

Where,

k is selection differential expressed in terms of phenotypic standard deviation, using 5 *per* cent selection in a large sample from a normally and independently distributed population, the value of selection intensity ***(k)*** is equal to **2.06**at5% level of significance.

σp =Phenotypic standard deviation

h^2 =Heritability is broad sense, and

$\bar{X}$ =Mean value for that character over all the genotypes.

3.5.5 Association studies

a) Correlation coefficient analysis

To determine the degree of association of characters with yield, yield components and physiological characters the correlation coefficients were calculated. Coefficients of correlation between characters were determined by using the variance and covariance componentsas suggested by (Al-jibouri *et al.*, 1958).

$$r_g(x,y) = \frac{cov_g(x,y)}{\sqrt{\sigma_g^2(x) + \sigma_g^2(y)}} r_p(x,y) = \frac{cov_p(x,y)}{\sqrt{\sigma_p^2(x) + \sigma_p^2(y)}}$$

Where,

$r_g(x,y)$and$r_p(x,y)$ are the genotypic and phenotypic correlation coefficients

$cov_g$and$cov_p$are the genotypic and phenotypic covariance, respectively

σ_g^2andσ_p^2 are the genotypic and phenotypic variance, respectively

b) Path coefficient analysis

The genotypic correlation coefficients were used to work out path coefficient analysis. Path coefficients were obtained according to Dewey and Lu, (1959).A set of simultaneous equations in the following form were solved:

$$r_{ny} = p_{ny} + r_{n2}p_{2y} + r_{n3}p_{3y} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_{nx}p_{xy}$$

Where,

r_{ny} = correlation coefficient of one character and yield

p_{ny} = path coefficient between the character and yield

r_{n2}, r_{n3} ……… r_{nx} = represent the correlation coefficient of that character with yield and other components in turn

The following correlation matrices were formed:

A		B		
r1y	r11	r12	r13	……r1j
r2y	r21	r22	r23	……r2j
r3y	r31	r32	r33	……r3j
riy	ri1	ri2	ri3	…... rij

The technique given by (Goulden, 1954) was followed for inversion (B^{-1}) of B matrix. Path coefficients $\mathbf{P_{jy}}$were obtained as follows:

$$\mathbf{P_{jy} = (B^{-1}) \times (A)}$$

The indirect effect for a particular character through other character was obtained by multiplication of direct path and particular correlation coefficient between those two characters, respectively.

$$\textbf{Indirect effect} = \mathbf{r_{ij} \times P_{jy}}$$

Where,

$i = 1, 2 \ldots\ldots\ldots\ldots n$

$j = 1, 2 \ldots\ldots\ldots\ldots n$ and

$P_{jy} = P_{1y}, P_{2y} \ldots\ldots\ldots\ldots P_{ny}$

The residual factor, *i.e.*, the variation in yield unaccounted for (by such characters which could not be studied) was calculated as:

$$\textbf{Residual factor (x)} = \mathbf{1-R^2}$$

Where,

$R^2 = P1y\ r1y + P2y\ r2y + \ldots\ldots\ldots\ P_{ny}r_{ny}$

R^2 = Squared multiple correlation coefficients and the amount of variation in yield that can be accounted for by the yield component character

3.6 Molecular analysis

Molecular analysis of 25 cluster bean genotypes was done using standard protocols as described below.

Glassware and reagents All the glassware used, were of the borosilicate quality and obtained from Borosil Glass Works Ltd., Mumbai or Corning Glass Company, USA. The chemicals used for preparing different solutions or buffers like DNA extraction buffer and PCR amplification buffer were obtained from Sigma Chemicals Co. USA, Life Technologies (India) Pvt. Ltd., Imperial Bio Medics (Chandigarh, India) and SRL Pvt. Ltd. Mumbai, Maharashtra, India. All other chemicals used in this study were of molecular biology grade or analytical grade and procured from Sigma Chemicals Co. and E. Merck Ltd. (Worli, Mumbai-400018, India).

3.6.3 Preparation of chemicals, reagents, buffers and solutions

(a)1M Tris-HCl (pH 8.0)

Tris base	121.1 g
Final volume (distilled water) 1000 ml	
pH	8.0

- Sterilization by autoclaving

(b) 0.5 M EDTA (pH 8.0)

EDTA	186.12g
Final volume (distilled water) 1000 ml	
pH	8.0

- Sterilization by autoclaving

(c) 5 M NaCl

Sodium chloride (NaCl)	292.2 g
Final volume (distilled water)	1000 ml

(d) 2% CTAB

Dissolve 2 g of CTAB in 100 ml of dd H_2O

(e) 10X TBE buffer

Tris108.0 g

Boric acid 55.0 g

0.5M EDTA (pH 8.0) 40 ml

Final volume (distilled water) 1000 ml

(f) RNase stock (10mg/ml)

NaCl (15mM) 500 µl

Tris (10mM, pH 8.0) 500 µl

RNase 10 mg

- RNase stock solution was prepared by boiling the solution (containing the above components) for 15 min. at 100°C, cooled and stored at 4°C till further use.

(g) 6X Loading dye

Sucrose 4.0 g

Bromophenol blue 0.025 g

Xylene cyanol0.025 g

Final volume (distilled water) 10 ml

- Loading dye solution was stored at 4°C in the refrigerator

(h) CTAB extraction buffer

Tris (pH 8.0) 1 M

EDTA (pH 8.0) 0.5 M

Sodium chloride 5 M

CTAB2%

PVP (Polyvinyl pyrrolidone) 2%

β-Mercaptoethanol2%(Added just before use)

(i) TE buffer

Tris (pH 8.0) 10 mM

EDTA (pH 8.0) 1 mM

(j) Acrylamide-bisacrylamide solution for 8% PAGE

Acryamide76 g

Bisacrylamide 4 g

Final volume (0.5X TBE) 1000 ml

3.6.4 Genomic DNA isolation

Genomic DNA was isolated from the young leaves of plants using CTAB extraction method of Murray and Thompson (1980) modified by Saghai-Maroof *et al.* (1984). The DNA isolation protocol involved four main phases: homogenization, solvent extraction, DNA precipitation and re-suspension of DNA.

Preparation of DNA extraction buffer: To make 100 ml extraction buffer, 20 ml of 1M Tris, 28 ml of 5M NaCl, 4 ml of 0.5M EDTA, 46 ml of distilled water, 2 g of CTAB and 2 g of PVP and were added, components were dissolved by incubating at 65ºC. 2 ml of β-mercaptoethanol was added after cooling at room temperature and.

Homogenization and incubation

- Leaf samples were taken from 3-4week old plant. Homogenization of one gram of fresh leaf tissue to fine powder in liquid nitrogen was done by using sterilized pre-chilled mortar andpestle.
- 15 ml CTAB buffer was added to sterilized 50 ml Oakridge tubes.
- Ground samples were transferred to the tubes and mix them gently by gently tilting the tubes and then incubated for 45 minutes to 1hr at 65ºC. Mixing of thecontents was done occasionally, by gently inverting the tubes at an interval of 15-20 min.

Solvent extraction:

- Added phenol: chloroform: isoamylalcohol (25:24:1) to the samples in equal volume and mixed them gently.
- Centrifugation of the content was done at 8000 rpm for 10 min and then upper aqueous layer was collected in another pre-sterilized oakridge tube.

- Again chloroform: isoamylalcohol (24:1) was added in aqueous phase and mixed thesamples gently. The samples were centrifuged again at 8000 rpm for 10 minutes.

DNA precipitation

- The aqueous layer was taken and equal volume of chilled isopropanol was addedand incubated at -20ºC for 1hr.
- Centrifugation of the samples was done at 8000 rpm for 10 minutes and then supernatant was removed supernatant and pellet was saved.
- 70% ethanol was added for 2 minutes for washing and then ethanol was discarded.Ethanol and the pellet was kept drying overnight.

Qualitative and Quantitative estimation of genomic DNA

An aliquot of DNA was suitably diluted, and its quality and quantity were assessed by both nanodrop and agarose gel electrophoresis. Intensity of bands was visually analysed by comparing it with intensity of Lambda DNA of know concentration in 0.8% agarose gel electrophoresis. One ml of preheated (65ºC) CTAB buffer was added to Eppendorf tube and the samples.

Table 3.4: Reagents used for DNA extraction, dilution, and gel electrophoresis

Reagents	**Amount to add for 100 ml**
Composition of CTAB extraction buffer	
Tris-HCl (1 M,pH8.0)	20ml
EDTA(disodium, 0.5M, pH8.0)	4ml
NaCl (5M)	28ml
CTAB	2 g
β-mercaptoethanol (Added just before use)	200 µl
Sterile distilled water	46ml
Composition of T.E. buffer (pH8.0)	
Tris (1M;pH8.0)	1ml
EDTA(disodium,0.5M;pH8.0)	200 µl
Composition of 10X TBE buffer (pH8.0)	
Tris	108g
Boric acid	55g
EDTA(disodium)	40ml
Composition of 6X loading dye (pH8.0)	
Sucrose	4 g
Bromophenol blue	0.025 g
Xylenecyanol	0.025 g

3.6.5 RNase Treatment

I. For removing RNA contamination, 1 µl of 10 mg/ml RNase was added in the DNA samples, dissolved in20 µl T.E. buffer.

II. The samples were gently mixed and incubated in water bath at 37ºC for 2-3 hours. DNA was again extracted by adding equal volume of chloroform: isoamyl alcohol (24:1) mixture.

III. Samplesweremixedwellandthencentrifugedat10,000rpmfor10-15minutes.Supernatant was transferred to sterilized new eppendorf tubes.

IV. DNA was precipitated down by adding 1/10th volume of 5M sodium chloride and 2volumes of chilled absolute alcohol followed by centrifugation at 10,000 rpm for 10 min. Pellet was then washed with 70% alcohol, air-dried, and finally dissolved in T.E. buffer for keeping as stock solution.

3.6.6 Molecular markers

A total of 102 SSR (simple sequence repeat) markers were used for studying molecular polymorphism among 25 cluster bean genotypes. All these primers were synthesized from IDT lnc. USA. A brief description of polymorphic SSR markers is given in the Table 3.6.

3.6.7 Polymerase Chain Reaction (PCR) Amplification

PCR amplifications were carried out using My-CYCLER (programmable thermal cycler from BIORAD^{TM} INTERNATIONAL). PCR conditions were optimized by varying concentration of gradients, temperature and time intervals during denaturation, annealing and elongation steps for obtaining better amplification, banding pattern and reproducibility. A tabular summery of all components and the steps of a standardized reaction are given in Table3.5.

Table 3.5: Components and protocol of a standardized PCR reaction

Sr. No.	Basic Components	Volume(µl)
1.	Sterile distilled water	6.7
2.	10X PCR buffer	1.0
3.	dNTPs mix(10µM)	0.4
4.	Forward primer(10µM)	0.4
5.	Reverse primer(10µM)	0.4
6.	$MgCl_2$ 50mM	1.0
7.	Taq DNA Polymerase (3U/µl)	0.1
8.	DNA template (100ng)	2.0

Optimized different steps of PCR

i. 95°C for 4 minutes (initial denaturation)

ii. 94°C for 1 minute (denaturation)

iii. 47– 69°C for 50 seconds (primer specific temperature for annealing)

iv. 72°C for 1 minute (primer extension)

v. 72°C for 15 minutes (final primer extension)

Thirty-five cycles were setup to repeat the step (ii) to (iv) in the amplification reaction and finally amplified products were stored at-20ºC for further use.

Table 3.6: A brief description of SSR markers used for screening

S. No.	Marker	Forward primer 5’→3’	Reverse primer 5’→3’	Tm (ºC)
1	GDR1	CTGCTCGCTGCAATTCTTG	GAATTCCTCGATGCTGCCTA	54.65
2	GDR2	GACGATGGAACCCTTCTGAT	CGTAGTAGCTGGTAGCATGCAG	55.85
3	GDR3	TTTCCCCTCATCCTTCTTCA	TATCATCGTCCCCATCGTTT	53.35
4	GDR4	GCCCAAAACTTACCGAGTTG	CAGAACCCCCTCTCACTGAC	55.65
5	GDR5	TTGCTCTCATTGCCATTGTC	AAATCCCAAGCGTCAATCTG	53.40
6	GDR6	GGCACCGCCATTGTTATTAT	CCAAAATGGACATGTGTTTGG	53.05
7	GDR7	GACCTTGCCCGAGAATACAT	CTTCCCAGCTTCACCAAGAG	55.10
8	GDR8	GGAAAAGCGGTGAGAGTGAG	TGCCTTATCTTGGCAAATGTC	54.60
9	GDR9	CACGAGGCCTGAATCAATCT	TGAGGAACAGGGAGCCTATG	55.50
10	GDR10	CCCTAAATCAAACGCAACAGA	GGACGTGGGTGGTGTAACTC	55.50
11	GDR11	GGTTTACACGCAGGTGGTTT	TTCCACTCGCATTACCCAGT	56.10
12	CTN01	TCAAGCTTCCGTTAAAGCGT	CACATCCATGAACTCCAACG	54.30
13	CTN02	AAATGGCTTTGGCCCTAACT	TGTGCCAACCACCTCTACAA	55.70
14	CTN03	GTTGGGGAGTTATGATGAGA	TTCCAGTCTTTTTGTCGAGT	51.55
15	CTN04	GGAGATAGTTGCAAACAAGG	TGCTTGAACAACACTCTTTG	51.25
16	CTN05	GCCTGCAACAGAAGATAGAC	GACTGAGAAGCTTGGAAATG	52.25
17	CTN06	GGGTTCTCTTGAGTGTCTTG	GGTAGCGTGACTATTCCAAA	52.50
18	CTN07	TAAACTCATGAAAGGCTCGT	CTTGAATGTGCTTTAGGACC	51.35
19	CTN08	ACCCCTCGTATCCTCATTAT	AGTTCATTTGCAACATCCTC	51.60
20	CTN09	GTTCTCACTCTTTCCGTGAG	AGTTTCTTCCTGTTTCCCTC	52.45
21	CTN10	GAGGGAAACAGGAAGAAACT	GTTCAAAGTCCAACTCAAGC	52.00
22	CTN11	CACAAGCAAGGAAAGCTAAT	AACATTCAGCATCCCACTAC	51.70
23	CTN12	GCTTCACAGTATCTTCAGGG	TCCATTGGAGGACAGATAAG	51.95
24	CTN14	AATGAGCTGCAATTACCAGT	CAATTCGTTAGTGGTTGGAT	51.30

25	CTN15	TTCTGAGGAAAGCTGAAGAG	CAGGGTATCCCAAGACATTA	51.50
26	CTN16	GTGAGAGTCAGAAGCCTGTC	GCTACTTGTAATGGTGGTCC	53.95
27	CTN17	ATACAAGGAAGGGCCTAAAC	CTGAGAAAGAACTTGGTTGG	51.55
28	CTN18	ATATTCTCCGTGACATCCAG	TTAGGCTACACGTCAAGGTT	52.50
29	CTN23	TTAGGCTACACGTCAAGGTT	GACATCCAGAAGGTCAGAGA	53.35
30	CTN24	CCAGTTTCAACTCAAACCAT	GTGTTCTCTCCCAAACCATA	51.35
31	CTN25	GAAGGCAATAGATGATGGAG	TTCTTTCTGGTAAGGAGCTG	51.05
32	CTN26	CATGCAAGAACTAAGGAAGG	TTCAAGCTCTGAGTTCCAAT	51.30
33	CTN27	GATTTCATGGTCATTTCCAC	GTAGTGGGATGCTGAATGTT	50.90
34	CTN28	GTTACTAATCGCCTGAGTGC	TTGCCAATAAAGTATCCACC	51.70
35	CTN35	GCCTGAACTGTTCCAAGAGC	TTTTGCAGTGACCAACTTGC	55.35
36	CTN36	ATGCAATCTCTAGTCGGAGA	GCAAGGGAATCTGTGAGATA	52.15
37	CTN37	CAAAAGCTTACGAGCTTGAT	AAGTCCAGTGGTAGCAAGAA	52.25
38	CTN40	TAACACCACACTTGTTCCAA	ACTCGTTGTATGCATCCTTT	51.90
39	CTN35	GCCTGAACTGTTCCAAGAGC	TTTTGCAGTGACCAACTTGC	55.35
40	CT223	CAA ATT TTT GCA GAG GCA GA	GGC TTT GAT GAG ACC AGC TC	53.80
41	CT224	CTG CAC CAT TGA TTG CAA GA	CGA ATC GAT CAG TCA CAA CC	53.60
42	CT225	CTC CTG GCT TCT TCA TCC AC	CAC GAT TCC ATT TCC AAA CC	53.70
43	CT226	AGC AGC TTG GGC ACT TGT AT	CCA CCC AAA GAA GAG GAT GA	55.75
44	CT227	GAC TTA AAC GAT GGG GTC CA	CAT CAA TTA GCG GCT TCT CC	54.05
45	CT228	CAC GAG GGT TGT TCA ATT TTC	AAG AGC GCG ATT TCA CAG AG	53.90
46	CT229	AGG GTC CTT TCC AAC ACA CA	CAC TGC CAT TGA AGA TCA GG	55.05
47	CT230	TCG TCC TTT CTT TCC ACT GC	GCT ACA GCC ATG CAT CTT CA	55.25
48	CTF231	GTC CCA GAA TGG TTC ATT GG	ATA CTG CTC GAG GGA GCT GA	55.60
49	CTF232	TGG AAC CTC GAC AGA CAC TG	AAT TCT AGG GCC AGG GAC AC	56.70
50	CTF233	GTG ACA AGG CAA GGC AAA TG	TCC CTC CAT CTG AAA GAG GTT	55.25

51	CTF234	ACG ACG TTC CTG ACC AAA AC	CAA ATC CTG GCT GCT AGC TC	55.70
52	CTF235	TGT TGG GTT GAT GGA GAA CA	TGA CAC GGA CAA CAC CTC AT	55.25
53	CTF236	CAC GAG GCT GTC TCT CAT CTT	GGT CGA CGG AGA TCT GAA AA	55.40
54	CTF237	AGC TGT TTT CTG GGT TCG AG	GCT TTT GGT TGA AAG GGT GA	54.45
55	CTF238	TGG TGT GCA TTA ACG ATG CT	ATG CTG GAA ATG ACG AAG GT	54.75
56	CTF239	CAC GAG GGA GCA GTG TCA T	GAA AAA TCA AGG CGT TCG AG	54.65
57	CTF240	CAC CGA AAA CAC AGT CAT CG	ATA GGG ACG AAG CAG AAG CA	55.05
58	Ct_SSR_1	GGAAATGGAAACTGAAGGA	CTATGAACACATTACAGAACAG	49.30
59	Ct_SSR_5	TCCTCCAATCCTTCGTAAA	CACCAGCATAGGGAGAAT	50.85
60	Ct_SSR_12	CCTTGTCTTGTGGTAGGCATATT	GTCTTCCTCTCATCAAGATTTCCC	55.00
61	Ct_SSR_118	AGAGGAGGTCCTTAGCTTTCT	GTGGCTTCATCTGCTCTGTAA	54.80
62	Ct_SSR_128	GCAGACCAACTCCAAATCAAG	GCGGTCTATCCGTCACAAT	54.40
63	Ct_SSR_139	GCCACTAGGTGGTTGAAGAG	CAGTGTTAGAGAAGAAGGACTGTAA	54.60
64	Ct_SSR_140	GGACAGAAGCCATCGACAAG	TCTATGCGCATTCTCCATTCTC	55.30
65	Ct_SSR_154	GGAGTACTTCATAAAGTTATACAAGCTG	CCGTAGATAGATAGGGCAGTGA	54.40
66	Ct_SSR_166	TCTCTCTCTCTCTCTCTCTCTCT	GTTCACCTGTTCGCATTCATC	54.50
67	Ct_SSR_167	AGGAACTTGCATAAGATCGATGA	GAGAGAGACAGAGAGACAGAGAG	54.50
68	CTGM_1	CAGAGGAGTTCTTAACACTCTGAAA	TTTTTTTTTAACTTTGACCATTGAA	49.00
69	CTGM_4	TTTAACTTTGTTGGACAGCCC	AATTTAGGTGGCATTACATTAGGAA	53.15
70	CTGM_5	CACATAAAAACATAAATGTGTGGG	AGGAATAAATGGAGGTTGCTTTT	51.95
71	CTGM_6	AAATTCAATTCCAATTTTTCAACTC	AACTTTTTGGCTCTAAATACCACG	51.65
72	CTGM_8	TGGAAATAGGAATAATGGTGGTG	TTTTTGGCCACCATACCATT	52.75
73	CTGM_9	TTAATCTCATCTTATGGGTCGGA	GCACGCACGCTCCTATCTA	55.05
74	CTGM_11	AAATTTAATATTTGGATGGAACAA	CACCATCCATCTTCTCTAAGCA	50.85
75	CTGM_12	TTATCGCATCCCTTCCTCAT	TGAGAAATTTTGGATGTGGCT	53.00
76	CTGM_16	CAATGACACAAATGCTTGGC	AACCAGGTGGTAGCGGAGTT	55.85

77	CTGM_17	AAGAGAGAGAGCTGGAGAAGCA	TCTACTCTTCTTCCTCATCATCAA	55.15
78	CTGM_18	TGATACAATTTTTTGATACATGGAA	TCCAAAAAAATTGATTTATCTTCAC	49.20
79	CTGM_20	CAATGAAACGGTAGGTTTTCTGA	CATGCATTTGTGATCAATTAAGTTT	52.30
80	CTGM_22	ACCCACAAACTCACTACCACG	AAGGCCTTAAGGGGATCTTAT	55.05
81	CTGM_24	AATATTTCATTCATCACCTGCATT	AAGATTTTATCAAAACTGCCCAAA	51.55
82	CTGM_25	GGCGGGCCAATATAAAATAG	CCCGTTAAGCTTTTCACGTT	52.45
83	CTGM_31	TGAGTTCCTCGCTGTTTGG	AGCTTGATCTCGATTAGAGGGT	55.15
84	CTGM_37	TTAATTAAGCTGTGTACCCAAACA	GGTGTAGCTTGCTAACGCACT	55.15
85	CTGM_40	GGGCCTAAAGCCCTTGTTT	TTATTTTTGTTGTCGTTATTGTTGA	52.95
86	CTGM_42	TTGAGTTTCCTAACCTGTGCAGT	AATCAAGCTTGTCTTCATTCATCA	53.80
87	CTGM_44	TGATAATTTTGGTATGTGTGCCA	ACCGGTGTAAGTTGATCTCTCTC	54.40
88	CTGM_46	AAGTGGGTGTACGTTAGTAAGCC	TGTACTTCCGACTTCGGTTTG	55.20
89	SSR1	CTTCGTCTCTTCTCACTACCC	TTCTCGACGAGCTTCTTG	53.00
90	SSR2	AGAAGACTGGGAGAAGAAGC	TCAGTTCCAGACTCTGTTCG	53.95
91	SSR3	GAGCGTCACATGAACAGAG	CACTGGTCTCTTTGTTGGTC	53.35
92	SSR4	CGTCACATGAACAGAGGAC	CTCACTTGCACTGGTCTCTT	53.80
93	SSR5	CTCTTCTGTGTCACTGTCCTC	AGCTAACTGGTGACAACGTC	54.70
94	SSR6	CTTCAGTTTCCTGCTCTGAC	GAGAGCTTACCGGAGACAA	53.40
95	SSR7	CCAGAGATGGCATCCTTA	CTCTCCCGAAGTATCAAGC	51.65
96	SSR8	GAGGGATTGGAGTGGTTT	GGCCATGATAGAGTGAGTGA	52.75
97	SSR9	GTGCCGTTGTTGTCGTTT	GAGAGAGGGAGAATCTCTCAG	53.70
98	SSR10	ATCGCTGCCATGAGATAG	GCATATGGCTGCATCTGT	52.20
99	SSR11	GAAAGACCATTGGACAGACC	GAAAGGGTCCCCAAATTC	51.95
100	SSR12	CCATTGCTCTCTTTGGTC	GGCTTCCAGCATGATCTAAC	52.05
101	SSR13	CACTCTCACCACACTCACTCT	ACGAGGGGGTTTTTGTAG	54.05
102	SSR14	CTGAACCCTTGTTTGCTG	GGTGGAAGTGGAAGACATAG	52.00

3.6.8 Agarose gel electrophoresis

- To visualize amplified DNA fragments 2% (w/v) agarose solution was prepared in 1X TBE and then ethidium bromide (0.5µg/ml) was added in the gel and mixed gently.
- Gel was then poured in casting plate with appropriate comb of required well number and size.
- The PCR amplification products were mixed with 2µl of 6X loading dye solution and loaded on wells using micropipette.
- Electrophoresis was done using 1X TBE as running buffer at constant voltage (5volt/cmof the gel). PCR amplification products were visualized under UV light and photographed using gel documentation system.

3.6.9 Statistical analysis

3.6.9.1 The polymorphism information content (PIC) was estimated according to Botstein et al. (1980) using the following equations:

$$PIC_i = 1 - \sum_{j=1}^{n} P_{ij}^2$$

Where,

PIC_i = polymorphic information content of a marker i,

P_{ij} = frequency of the jth pattern for marker i,

The summation extends over n patterns

3.6.9.2 The expected heterozygosity /gene diversity (He) values of each primer were determined according to Liu (1994) using the equation:

$$Expected\ heterozygosity/gene\ diversity\ (H_e) = 1 - \sum_{i=1}^{n} P_{ij}^2$$

Where,

P_i is the frequency of the ith allele

n_i is the total number of alleles at all loci

3.6.9.3 Genetic dissimilarity and factorial analysis

To determine the genetic dissimilarities and factorial analysis among the genotypes, the 48 polymorphic SSR marker data were analyzed with the help of DARwin 6.0 program (Perrier and Jacquemoud-Collet, 2006). The obtained dissimilarity matrix was used to create a un-weighted neighbor-joining (UNJ) tree at value of 30,000 bootstraps. In addition, Bayesian model-based cluster analysis was also conducted via STRUCTURE v.2.3.4 program to specify the population structure and identify the number of gene pools (Pritchard *et al.*, 2000). The assumed population numeral (K) was set at 1 - 10. For each fixed K, ten unbiased runs were tested, and each run comprised of 50,000 burn-in times and 100,000 iterations. Using Structure Harvester v6.0 (Earl and Vonholdt, 2012), the peak value of K was estimated by evaluating ΔK statistics and L (K) (Evanno *et al.*, 2005).

3.7 Stability analysis

3.7.1 Eberhart and Russell's (1966) Model

To analyze the data over eight environments the stability model proposed by Eberhart and Russell's (1966) was adopted. This model involves the estimation of three parameters which are defined by a mathematical formula.

$$Y_{ij} = \mu_i + \beta_i I_j + S_{ij}$$

Where,

Y_{ij} = Mean of the i^{th} variety at the j^{th} environment

μ_i = Mean of i^{th} variety over all environments

β_i = The regression coefficient that measures the response of i^{th} variety to varyingenvironments

S_{ij} = The deviation from regression of the i^{th} variety at the j^{th} environment and

Ij = The environmental index obtained by subtracting the grand mean from the meanof all varieties at the j^{th} environment

These parameters were calculated as follows

(i) Environmental index

$$I_j = \Sigma_j Y_{ij}/T - \Sigma_i \Sigma_j Y_{ij}/t.s$$

Where,

t = Number of varieties

s = Number of environments

$$\Sigma_j I_j = 0$$

(ii) The regression coefficient for each variety (bi)

$$b_i = \Sigma_j Y_{ij} I_j / \Sigma_j I^2_j$$

(iii) Deviation from regression

$$S^2 d_i = \Sigma_j \delta^2_{ij}/(S-2) - S^2 e/R$$

Where, S^2e/R= Mean square for (estimate of) pooled error

Analysis of variance for stability

In this model the variance due to environments and genotype x environment are partitioned into environment (linear), genotype x environment (linear) and deviation from the regression coefficient.

Table 3.7.1: Analysis of variance for stability–Eberhart &Russell's Model (1966)

Source of variation	Degree of freedom	M.S.	F value
Genotype (G)	(g-1)	MS_1	MS_1/MS_3
Environment (E)	(n-1)		
G X E	(g-1)(n-1)		
Environment (Linear)	1		
Genotype X Environment (Linear)	(g-1)	MS_2	MS_2/MS_3

Pooled deviation	g(n-2)	MS_3	MS_3/MS_4
Genotype 1	(n-2)		
Genotype 2	(n-2)		
Pooled error	n(g-1)(r-1)	MS_4	
Total	(ng-1)	TSS	

Where,

n = number of environments

r = number of replications

g = number of genotypes

CF = Correction factor

Test of Significance

The mean sum of squares due to genotypes, environments, G x E interaction, Environment (linear) and G x E (linear) was tested against pooled deviation. If pooled deviation is non-significant all these components were tested against pooled error. Mean sum of squares due to pooled deviations were tested against pooled error.

(i) To test the significance of pooled deviation mean square against the pooled error mean square

$$F = MS_3/ MS_4$$

(ii) To test the significance of the differences among the means of genotypes

$$F = MS_1/MS_3$$

(iii) To test that the genotypes do not differ for their regression on environmental index

$$F = MS_2/MS_3$$

Further,‘t‘test is used to test the significance of deviation of ‘bi‘ from unity

$$t = | 1- bi |/S.E (bi)$$

$$SE\ \ bi\ = \frac{\sqrt{{}_j\frac{\delta_{ij}^2}{n} - 2}}{{}_j I_j^2}$$

Where,

δ^2ij is the deviation of i^th variety in j^th environment from regression

(iv) To test individual deviation from linear regression

$$F = (\Sigma_j\delta^2ij/n-2)/\text{Pooled error mean square}$$

A joint consideration of three parameters, that is

a) The mean performance of the genotype over environments

b) Regression co-efficient bi

c) The deviation from linear regression S^2di were used to define stability of genotype (variety).

The estimate of deviation from regression suggests the degree of reliance that should be put to linear regression in interpretation of data. If these values are significantly deviating from zero, the expected phenotype cannot be predicted satisfactorily. When deviations are non-significant, the conclusions may be drawn by joint consideration of mean yield and regression values (Finlay and Wilkinson, 1963 and Eberhart and Russell, 1966) as below.

Regression	**Stability**	**Mean yield**	**Remarks**
$b_i = 1$	Average	High	Well adapted to all the environments
$b_i = 1$	Average	Low	Low Poorly adapted to all environments
$bi> 1$	Below average	High	Specifically adapted to favourable environments
$bi< 1$	Above average	High	Specifically adapted to unfavourable environments

Stable Genotype:

A Genotype with high mean value, unit regression coefficient and deviation not significantly differing from zero ($S^{-2}di=0$) was taken as stable genotype.

3.7.2 AMMI Model

The AMMI model for 'g' genotypes and 'i' environments is given as

$$Yij = \mu + gi + ej + \Sigma\ \lambda n \alpha in \gamma jn + \theta ij$$

Where,

Y_{ij} = mean yield of i_{th} genotype in the j_{th} environment

μ = general mean

g_i = i^{th}genotypic effect

e_j = j^{th}location effect

λ_n = eigen value of the Principal Component Axis n

$\alpha_{in}\gamma_{jn}$= i^{th}genotype, j^{th}environment Principle component analysis (PCA) scores for the PCA axis n

θ_{ij} = residual

n = number of PCA axes retained in the model.

Ordinarily the number n is judged on the basis of empirical consideration of F-test of significance (Gauch 1988). The residual combines the PCA scores from the N - n'discarded axes, where N = min (G-1, E-1). The number of PCA axes to be retained is determined by testing the mean square of each axis with the estimate of residual through F-statistic (Gollob, 1968, Gauch, 1988). The mean sum of squares of each PCA axis is equal to the ratio of square of corresponding eigen value and degree of freedom of each axis obtained as G + E –1 –2n.

The member of the AMMI family with 1 PCA axis (while relegating all higher axes to the residual) is denoted AMMI 1, while AMMI 2 retain 2 PCA axes and so on, In general, AMMI N denotes the AMMI model with IPCA axes 1 to N, AMMI 0 has no IPCA axes and is identically ANOVA (Table 3.4.2). The full model with minimum (G-1, E-1) Interaction

Principal Component Axis, is denoted by AMMI E. The equation, except that it deletes the residual and error and that it stipulates a specific AMMI model rather than the entire AMMI family.

Step in computation

Environment-wise analysis and pooled analysis of variance were conducted as per normal procedure. If genotypes, environments, and G x E interaction are significant, the analysis may proceed further for AMMI analysis.

Table: 3.7.2 Analysis of variance for stability – AMMI Model

Source	**Degree of freedom**	**MSS**	**F**
Total	(ger-1)		
Treatment	(ge-1)		
Genotypes	(g-1)	MS1	MS1/MS3
Environment	(e-1)	MS2	MS2/MS3
Genotype x Environment	(g-1)(e-1)	MS3	MS3/Mse
IPCA1	(G+E-1-2n)	MS4	MS4/Mse
IPCA2	(G+E-1-2n)		
Residual			
Blocks	(r-1)		
Error	(r-1)(ge-1)	Mse	

If IPCA mean sum of square are significant and residual mean square is non-significant, the step may be conducted for development of biplot. The AMMI biplot is developed by placing both genotype and environment mean value on X-axis and the respective IPCA axis Eigen vector on the Y-axis.

Interpretation of Biplot

In biplot displacements along the X-axis indicate differences in main (additive) effects, whereas displacement along the ordinate (Y-axis) indicate differences in interaction effects. For the points of different kinds, the AMMI model equation provides the expected yield values. The biplot has another important interpretation. The main effect for genotypes reflects breeding advances. Similarly, the main effects for environments reflect overall comparison of environments.

From the values of mean and IPCA1, the genotypes were classified under four distinct classes.

Class 1: Genotypes with high mean and positive IPCA1

Class 2: Genotypes with high mean and negative IPCA1

Class 3: Genotypes with low mean and negative IPCA1

Class 4: Genotypes with low mean and positive IPCA1

In AMMI 2 interaction biplot between IPAC1 and IPAC2, the environmental scores are joined to the origin by environment lines. Environments with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction. The genotypes occurring close together on the plot will tend to have similar yields in all environments, while genotypes far apart may either differ in mean yield or show a different pattern of response over the environments. Hence, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction. Genotypes and environments that fall in the same sectors interact positively; in contrast, if they fall in opposite sectors interact negatively. If they fall into adjacent sectors, interaction is somewhat more complex.

CHAPTER-IV

EXPERIMENTAL RESULTS

The results of the present research work entitled **"Molecular diversity and stability analysis for seed yield and its components in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]"**have been described under following categories.

4.1 Characterization of cluster bean genotypes based on morphological characters

4.2 Analysis of variance (ANOVA) for individual environment

4.3 Mean performance and range across the environments for different quantitative characters

4.4 Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean for different quantitative characters

4.5 Phenotypic correlation coefficient analysis

  4.5.1 Phenotypic correlation coefficient analysis for yield and component characters

  4.5.2 Phenotypic correlation coefficient analysis for bacterial leaf blight intensity andquality characters

4.6. Path coefficient analysis

  4.6.1 Path coefficient analysis for yield and component characters

  4.6.2 Path coefficient analysis for bacterial leaf blight intensity and quality characters

4.7 Stability analysis based on Eberhart and Russell‘s model, 1966

  4.7.1 Pooled analysis of variance

  4.7.2 Stability parameters

  4.7.3 Environmental indices

4.8 Stability analysis based on AMMI model, 1997

  4.8.1 Pooled analysis of variance

  4.8.2 Stability parameters

4.9 Molecular diversity analysis using SSR markers

4.1 Characterization of cluster bean genotypes based on morphological characters

Based on the observations recorded for ten qualitative characters in eight environments the 25 genotypes of cluster bean were visually classified and categorized into different groups. There was no variation found for these characters over different environments. However, two characters namely, position of first trifoliate leaf and first cluster from bottom were found inconsistent within the replication for each genotype in each environment. Therefore, the characterization of genotypes on the basis of these two characters was not possible. The characterization and grouping of genotypes have been presented in Table 4.1 and these characters have been shown in Figure 4.1.

4.1.1 Plant Growth Habit

The 25 genotypes of cluster bean were classified into three groups *i.e.,* unbranched (0-1 branch), sparsely branched (2-5 branches) and branched (> 5 branches) types for plant grow habit. There were three genotypes each with unbranched and sparsely branched grow habit and remaining 19 genotypes were branched (Table 4, Figure 4.1.1).

4.1.2 Leaf pubescence

Leaf pubescence is dominant among the released varieties of cluster bean. Leaf pubescence protects the plant during various abiotic stresses, namely ultra-violet injury, drought tolerance, radiation heat load reduction *etc.* Based on the presence/absence of leaf pubescence the genotypes are divided into two groups *i.e.* pubescent and glabrous. Out of 25 genotypes 22 were found pubescent while, three were found with glabrous leaves (Table 4.1, Figure 4.1.2).

4.1.3 Leaf margin

Two types of leaf margin were observed among 25 genotypes *i.e.* serrated and smooth. Out all the genotypes 17 were found with serrated leaf margin and remaining eight were found with smooth leaf margin (Table 4.1, Figure 4.1.2).

4.1.4 Leaf colour

Two types of leaf colours were observed among 25 genotypes *i.e.* dark green and light green. Out all the genotypes dark green coloured leaves were found in 21 genotypes while four genotypes were observed with light green coloured leaves (Table 4.1, Figure 4.1.3).

4.1.5 Flower colour

Two types of flower colours were observed among 25 genotypes *i.e.* pink and white. Out all the genotypes pink coloured flowers were found in 20 genotypes while, five genotypes were observed with white coloured flowers (Table 4.1, Figure 4.1.3).

4.1.6 Pod pubescence

Based on the presence/absence of pod pubescence the genotypes are divided into two groups *i.e.* pubescent and glabrous. Out of 25 genotypes 21 were found pubescent while, four were found glabrous pods (Table 4.1, Figure 4.1.4).

4.1.7 Seed Shape

The seed shape under present study was grouped into two categories *i.e*. square and flat & round. Out of 25 genotypes 21 genotypes were found with square shaped seed while, four genotypes had flat & square seed shape (Table 4.1, Figure 4.1.5).

4.1.8 Seed Colour

The genotypes were grouped into five categories *i.e*., pale yellow pink, moderate orange, medium grey, light grey and light greenish grey with the help of Lilac colour groups by Royal Horticultural Society colour chart. Out of 25 genotypes the seed colour of four genotypes each was found pale yellow pink and medium grey, moderate orange was in three genotypes, nine genotypes had light grey coloured seed and light greenish grey seed colour was found in five genotypes (Table 4.1, Figure 4.1.6).

Table 4.1: Classification and grouping of 25 cluster bean genotypes based on qualitative characters

Diagnostic Characters	Descriptors	Number of genotypes	Name of genotypes
1.Plant growth habit	Unbranched	3	FS 277, PNB and RGC 1066
	Sparsely Branched	3	HG 6, HVG 2-30 and M 83
	Branched	19	HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 100, X 10, GG1, GG 2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, HG 75 and RGC 1033
2. Leaf pubescence	Pubescent	22	HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X 10, GG1, GG 2, RGC 1017, FS 277, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, RGC 1066, HG 75 and RGC 1033
	Glabrous	3	HVG 2-30, PNB and M 83
3.Leaf margin	Serrated	17	HG 2-20, HG 884, HG 365, HG 3-52, HG 6, GG 2, RGC 1017, FS 277, RGC 1038, RGC 936, HVG 2-30, PNB, M 83, RGC 1055, RGC 1002, RGC 1003, RGS 3 and RGC 1066
	Smooth	8	HG 870, HG 563, HG 100, X 10, GG 1, RGC 1003, HG 75 and RGC 1033
4.Leaf colour	Dark green	21	HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X 10, GG1, GG 2, RGC 1017, FS 277, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, RGC 1066 and RGC 1033
	Light green	4	HVG 2-30, PNB, HG 75 and M 83
5.Flower colour	Pink	20	HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X 10, GG 1, RGC 1017, PNB, FS 277, RGC 1038, RGC 1055, RGC 1002, RGC 1003, RGS 3, RGC 1066 and RGC 1033
	White	5	HVG 2-30, GG 2, RGC 936, HG 75 and M 83
6. Pod pubescence	Pubescent	21	HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X 10, GG1, GG 2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, RGC 1066, HG 75 and RGC 1033
	Glabrous	4	HVG 2-30, FS 277, PNB and M 83
7. Seed shape	Square	21	HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X 10, GG1, RGC 1017, FS 277, RGC 1038, RGC 936, RGC 197, RGC 1055, RGC 1002, RGC 1003, RGS 3, RGC 986, RGC 1066, HG 75 and RGC 1033
	Flat & Round	4	HVG 2-30, GG 2, PNB and M 83
8. Seed colour	Pale yellow pink	4	HG 563, RGC 936, HG 75 and M 83
	Moderate orange	3	HG 365, X 10 and GG 2
	Medium grey	4	HG 884, RGC 1017, RGC 1002 and RGC 1033
	Light grey	9	HG 2-20, HG 870, HG 3-52, HG 6, HVG 2-30, FS 277, PNB, RGC 1003 and RGS 3
	Light greenish grey	5	HG 100, GG 1, RGC 1038, RGC 1055, RGC 1066

Figure 4.1: Variation showing for eight qualitative characters among 25 genotypes

Figure 4.1.1: Plant growth habit

		
1: Unbranched	2: Sparsely branched	3: Branched

Figure 4.1.2: Leaf pubescence and leaf margin

			
1: Pubescent	2: Glabrous	3: Serrated	4: Non-serrated

Figure 4.1.3: Leaf and flower colour

			
1: Dark green	2: Light green	3: Pink	4: White

Figure 4.1.4: Pod Pubescence

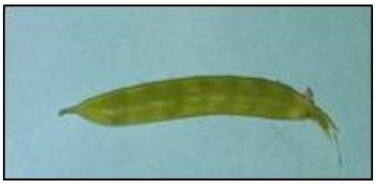	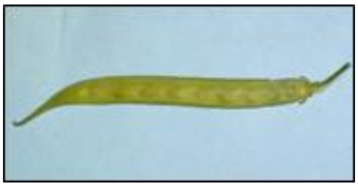
1: Pubescent	2: Glabrous

Figure 4.1.5: Seed shape

	
1: Square	2: Round and flat

Figure 4.1.6: Seed colour

		
1: Pale yellow pink	2: Moderate orange	3: Medium grey
		
4: Light grey		5: Light greenish grey

4.2 Analysis of variance (ANOVA) for individual environment

The data presented in table 4.2 a to h, revealed that the mean sum of squares due to genotypes were significant for all the characters under all the environments indicating the sufficient variation available in the cluster bean genotypes studied.

4.3 Mean performance and range across the environments for different quantitative characters

4.3.1 Plant height

Plant height in HS 19 ranged from 60.33 cm (HG 6) to 168.13 cm (FS 277) with mean 104.21 cm; in BS 19 from 67.27 cm (HG 6) to170.80 cm (FS 277) with mean 105.55 cm; in HK 19 from 67.80 cm (HG 6) to170.33 cm (FS 277) with mean 106.93 cm; in BK 19 from 67.40 cm (HG 6) to 153.27 cm (FS 277) with mean 102.88 cm; in HS 20 from 64.65 cm (HG 6) to 160.40 cm (FS 277) with mean 104.18 cm; in BS 20 from 59.07 cm (HG 6) to 159.20 cm (FS 277) with mean 101.80 cm; in HK 20 from 68.87 cm (HG 6) to 178.07 cm (FS

277) with mean 105.66 cm and in BK 20 from 68.60 cm (HG 6) to 148.78 cm (FS 277) with mean 103.58 cm (Table 4.3.1).

On the basis of overall performance, 20, 19, 19, 20, 19, 20, 19 and 20 (Number in each environment) showed minimum plant height than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. HG 6 (60.33 cm) was found to be dwarf in HS 19 followed by HG 870 (92.13 cm), and HG 884 (94.67 cm); HG 6 (67.27 cm) in BS 19 followed by HG 870 (96.13 cm) and HG 563 (97.93 cm); HG 6 (67.80 cm) in HK 19 followed HG 365 (99.93 cm) and GG 1 (100.47 cm); HG 6 (67.40 cm) in BK 19 followed by RGS 3 (96.13 cm) and GG 2 (96.27 cm); HG 6 (64.65 cm) in HS 20 followed by HG 884 (98.30 cm) and HG 870 (98.55 cm); HG 6 (59.07 cm) in BS 20 followed HG 365 (94.20 cm) and RGS 3 (94.87 cm); HG 6 (68.87 cm) in HK 20 followed by GG 1 (90.67 cm) and RGC 1003 (97.40 cm); HG 6 (68.60 cm) in BK 20 followed HG 365 (96.13 cm) and RGC 1033 (96.87 cm).

On the basis of overall mean across the environments HG 6 (65.50 cm) was found to be the most dwarf genotypes followed by HG 870 (98.39 cm), HG 884 and HG 365 (98.71 cm). Among the environments HS 19, BK 19, HS 20, BS 20 and BK 20 showed significantly shorter plants than grand mean.

4.3.2 Days to 50% flowering

Days to 50% flowering in HS 19 ranged from 35 (HG 6 and RGC 1033) to 42 (PNB) days with mean 37 days; in BS 19 from 30 (HG 6) to 42 (PNB) days with mean 34 days; in HK 19 from 29 (HG 6) to 44 (PNB) days with mean 35 days; in BK 19 from 31 (HG 884 and HG 6) to 44 (PNB) days with mean 34 days; in HS 20 from 32 (HG 884, HG 6 and RGS 3) to 45 (PNB) days with mean 35 days; in BS 20 from 32 (HG 6) to 40 (PNB and FS 277) days with Mean 35 days; in HK 20 from 29 (HG 6) to 43 (FS 277 and PNB) days with mean 34 days and in BK 20 from 31 (HG 6) to 41 (PNB and RGC 936) with mean 35 days (Table 4.3.2).

Table 4.2 (a): Analysis of variance for various characters under summer cultivation of 25 cluster bean genotypes at Hisar during year, 2019

Source of Variation	**D.F.**	**PH**	**DFF**	**DM**	**PMS**	**PPP**	**PPC**	**SPP**	**PL**	**BPP**
Replication	**2**	0.264	0.213	30.413	1.238	7.626	6.63	-0.001	0.025	1.032
Genotype	**24**	1161.738**	7.130**	222.806**	2659.990**	9855.413**	11.316**	1.601**	2.194**	55.070**
Error	**48**	6.576	1.005	4.802	5.571	15.724	0.293	0.293	0.033	2.178
Source of Variation	**D.F.**	**100 SW**	**BMPP**	**HI**	**CPP**	**SYPP**	**GC**	**PC**	**TSS**	**RS**
Replication	**2**	0.005	0.044	0.001	10.255	0.004	1.293	1.275	31.251	0.342
Genotype	**24**	0.280**	2.003**	0.007**	901.643**	0.305**	38.774**	10.963**	196.743**	6.207**
Error	**48**	0.045	0.055	0.001	7.849	0.014	1.912	0.926	13.400	0.860
Source of Variation	**D.F.**	**NRS**	**ADF**	**Lignin**	**CellC**	**Silica**	**NDF**	**HCellC**	**BLBI**	
Replication	**2**	25.642	0.247	0.025	0.190	0.003	0.120	0.024	3.876	
Genotype	**24**	206.537**	0.678**	0.131**	0.467**	0.221**	0.678**	0.034**	38.942**	
Error	**48**	14.551	0.213	0.015	0.206	0.001	0.232	0.018	3.790	

Table 4.2 (b): Analysis of variance for various characters under Summer Cultivation of 25 cluster bean genotypes at Bawal during year, 2019

Source of Variation	**D.F.**	**PH**	**DFF**	**DM**	**PMS**	**PPP**	**PPC**	**SPP**	**PL**	**BPP**
Replication	**2**	0.094	1.773	1.693	7.313	10.051	0.434	0.476	0.001	0.164
Genotype	**24**	1163.983**	19.637**	264.469**	1711.017**	3592.945**	11.529**	1.108**	1.954**	57.547**
Error	**48**	4.875	1.982	3.332	3.58	20.503	0.187	0.157	0.024	1.321
Source of Variation	**D.F.**	**100 SW**	**BMPP**	**HI**	**CPP**	**SYPP**	**GC**	**PC**	**TSS**	**RS**
Replication	**2**	0.021	0.018	0.000	14.848	0.003	3.246	0.566	14.506	0.242
Genotype	**24**	0.578**	0.447**	0.022	464.377**	0.078**	24.691**	14.450**	121.976**	5.245**
Error	**48**	0.013	0.02	0.001	3.816	0.003	1.701	0.797	10.306	0.258
Source of Variation	**D.F.**	**NRS**	**ADF**	**Lignin**	**CellC**	**Silica**	**NDF**	**HCellC**	**BLBI**	
Replication	**2**	11.27	0.319	0.047	0.133	0.004	0.751	0.113	5.545	
Genotype	**24**	89.900**	3.191**	0.203**	2.326**	0.099**	3.178**	1.040**	50.723**	
Error	**48**	9.884	0.107	0.016	0.113	0.001	0.098	0.138	4.225	

PH- Plant height, DFF- Days to 50% flowering, DM- Days to maturity, PMS- Pods on main stem, PPP- Pods per plant, PPC- Pods per cluster, SPP- Seeds per pod, PL- Pod length, BPP- Branches per plant, 100SW- 100 seed weight, BMPP- Biomass per plot, HI- Harvest index, CPP- Clusters per plant, SYPP- Seed yield per plot, GC- Gum content, PC- Protein content, TSS- Total soluble sugar, RS- Reducing sugar, NRS- Non-reducing sugar, ADF- Acid detergent fibre, Lignin- Lignin content, CellC- Cellulose content, Silica- Silica content, NDF- Neutral detergent fibre, HCellC- Hemicellulose content, BLBI- Bacterial leaf blight content

Table 4.2 (c): Analysis of variance for various characters under *Kharif* Cultivation of 25 cluster bean genotypes at Hisar during year, 2019

Source of Variation	**D.F.**	**PH**	**DFF**	**DM**	**PMS**	**PPP**	**PPC**	**SPP**	**PL**	**BPP**
Replication	**2**	0.077	0.173	0.360	6.852	8.568	0.013	0.028	0.003	0.127
Genotype	**24**	1132.762**	29.152**	292.774**	1830.659**	5881.757**	9.954**	0.744**	1.069**	44.898**
Error	**48**	4.115	1.021	1.221	3.636	7.365	0.111	0.143	0.115	0.522
Source of Variation	**D.F.**	**100 SW**	**BMPP**	**HI**	**CPP**	**SYPP**	**GC**	**PC**	**TSS**	**RS**
Replication	**2**	0.004	0.009	0.000	3.973	0.002	0.058	0.883	22.181	0.027
Genotype	**24**	0.074**	0.831**	0.004**	581.835**	0.087**	34.694**	6.888**	155.020**	9.065**
Error	**48**	0.008	0.016	0.001	3.529	0.002	1.586	0.503	12.569	0.427
Source of Variation	**D.F.**	**NRS**	**ADF**	**Lignin**	**CellC**	**Silica**	**NDF**	**HCellC**	**BLBI**	
Replication	**2**	21.697	0.715	0.190	0.551	0.006	0.538	0.037	0.209	
Genotype	**24**	115.291**	1.312**	0.062*	0.896**	0.166**	1.473**	0.214**	53.470**	
Error	**48**	13.034	0.115	0.037	0.154	0.001	0.109	0.028	1.845	

Table 4.2 (d): Analysis of variance for various characters under *Kharif* Cultivation of 25 cluster bean genotypes at Bawal during year, 2019

Source of Variation	**D.F.**	**PH**	**DFF**	**DM**	**PMS**	**PPP**	**PPC**	**SPP**	**PL**	**BPP**
Replication	**2**	22.022	3.720	1.013	2.709	3.030	0.081	0.318	0.005	0.165
Genotype	**24**	838.970**	25.553**	242.002**	1051.030**	1645.861**	7.131**	0.826**	1.372**	31.236**
Error	**48**	4.534	0.637	1.444	1.152	2.724	0.540	0.171	0.015	0.940
Source of Variation	**D.F.**	**100 SW**	**BMPP**	**HI**	**CPP**	**SYPP**	**GC**	**PC**	**TSS**	**RS**
Replication	**2**	0.158	0.010	0.001	0.658	0.002	9.108	0.440	3.368	0.158
Genotype	**24**	0.054**	0.452**	0.011**	166.521**	0.067**	22.383**	6.468**	119.718**	6.948**
Error	**48**	0.020	0.012	0.001	2.008	0.001	1.293	0.420	7.435	0.245
Source of Variation	**D.F.**	**NRS**	**ADF**	**Lignin**	**CellC**	**Silica**	**NDF**	**HCellC**	**BLBI**	
Replication	**2**	2.839	0.426	0.154	0.284	0.003	0.431	0.002	0.680	
Genotype	**24**	115.022**	1.968**	0.122**	1.464**	0.112**	3.099**	0.275**	38.861**	
Error	**48**	8.338	0.041	0.007	0.048	0.000	0.041	0.039	2.394	

PH- Plant height, DFF- Days to 50% flowering, DM- Days to maturity, PMS- Pods on main stem, PPP- Pods per plant, PPC- Pods per cluster, SPP- Seeds per pod, PL- Pod length, BPP- Branches per plant, 100SW- 100 seed weight, BMPP- Biomass per plot, HI- Harvest index, CPP- Clusters per plant, SYPP- Seed yield per plot, GC- Gum content, PC- Protein content, TSS- Total soluble sugar, RS- Reducing sugar, NRS- Non-reducing sugar, ADF- Acid detergent fibre, Lignin- Lignin content, CellC- Cellulose content, Silica- Silica content, NDF- Neutral detergent fibre, HCellC- Hemicellulose content, BLBI- Bacterial leaf blight content

Table 4.2 (e): Analysis of variance for various characters under Summer Cultivation of 25 cluster bean genotypes at Hisar during year, 2020

Source of Variation	**D.F.**	**PH**	**DFF**	**DM**	**PMS**	**PPP**	**PPC**	**SPP**	**PL**	**BPP**
Replication	**2**	3.250	0.120	4.120	11.103	17.829	0.707	0.054	0.003	0.258
Genotype	**24**	805.839**	29.389**	218.417**	3319.574**	7918.880**	8.299**	1.334**	1.779**	53.188**
Error	**48**	3.089	0.384	1.078	3.644	9.001	0.223	0.135	0.007	1.150
Source of Variation	**D.F.**	**100 SW**	**BMPP**	**HI**	**CPP**	**SYPP**	**GC**	**PC**	**TSS**	**RS**
Replication	**2**	0.060	0.005	0.001	4.396	0.009	0.528	0.258	27.151	0.220
Genotype	**24**	0.224**	0.465**	0.005**	322.743**	0.077**	33.395**	6.387**	177.584**	6.591**
Error	**48**	0.025	0.019	0.000	4.350	0.004	1.521	0.290	23.802	0.309
Source of Variation	**D.F.**	**NRS**	**ADF**	**Lignin**	**CellC**	**Silica**	**NDF**	**HCellC**	**BLBI**	
Replication	**2**	28.545	0.047	0.030	0.149	0.000	0.107	0.020	9.039	
Genotype	**24**	160.489**	4.812**	0.427**	2.598**	0.080**	4.940**	0.180**	46.405**	
Error	**48**	23.250	0.065	0.041	0.101	0.001	0.072	0.045	4.765	

Table 4.2 (f): Analysis of variance for various characters under Summer Cultivation of 25 cluster bean genotypes at Bawal during year, 2020

Source of Variation	**D.F.**	**PH**	**DFF**	**DM**	**PMS**	**PPP**	**PPC**	**SPP**	**PL**	**BPP**
Replication	**2**	25.773	0.173	0.413	7.653	0.071	8.939	0.131	0.074	0.638
Genotype	**24**	950.399**	12.722**	175.998**	1671.966**	10.911**	3270.373**	0.679**	1.385**	38.963**
Error	**48**	6.008	0.437	2.024	3.345	0.246	11.231	0.132	0.039	0.960
Source of Variation	**D.F.**	**100 SW**	**BMPP**	**HI**	**CPP**	**SYPP**	**GC**	**PC**	**TSS**	**RS**
Replication	**2**	0.116	0.083	0.001	4.249	0.005	2.972	0.156	4.786	0.201
Genotype	**24**	0.148**	0.783**	0.005**	360.404**	0.087**	27.612**	4.730**	95.502**	7.182**
Error	**48**	0.028	0.019	0.000	4.213	0.001	1.483	0.128	5.571	0.189
Source of Variation	**D.F.**	**NRS**	**ADF**	**Lignin**	**CellC**	**Silica**	**NDF**	**HCellC**	**BLBI**	
Replication	**2**	5.074	0.131	0.006	0.094	0.004	0.111	0.001	10.788	
Genotype	**24**	58.136**	2.170**	0.069**	1.516**	0.153**	2.168**	0.278**	46.356**	
Error	**48**	5.790	0.038	0.015	0.045	0.010	0.041	0.054	2.467	

PH- Plant height, DFF- Days to 50% flowering, DM- Days to maturity, PMS- Pods on main stem, PPP- Pods per plant, PPC- Pods per cluster, SPP- Seeds per pod, PL- Pod length, BPP- Branches per plant, 100SW- 100 seed weight, BMPP- Biomass per plot, HI- Harvest index, CPP- Clusters per plant, SYPP- Seed yield per plot, GC- Gum content, PC- Protein content, TSS- Total soluble sugar, RS- Reducing sugar, NRS- Non-reducing sugar, ADF- Acid detergent fibre, Lignin- Lignin content, CellC- Cellulose content, Silica- Silica content, NDF- Neutral detergent fibre, HCellC- Hemicellulose content, BLBI- Bacterial leaf blight content

Table 4.2 (g): Analysis of variance for various characters under *Kharif* Cultivation of 25 cluster bean genotypes at Hisar during year, 2020

Source of Variation	**D.F.**	**PH**	**DFF**	**DM**	**PMS**	**PPP**	**PPC**	**SPP**	**PL**	**BPP**
Replication	**2**	0.197	0.173	0.640	0.117	1.416	0.129	0.273	0.046	0.668
Genotype	**24**	1053.643**	25.041**	287.139**	1992.666**	4576.610**	5.171**	1.060**	1.545**	45.643**
Error	**48**	5.206	0.618	1.529	3.681	9.186	0.231	0.375	0.022	1.174
Source of Variation	**D.F.**	**100 SW**	**BMPP**	**HI**	**CPP**	**SYPP**	**GC**	**PC**	**TSS**	**RS**
Replication	**2**	0.019	0.083	0.001	2.142	0.000	4.504	0.200	9.913	0.406
Genotype	**24**	0.156**	0.783**	0.005**	280.910**	0.082**	30.459**	18.740**	189.210**	36.580**
Error	**48**	0.011	0.019	0.000	3.265	0.001	1.709	0.789	17.336	1.296
Source of Variation	**D.F.**	**NRS**	**ADF**	**Lignin**	**CellC**	**Silica**	**NDF**	**HCellC**	**BLBI**	
Replication	**2**	7.919	0.037	0.006	0.064	0.011	0.022	0.003	10.788	
Genotype	**24**	64.206**	1.833**	0.119**	1.190**	0.117**	1.903**	0.642**	46.356**	
Error	**48**	18.702	0.037	0.025	0.051	0.004	0.042	0.037	2.467	

Table 4.2 (h): Analysis of variance for various characters under *Kharif* Cultivation of 25 cluster bean genotypes at Bawal during year, 2020

Source of Variation	**D.F.**	**PH**	**DFF**	**DM**	**PMS**	**PPP**	**PPC**	**SPP**	**PL**	**BPP**
Replication	**2**	1.344	1.720	0.360	1.282	9.628	0.644	0.400	0.002	1.109
Genotype	**24**	730.727**	15.944**	221.803**	1048.601**	1691.084**	7.736**	0.814**	1.382**	34.068**
Error	**48**	5.787	0.789	1.443	1.749	5.555	0.340	0.137	0.013	0.793
Source of Variation	**D.F.**	**100 SW**	**BMPP**	**HI**	**CPP**	**SYPP**	**GC**	**PC**	**TSS**	**RS**
Replication	**2**	0.021	0.021	0.000	10.611	0.000	7.383	0.716	45.311	0.271
Genotype	**24**	0.578**	0.578**	0.013**	237.473**	0.096**	40.445**	12.415**	296.245**	5.274**
Error	**48**	0.013	0.013	0.000	2.043	0.001	1.375	0.660	32.880	1.014
Source of Variation	**D.F.**	**NRS**	**ADF**	**Lignin**	**CellC**	**Silica**	**NDF**	**HCellC**	**BLBI**	
Replication	**2**	49.967	0.031	0.052	0.025	0.001	0.039	0.001	4.490	
Genotype	**24**	229.582**	3.029**	0.142**	3.160**	0.040**	3.040**	0.006**	44.512**	
Error	**48**	32.336	0.042	0.032	0.077	0.002	0.042	0.002	1.825	

PH- Plant height, DFF- Days to 50% flowering, DM- Days to maturity, PMS- Pods on main stem, PPP- Pods per plant, PPC- Pods per cluster, SPP- Seeds per pod, PL- Pod length, BPP- Branches per plant, 100SW- 100 seed weight, BMPP- Biomass per plot, HI- Harvest index, CPP- Clusters per plant, SYPP- Seed yield per plot, GC- Gum content, PC- Protein content, TSS- Total soluble sugar, RS- Reducing sugar, NRS- Non-reducing sugar, ADF- Acid detergent fibre, Lignin- Lignin content, CellC- Cellulose content, Silica- Silica content, NDF- Neutral detergent fibre, HCellC- Hemicellulose content, BLBI- Bacterial leaf blight content

Table 4.3.1: Mean performance of cluster bean genotypes under different environments for plant height (cm)

Genotypes	**HS 19**	**BS 19**	**HK19**	**BK 19**	**HS 20**	**BS 20**	**HK 20**	**BK 20**	**Over all Mean**
HG 2-20	95.27	98.80	102.17	99.53	99.33	98.93	106.67	98.80	99.94
HG 884	94.67	99.60	102.07	98.80	98.30	97.13	100.47	98.67	98.71
HG 870	92.13	96.13	100.80	96.73	98.55	99.00	105.00	98.80	98.39
HG 563	97.67	97.93	101.33	96.80	101.01	96.87	104.67	98.73	99.38
HG 365	97.87	98.27	99.93	98.73	100.63	94.20	103.93	96.13	98.71
HG 3-52	101.00	100.00	103.13	97.80	100.09	96.07	100.40	99.47	99.75
HG 6	60.33	67.27	67.80	67.40	64.65	59.07	68.87	68.60	65.50
HVG 2-30	105.07	111.40	115.00	113.73	111.80	109.13	111.53	112.60	111.28
HG 100	102.47	102.27	102.33	97.20	101.34	100.13	100.27	98.87	100.61
FS 277	168.13	170.80	170.33	153.27	160.40	159.20	178.07	148.73	163.62
X-10	97.93	98.60	101.00	98.87	99.32	96.07	100.20	97.47	98.68
PNB	154.93	159.67	160.87	150.80	140.37	145.53	141.87	148.40	150.31
GG-1	102.33	99.80	100.47	97.27	101.19	90.67	99.93	100.80	99.06
GG-2	100.13	101.07	102.67	96.27	99.36	96.73	99.00	100.33	99.45
RGC 1017	100.47	100.60	101.87	97.40	100.03	98.80	99.47	99.47	99.76
RGC 1038	101.07	102.80	102.53	102.00	99.88	98.07	99.53	99.20	100.64
RGC 936	99.20	99.13	101.87	96.60	100.54	97.33	99.67	102.73	99.63
RGC 1055	99.93	100.93	101.87	99.47	101.13	98.00	100.67	99.93	100.24
RGC 1002	101.40	102.27	101.93	98.53	100.18	99.67	100.67	100.87	100.69
RGC 1003	101.67	102.40	102.20	97.67	98.85	98.87	97.40	100.93	100.00
RGC 1066	108.53	106.67	108.13	106.00	108.90	108.00	108.87	100.93	107.00
RGS 3	98.07	100.67	101.00	96.13	99.83	94.87	99.67	99.60	98.73
M-83	110.47	110.80	110.80	101.87	107.24	104.07	104.80	110.93	107.62
RGC 1033	102.67	101.33	100.93	103.53	104.15	102.93	102.40	96.87	101.85
HG 75	111.73	109.60	110.20	109.67	107.29	105.60	107.60	111.53	109.15
Over all Mean	**104.21**	**105.55**	**106.93**	**102.88**	**104.18**	**101.80**	**105.66**	**103.58**	**104.35**
C.D.	**4.22**	**3.64**	**3.34**	**3.51**	**2.89**	**4.03**	**3.76**	**3.96**	
C.V. at 5%	**2.46**	**2.09**	**1.90**	**2.07**	**1.69**	**2.40**	**2.16**	**2.32**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

Table 4.3.2: Mean performance of cluster bean genotypes under different environments for days to 50% flowering

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	37	34	33	33	34	34	33	34	34
HG 884	37	34	33	31	32	33	33	33	33
HG 870	37	33	34	32	33	33	32	32	33
HG 563	37	33	34	33	34	35	32	33	34
HG 365	36	34	32	32	33	34	33	33	33
HG 3-52	37	34	35	35	35	36	33	34	35
HG 6	35	30	29	31	32	32	29	31	31
HVG 2-30	38	34	34	37	38	37	34	37	36
HG 100	37	35	35	33	33	36	33	33	34
FS 277	41	41	43	40	42	40	43	41	41
X-10	37	34	33	34	35	33	33	34	34
PNB	42	42	44	44	45	40	43	36	42
GG-1	37	33	34	33	34	33	32	35	34
GG-2	36	33	34	32	34	34	33	34	34
RGC 1017	37	34	33	33	34	35	33	34	34
RGC 1038	37	34	34	34	35	35	33	34	35
RGC 936	38	34	34	36	38	37	34	41	37
RGC 1055	39	35	35	33	34	35	35	34	35
RGC 1002	38	34	35	36	36	35	34	35	35
RGC 1003	36	32	33	33	34	34	33	34	34
RGC 1066	37	32	33	33	34	34	33	33	34
RGS 3	39	34	35	34	32	33	35	34	35
M-83	38	34	36	37	38	36	35	35	36
RGC 1033	35	32	33	33	34	34	33	34	34
HG 75	39	38	40	37	37	37	35	36	37
Over all Mean	**37**	**34**	**35**	**34**	**35**	**35**	**34**	**35**	**35**
C.D.	**1.65**	**2.32**	**1.66**	**1.31**	**1.02**	**1.08**	**1.29**	**1.46**	
C.V. at 5%	**2.68**	**4.10**	**2.92**	**2.32**	**1.76**	**1.88**	**2.31**	**2.57**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

On the basis of overall performance, 1, 21, 20, 18, 17, 15, 22 and 18 (Number in each environment) genotypes showed earlier flowering than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. HG 6 and RGC 1033 (35 days) took minimum days to 50% flowering in HS 19 followed by HG 365, GG 2 and RGC 1003 (36 days); HG 6 (30 days) in BS 19 followed by RGC 1003, RGC 1066 and RGC 1033 (32 days); HG 6 (29 days) in HK 19 followed HG 365 (32 days), HG 2-20, HG 884, X 10, RGC 1017, RGC 1003, RGC 1066 and RGC 1033 (33 days); HG 6 and HG 884 (31 days) in BK 19 followed HG 870, HG 365 and GG 2 (32 days); HG 6, HG 884 and RGS 3 (32 days) in HS 20 followed by HG 870, HG 365 and HG 100 (33 days); HG 6 (32 days) in BS 20 followed HG 884, HG 870, X 10, GG 1 and RGS 3 (33 days); HG 6 (29 days) in HK 20 followed by HG 870, GG 1 and HG 563 (32 days); HG 6 (31 days) in BK 20 followed HG 870 (32 days), HG 884, HG 563, HG 365, HG 100 and HG 1066 (33 days).

On the basis of overall mean across the environments HG 6 (31 days) had shown earlier flowering followed by HG 884, HG 870 and HG 365 (33 days). Among the environments BS 19, BK 19 and HK 20 showed earlier flowering than grand mean.

4.3.3 Days to maturity

Days to maturity in HS 19 ranged from 87 (HG 6) to 132 (FS 277) days with mean 104 days; in BS 19 from 86 (HG 6) to135 (FS 277) days with mean 105 days; in HK 19 from 84 (HG 6) to137 (FS 277) days with mean 105 days; in BK 19 from 82 (HG 6) to112 (FS 277) days with mean 102 days; in HS 20 from 89 (HG 6) to 131 (FS 277) days with mean 106 days; in BS 20 from 88 (HG 6) to127 (FS 277) days with mean 104 days; in HK 20 from 84 (HG 6) to136 (FS 277) days with mean 105 days and in BK 20 from 82 (HG 6) to 131 (FS 277) with mean 104 days (Table 4.3.3).

On the basis of overall performance, 19, 19, 16, 20, 14, 19, 19 and 19 (Number in each environment)genotypes showed earlier maturity than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20, respectively. HG 6 (87 days) earliest in maturity in HS 19 followed by M 83 (95 days), HG 365 and RGC 1017 (98 days); HG 6 (86 days) in BS 19 followed by M 83 (98 days) and X 10 (100 days); HG 6 (84 days) in HK 19 followed by HG 2-20, HG 884, HG 870, HG 365, HG 100 and RGC 1033 (101 days); HG 6 (82 days) in BK 19 followed by HG 563 and X 10 (97 days); HG 6 (89 days) in HS 20 followed by HG 563, HG 365 and RGC 1003 (101 days); HG 6 (88 days) in BS 20 followed HG 884 and RGS 3 (99 days); HG 6 (84 days)in HK 20 followed by HG 2-20, HG 563, GG 1, RGC 1017, RGC 936, RGC 1002 (101 days); HG 6 (82 days)in BK 20 followed HG 870 (99 days), HG 2-20, HG 884 and HG 563 (100 days).

On the basis of overall mean across the environments HG 6 (85 days) had shown earliest maturity followed by HG 2-20, HG 884, HG 870, HG 563, HG 365, X 10 and RGC 1017 (101 days). Among the environments BK 19, BS 20 and BK 20 took less days to maturity than grand mean.

Table 4.3.3: Mean performance of cluster bean genotypes under different environments for days to maturity

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	102	102	101	101	103	101	101	100	101
HG 884	101	104	101	98	102	99	103	100	101
HG 870	101	102	101	100	102	100	103	99	101
HG 563	101	102	103	97	101	101	101	100	101
HG 365	99	102	101	98	101	103	102	101	101
HG 3-52	102	102	102	101	103	105	104	101	102
HG 6	87	86	84	82	89	88	84	82	85
HVG 2-30	114	118	120	110	121	113	120	111	116
HG 100	103	102	101	102	105	102	102	101	102
FS 277	132	135	137	132	131	127	136	131	132
X-10	100	101	102	97	102	101	102	101	101
PNB	123	126	127	123	126	124	127	107	123
GG-1	105	103	102	99	106	100	101	101	102
GG-2	103	104	105	99	103	103	102	105	103
RGC 1017	99	100	101	102	103	101	101	101	101
RGC 1038	101	103	104	101	102	103	102	102	102
RGC 936	102	103	104	101	103	101	101	104	102
RGC 1055	103	103	103	101	104	101	102	102	102
RGC 1002	103	102	102	101	104	101	101	103	102
RGC 1003	101	102	103	100	101	101	102	104	102
RGC 1066	100	101	103	99	104	104	103	102	102
RGS 3	103	104	104	102	105	99	104	101	103
M-83	95	98	105	104	109	105	104	123	105
RGC 1033	105	105	101	101	104	103	103	102	103
HG 75	109	110	111	107	111	106	109	106	109
Over all Mean	**104**	**105**	**105**	**102**	**106**	**104**	**105**	**104**	**104**
C.D.	**3.61**	**3.01**	**1.82**	**1.98**	**1.71**	**2.34**	**2.04**	**1.98**	
C.V. at 5%	**2.11**	**1.74**	**1.05**	**1.18**	**0.98**	**1.37**	**1.18**	**1.16**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

4.3.4 Pods on main stem

Number of pods on main stem in HS 19 ranged from 21.87 (RGC 936) to 179.20 (RGC 1066) with mean 49.83 ; in BS 19 from 28.20 (HVG 2-30) to 146.87 (RGC 1066) with mean 48.27; in HK 19 from 27.80 (HG 75) to 149.47 (RGC 1066) with mean 47.93; in BK 19 from 16.77 (RGC 936) to 109.03(RGC 1066) with mean 32.18; in HS 20 from 12.60 (GG 1) to 198.93 (RGC 1066) with mean 45.03; in BS 20 from 24.93 (RG 936) to 138.60 (RGC 1066) with mean 39.38; in HK 20 from 16.80 (M 83) to 153.27 (RGC 1066) with mean 39.03 and in BK 20 from 21.30 (M 83) to 114.00 (RGC 1066) with mean 37.05 (Table 4.3.4).

On the basis of overall performance, 16, 13, 13, 2, 10, 7, 4 and 2 (Number in each environment) genotypes showed maximum number of pods on main stem than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. RGC 1066 (179.20) showed highest pod bearing on main stem in HS 19 followed by FS 277 (80.73) and HG 563 (58.67); RGC 1066 (146.87) in BS 19 followed by FS 277 (90.33) and HG 870 (54.87); RGC 1066 (149.47) in HK 19 followed FS 277 (90.33) and HG 2-20 (54.71); RGC 1066 (109.03) in BK 19 followed by FS 277 (63.40) and PNB (41.77); RGC 1066 (198.93) in HS 20 followed by FS 277 (56.00) and PNB (51.80); RGC 1066 (138.60) in BS 20 followed FS 277 (76.80) and HG 2-20 (47.87); RGC 1066 (153.27) in HK 20 followed by FS 277 (69.93) and HG 2-20 (44.33); RGC 1066 (114.00) in BK 20 followed FS 277 (69.70) and HG 2-20 (41.10).

On the basis of overall mean across the environments in RGC 1066 (148.67) highest number of pods was found on main stem followed by FS 277 (74.65) and HG 2-20 (48.13).Among the environments HS 19, BS 19 and HK 19 showed highest number of pods on main stem than grand mean.

4.3.5 Pods on per plant

Number of pods per plant in HS 19 ranged from 56.33 (PNB) to 245.47 (HG 563) with mean 154.65; in BS 19 from 46.45 (PNB) to 170.80 (HG 563) with mean 125.55; in HK 19 from 46.37 (PNB) to 194.33 (HG 2-20) with mean 137.05; in BK 19 from 50.17 (HVG 2-30) to HG 2-20 (128.60) with mean 95.93; in HS 20 from 62.80 (FS 277) to 212.73 (HG 2-20) with mean 148.31; in BS 20 from 37.40 (PNB) to 168.33 (HG 2-20) with mean 126.28; in HK 20 from 42.47 (PNB) to 180.87 (HG 2-20) with mean 129.35 and in BK 20 from 48.60 (PNB) to 131.20 (HG 2-20) with mean 97.39 (Table 4.3.5).

On the basis of overall performance, 18, 18, 18, 8, 18, 0, 18 and8 (Number in each environment) shown maximum number of pods per plant than grand mean

Table 4.3.4: Mean performance of cluster bean genotypes under different environments for pods on main stem

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	58.20	53.73	54.71	37.27	47.80	47.87	44.33	41.10	48.13
HG 884	46.33	52.60	51.07	32.63	44.33	39.27	38.93	37.40	42.82
HG 870	45.40	54.87	48.07	34.23	41.87	46.07	40.33	40.80	43.96
HG 563	58.67	51.07	52.60	34.80	46.40	44.73	42.20	37.27	45.97
HG 365	49.60	50.60	50.60	33.93	40.73	43.13	38.27	37.70	43.07
HG 3-52	49.60	40.00	41.27	25.93	33.67	30.07	32.20	29.43	35.27
HG 6	44.33	37.93	37.93	21.33	43.13	26.33	34.00	27.03	34.00
HVG 2-30	40.93	28.20	28.20	24.30	37.47	29.53	28.60	40.40	32.20
HG 100	39.73	41.27	40.00	26.50	34.00	33.80	34.13	31.53	35.12
FS 277	80.73	90.33	90.33	63.40	56.00	76.80	69.93	69.70	74.65
X-10	56.87	48.07	54.87	34.30	48.73	43.00	43.40	38.00	45.91
PNB	48.33	39.87	37.67	41.77	51.80	28.80	33.40	40.87	40.31
GG-1	28.60	33.13	25.07	17.77	12.60	26.27	28.67	27.03	24.89
GG-2	29.40	43.13	44.73	21.37	32.20	25.27	32.60	27.13	31.98
RGC 1017	51.20	43.80	43.80	26.87	38.87	31.20	28.80	31.90	37.06
RGC 1038	47.07	44.73	43.13	32.77	43.27	41.27	33.73	30.60	39.57
RGC 936	21.87	34.40	34.40	16.77	30.40	24.93	20.27	24.07	25.89
RGC 1055	44.40	46.73	46.73	23.80	36.60	29.00	35.53	33.97	37.10
RGC 1002	39.93	38.27	39.20	20.83	33.07	27.53	26.00	26.37	31.40
RGC 1003	53.33	39.20	38.27	21.13	32.07	26.87	27.73	27.23	33.23
RGC 1066	179.20	146.87	149.47	109.03	198.93	138.60	153.27	114.00	148.67
RGS 3	36.00	35.40	35.40	27.83	35.93	35.60	29.53	30.57	33.28
M-83	42.40	33.40	33.40	19.07	33.93	25.07	16.80	21.30	28.17
RGC 1033	31.60	49.47	49.47	30.57	43.60	37.73	31.07	38.33	38.98
HG 75	22.13	29.80	27.80	26.33	28.33	25.80	32.00	22.63	26.85
Over all Mean	**49.83**	**48.27**	**47.93**	**32.18**	**45.03**	**39.38**	**39.03**	**37.05**	**42.34**
C.D.	**3.89**	**3.12**	**3.14**	**1.77**	**3.14**	**3.01**	**3.16**	**2.18**	
C.V. at 5%	**4.74**	**3.92**	**3.98**	**3.34**	**4.24**	**4.64**	**4.92**	**3.57**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

Table 4.3.5: Mean performance of cluster bean genotypes under different environments for pods per plant

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	224.27	168.07	194.34	128.60	212.73	168.33	180.87	131.20	176.05
HG 884	207.53	158.60	190.43	118.17	203.33	150.13	170.27	117.83	164.54
HG 870	222.93	166.93	183.30	122.27	205.27	164.73	171.10	128.40	170.62
HG 563	245.47	170.80	188.73	122.27	212.67	161.47	178.47	125.77	175.71
HG 365	220.60	161.33	183.57	118.63	195.93	156.87	166.63	123.43	165.87
HG 3-52	170.73	133.47	142.30	102.23	149.60	131.40	137.53	100.10	133.42
HG 6	100.93	121.27	110.80	85.87	105.53	112.13	109.60	90.63	104.60
HVG 2-30	94.00	61.87	73.07	50.17	93.53	68.93	71.63	65.00	72.28
HG 100	169.42	127.40	151.87	103.07	164.27	138.80	149.67	100.60	138.14
FS 277	87.40	93.67	95.40	67.37	62.80	80.33	75.57	74.10	79.58
X-10	196.33	155.13	191.57	121.33	210.07	157.20	175.50	124.47	166.45
PNB	56.33	46.45	46.37	51.53	63.00	37.40	42.47	48.60	49.02
GG-1	81.40	111.13	66.33	73.80	74.87	118.33	114.47	83.50	90.48
GG-2	117.33	130.87	147.13	85.13	136.60	114.93	128.53	88.83	118.67
RGC 1017	225.96	140.80	154.37	105.43	163.00	135.33	132.13	108.10	145.64
RGC 1038	181.93	145.13	164.93	116.37	199.13	152.53	156.70	106.33	152.88
RGC 936	126.87	99.73	119.33	74.37	134.93	113.73	95.03	76.23	105.03
RGC 1055	179.93	150.53	165.63	96.53	170.60	128.53	150.93	109.30	144.00
RGC 1002	176.13	114.87	129.07	89.90	131.93	123.53	113.97	85.77	120.65
RGC 1003	169.67	120.07	125.13	88.07	129.20	120.87	116.10	89.83	119.87
RGC 1066	180.53	148.60	151.70	117.97	201.67	150.80	162.57	119.47	154.16
RGS 3	169.87	120.40	135.03	105.00	150.20	142.67	128.37	101.67	131.65
M-83	86.60	81.27	80.53	59.70	80.33	74.20	59.87	59.50	72.75
RGC 1033	115.53	143.20	164.00	111.73	178.93	146.73	144.37	114.40	139.86
HG 75	58.60	67.27	71.23	82.67	77.73	107.00	101.50	61.60	78.45
Over all Mean	**154.65**	**125.55**	**137.05**	**95.93**	**148.31**	**126.28**	**129.35**	**97.39**	**126.81**
C.D.	**6.53**	**7.46**	**4.47**	**2.18**	**4.94**	**5.51**	**4.99**	**3.88**	
C.V. at 5%	**2.56**	**3.61**	**1.98**	**1.72**	**2.02**	**2.65**	**2.34**	**2.42**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

genotypes in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. HG 563 (245.47) showed highest number of pods per plant in HS 19 followed by RGC 1017(225.96) and HG 2-20 (224.27); HG 563 (170.80) in BS 19 followed by HG 2-20(168.07) and HG 870 (166.93); HG 2-20 (194.34) in HK 19 followed X 10(191.57) and HG 884 (190.43); HG 2-20 (128.60) in BK 19 followed by HG 870, HG 563 (122.27) and X 10 (121.33); HG 2-20(212.73) in HS 20 followed by HG 563(212.67) and X 10 (210.67); HG 2-20(168.33) in BS 20 followed HG 870 (164.73) and HG 563 (161.47); HG 2-20 (180.87) in HK 20 followed by HG 563 (178.47) and X 10 (175.50); HG 2-20 (131.20) in BK 20 followed HG 870(128.40) and HG 563 (125.77).

On the basis of overall mean across the environments in HG 2-20 (176.05) highest numbers of pods per plant were found followed by HG 563 (175.71) and HG 870 (170.62). Among the environments HS 19, HK 19, HS 20 and HK 20 showed highest number of pods per plant than grand mean.

4.3.6 Pods per cluster

Number of pods per cluster in HS 19 ranged from 3.67 (GG 2) to 12.87 (FS 277) with mean 6.13 ; in BS 19 from 3.53 (HG 75) to 12.20 (FS 277) with mean 5.82; in HK 19 from 4.20 (HG 75) to 11.93 (FS 277) with mean 5.95; in BK 19 from 3.27 (GG 1) to11.00 (PNB) with mean 4.51; in HS 20 from 4.07 (GG 2) to 11.33 (FS 277) with mean 5.49; in BS 20 from 3.20 (GG 1) to11.33 (FS 277) with mean 5.32; in HK 20 from 4.00 (GG 1) to 9.40 (FS 277) with mean 5.26 and in BK 20 from 3.80 (RGC 1033) to 11.47 (FS 277) with mean 5.20 (Table 4.3.6).

On the basis of overall performance, the genotypes 11, 13, 15, 22, 17, 20, 19 and 22 (Number in each environment) shown minimum number of pods per cluster than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. GG 2 (3.67) showed lowest number of pods per cluster in HS 19 followed by HG 365 (3.73) and RGC 936 (4.47); HG 75 (3.53) in BS 19 followed by GG 1(4.00) and RGC 936 (4.33); HG 75(4.20) in HK 19 followed GG 1(4.67) and GG 2 (4.80); GG 1 (3.27) in BK 19 followed by RGC 936 (3.33) and RGC 1003 (3.47); GG 2 (4.07) in HS 20 followed by HG 3-52 and HG 365 (4.27); GG 1 (3.20) in BS 20 followed HG 6 (4.00) and GG 2 (4.07); GG 1 (4.00) in HK 20 followed by RGC 936 (4.07) and RGC 1003 (4.40); RGC 1033 (3.80) in BK 20 followed RGC 936 (4.00) and GG 1 (4.13).

On the basis of overall mean across the environments in RGC 936 (4.22) lowest number of pods per cluster was found followed by GG 2 (4.26) and GG 1 (4.30). Among the environments BK 19, BS 20, HK 20 and BK 20 showed lowest number of pods per cluster than grand mean.

Table 4.3.6: Mean performance of cluster bean genotypes under different environments for pods per cluster

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	5.07	4.87	5.13	4.40	4.93	5.33	4.87	4.87	4.93
HG 884	4.80	4.47	5.00	4.33	5.00	4.67	4.73	4.87	4.73
HG 870	5.67	5.47	5.20	4.20	4.47	4.87	4.93	4.20	4.88
HG 563	6.00	5.53	5.60	4.93	5.00	4.93	5.27	4.93	5.27
HG 365	3.73	4.80	5.13	4.27	4.33	4.53	4.67	4.33	4.47
HG 3-52	5.40	5.13	5.27	4.00	4.27	4.27	4.73	4.20	4.66
HG 6	5.07	4.67	5.13	3.93	4.67	4.00	4.67	4.93	4.63
HVG 2-30	5.73	5.40	5.40	3.80	6.07	4.93	5.33	5.40	5.26
HG 100	6.47	5.67	5.33	4.07	4.53	5.00	4.80	4.93	5.10
FS 277	12.87	12.20	11.93	8.00	11.33	11.33	9.40	11.47	11.07
X-10	5.27	5.40	5.40	4.60	5.20	4.80	4.73	5.00	5.05
PNB	9.13	10.87	11.00	10.00	8.33	10.93	8.93	8.60	9.72
GG-1	6.47	4.00	4.67	3.27	4.67	3.20	4.00	4.13	4.30
GG-2	3.67	4.53	4.80	3.67	4.07	4.07	4.53	4.73	4.26
RGC 1017	5.67	5.80	5.87	4.00	4.73	4.40	5.80	5.07	5.17
RGC 1038	6.40	6.00	5.80	4.07	4.67	4.73	4.87	5.13	5.21
RGC 936	4.47	4.33	4.93	3.33	4.27	4.33	4.07	4.00	4.22
RGC 1055	5.33	4.93	5.20	4.07	4.53	4.67	4.67	5.33	4.84
RGC 1002	7.33	6.47	6.13	3.53	6.40	6.20	4.73	4.53	5.67
RGC 1003	7.67	6.33	6.27	3.47	5.47	5.80	4.40	4.73	5.52
RGC 1066	8.67	7.87	7.93	6.67	8.13	7.13	6.47	5.13	7.25
RGS 3	4.80	4.93	5.07	3.73	4.67	4.47	4.47	4.60	4.59
M-83	7.07	6.80	6.73	3.53	6.80	5.20	6.13	6.47	6.09
RGC 1033	5.67	5.60	5.53	5.00	4.73	4.67	5.67	3.80	5.08
HG 75	4.87	3.53	4.20	4.00	6.07	4.47	4.67	4.60	4.55
Over all Mean	**6.13**	**5.82**	**5.95**	**4.51**	**5.49**	**5.32**	**5.26**	**5.20**	**5.46**
C.D.	**0.89**	**0.71**	**0.55**	**1.21**	**0.78**	**0.81**	**0.79**	**0.96**	
C.V. at 5%	**8.83**	**7.43**	**5.61**	**16.28**	**8.60**	**9.33**	**9.13**	**11.22**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

Table 4.3.7: Mean performance of cluster bean genotypes under different environments for seeds per pod

Genotypes	**HS 19**	**BS 19**	**HK19**	**BK 19**	**HS 20**	**BS 20**	**HK 20**	**BK 20**	**Over all Mean**
HG 2-20	9.27	8.80	8.97	8.73	10.00	8.80	9.07	8.72	9.05
HG 884	9.20	8.73	8.77	8.70	8.93	9.20	9.07	8.27	8.86
HG 870	9.20	8.60	8.57	8.73	9.07	9.53	8.67	8.40	8.85
HG 563	9.20	9.20	8.87	8.00	9.30	8.73	9.07	8.27	8.83
HG 365	9.20	8.60	8.60	8.23	8.93	8.67	8.73	8.27	8.65
HG 3-52	8.93	8.27	8.60	8.47	8.77	8.53	9.27	8.13	8.62
HG 6	8.67	8.27	8.47	7.93	8.63	8.87	8.27	8.73	8.48
HVG 2-30	8.80	8.40	8.43	7.73	8.70	8.67	9.20	8.13	8.51
HG 100	9.47	8.60	8.47	8.00	8.87	8.80	8.73	8.20	8.64
FS 277	8.20	8.00	7.77	7.53	8.23	8.20	9.60	7.93	8.18
X-10	9.33	8.60	8.43	8.53	9.17	8.87	8.80	8.73	8.81
PNB	9.13	8.53	7.90	7.73	10.67	8.73	10.07	8.47	8.90
GG-1	8.33	8.27	8.17	7.87	8.30	8.93	8.27	7.80	8.24
GG-2	8.87	8.47	8.53	8.00	8.60	8.67	8.73	8.00	8.48
RGC 1017	11.53	8.73	9.33	8.27	8.67	8.67	8.07	7.53	8.85
RGC 1038	9.13	8.47	8.60	8.53	8.80	8.53	9.13	8.07	8.66
RGC 936	8.33	8.40	8.17	7.80	8.23	8.80	7.27	7.80	8.10
RGC 1055	10.33	8.47	8.60	8.27	9.40	8.80	8.07	8.13	8.76
RGC 1002	8.53	8.33	8.33	7.93	8.23	8.93	8.07	7.60	8.24
RGC 1003	8.67	8.40	8.03	7.93	8.53	9.13	8.53	10.07	8.66
RGC 1066	10.20	9.53	10.27	8.67	10.63	10.80	9.67	8.20	9.75
RGS 3	8.53	8.33	8.23	7.87	8.30	8.87	9.00	8.00	8.39
M-83	8.47	11.13	8.43	10.07	8.87	8.67	8.73	8.67	9.13
RGC 1033	9.07	8.60	8.73	8.43	8.63	8.60	8.47	9.00	8.69
HG 75	8.53	8.20	8.07	7.80	8.37	8.60	8.67	7.93	8.27
Over all Mean	**9.09**	**8.64**	**8.53**	**8.23**	**8.91**	**8.86**	**8.77**	**8.28**	**8.66**
C.D.	**0.89**	**0.65**	**0.62**	**0.68**	**0.60**	**0.59**	**1.01**	**0.61**	
C.V. at 5%	**5.96**	**4.59**	**4.43**	**5.03**	**4.12**	**4.10**	**6.99**	**4.47**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

4.3.7 Seeds per pod

Number of seeds per pod in HS 19 ranged from 8.20 (FS 277) to 11.53 (RGC 1017) with mean 9.09; in BS 19 from 8.00 (FS 277) to 11.13 (M 83) with mean 8.64; in HK 19 from 7.77 (FS 277) to10.27 (RGC 1066) with mean 8.53; in BK 19 from 7.53 (FS 277) to 10.07 (M 83) with mean 8.23; in HS 20 from 8.23 (FS 277, RGC 936 and RGC 1002) to 10.67 (PNB) with mean 8.91; in BS 20 from 8.20 (FS 277) to 10.80 (RGC 1066) with mean 8.86; in HK 20 from 7.27 (RGC 936) to 10.07 (PNB) with mean 8.77 and in BK 20 from 7.53 (RGC 1017) to 10.07 (RGC 1003) with mean 8.28 (Table 4.3.7).

On the basis of overall performance, 18, 6, 6, 5, 15, 20, 17 and 6 (Number in each environment) genotypes shown maximum number of seeds per pod than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. RGC 1017(11.53) showed highest number of seeds per pod in HS 19 followed by RGC 1055 (10.33) and RGC 1066 (10.20); M 83 (11.13) in BS 19 followed by RGC 1066 (9.53) and HG 563 (9.20); RGC 1066(10.27) in HK 19 followed RGC 1017 (9.33) and HG 2-20 (8.97); M 83 (10.07) in BK 19 followed by HG 2-20, HG 870 (8.73) and HG 884 (8.70); PNB (10.67) in HS 20 followed by RGC 1066 (10.63) and HG 2-20 (10.00); RGC 1066 (10.80) in BS 20 followed HG 870 (9.53) and HG 884 (9.20); PNB (10.07) in HK 20 followed by RGC 1066 (9.67) and FS 277 (9.60); RGC 1003 (10.07) in BK 20 followed RGC 1033 (9.00), HG 6 and X 10 (8.73).

On the basis of overall mean across the environments in RGC 1066 (9.75) highest number of seeds per pod was found followed by RGC 1033 (9.13) and HG 2-20 (9.04). Among the environments HS 19, HS 20, BS 20 and HK 20 showed highest number seeds per pod than grand mean.

4.3.8 Pod length

Pod length in HS 19 ranged from 5.14 cm (HG 6) to 9.06cm (PNB) with mean 6.03 cm ; in BS 19 from 5.13 cm (HG 75) to 8.79cm (PNB) with mean 5.93 cm; in HK 19 from 5.39 cm (GG 2) to 8.09cm (PNB) with mean 5.89 cm; in BK 19 from 4.87 cm (RGC 936) to 8.20 cm (PNB) with mean 5.40 cm; in HS 20 from 5.27 cm (RGC 1003) to 8.74 cm (PNB) with mean 5.95 cm; in BS 20 from 5.38cm (HG 6) to 8.34 cm (PNB) with mean 5.87 cm; in HK 20 from 5.35 cm (GG 2) to 8.51 cm (PNB) with mean 5.83 cm and in BK 20 from 4.92 cm (FS 277) to 8.33 cm (PNB) with mean 5.44 cm(Table 4.3.8).

On the basis of overall performance, 14, 17, 15, 22, 15, 18, 19 and22 (Number in each environment) genotypes showed shorter pods than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. HG 6(5.14 cm) showed shortest pods in HS 19 followed by RGC 1003 (5.27 cm) and GG 2 (5.33 cm); HG 75 (5.13 cm) in BS 19 followed by RGS 3 (5.32 cm) and RGC 1003 (5.40 cm) ; GG 2 (5.39 cm) in HK 19 followed RGC 1003 (5.40 cm) and HG 100 (5.52 cm); RGC 936 (4.87 cm) in BK 19 followed by HG 75 (4.95 cm) and HG (4.96 cm); RGC 1003 (5.27 cm) in HS 20 followed by GG 2 (5.354 cm)

Table 4.3.8: Mean performance of cluster bean genotypes under different environments for pod length

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	5.85	5.79	5.84	5.27	5.89	5.72	5.83	5.31	5.69
HG 884	5.49	5.62	5.67	5.16	5.65	5.59	5.59	5.13	5.49
HG 870	6.22	6.21	6.02	5.34	6.10	5.82	6.05	5.13	5.86
HG 563	5.62	5.69	5.65	5.42	5.63	5.71	5.65	5.14	5.56
HG 365	5.58	5.57	5.67	5.29	5.70	5.61	5.67	5.13	5.53
HG 3-52	5.60	5.60	5.72	5.20	5.77	5.58	5.61	5.34	5.55
HG 6	5.14	5.62	5.85	4.97	5.48	5.38	5.65	4.95	5.38
HVG 2-30	7.48	7.73	7.10	6.25	7.51	7.45	7.30	6.33	7.14
HG 100	5.57	5.68	5.52	5.17	5.55	5.56	5.45	5.15	5.46
FS 277	6.05	5.96	5.84	5.17	5.95	5.76	5.73	4.92	5.67
X-10	5.59	5.69	6.01	5.22	5.51	5.61	5.49	5.16	5.54
PNB	9.06	8.79	8.09	8.20	8.74	8.34	8.51	8.33	8.51
GG-1	5.65	5.51	5.47	5.15	5.57	5.53	5.39	5.16	5.43
GG-2	5.33	5.44	5.39	5.19	5.34	5.57	5.35	5.17	5.35
RGC 1017	6.25	5.77	5.69	5.16	5.88	5.68	5.54	5.30	5.66
RGC 1038	6.31	5.78	5.70	5.16	5.92	5.65	5.49	5.20	5.65
RGC 936	5.69	5.63	5.73	4.87	5.54	5.43	5.47	5.61	5.50
RGC 1055	6.19	5.79	5.79	5.14	5.99	5.95	5.62	5.21	5.71
RGC 1002	6.08	5.62	5.59	5.12	5.72	5.53	5.42	5.56	5.58
RGC 1003	5.27	5.43	5.40	5.08	5.27	5.52	5.43	5.47	5.36
RGC 1066	6.21	6.13	5.98	5.58	6.12	5.89	6.01	5.56	5.94
RGS 3	5.69	5.32	5.77	5.09	5.62	5.55	5.47	5.22	5.47
M-83	7.51	7.15	6.76	6.32	7.14	6.80	6.84	6.07	6.82
RGC 1033	5.68	5.71	5.56	5.46	5.57	5.87	5.60	5.26	5.59
HG 75	5.57	5.13	5.53	4.95	5.47	5.56	5.46	5.28	5.37
Over all Mean	**6.03**	**5.93**	**5.89**	**5.40**	**5.95**	**5.87**	**5.83**	**5.44**	**5.79**
C.D.	**0.30**	**0.25**	**0.56**	**0.20**	**0.13**	**0.32**	**0.24**	**0.19**	
C.V. at 5%	**3.04**	**2.59**	**5.76**	**2.24**	**1.37**	**3.37**	**2.55**	**2.13**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

and HG 6 (5.48 cm); HG 6 (5.38 cm) in BS 20 followed RGC 936 (5.43 cm) and RGC 1003 (5.52 cm); GG 2 (5.35 cm) in HK 20 followed by GG 1 (5.39 cm) RGC 1002 (5.42 cm)FS 277 (4.92 cm) in BK 20 followed HG 6 (4.95 cm) and HG 884, HG 870 and HG 365 (5.13 cm).

On the basis of overall mean across the environments in GG 2 (5.35 cm)shortest pods were observed followed by RGC 1003 (5.36 cm) and HG 75 (5.37 cm). Among the environments BK 19 and BK 20 showed shorter pods than grand mean.

4.3.9 Branches per plant

Number of branches per plant in HS 19 ranged from 0.47 (RGC 1066) to 13.13 (RGC 1003) with mean 9.27 ; in BS 19 from 0.40 (RGC 1066) to 12.60 (X 10 and GG 1) with mean 9.09; in HK 19 from 1.01 (PNB) to 11.73 (X 10) with mean 8.63; in BK 19 from 0.80 (RGC 1066) to 10.13 (RGC 1038) with mean 7.35; in HS 20 from 1.00 (PNB) to 13.47 (RGC 1003) with mean 9.52; in BS 20 from 1.00 (RGC 1066) to 12.07 (RGC 1038) with mean 8.16; in HK 20 from 0.87 (RGC 1066) to 13.13 (RGC 1017) with mean 8.62 and in BK 20 from 1.14 (RGC 1066) to 11.45 (GG 1) with mean 8.21 (Table 4.3.9).

On the basis of overall performance, 18, 18, 18, 15, 18, 18, 18 and17 (Number in each environment) genotypes showed maximum number of branches per plant than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. RGC 1003 (13.13) exhibited maximum number of branches per plant in HS 19 followed by HG 2-20 (13.00) and RGC 1002 (12.93); X 10 and GG 1 (12.60) in BS 19 followed by HG 365 (12.40) and RGC 1017 (12.33); X 10 (11.73) in HK 19 followed HG 100 (11.59) and RGS 3 and HG 2-20 (11.31); RGC 1038 (10.13) in BK 19 followed by RGC 1055, RGC 1003 and RGC 1033 (9.87); RGC 1003 (13.47) in HS 20 followed by RGS 3 (12.80) and HG 2-20 (12.67); RGC 1038 (12.07) in BS 20 followed HG 2-20 (11.53), GG 1 and HG 100 (11.00); RGC 1017 (13.13) in HK 20 followed by HG 3-52 (12.13) and GG 1 (11.73); GG 1 (11.45) in BK 20 followed RGC 1038 (11.38) and HG 563 (10.86).

On the basis of overall mean across the environments, maximum number of branches per plant were observed in RGC 1038 (11.51) followed by HG 2-20 (11.23) and RGC 1003 (11.20). Among the environments HS 19, BS 19, HK 19, HS 20 and HK 20 showed maximum number of branches per plant than grand mean.

4.3.10 100 seed weight

100 seed weight in HS 19 ranged from 2.02 g (PNB) to 3.17g (X 10) with mean 2.69 g; in BS 19 from 1.56 g (HG 75) to 3.14 g (RGC 1038 and HG 3-52) with mean 2.10 g; in HK 19 from 2.07 g (HVG 2-30) to 2.71 g (HG 884 and HG 3-52) with mean 2.47 g; in BK 19 from 2.60 g (RGC 936) to 3.22 g (PNB) with mean 2.89 g; in HS 20 from 2.28 g (RGC 1055) to 3.27 g (RGC 1066) with mean 2.73 g; in BS 20 from 1.84 g (HVG 2-30) to 2.52 g (HG 6) with mean 2.16 g; in HK 20 from 1.78 g (PNB) to 2.61 g (HG 3-52) with mean 2.26 g and in BK 20 from 1.56 g (RGC 936) to 3.14 g (X 10 and RGC 1033) with mean 2.10 g (Table 4.3.10).

Table 4.3.9: Mean performance of cluster bean genotypes under different environments for branches per plant

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	13.00	12.20	11.31	8.60	12.67	11.53	10.13	10.42	11.23
HG 884	11.60	11.40	10.99	9.67	12.53	10.27	10.53	9.76	10.84
HG 870	11.53	10.93	10.83	9.00	11.13	10.87	10.80	10.57	10.71
HG 563	9.73	10.47	10.15	9.53	11.07	9.40	10.33	10.86	10.19
HG 365	10.47	12.40	11.08	9.60	11.07	9.47	10.87	9.83	10.60
HG 3-52	12.60	12.00	10.42	8.47	11.60	9.33	12.13	8.83	10.67
HG 6	4.33	5.33	5.05	3.80	4.27	4.80	5.73	4.75	4.76
HVG 2-30	2.60	2.07	1.60	1.53	2.80	2.40	1.80	2.78	2.20
HG 100	12.87	11.80	11.59	9.40	11.80	11.00	10.13	8.52	10.89
FS 277	1.07	0.53	1.27	1.13	1.47	1.20	1.00	1.99	1.21
X-10	11.60	12.60	11.73	8.00	11.60	9.60	10.93	8.92	10.62
PNB	0.67	0.47	1.01	1.07	1.00	1.40	1.00	1.55	1.02
GG-1	11.40	12.60	10.56	8.27	11.53	11.00	11.73	11.45	11.07
GG-2	11.67	11.73	10.33	7.87	11.60	10.67	11.67	10.27	10.73
RGC 1017	11.60	12.33	10.86	8.80	12.20	10.73	13.13	9.37	11.13
RGC 1038	11.20	12.07	11.25	10.13	12.60	12.07	11.40	11.38	11.51
RGC 936	11.13	12.27	11.25	9.40	12.07	8.80	10.73	10.23	10.74
RGC 1055	10.60	10.47	10.57	9.87	11.53	9.47	10.40	10.42	10.42
RGC 1002	12.93	11.20	10.66	9.73	11.40	10.53	9.47	10.66	10.82
RGC 1003	13.13	10.73	11.10	9.87	13.47	10.93	9.93	10.43	11.20
RGC 1066	0.47	0.40	1.03	0.80	1.53	1.00	0.87	1.14	0.91
RGS 3	11.53	12.20	11.31	9.47	12.80	9.07	10.47	10.12	10.87
M-83	3.87	4.73	5.15	4.13	3.60	4.07	3.40	5.57	4.32
RGC 1033	12.13	10.27	10.27	9.87	12.47	9.73	10.33	10.73	10.73
HG 75	7.93	3.93	4.37	5.80	8.07	4.67	6.47	4.80	5.76
Over all Mean	**9.27**	**9.09**	**8.63**	**7.35**	**9.51**	**8.16**	**8.62**	**8.21**	**8.60**
C.D.	**2.43**	**1.89**	**1.19**	**1.60**	**1.77**	**1.61**	**1.78**	**1.47**	
C.V. at 5%	**15.92**	**12.65**	**8.38**	**13.19**	**11.27**	**12.00**	**12.58**	**10.84**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

Table 4.3.10: Mean performance of cluster bean genotypes under different environments for 100 seed weight

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	3.13	2.17	2.64	3.01	2.62	2.35	2.15	2.60	2.58
HG 884	3.08	1.90	2.71	2.89	2.84	2.48	2.16	2.35	2.55
HG 870	3.15	1.82	2.49	2.81	3.05	2.24	1.99	2.69	2.53
HG 563	2.83	2.35	2.59	3.04	2.76	2.34	2.38	2.40	2.59
HG 365	3.06	2.38	2.60	2.87	2.82	2.07	2.03	2.38	2.53
HG 3-52	2.70	3.14	2.71	2.81	3.14	2.48	2.61	2.27	2.73
HG 6	2.42	2.01	2.49	2.77	3.12	2.52	2.33	1.90	2.45
HVG 2-30	2.44	1.64	2.07	2.67	2.73	1.84	2.05	1.89	2.17
HG 100	2.69	2.40	2.47	2.78	2.57	2.34	2.57	2.01	2.48
FS 277	2.39	2.05	2.35	2.79	2.33	2.00	2.37	1.64	2.24
X-10	3.17	2.27	2.44	2.80	2.94	2.12	2.24	3.14	2.64
PNB	2.02	2.05	2.33	3.22	2.55	1.92	1.78	1.58	2.18
GG-1	2.56	1.58	2.40	2.84	2.63	1.92	2.53	1.86	2.29
GG-2	2.68	1.87	2.48	2.89	2.43	1.87	2.52	1.87	2.33
RGC 1017	3.11	2.69	2.58	2.98	2.68	2.32	2.31	2.07	2.59
RGC 1038	2.83	3.14	2.58	3.06	3.04	2.10	2.23	2.17	2.64
RGC 936	2.58	2.07	2.36	2.60	2.46	2.00	2.04	1.56	2.21
RGC 1055	2.72	1.86	2.49	2.75	2.28	1.91	2.53	2.05	2.32
RGC 1002	2.55	1.78	2.30	3.04	2.47	2.21	2.36	1.82	2.32
RGC 1003	2.62	1.70	2.56	3.00	2.75	1.96	2.24	1.80	2.33
RGC 1066	2.77	2.60	2.54	2.99	3.27	2.47	2.34	2.05	2.63
RGS 3	2.46	1.80	2.29	2.93	3.10	1.90	1.85	1.78	2.26
M-83	2.24	1.67	2.25	2.87	2.56	2.13	2.04	1.70	2.18
RGC 1033	2.74	1.89	2.63	2.91	2.67	2.38	2.25	3.14	2.58
HG 75	2.38	1.56	2.31	2.88	2.46	1.99	2.52	1.67	2.22
Over all Mean	**2.69**	**2.10**	**2.47**	**2.89**	**2.73**	**2.15**	**2.26**	**2.10**	**2.42**
C.D.	**0.35**	**0.19**	**0.15**	**0.24**	**0.26**	**0.27**	**0.17**	**0.19**	
C.V. at 5%	**7.87**	**5.37**	**3.58**	**4.94**	**5.73**	**7.78**	**4.67**	**5.37**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

On the basis of overall performance, the genotypes 20, 4, 16, 25, 23, 4, 6, 4 (Number in each environment) highest 100 seed weight than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. X 10 (3.17 g) exhibited highest 100 seed weight in HS 19 followed by HG 870 (3.15 g) and HG 2-20 (3.13 g); HG 3-52 and RGC 1038 (3.14 g) in BS 19 followed by RGC 1017 (2.69 g) and RGC 1066 (2.60 g); HG 3-52 and HG 884 (2.71g) in HK 19 followed HG 2-20 (2.64g) and RGC 1033 (2.63 g); PNB (3.22 g) in BK 19 followed by RGC 1038 (3.06 g), HG 563 and RGC 1002 (3.04 g); RGC 1066 (3.27 g) in HS 20 followed by HG 3-52 (3.14 g) and HG 6 (3.12 g); HG 6 (2.52 g) in BS 20 followed HG 884 and HG 3-52 (2.48 g) and RGC 1066 (2.47 g); HG 3-52 (2.61 g) in HK 20 followed by HG 100 (2.57 g), RGC 936 and GG 1 (2.53 g); X 10 and RGC 1033 (3.14 g) in BK 20 followed HG 870 and HG 2-20 (2.60 g).

On the basis of overall mean across the environments in HG 3-52 (2.73 g) highest 100 seed weight were observed followed by RGC 1038 (2.65 g) and X 10 (2.64 g). Among the environments HS 19, HK 19, BK 19 and HS 20 showed highest 100 seed weight than grand mean.

4.3.11 Biomass per plot

Biomass per plot in HS 19 ranged from 1.30 kg (PNB) to 4.42 kg (HG 2-20) with mean 3.07 kg ; in BS 19 from 1.04 kg (PNB) to 2.36 kg (HG 870) with mean 1.70 kg; in HK 19 from 1.33 kg (PNB) to 3.30 kg (HG 2-20) with mean 2.39 kg; in BK 19 from 1.02 kg (RGC 936) to 2.76 kg (FS 277) with mean 1.70 kg; in HS 20 from 2.38 kg (GG 1) to 3.84 kg (HG 2-20) with mean 2.99 kg; in BS 20 from 1.15 kg (HG 75) to 3.10 kg (FS 277) with mean 2.30 kg; in HK 20 from 1.41 kg (PNB) to 3.05 kg (FS 277) with mean 2.38 kg and in BK 20 from 1.56kg (RGC 1002) to 3.14 kg (X 10 and FS 277) with mean 2.10 kg (Table 4.3.11).

On the basis of overall performance, 19, 1, 132, 25, 12, 13 and7 (Number in each environment) genotypes exhibited biomass per plot than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. HG 2-20 (4.42 kg) exhibited highest biomass per plot in HS 19 followed by HG 884 (4.00 kg) and HG 870 (3.95 kg); HG 870 (2.36 kg) in BS 19 followed by HG 2-20 (2.24 kg) and HG 563 and FS 277 (2.16 kg); HG 2-20 (3.30 kg) in HK 19 followed X 10 (3.19 kg) and HG 563 (3.13 kg);FS 277 (2.76 kg) in BK 19 followed by HG 884 (2.37 kg) and X 10 (2.07); HG 2-20 (3.84 kg) in HS 20 followed by HG 563 (3.78 kg) and HG 870 (3.49 kg);FS 277 (3.10 kg)in BS 20 followed HG 2-20 (3.01 kg) and X 10 (2.96 kg); FS 277 (3.05 kg) in HK 20 followed by HG 2-20 and HG 563 (3.02 kg); FS 277 and X 10 (3.14 kg) in BK 20 followed HG 2-20 (2.69 kg) and HG 870 (2.60 kg).

On the basis of overall mean across the environments in HG 2-20 (3.07 kg) highest biomass per plot were observed followed by X 10 (2.97 kg) and HG 563 (2.90 kg). Among the environments HS 19, HK 19, HS 20 and HK 20 showed highest biomass per plot than grand mean.

Table 4.3.11:Mean performance of cluster bean genotypes under different environments for biomass per plot

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	4.42	2.24	3.30	2.04	3.84	3.01	3.02	2.69	3.07
HG 884	4.00	2.01	3.09	2.37	3.20	2.68	2.81	2.27	2.81
HG 870	3.95	2.36	3.09	1.89	3.49	2.86	2.81	2.60	2.88
HG 563	3.80	2.16	3.13	2.01	3.78	2.90	3.02	2.35	2.90
HG 365	3.77	2.03	2.48	1.84	3.14	2.72	2.75	2.38	2.64
HG 3-52	3.47	1.46	2.20	1.75	2.97	2.30	2.45	1.90	2.31
HG 6	1.73	1.20	2.05	1.44	2.62	1.91	2.13	1.64	1.84
HVG 2-30	2.02	1.23	1.53	1.18	2.55	1.80	1.83	1.80	1.74
HG 100	3.15	1.70	2.19	1.48	2.85	2.55	2.69	2.17	2.35
FS 277	2.80	2.16	2.07	2.76	3.25	3.10	3.05	3.14	2.79
X-10	3.85	2.07	3.19	2.07	3.45	2.96	2.99	3.14	2.97
PNB	1.30	1.04	1.33	1.94	2.98	1.31	1.41	1.82	1.64
GG-1	2.06	1.82	1.97	1.49	2.38	1.99	1.86	1.86	1.93
GG-2	3.48	1.83	2.53	1.51	2.80	2.00	2.19	1.78	2.27
RGC 1017	3.66	1.81	2.59	1.60	3.10	2.27	2.23	2.05	2.42
RGC 1038	3.31	1.80	2.31	1.67	3.18	2.58	2.62	1.87	2.42
RGC 936	3.33	1.77	2.61	1.02	2.91	2.06	1.92	2.01	2.20
RGC 1055	3.04	1.28	2.43	1.52	2.89	2.09	2.22	1.89	2.17
RGC 1002	3.02	1.21	2.17	1.28	2.52	2.07	2.07	1.56	1.99
RGC 1003	3.18	1.05	2.03	1.24	2.52	2.12	2.11	1.70	2.00
RGC 1066	3.55	1.69	2.40	2.01	3.17	2.42	2.49	2.05	2.47
RGS 3	2.82	1.78	2.21	1.55	3.33	2.52	2.43	2.07	2.34
M-83	1.93	1.66	2.90	1.70	2.76	1.70	1.79	1.58	2.00
RGC 1033	3.24	1.81	2.45	1.74	2.66	2.53	2.62	2.40	2.43
HG 75	1.92	1.26	1.55	1.39	2.53	1.15	2.00	1.67	1.68
Over all Mean	**3.07**	**1.70**	**2.39**	**1.70**	**2.99**	**2.30**	**2.38**	**2.10**	**2.33**
C.D.	**0.39**	**0.24**	**0.21**	**0.18**	**0.23**	**0.23**	**0.19**	**0.19**	
C.V. at 5%	**7.61**	**8.43**	**5.35**	**6.46**	**4.65**	**6.00**	**4.95**	**5.37**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

4.3.12 Harvest index

Harvest index in HS 19 ranged from 16.07% (FS 277) to 38.82% (RGC 1055) with mean 30.64%; in BS 19 from 12.96% (FS 277) to52.38% (RGC 1003) with mean 35.50%; in HK 19 from 19.32% (FS 277) to34.63% (HG 6) with mean 30.95%; in BK 19 from 14.13% (FS 277) to 38.73% (HG 2-20) with mean 31.84%; in HS 20 from 16.31% (FS 277) to 33.46% (RGC 1033) with mean 27.17%; in BS 20 from 14.19% (FS 277) to 31.40 % (RGC 1066) with mean 26.73%; in HK 20 from 14.75% (FS 277) to 35.50% (HG 75) with mean 28.87% and in BK 20 from 12.74 (FS 277) to 39.02% (RGC 1066) with mean 30.97% (Table 4.3.12).

On the basis of overall performance, 15, 20, 19, 18, 1, 1, 6 and 18 (Number in each environment) genotypes showed highest harvest index than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. RGC 1055 (38.82%) exhibited highest harvest index in HS 19 followed by RGC 1017 (36.07%) and HG 563 (36.05%); RGC 1003 (52.38%) in BS 19 followed by RGC 1055 (50.78%) and HG 6 (46.67%); HG 6 (34.63%) in HK 19 followed HG 100 (34.25%) and RGC 1066 (34.17%); HG 2-20 (38.73%) in BK 19 followed by HG 563 (36.82%) and RGC 1038 (36.53%); RGC 1033 (33.46%) in HS 20 followed by HG 6 (30.15%) and RGC 1055 (33.10%); RGC 1066 (31.40%) in BS 20 followed RGC1055 (29.67%) and HG 870 (29.37%); RGC 1055 and HG 75 (35.50%) in HK 20 followed by RGC 1055 (35.14%) and GG 1 (34.41%); RGC 1066 (39.02%) in BK 20 followed HG 6 (35.98%) and HG 3-52 (35.79%).

On the basis of overall mean across the environments in RGC 1055 (36.00%) highest harvest index were observed followed by HG 6 (35.11%) and RGC 1066 (34.45%). Among the environments HS 19, BS 19, HK 19, BK 19 and BK 20 showed highest harvest index than grand mean.

4.3.13 Clusters per plant

Number of clusters per plant in HS 19 ranged from 10.27 (FS 277) to 68.37 (HG 563) with mean 43.48 ; in BS 19 from 7.47 (FS 277) to 52.60 (HG 870) with mean 35.39; in HK 19 from 11.83 (FS 277) to 60.40 (HG 2-20) with mean 40.07; in BK 19 from 16.63 (FS 277) to 42.23 (HG 2-20) with mean 30.62; in HS 20 from 15.33 (FS 277) to 57.27 (HG 2-20) with mean 37.65; in BS 20 from 8.70 (FS 277) to 48.07 (HG 2-20) with mean 33.29; in HK 20 from 18.27 (M 83) to 51.60 (HG 2-20) with mean 35.65 and in BK 20 from 13.70 (PNB) to 45.23 (HG 870) with mean 31.28 (Table 4.3.13).

On the basis of overall performance, 18, 12, 18, 7, 13, 12, 13 and 8 (Number in each environment) genotypes showed highest number of clusters per plant than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. HG 563 (68.37) exhibited highest number of clusters per plant in HS 19 followed by RGC 1017 (67.20) and

Table 4.3.12:Mean performance of cluster bean genotypes under differentenvironments for harvest index

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	30.32	40.18	31.82	38.73	29.17	28.24	30.13	31.97	32.57
HG 884	30.75	37.31	30.74	34.60	29.38	27.24	29.89	35.68	31.95
HG 870	30.38	35.59	30.10	34.39	27.51	29.37	29.54	33.46	31.29
HG 563	36.05	37.04	28.75	36.82	28.31	28.28	31.13	34.89	32.66
HG 365	33.95	33.99	33.87	36.41	28.98	29.04	29.45	34.87	32.57
HG 3-52	33.14	41.78	34.09	33.14	27.61	28.26	32.24	35.79	33.26
HG 6	35.84	46.67	34.63	34.03	30.15	29.32	34.27	35.98	35.11
HVG 2-30	25.25	26.83	31.37	27.97	24.31	27.22	27.32	26.11	27.05
HG 100	30.79	32.35	34.25	35.81	29.47	26.67	30.11	35.48	31.87
FS 277	16.07	12.96	19.32	14.13	16.31	14.19	14.75	12.74	15.06
X-10	34.81	37.68	31.03	34.30	29.28	27.03	29.10	28.66	31.49
PNB	32.31	28.85	28.57	20.10	19.80	19.85	29.79	20.33	24.95
GG-1	28.64	24.73	30.46	30.20	28.57	25.63	34.41	30.11	29.09
GG-2	25.86	33.88	31.23	31.13	27.86	26.00	31.51	32.02	29.93
RGC 1017	36.07	36.46	31.27	35.00	27.42	29.07	30.04	34.63	32.50
RGC 1038	32.93	35.56	33.33	36.53	28.93	28.68	29.39	33.16	32.31
RGC 936	23.42	21.47	25.67	27.45	22.34	26.70	19.79	21.89	23.59
RGC 1055	38.82	50.78	32.92	36.18	30.10	29.67	35.14	34.39	36.00
RGC 1002	33.11	43.80	31.80	32.03	29.76	28.99	29.95	31.41	32.61
RGC 1003	32.39	52.38	33.99	34.68	28.17	27.83	26.54	32.35	33.54
RGC 1066	32.96	39.64	34.17	34.33	29.97	31.40	34.14	39.02	34.45
RGS 3	28.37	33.71	32.13	32.26	26.73	27.78	24.28	35.75	30.12
M-83	25.39	31.33	23.45	20.00	18.48	17.06	21.23	17.09	21.75
RGC 1033	27.78	37.02	33.88	33.91	33.46	28.06	28.63	35.42	32.27
HG 75	28.13	41.27	33.55	30.22	29.25	26.96	35.50	31.14	32.00
Over all Mean	**30.64**	**35.50**	**30.95**	**31.84**	**27.17**	**26.73**	**28.87**	**30.97**	**30.33**
C.D.	**5.00**	**5.00**	**4.00**	**5.00**	**3.00**	**3.00**	**3.00**	**3.00**	
C.V. at 5%	**9.53**	**8.17**	**7.38**	**8.73**	**7.28**	**7.29**	**7.40**	**6.72**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

Table 4.3.13: Mean performance of cluster bean genotypes under different environments for cluster per plant

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	65.93	52.13	60.40	42.23	57.27	48.07	51.60	44.63	52.78
HG 884	58.73	49.67	53.90	40.07	49.20	42.20	47.73	39.63	47.64
HG 870	54.33	52.60	50.00	38.40	46.53	44.33	43.47	45.23	46.86
HG 563	68.37	48.47	59.72	39.43	53.33	45.40	49.23	40.57	50.57
HG 365	59.93	45.67	51.80	38.93	45.47	44.13	43.20	39.33	46.06
HG 3-52	49.20	35.33	43.57	33.20	38.33	36.53	40.23	30.67	38.38
HG 6	42.33	35.93	38.20	28.53	35.67	31.87	35.07	30.97	34.82
HVG 2-30	17.73	20.07	18.83	18.80	25.40	25.07	19.33	19.93	20.65
HG 100	48.73	26.93	45.37	31.30	42.13	37.80	41.20	28.83	37.79
FS 277	10.27	7.47	11.83	16.63	15.33	8.70	21.83	15.23	13.41
X-10	62.27	50.73	52.30	39.73	45.20	44.87	43.70	44.17	47.87
PNB	10.60	8.00	15.43	26.53	21.40	8.73	18.57	13.70	15.37
GG-1	15.53	31.27	21.90	25.27	33.47	31.73	31.23	27.30	27.21
GG-2	43.87	41.93	41.03	26.33	35.53	26.67	33.27	30.37	34.88
RGC 1017	67.20	42.53	54.97	33.67	43.00	37.93	36.73	35.57	43.95
RGC 1038	49.00	38.00	46.53	36.83	44.80	43.20	40.33	32.23	41.37
RGC 936	42.07	28.20	32.77	19.20	23.27	25.33	21.47	22.77	26.89
RGC 1055	51.47	43.67	45.97	33.10	42.33	35.47	38.73	31.30	40.26
RGC 1002	46.47	27.93	40.23	29.47	33.60	34.80	32.43	24.97	33.74
RGC 1003	48.37	34.73	41.45	26.40	35.40	32.20	32.07	29.87	35.06
RGC 1066	29.00	30.27	28.97	25.03	40.33	26.00	43.57	37.70	32.61
RGS 3	45.60	33.80	39.40	34.07	33.20	40.73	32.30	32.23	36.42
M-83	23.17	25.27	19.58	19.23	22.20	19.33	18.27	20.23	20.91
RGC 1033	43.73	45.93	51.67	35.40	44.87	40.60	40.13	40.07	42.80
HG 75	33.13	28.33	36.00	27.80	33.87	20.53	35.63	24.47	29.97
Over all Mean	**43.48**	**35.39**	**40.07**	**30.62**	**37.65**	**33.29**	**35.65**	**31.28**	**35.93**
C.D.	**4.61**	**3.22**	**3.09**	**2.33**	**3.44**	**3.38**	**2.98**	**2.35**	
C.V. at 5%	**6.44**	**5.52**	**4.69**	**4.63**	**5.54**	**6.17**	**5.07**	**4.57**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

HG 2-20 (65.93); HG 870 (52.60) in BS 19 followed by HG 2-20 (52.13) and X 10 (50.73); HG 2-20 (60.40) in HK 19 followed HG 563 (59.72) and RGC 1017 (54.97); HG 2-20 (42.33) in BK 19 followed by HG 884 (40.07) and HG 563 (39.43); HG 2-20 (57.27) in HS 20 followed by HG 563 (53.33) and HG 884 (49.20); HG 2-20 (48.07) in BS 20 followed HG 563 (45.40) and X 10 (44.87); HG 2-20 (51.60) in HK 20 followed by HG 563 (49.23) and HG 884 (47.73); HG 870 (45.23) in BK 20 followed HG 2-20 (44.63) and X 10 (44.17).

On the basis of overall mean across the environments in HG 2-20 (52.78) highest number of clusters per plant was observed followed by HG 563 (50.57) and X 10 (47.87). Among the environments HS 19, HK 19 and HS 20showed high number of clusters per plant than grand mean.

4.3.14 Seed yield per plot

Seed yield per plot in HS 19 ranged from 0.42 kg (PNB) to 1.37 kg (HG 563) with mean 0.95 kg ; in BS 19 from 0.28 kg (FS 277) to 0.90 kg (HG 2-20) with mean 0.59 kg; in HK 19 from 0.38 kg (PNB) to 1.05 kg (HG 2-20) with mean 0.74 kg; in BK 19 from 0.28 kg (RGC 936) to 0.82 kg (HG 884) with mean 0.54 kg; in HS 20 from 0.51 (M 83) to 1.12 kg (HG 2-20) with mean 0.82 kg; in BS 20 from 0.26 (PNB) to 0.85 (HG 2-20) with mean 0.62 kg; in HK 20 from 0.38 kg (RGC 936 and M 83) to 0.94 kg (HG 563) with mean 0.69 kg and in BK 20 from 0.27 kg (M 83) to 0.90 kg (X 10) with mean 0.65 kg (Table 4.3.14).

On the basis of overall performance, 18, 5, 16, 4, 19, 9, 14 and 11 (Number in each environment) genotypes highest seed yield per plot than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. HG 563 (1.37 kg) exhibited highest seed yield per plot in HS 19 followed by HG 2-20 and X 10 (1.34 kg); HG 2-20 (0.90 kg) in BS 19 followed by HG 870 (0.84 kg) and HG 563 (0.80 kg); HG 2-20 (1.05 kg) in HK 19 followed X 10 (0.99 kg) and HG 884 (0.95 kg); HG 884 (0.82 kg) in BK 19 followed by HG 2-20 (0.79 kg) and HG 563 (0.74 kg); HG 2-20 (1.12 kg) in HS 20 followed by HG 563 (1.07 kg) and X 10 (1.01 kg); HG 2.20 (0.85 kg) in BS 20 followed HG 870 (0.84 kg) and HG 563 (0.82 kg); HG 563 (0.94 kg) in HK 20 followed by HG 2-20 (0.91 kg) and X 10 (0.87 kg); X 10 (0.90 kg) in BK 20 followed HG 870 (0.87 kg) and HG 2-20 (0.86 kg).

On the basis of overall mean across the environments in HG 2-20 (0.98 kg) highest seed yield per plot was observed followed by HG 563 (0.93 kg) and X 10 (0.93 kg). Among the environments HS 19, HK 19 and HS 20 showed highest seed yield per plot than grand mean.

4.3.15 Gum content

Gum content in HS 19 ranged from 19.55% (PNB) to 32.60% (HG 884 and HG 3-52) with mean 28.74%; in BS 19 from 22.10% (PNB) to 33.60% (HG 3-52) with mean 28.38%; in HK 19 from 19.55% (PNB) to 31.95% (RGC 1066) with mean 27.01%; in BK 19 from

Table 4.3.14: Mean performance of cluster bean genotypes under different environments for seed yield per plot

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	1.34	0.90	1.05	0.79	1.12	0.85	0.91	0.86	0.98
HG 884	1.23	0.75	0.95	0.82	0.94	0.73	0.84	0.81	0.88
HG 870	1.20	0.84	0.93	0.65	0.96	0.84	0.83	0.87	0.89
HG 563	1.37	0.80	0.90	0.74	1.07	0.82	0.94	0.82	0.93
HG 365	1.28	0.69	0.84	0.67	0.91	0.79	0.81	0.83	0.85
HG 3-52	1.15	0.61	0.75	0.58	0.82	0.65	0.79	0.68	0.75
HG 6	0.62	0.56	0.71	0.49	0.79	0.56	0.73	0.59	0.63
HVG 2-30	0.51	0.33	0.48	0.33	0.62	0.49	0.50	0.47	0.47
HG 100	0.97	0.55	0.75	0.53	0.84	0.68	0.81	0.77	0.74
FS 277	0.45	0.28	0.40	0.39	0.53	0.44	0.45	0.40	0.42
X-10	1.34	0.78	0.99	0.71	1.01	0.80	0.87	0.90	0.93
PNB	0.42	0.30	0.38	0.39	0.59	0.26	0.42	0.37	0.39
GG-1	0.59	0.45	0.60	0.45	0.68	0.51	0.64	0.56	0.56
GG-2	0.90	0.62	0.79	0.47	0.78	0.52	0.69	0.57	0.67
RGC 1017	1.32	0.66	0.81	0.56	0.85	0.66	0.67	0.71	0.78
RGC 1038	1.09	0.64	0.77	0.61	0.92	0.74	0.77	0.62	0.77
RGC 936	0.78	0.38	0.67	0.28	0.65	0.55	0.38	0.44	0.52
RGC 1055	1.18	0.65	0.80	0.55	0.87	0.62	0.78	0.65	0.76
RGC 1002	1.00	0.53	0.69	0.41	0.75	0.60	0.62	0.49	0.64
RGC 1003	1.03	0.55	0.69	0.43	0.71	0.59	0.56	0.55	0.64
RGC 1066	1.17	0.67	0.82	0.69	0.95	0.76	0.85	0.80	0.84
RGS 3	0.80	0.60	0.71	0.50	0.89	0.70	0.59	0.74	0.69
M-83	0.49	0.52	0.68	0.34	0.51	0.29	0.38	0.27	0.44
RGC 1033	0.90	0.67	0.83	0.59	0.89	0.71	0.75	0.85	0.77
HG 75	0.54	0.52	0.52	0.42	0.74	0.31	0.71	0.52	0.54
Over all Mean	**0.95**	**0.59**	**0.74**	**0.54**	**0.82**	**0.62**	**0.69**	**0.65**	**0.70**
C.D.	**0.20**	**0.09**	**0.08**	**0.05**	**0.10**	**0.06**	**0.06**	**0.06**	
C.V. at 5%	**12.57**	**9.64**	**6.65**	**5.45**	**7.26**	**5.98**	**5.17**	**5.26**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

Table 4.3.15: Mean performance of cluster bean genotypes under different environments for gum content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	31.90	31.55	30.25	29.30	31.60	29.95	31.25	32.60	31.05
HG 884	32.60	30.30	29.95	28.35	31.25	29.30	29.95	31.95	30.46
HG 870	32.25	31.25	29.65	29.60	30.60	30.90	32.60	31.25	31.01
HG 563	30.95	29.95	28.65	28.35	29.95	28.95	29.60	30.90	29.66
HG 365	30.60	29.65	29.00	29.00	29.00	30.30	30.30	29.60	29.68
HG 3-52	32.60	33.60	31.25	30.25	32.90	31.60	31.95	33.30	32.18
HG 6	29.95	27.75	27.43	27.13	27.13	26.83	28.35	29.00	27.95
HVG 2-30	20.95	24.98	19.85	25.00	21.80	21.80	23.80	21.80	22.50
HG 100	29.30	28.65	28.35	26.83	27.45	27.12	28.05	26.80	27.82
FS 277	24.10	25.88	21.50	21.80	23.50	22.95	24.43	21.20	23.17
X-10	31.60	30.95	29.30	30.60	30.30	29.73	32.25	30.30	30.63
PNB	19.55	22.10	19.55	20.65	21.20	22.35	20.40	22.05	20.98
GG-1	29.65	28.35	25.63	27.45	28.05	27.43	27.43	27.45	27.68
GG-2	30.30	29.30	27.12	28.05	28.65	28.35	26.83	26.22	28.10
RGC 1017	27.13	28.65	26.83	26.18	26.50	26.52	29.00	27.13	27.24
RGC 1038	31.25	29.60	30.60	28.35	29.60	28.65	30.90	31.60	30.07
RGC 936	26.83	22.65	24.43	21.20	22.95	24.10	25.93	25.63	24.22
RGC 1055	28.65	30.60	28.65	27.75	28.35	28.05	29.30	32.25	29.20
RGC 1002	27.43	27.43	25.23	24.68	25.63	25.88	26.18	25.88	26.04
RGC 1003	28.05	26.50	24.68	25.88	24.98	24.43	25.23	24.43	25.52
RGC 1066	32.25	31.90	31.95	29.95	31.95	29.60	31.60	29.95	31.14
RGS 3	28.35	28.05	26.52	25.63	26.83	26.18	26.80	24.98	26.67
M-83	22.95	23.80	22.35	24.43	22.05	19.85	22.10	21.80	22.42
RGC 1033	31.60	28.95	28.65	28.70	29.30	27.75	28.65	27.75	28.92
HG 75	27.75	27.13	27.75	26.52	26.22	25.63	27.13	26.50	26.83
Over all Mean	**28.74**	**28.38**	**27.01**	**26.87**	**27.51**	**26.97**	**28.00**	**27.69**	**27.65**
C.D.	**2.28**	**2.15**	**2.07**	**1.87**	**2.03**	**2.01**	**2.15**	**1.93**	
C.V. at 5%	**4.81**	**4.60**	**4.66**	**4.23**	**4.48**	**4.52**	**4.67**	**4.24**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

20.65% (PNB) to 30.60% (X 10) with mean 26.87%; in HS 20 from 21.20% (PNB) to 32.90% (HG 3-52) with mean 27.51%; in BS 20 from 19.85% (M 83) to 31.60% (HG 3-52) with mean 26.97%; in HK 20 from 20.40% (PNB) to HG 870 (32.60%) with mean 28.00% and in BK 20 from 21.20% (FS 277) to 32.60% (HG 2-20) with mean 27.69% (Table 4.3.15).

On the basis of overall performance, 18, 17, 13, 12, 13, 12, 14 and12 (Number in each environment) genotypes showed highest gum content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. HG 3-52 and HG 884 (32.60%) exhibited highest gum content in HS 19 followed by HG 870 and RGC 1066 (32.25%); HG 3-52 (33.60%) in BS 19 followed by RGC 1066 (31.90%) and HG 2-20 (31.55%); RGC 1066 (31.95%) in HK 19 followed HG 3-52 (31.25%) and RGC 1038 (30.60%); X 10 (30.60%) in BK 19 followed by HG 3-52 (30.25%) and RGC 1066 (29.95%); HG 3-52 (32.90%) in HS 20 followed by RGC 1066 (31.95%) and HG 2-20 (31.60%); HG 3-52 (31.60%) in BS 20 followed HG 870 (30.90%) and HG 365 (30.30%); HG 870 (32.60%) in HK 20 followed by X 10 (32.25%) and HG 3-52 (31.95%); HG 3-52 (33.30%) in BK 20 followed HG 2-20 (32.60%) and RGC 1055 (32.25%).

On the basis of overall mean across the environments in HG 3-52 (32.18%) highest gum content was observed followed by RGC 1066 (31.14%) and HG 2-20 (31.05%). Among the environments HS 19, BS 19, HK 20 and BK 20 showed high gum content than grand mean.

4.3.16 Protein content

Protein content in HS 19 ranged from 15.96% (RGS 3) to 24.19% (HG 563) with mean 21.39% ; in BS 19 from 17.10% (GG 1) to 25.02% (RGC 1038) with mean 21.71%; in HK 19 from 18.82% (RGC 1033) to 24.50% (RGC 1038) with mean 21.55%; in BK 19 from 17.22% (RGC 1033) to 24.30% (HG 6) with mean 21.30%; in HS 20 from 17.96% (RGC 1017) to 23.74% (HG 365) with mean 21.43%; in BS 20 from 19.50% (HG 884) to 24.18% (RGC 1055) with mean 22.07%; in HK 20 from 16.15% (GG 1) to 24.06 (RGC 1017) with mean 20.36% and in BK 20 from 17.67% (RGC 936) to 24.96% (HG 365) with mean 22.50% (Table 4.3.16).

On the basis of overall performance, 12, 13, 11, 9, 13, 18, 10 and17 (Number in each environment) genotypes showed highest protein content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 20 and BK 20 respectively. HG 563 (24.19%) exhibited highest protein content in HS 19 followed by RGC 1038 (23.98%) and RGC 1055 (23.67%); RGC 1038 (25.02%) in BS 19 followed by RGC 1055 (24.50%) and HG 365 (24.19%); RGC 1038 (24.50%) in HK 19 followed RGC 1055 (24.08%) and FS 277 (23.46%); HG 6 (24.30%) in BK 19 followed by RGC 1055 (24.15%) and M 83 (23.11%); HG 365 (23.74%) in HS 20 followed by RGC 1055 (23.73%) and RGS 3 (23.41%); RGC 1055 (24.18%) in BS 20 followed HG 563

Table 4.3.16: Mean performance of cluster bean genotypes under differentenvironments for protein content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	21.27	23.04	22.16	20.24	21.03	22.00	20.11	22.67	21.57
HG 884	21.17	21.06	21.11	20.14	20.92	19.50	18.44	22.15	20.56
HG 870	18.57	21.90	20.23	21.18	21.37	22.32	19.69	22.04	20.91
HG 563	24.19	17.94	21.06	20.76	20.48	23.82	19.48	21.21	21.12
HG 365	20.02	24.19	22.10	20.86	23.74	22.07	17.71	24.96	21.96
HG 3-52	20.54	20.65	20.59	21.39	21.25	21.74	16.61	23.08	20.73
HG 6	19.50	23.46	21.48	24.30	22.71	23.18	23.34	21.94	22.49
HVG 2-30	22.63	20.86	21.74	22.17	22.17	23.09	22.40	24.02	22.39
HG 100	22.21	19.61	20.91	19.98	20.16	20.89	20.73	20.69	20.65
FS 277	23.15	23.77	23.46	21.70	22.24	22.82	22.92	24.65	23.09
X-10	21.06	20.33	20.70	21.39	21.50	21.20	18.02	21.32	20.69
PNB	23.35	23.35	23.35	21.96	21.99	22.08	21.56	24.33	22.75
GG-1	21.38	17.10	19.24	20.34	19.82	21.01	16.15	19.54	19.32
GG-2	19.61	18.98	19.29	19.67	19.88	21.65	16.27	24.54	19.99
RGC 1017	22.00	19.50	20.75	22.90	17.96	19.69	24.06	18.82	20.71
RGC 1038	23.98	25.02	24.50	20.81	20.42	21.87	18.75	22.25	22.20
RGC 936	20.85	22.84	21.84	21.54	22.02	22.83	21.36	17.67	21.37
RGC 1055	23.67	24.50	24.08	24.15	23.73	24.18	23.85	23.40	23.95
RGC 1002	21.90	21.06	21.48	21.96	21.88	22.84	21.04	24.75	22.11
RGC 1003	23.04	22.52	22.78	21.96	21.68	23.16	22.71	24.23	22.76
RGC 1066	21.06	21.48	21.27	21.07	21.58	20.22	20.42	21.52	21.08
RGS 3	15.96	23.36	19.66	21.49	23.41	23.41	16.46	24.23	21.00
M-83	21.79	23.87	22.83	23.11	22.68	22.64	22.08	24.13	22.89
RGC 1033	18.98	18.67	18.82	17.22	18.49	20.43	23.02	24.44	20.01
HG 75	22.84	23.56	23.20	20.19	22.65	23.06	21.77	19.96	22.15
Over all Mean	**21.39**	**21.71**	**21.55**	**21.30**	**21.43**	**22.07**	**20.36**	**22.50**	**21.54**
C.D.	**1.59**	**1.47**	**1.17**	**1.07**	**0.89**	**0.59**	**1.46**	**1.34**	
C.V. at 5%	**4.50**	**4.11**	**3.29**	**3.04**	**2.51**	**1.62**	**4.36**	**3.61**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

(23.82%) and RGS 3 (23.41%); RGC 1017 24.06%) in HK 20 followed byRGC 1055 (23.85%) and HG 6 (23.34%); HG 365 (24.96%) in BK 20 followed RGC 1002 (24.75%) and FS 277 (24.65%).

On the basis of overall mean across the environments in RGC 1055 (23.95%) highest protein content was observed followed by FS 277 (23.09%) and M 83 (22.89%).Among the environments BS 19, HK 19, BS 20 and BK 20 showed high protein content than grand mean.

4.2.17 Total soluble sugar content (TSS)

Total soluble sugar content (TSS) in HS 19 ranged from 100.98 mg/g dry weight (GG 2) to 125.17 mg/g dry weight (HG 365) with overall mean 112.08 mg/g dry weight; in BS 19 from 101.60 mg/g dry weight (HG 3-52) to 122.49 mg/g dry weight (M 83) with overall mean 111.23 mg/g dry weight; in HK 19 from 98.73 mg/g dry weight (GG 2) to 122.98 mg/g dry weight (PNB) with overall mean 108.74 mg/g dry weight; in BK 19 from 100.05mg/g dry weight (HG 3-52) to 120.66 mg/g dry weight (HVG 2-30) with overall mean 107.53 mg/g dry weight; in HS 20 from 98.25 mg/g dry weight (HG 365) to 123.99 mg/g dry weight (FS 277) with overall mean 108.36 mg/g dry weight; in BS 20 from 100.62 mg/g dry weight (RGC 1003) to 119.16 mg/g dry weight (RGC 1002) with overall mean 109.46 mg/g dry weight; in HK 20 from 99.50mg/g dry weight (HG 563) to 122.09 mg/g dry weight (HVG 2-30) with overall mean 111.31 mg/g dry weight; in BK 20 from 93.85 mg/g dry weight (HG 870) to 126.70 mg/g dry weight (RGC 1003) with overall mean 107.12 mg/g dry weight (Table 4.2.17).

On the basis of overall performance, 14, 11, 16, 18, 16, 15, 10 and15 (Number in each environment) genotypes exhibited least TSS content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. GG 2 (100.98 mg/g dry weight) showed least TSS content in HS 19 followed by RGC 1033 (102.48 mg/g dry weight)and HG 563 (102.51 mg/g dry weight); HG 3-52 (101.60 mg/g dry weight) in BS 19 followed by HG 563 (102.02 mg/g dry weight) and RGC 936 (102.64 mg/g dry weight); GG 2 (98.73 mg/g dry weight) in HK 19 followed RGC 1033 (99.00 mg/g dry weight) and RGC 1066 (99.62 mg/g dry weight); HG 3-52 (100.05 mg/g dry weight) in BK 19 followed by HG 75 (100.42 mg/g dry weight) and HG 563 (100.79 mg/g dry weight); HG 365 (98.25 mg/g dry weight) in HS 20 followed by HG 884 (98.66 mg/g dry weight) and RGC 1038 (98.92 mg/g dry weight); RGC 1003 (100.62 mg/g dry weight) in BS 20 followed HG 563 (102.19 mg/g dry weight) and HG 365 (103.58 mg/g dry weight); HG 563 (99.50 mg/g dry weight) in HK 20 followed by RGC 1033 (99.89 mg/g dry weight) and GG 2 (101.74 mg/g dry weight); HG 870 (93.85 mg/g dry weight) in BK 20 followed X 10 (95.37 mg/g dry weight) and HG 75 (95.59 mg/g dry weight).

On the basis of overall mean across the environments HG 563 (102.64 mg/g dry weight) had shown least TSS content followed by RGC 1033 (103.26 mg/g dry weight) and HG 75

Table 4.3.17: Mean performance of cluster bean genotypes under different environments for TSS content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	106.61	108.34	105.34	103.13	102.68	109.74	116.17	100.53	106.57
HG 884	103.29	116.7	101.27	105.18	98.66	106.38	103.92	100.64	104.51
HG 870	107.01	106.7	106.62	101.19	104.68	109.25	109.83	93.85	104.89
HG 563	102.51	102.02	104.00	100.79	108.44	102.19	99.50	101.70	102.64
HG 365	125.17	108.74	105.38	103.75	98.25	103.58	102.29	99.25	105.80
HG 3-52	108.18	101.6	105.63	100.05	123.86	105.78	109.6	110.63	108.17
HG 6	124.78	114.45	117.45	109.21	101.61	116.46	121.53	125.46	116.37
HVG 2-30	107.19	117.75	121.45	120.66	113.00	105.97	122.09	112.33	115.06
HG 100	108.54	114.20	107.42	104.10	101.87	117.25	107.35	98.00	107.34
FS 277	119.93	122.32	115.28	117.20	123.99	118.45	121.28	118.58	119.63
X-10	106.92	113.56	102.47	112.34	111.45	113.18	102.41	95.37	107.21
PNB	124.93	117.68	122.98	114.34	113.18	117.00	120.23	112.39	117.84
GG-1	120.77	116.85	116.48	115.44	121.85	107.79	113.14	108.50	115.10
GG-2	100.98	113.8	98.73	109.00	103.19	105.57	101.74	123.86	107.11
RGC 1017	107.94	107.15	101.12	118.17	111.58	106.50	109.55	106.20	108.53
RGC 1038	116.02	105.79	106.96	102.01	98.92	109.71	115.17	109.52	108.01
RGC 936	115.78	102.64	113.88	105.82	108.31	118.34	103.01	111.74	109.94
RGC 1055	116.4	107.11	105.28	105.25	102.95	103.8	116.83	105.57	107.90
RGC 1002	107.69	109.61	113.79	105.35	108.66	119.16	121.30	102.55	111.01
RGC 1003	113.52	120.95	109.39	116.92	102.28	100.62	121.06	126.70	113.93
RGC 1066	106.89	111.11	99.62	102.49	120.37	106.63	106.85	100.59	106.82
RGS 3	122.90	103.59	112.00	105.05	108.41	106.32	116.34	101.46	109.51
M-83	122.58	122.49	119.86	101.68	111.10	106.16	118.92	121.40	115.52
RGC 1033	102.48	111.06	99.00	108.65	104.25	105.92	99.89	95.61	103.36
HG 75	103.10	104.59	107.03	100.42	105.39	114.83	102.69	95.59	104.21
Over all Mean	**112.08**	**111.23**	**108.74**	**107.53**	**108.36**	**109.46**	**111.31**	**107.12**	**109.48**
C.D.	**6.03**	**5.29**	**5.84**	**4.49**	**8.03**	**3.89**	**6.86**	**9.44**	
C.V. at 5%	**3.27**	**2.89**	**3.26**	**2.54**	**4.5**	**2.16**	**3.74**	**5.35**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

(104.21 mg/g dry weight).Among the environments HK 19, BK 19, HS 20 and BK 20 showed least TSS content than grand mean.

4.2.18 Reducing sugar content

Reducing sugar content in HS 19 ranged from 13.32 mg/g dry weight (HG 75) to 18.72 mg/g dry weight (HG 870) with overall mean 16.00 mg/g dry weight; in BS 19 from 13.71 mg/g dry weight (HG 75) to 18.03 mg/g dry weight (HVG 2-30 and FS 277) with overall mean 15.57 mg/g dry weight; in HK 19 from 12.95 mg/g dry weight (HG 884) to 19.33 mg/g dry weight (HVG 2-30) with overall mean 16.14 mg/g dry weight; in BK 19 from 13.10 mg/g dry weight (HG 75) to 18.39 mg/g dry weight (RGC 936) with overall mean 15.91 mg/g dry weight; in HS 20 from 12.29 mg/g dry weight (HG 870) to 18.82 mg/g dry weight (RGS 3) with overall mean 14.79 mg/g dry weight; in BS 20 from 13.76 mg/g dry weight (RGC 1003) to 19.59 mg/g dry weight (FS 277) with overall mean 17.17mg/g dry weight; in HK 20 from 11.43 mg/g dry weight (HG 563) to 22.36 mg/g dry weight (HG 6) with overall mean 17.71 mg/g dry weight; in BK 20 from 12.00 mg/g dry weight (HG 870) to 17.42 mg/g dry weight (HG 6) with overall mean 15.29 mg/g dry weight (Table 4.2.18).

On the basis of overall performance, 10, 17, 13, 12, 22, 5, 9 and 19(Number in each environment) genotypes exhibited least reducing sugar content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. HG 75 (13.32 mg/g dry weight) showed least reducing sugar content in HS 19 followed by GG 1 (13.60 mg/g dry weight) and M 83 (14.10 mg/g dry weight); HG 75 (13.71 mg/g dry weight) in BS 19 followed by RGC 1003 (13.82 mg/g dry weight) and RGC 936 (13.86 mg/g dry weight); HG 884 (12.95 mg/g dry weight) in HK 19 followed by X 10 (12.98 mg/g dry weight) and RGS 3 (13.47 mg/g dry weight); HG 75 (13.10 mg/g dry weight) in BK 19 followed by RGC 1033 (13.56 mg/g dry weight) and X 10 (13.89 mg/g dry weight); HG 870 (12.29 mg/g dry weight) in HS 20 followed by HG 563 (13.39 mg/g dry weight) and M 83 (13.53 mg/g dry weight); RGC 1003 (13.76 mg/g dry weight) in BS 20 followed RGC 1055 (14.14 mg/g dry weight) and HG 563 (14.67 mg/g dry weight); HG 563 (11.43 mg/g dry weight) in HK 20 followed by RGC 1033 (11.90 mg/g dry weight) and GG 2 (12.53 mg/g dry weight); HG 870 (12.00 mg/g dry weight) in BK 20 followed HG 75 (12.60 mg/g dry weight) and X 10 (14.01 mg/g dry weight).

On the basis of overall mean across the environments HG 563 (14.20 mg/g dry weight) had shown least reducing sugar content followed by HG 75 (14.38 mg/g dry weight) and HG 365 (14.69 mg/g dry weight). Among the environments HS 19, BS 19, BK 19, HS 20 and BK 20 showed least reducing sugar content than grand mean.

4.2.19 Non Reducing sugar content

Non Reducing sugar content in HS 19 ranged from 84.10 mg/g dry weight (GG 2) to 110.27 mg/g dry weight (HG 365) with overall mean 96.08mg/g dry weight; in BS 19 from

Table 4.3.18: Mean performance of cluster bean genotypes under differentenvironments for reducing sugar content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	16.16	14.58	15.72	14.67	14.14	18.03	19.50	14.81	15.95
HG 884	14.31	16.25	12.95	16.44	14.10	17.23	15.46	14.90	15.21
HG 870	18.72	14.60	16.92	16.83	12.29	16.88	19.08	12.00	15.92
HG 563	16.17	14.15	13.89	15.05	13.39	14.67	11.43	14.87	14.20
HG 365	14.90	15.32	14.24	16.96	13.81	15.11	12.69	14.52	14.69
HG 3-52	16.67	13.95	16.56	16.02	14.74	16.62	16.86	15.52	15.87
HG 6	17.07	16.11	18.16	15.69	15.45	19.57	22.36	17.42	17.73
HVG 2-30	17.42	18.03	19.33	16.64	13.58	16.85	21.97	15.68	17.44
HG 100	16.41	16.48	15.91	14.63	16.03	17.77	15.95	14.46	15.96
FS 277	18.15	18.03	18.14	18.02	18.37	19.59	21.79	17.07	18.65
X-10	14.89	16.02	12.98	13.89	15.96	18.22	14.29	14.01	15.03
PNB	18.28	18.02	17.31	17.32	16.39	18.60	21.04	16.47	17.93
GG-1	13.60	16.31	17.35	15.49	15.57	17.58	18.95	15.36	16.28
GG-2	16.88	16.06	15.73	13.91	14.61	16.66	12.53	17.09	15.43
RGC 1017	16.14	15.15	14.71	16.65	15.05	17.58	17.40	15.48	16.02
RGC 1038	15.99	14.34	15.76	16.72	14.14	18.06	20.02	15.90	16.37
RGC 936	16.68	13.86	17.34	18.39	15.02	18.40	15.47	16.02	16.40
RGC 1055	14.76	14.53	17.77	17.04	13.61	14.14	20.02	15.46	15.92
RGC 1002	15.52	15.63	17.70	14.17	14.41	18.61	21.04	15.25	16.54
RGC 1003	16.07	13.82	15.60	17.38	14.73	13.76	20.80	17.37	16.19
RGC 1066	17.12	16.07	15.10	17.00	13.93	17.83	16.69	14.46	16.03
RGS 3	14.44	15.58	13.47	14.35	18.82	16.19	20.74	15.10	16.09
M-83	14.10	17.04	18.04	17.73	13.53	16.76	20.97	16.21	16.80
RGC 1033	16.25	15.64	16.91	13.56	14.06	16.05	11.90	14.18	14.82
HG 75	13.32	13.71	15.91	13.10	13.99	18.61	13.76	12.60	14.38
Over all Mean	**16.00**	**15.57**	**16.14**	**15.91**	**14.79**	**17.17**	**17.71**	**15.29**	**16.07**
C.D.	**1.53**	**0.84**	**1.08**	**0.82**	**0.92**	**0.72**	**1.88**	**1.66**	
C.V. at 5%	**5.80**	**3.26**	**4.05**	**3.11**	**3.76**	**2.53**	**6.43**	**6.59**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

Table 4.3.19: Mean performance of cluster bean genotypes under different environments for non-reducing sugar content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	90.45	93.76	89.63	88.46	88.54	91.71	96.67	85.71	90.62
HG 884	88.98	100.45	88.32	88.74	84.56	89.15	88.46	85.73	89.30
HG 870	88.29	92.09	89.70	84.37	92.39	92.37	90.74	81.84	88.97
HG 563	86.34	87.87	90.10	85.75	95.05	87.52	88.07	86.82	88.44
HG 365	110.27	93.42	91.14	86.80	84.44	88.46	89.59	84.73	91.11
HG 3-52	91.50	87.65	89.07	84.03	109.11	89.17	92.74	95.11	92.30
HG 6	107.71	98.34	99.29	93.52	86.16	96.89	99.17	108.04	98.64
HVG 2-30	89.77	99.71	102.12	104.02	99.42	89.12	100.11	96.65	97.62
HG 100	92.13	97.72	91.51	89.47	85.84	99.48	91.40	83.54	91.39
FS 277	101.77	104.28	97.13	99.17	105.62	98.86	99.49	101.51	100.98
X-10	92.03	97.54	89.48	98.45	95.49	94.97	88.12	81.36	92.18
PNB	106.65	99.66	105.67	97.02	96.79	98.40	99.19	95.93	99.91
GG-1	107.17	100.54	99.13	99.96	106.28	90.21	94.19	93.14	98.83
GG-2	84.10	97.74	83.00	95.09	88.58	88.91	89.20	106.77	91.67
RGC 1017	91.80	92.00	86.40	101.51	96.53	88.92	92.15	90.72	92.50
RGC 1038	100.04	91.45	91.20	85.30	84.78	91.65	95.15	93.62	91.65
RGC 936	99.10	88.78	96.54	87.43	93.29	99.94	87.54	95.72	93.54
RGC 1055	101.64	92.57	87.51	88.20	89.33	89.66	96.81	90.10	91.98
RGC 1002	92.17	93.98	96.08	91.18	94.25	100.55	100.26	87.29	94.47
RGC 1003	97.45	107.13	93.79	99.54	87.54	86.86	100.26	109.33	97.74
RGC 1066	89.77	95.04	84.52	85.50	106.44	88.80	90.16	86.14	90.80
RGS 3	108.46	88.01	98.53	90.70	89.58	90.13	95.60	86.36	93.42
M-83	108.48	105.45	101.82	83.95	97.57	89.40	97.96	105.19	98.73
RGC 1033	86.23	95.43	82.09	95.08	90.18	89.87	87.99	81.43	88.54
HG 75	89.78	90.88	91.11	87.32	91.40	96.22	88.93	82.99	89.83
Over all Mean	**96.08**	**95.66**	**92.60**	**91.62**	**93.57**	**92.29**	**93.60**	**91.83**	**93.41**
C.D.	**6.28**	**5.18**	**5.95**	**4.76**	**7.94**	**3.96**	**7.12**	**9.36**	
C.V. at 5%	**3.97**	**3.29**	**3.90**	**3.15**	**5.15**	**2.61**	**4.62**	**6.19**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

87.65 mg/g dry weight (HG 3-52) to 107.13 mg/g dry weight (RGC 1003) with overall mean 95.66 mg/g dry weight; in HK 19 from 82.09 mg/g dry weight (RGC 1033) to 105.67 mg/g dry weight (PNB) with overall mean 92.60 mg/g dry weight; in BK 19 from 83.95 (M 83) to 104.20 mg/g dry weight (HVG 2-30) with overall mean 91.62 mg/g dry weight; in HS 20 from 84.44 mg/g dry weight (HG 365) to 109.11 mg/g dry weight (HG 3-52) with overall mean 93.57mg/g dry weight; in BS 20 from 86.86 mg/g dry weight (RGC 1003) to 100.55 mg/g dry weight (RGC 1002) with overall mean 92.29 mg/g dry weight; in HK 20 from 87.54 mg/g dry weight (RGC 936) to 100.26mg/g dry weight (RGC 1002 and RGC 1003) with overall mean 93.60mg/g dry weight; in BK 20 from 81.36 (X 10) to 109.33 mg/g dry weight (RGC 1003) with overall mean 91.83 mg/g dry weight (Table 4.2.19).

On the basis of overall performance, 14, 9, 15, 15, 14, 17, 13 and15 (Number in each environment) genotypes exhibited least non reducing sugar content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. GG 2 (84.10 mg/g dry weight) showed least non reducing sugar content in HS 19 followed by RGC 1033 (86.23 mg/g dry weight) and HG 563 (86.34 mg/g dry weight); HG 3-52 (87.65 mg/g dry weight) in BS 19 followed by HG 563 (87.87 mg/g dry weight) and RGS 3 (88.01 mg/g dry weight); RGC 1003 (82.09 mg/g dry weight) in HK 19 followed GG 2 (83.00 mg/g dry weight) and RGC 1066 (84.52 mg/g dry weight); M 83 (83.95 mg/g dry weight) in BK 19 followed by HG 3-52 (84.03 mg/g dry weight) and HG 870 (84.37 mg/g dry weight); HG 365 (84.44 mg/g dry weight) in HS 20 followed by HG 884 (84.56 mg/g dry weight) and RGC 1038 (84.78 mg/g dry weight); RGC 1003 (86.86 mg/g dry weight) in BS 20 followed HG 563 (87.52 mg/g dry weight) and HG 365 (88.46 mg/g dry weight); RGC 936 (87.54 mg/g dry weight) in HK 20 followed by RGC 1033 (87.99 mg/g dry weight) and HG 563 (88.07 mg/g dry weight); X 10 (81.36 mg/g dry weight) in BK 20 followed RGC 1033 (81.43 mg/g dry weight) and HG 870 (81.84 mg/g dry weight).

On the basis of overall mean across the environments HG 563 (88.44 mg/g dry weight) had shown least non reducing sugar content followed by RGC 1033 (88.54 mg/g dry weight) and HG 870 (88.97 mg/g dry weight). Among the environments HK 19, BK 19, BS 20 and BK 20 showed least non reducing sugar content than grand mean.

4.2.20 Acid detergent fibre (ADF) content

Acid detergent fibre (ADF) content in HS 19 ranged from 9.11 % dry weight basis (HG 2-20) to 11.09% dry weight basis (RGS 3) with overall mean 10.24% dry weight basis; in BS 19 from 9.59 % dry weight basis (HVG 2-30) to 12.78% dry weight basis (HG 563) with overall mean 11.08% dry weight basis; in HK 19 from 8.37% dry weight basis(FS 277) to 11.38 % dry weight basis (HG 884) with overall mean 9.47% dry weight basis; in BK 19 from 9.68 % dry weight basis (FS 277) to 12.44% dry weight basis (HG 75) with overall mean 10.77% dry weight basis; in HS 20 from 8.29% dry weight basis(FS 277) to 12.49% dry

Table 4.3.20: Mean performance of cluster bean genotypes under differentenvironments for ADF content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	9.11	11.48	10.17	10.83	9.60	9.82	10.00	9.03	10.01
HG 884	10.27	10.10	11.38	10.68	9.34	10.21	10.44	9.26	10.21
HG 870	10.33	11.65	9.04	10.56	9.83	10.13	10.28	10.49	10.29
HG 563	10.08	12.78	10.17	11.68	11.65	10.78	10.95	9.62	10.96
HG 365	10.12	12.17	10.10	10.13	8.87	11.08	11.45	10.03	10.49
HG 3-52	9.92	12.51	9.36	10.66	9.42	10.07	10.26	10.88	10.39
HG 6	10.05	10.20	8.90	10.68	9.31	9.41	9.00	8.98	9.57
HVG 2-30	9.99	9.59	8.85	9.74	8.45	9.02	9.66	9.00	9.29
HG 100	10.32	10.08	9.53	9.90	11.31	11.02	10.40	11.41	10.50
FS 277	10.31	9.85	8.37	9.68	8.29	9.44	10.05	9.62	9.45
X-10	11.05	10.98	10.15	11.45	11.38	11.03	11.08	12.01	11.14
PNB	10.10	9.94	8.88	9.84	8.57	9.34	9.93	8.63	9.40
GG-1	10.02	10.18	9.33	10.70	8.44	10.13	10.39	11.32	10.06
GG-2	10.24	10.22	9.50	10.71	9.69	10.13	10.43	10.05	10.12
RGC 1017	10.73	12.41	9.89	10.41	10.92	9.85	10.17	11.34	10.72
RGC 1038	11.04	11.90	9.50	10.46	11.62	12.01	10.33	9.59	10.81
RGC 936	9.78	11.70	8.50	10.57	12.49	11.01	9.03	10.11	10.40
RGC 1055	9.81	11.49	9.01	9.93	9.54	9.48	9.45	8.64	9.67
RGC 1002	10.61	12.54	9.09	11.94	9.34	9.26	8.80	11.65	10.40
RGC 1003	10.12	12.22	9.90	12.40	10.48	9.60	9.83	10.09	10.58
RGC 1066	10.21	10.14	9.56	10.89	11.40	12.01	10.52	11.05	10.72
RGS 3	11.09	10.36	9.95	11.42	9.84	10.62	8.97	11.04	10.41
M-83	9.73	10.08	8.70	9.84	8.97	9.31	9.52	10.14	9.54
RGC 1033	9.90	10.65	9.49	11.78	11.47	11.00	11.53	9.53	10.67
HG 75	11.03	11.85	9.37	12.44	11.99	11.13	11.57	11.30	11.34
Over all Mean	**10.24**	**11.08**	**9.47**	**10.77**	**10.09**	**10.28**	**10.16**	**10.19**	**10.28**
C.D.	**0.76**	**0.54**	**0.56**	**0.33**	**0.42**	**0.32**	**0.32**	**0.34**	
C.V. at 5%	**4.51**	**2.95**	**3.58**	**1.88**	**2.53**	**1.89**	**1.89**	**2.01**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

weight basis (RGC 936) with overall mean 10.09% dry weight basis; in BS 20 from 9.02 % dry weight basis (HVG 2-30) to 12.01% dry weight basis (RGC 1066) with overall mean 10.28% dry weight basis; in HK 20 from 8.80% dry weight basis(RGC 1002) to 11.57% dry weight basis (HG 75) with overall mean 10.16% dry weight basis; in BK 20 from 8.63% dry weight basis (PNB) to 12.01% dry weight basis (X 10) with overall mean 10.19% dry weight basis (Table 4.2.20).

On the basis of overall performance, 9, 15, 1, 18, 10, 10, 11 and 10 (Number in each environment) genotypes exhibited higher ADF content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. RGS 3 (11.09 % dry weight basis) showed highest ADF content in HS 19 followed by X 10 (11.05 % dry weight basis) and RGC 1038 (11.04 % dry weight basis); HG 563 (12.78 % dry weight basis) in BS 19 followed by RGC 1002 (12.54 % dry weight basis) and HG 3-52 (12.51 % dry weight basis); HG 884 (11.38 % dry weight basis) in HK 19 followed HG 563 and HG 2-20 (10.17 % dry weight basis); HG 75 (12.44 % dry weight basis) in BK 19 followed by RGC 1003 (12.40 % dry weight basis) and RGC 1002 (11.94 % dry weight basis); RGC 936 (12.49 % dry weight basis) in HS 20 followed by HG 75 (11.99 % dry weight basis) and HG 563 (11.65 % dry weight basis); RGC 1038 and RGC 1066 (12.01 % dry weight basis) in BS 20 followed HG 75 (11.13 % dry weight basis) and HG 365 (11.08 % dry weight basis); HG 75 (11.57 % dry weight basis) in HK 20 followed by RGC 1033 (11.53 % dry weight basis) and HG 365 (11.45 % dry weight basis); X 10 (12.01 % dry weight basis) in BK 20 followed RGC 1002 (11.65 % dry weight basis) and HG 100 (11.41 % dry weight basis).

On the basis of overall mean across the environments HG 75 (11.34 % dry weight basis) had shown high ADF content followed by X 10 (11.14 % dry weight basis) and HG 563 (10.96 % dry weight basis). Among the environments BS 19 and BK 19 showed higher ADF content than grand mean.

4.2.21 Lignin content

Lignin content in HS 19 ranged from 2.54 % dry weight basis (HVG 2-30) to 3.23% dry weight basis (HG 870 and HG 75) with overall mean 2.89% dry weight basis; in BS 19 from 2.41% dry weight basis (M 83) to 3.16% dry weight basis (HG 563 and HG 3-52) with overall mean 2.89% dry weight basis; in HK 19 from 2.73 % dry weight basis (HVG 2-30) to 3.29% dry weight basis (HG 563) with overall mean 3.03% dry weight basis; in BK 19 from 2.34 % dry weight basis (HVG 2-30) to 3.07% dry weight basis (HG 75) with overall mean 2.77% dry weight basis; in HS 20 from 2.02 % dry weight basis(HVG 2-30) to 3.34% dry weight basis (RGC 936) with overall mean 2.68 % dry weight basis; in BS 20 from 2.68 % dry weight basis (RGC 1002) to 3.19% dry weight basis (HG 75) with overall mean 2.97% dry weight basis; in HK 20 from 2.56 % dry weight basis (HG 6) to 3.34% dry weight basis

Table 4.3.21: Mean performance of cluster bean genotypes under different environments for lignin content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	3.08	3.06	3.07	2.93	2.77	2.86	2.84	2.85	2.93
HG 884	2.81	2.82	3.23	2.74	2.60	3.02	3.12	2.95	2.91
HG 870	3.23	3.07	3.01	2.73	2.60	3.01	3.03	2.61	2.91
HG 563	2.81	3.16	3.29	2.95	3.27	3.06	3.13	3.12	3.10
HG 365	3.08	3.07	3.22	2.73	2.39	3.12	3.19	2.86	2.96
HG 3-52	2.82	3.16	2.98	2.75	2.50	2.90	2.94	2.85	2.86
HG 6	2.67	2.83	2.98	2.91	2.45	2.82	2.56	2.97	2.77
HVG 2-30	2.54	2.56	2.73	2.34	2.02	2.76	2.79	2.80	2.57
HG 100	3.09	2.55	3.05	2.52	2.80	3.11	3.02	2.85	2.87
FS 277	2.67	2.42	2.79	2.67	2.06	2.83	2.81	2.96	2.65
X-10	3.12	2.99	3.15	2.94	3.15	3.14	3.19	3.19	3.11
PNB	2.60	2.60	2.88	2.43	2.47	2.83	2.75	2.68	2.66
GG-1	2.59	2.70	2.89	2.92	2.27	2.93	2.96	2.85	2.76
GG-2	2.72	2.86	3.07	2.80	2.69	2.97	2.95	2.32	2.80
RGC 1017	2.94	3.14	3.10	2.72	2.85	2.94	2.85	2.83	2.92
RGC 1038	2.85	3.13	3.05	2.70	2.95	3.15	2.99	3.10	2.99
RGC 936	3.00	3.06	2.81	2.73	3.34	3.10	3.07	2.90	3.00
RGC 1055	2.82	3.26	2.98	2.72	2.59	2.89	2.75	2.93	2.87
RGC 1002	2.93	3.02	3.06	2.93	2.46	2.68	2.59	2.94	2.83
RGC 1003	2.99	2.45	3.21	2.52	2.72	2.85	2.88	3.15	2.85
RGC 1066	3.04	2.92	3.12	2.95	2.89	3.18	2.79	2.90	2.97
RGS 3	2.91	2.96	3.06	3.05	2.85	3.04	2.84	2.83	2.94
M-83	2.58	2.41	2.85	2.42	2.04	2.71	2.81	2.50	2.54
RGC 1033	3.13	3.00	3.05	3.01	3.05	3.11	3.29	3.38	3.13
HG 75	3.23	3.14	3.03	3.07	3.31	3.19	3.34	2.89	3.15
Over all Mean	**2.89**	**2.89**	**3.03**	**2.77**	**2.68**	**2.97**	**2.94**	**2.89**	**2.88**
C.D.	**0.20**	**0.21**	**N.S.**	**0.14**	**0.33**	**0.20**	**0.26**	**0.29**	
C.V. at 5%	**4.25**	**4.42**	**6.37**	**3.12**	**7.54**	**4.13**	**5.43**	**6.16**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

(HG 75) with overall mean 2.94% dry weight basis; in BK 20 from 2.32% dry weight basis (GG 2) to 3.38% dry weight basis (RGC 1033) with overall mean 2.89% dry weight basis (Table 4.2.21).

On the basis of overall performance, 13, 15, 20, 10, 7, 17, 13 and 13(Number in each environment) genotypes exhibited higher lignin content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. HG 870 and HG 75 (3.23 % dry weight basis) showed highest lignin content in HS 19 followed by RGC 1033 (3.13% dry weight basis) and X 10 (3.12 % dry weight basis); RGC 1055 (3.26) % dry weight basis in BS 19 followed by HG 3-52 and HG 563 (3.16 % dry weight basis); Hg 563 (3.29 % dry weight basis) in HK 19 followed HG 884 (3.23 % dry weight basis) and HG 365 (3.22 % dry weight basis); HG 75 (3.07 % dry weight basis) in BK 19 followed by RGS 3 (3.05 % dry weight basis) and RGC 1033 (3.01 % dry weight basis); RGC 936 (3.34 % dry weight basis) in HS 20 followed by HG 75 (3.31 % dry weight basis) and HG 563 (3.27 % dry weight basis); HG 75 (3.19 % dry weight basis) in BS 20 followed RGC 1066 (3.18 % dry weight basis) and RGC 1038 (3.15 % dry weight basis); HG 75 (3.34 % dry weight basis) in HK 20 followed by RGC 1033 (3.29 % dry weight basis), X 10 and HG 365 (3.19 % dry weight basis); RGC 1033 (3.38 % dry weight basis) in BK 20 followed X 10 (3.19 % dry weight basis) and RGC 1003 (3.15 % dry weight basis).

On the basis of overall mean across the environments HG 75 (3.15 % dry weight basis) had shown high lignin content followed by RGC 1033 (3.13 % dry weight basis) and X 10 (3.11 % dry weight basis).All the environments except BK 19 and HS 20 showed higher lignin content than grand mean.

4.2.22 Cellulose content

Cellulose content in HS 19 ranged from 6.56% dry weight basis (HVG 2-30) to HG 3-52% dry weight basis (8.28 % dry weight basis) with overall mean 7.35 % dry weight basis; in BS 19 from 7.03 % dry weight basis (HVG 2-30) to 9.77% dry weight basis (RGC 1003) with overall mean 8.19% dry weight basis; in HK 19 from 5.59% dry weight basis (FS 277) to 8.15% dry weight basis (HG 884) with overall mean 6.44% dry weight basis; in BK 19 from 7.02 % dry weight basis (FS 277) to 9.88% dry weight basis (RGC 1003) with overall mean 8.01% dry weight basis; in HS 20 from 6.10 % dry weight basis (PNB) to 9.16% dry weight basis (RGC 936) with overall mean 7.41% dry weight basis; in BS 20 from 6.26 % dry weight basis (HVG 2-30) to 8.85% dry weight basis (RGC 1038) with overall mean 7.31% dry weight basis; in HK 20 from 5.97 % dry weight basis (RGC 936) to 8.26% dry weight basis (HG 365) with overall mean 7.22% dry weight basis; in BK 20 from 5.71 % dry weight basis (RGC 1055) to 8.82% dry weight basis (X 10) with overall mean 7.30% dry weight basis (Table 4.2.22).

Table 4.3.22: Mean performance of cluster bean genotypes under different environments for cellulose content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	7.19	8.42	7.10	7.90	6.83	6.96	7.16	6.18	7.22
HG 884	7.31	7.28	8.15	7.94	6.74	7.19	7.32	6.32	7.28
HG 870	7.50	8.58	6.03	7.83	7.23	7.12	7.24	7.88	7.43
HG 563	7.80	9.61	6.87	8.73	8.37	7.72	7.82	6.50	7.93
HG 365	6.94	9.10	6.88	7.40	6.48	7.96	8.26	7.17	7.52
HG 3-52	8.28	9.35	6.38	7.90	6.92	7.17	7.32	8.03	7.67
HG 6	7.11	7.37	5.93	7.77	6.86	6.60	6.44	6.01	6.76
HVG 2-30	6.56	7.03	6.11	7.40	6.44	6.26	6.87	6.20	6.61
HG 100	7.22	7.53	6.48	7.38	8.51	7.91	7.38	8.56	7.62
FS 277	7.25	7.43	5.59	7.02	6.23	6.62	7.23	6.66	6.75
X-10	7.21	7.99	7.00	8.51	8.23	7.88	7.90	8.82	7.94
PNB	7.29	7.34	6.00	7.41	6.10	6.51	7.18	5.96	6.72
GG-1	7.22	7.48	6.44	7.78	6.17	7.20	7.43	8.47	7.27
GG-2	7.33	7.36	6.44	7.91	7.00	7.17	7.48	7.73	7.30
RGC 1017	8.10	9.28	6.79	7.69	8.07	6.92	7.32	8.50	7.83
RGC 1038	7.36	8.77	6.45	7.76	8.68	8.85	7.34	6.49	7.71
RGC 936	7.32	8.64	5.69	7.83	9.16	7.92	5.97	7.22	7.47
RGC 1055	7.17	8.23	6.03	7.21	6.95	6.58	6.70	5.71	6.82
RGC 1002	7.17	9.52	6.03	9.02	6.88	6.58	6.21	8.71	7.52
RGC 1003	7.13	9.77	6.69	9.88	7.75	6.75	6.95	6.94	7.73
RGC 1066	7.20	7.21	6.44	7.94	8.51	8.83	7.73	8.14	7.75
RGS 3	8.14	7.40	6.90	8.37	6.99	7.58	6.13	8.21	7.47
M-83	7.15	7.67	5.85	7.41	6.93	6.60	6.71	7.65	7.00
RGC 1033	6.95	7.64	6.45	8.77	8.42	7.89	8.24	6.16	7.57
HG 75	7.79	8.71	6.34	9.37	8.68	7.94	8.23	8.41	8.18
Over all Mean	**7.35**	**8.19**	**6.44**	**8.01**	**7.41**	**7.31**	**7.22**	**7.30**	**7.40**
C.D.	**0.75**	**0.55**	**0.65**	**0.36**	**0.52**	**0.35**	**0.37**	**0.46**	
C.V. at 5%	**6.17**	**4.10**	**6.09**	**2.73**	**4.29**	**2.91**	**3.14**	**3.79**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

On the basis of overall performance, 6, 18, 1, 20, 10, 10, 8 and 12 (Number in each environment) genotypes exhibited higher cellulose content than grand mean in HS 19, BS 19,

HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. HG 3-52 (8.28 % dry weight basis) showed highest cellulose content in HS 19 followed by RGS 3 (8.14 % dry weight basis) and RGC 1017 (8.10 % dry weight basis); RGC 1003 (9.77 % dry weight basis) in BS 19 followed by HG 563 (9.61 % dry weight basis) and RGC 1002 (9.52 % dry weight basis); HG 884(8.15 % dry weight basis) in HK 19 followed HG 2-20 (7.10 % dry weight basis) and X 10 (7.00 % dry weight basis); RGC 1003 (9.88 % dry weight basis) in BK 19 followed by HG 75 (9.37 % dry weight basis) and RGC 1002 (9.02 % dry weight basis); RGC 936 (9.16 % dry weight basis) in HS 20 followed by HG 75 and RGC 1038 (8.68 % dry weight basis); RGC 1038 (8.85 % dry weight basis) in BS 20 followed RGC 1066 (8.83 % dry weight basis) and HG 365 (7.96 % dry weight basis); HG 365 (8.26 % dry weight basis) in HK 20 followed by RGC 1033 (8.24 % dry weight basis) and HG 75 (8.23 % dry weight basis); X 10 (8.82 % dry weight basis) in BK 20 followed RGC 1002 (8.71 % dry weight basis) and HG 100 (8.56 % dry weight basis).

On the basis of overall mean across the environments HG 75 (8.18 % dry weight basis) had shown high cellulose content followed by X 10 (7.94 % dry weight basis) and HG 563 (7.93 % dry weight basis). Among the environments BS 19, BK 19 and HS 20 showed higher cellulose content than grand mean.

4.2.23 Silica content

Silica content in HS 19 ranged from 0.55 % dry weight basis (HVG 2-30) to 1.53 % dry weight basis (HG 870) with overall mean 0.74 % dry weight basis; in BS 19 from 0.57 % dry weight basis (FS 277) to 1.23 % dry weight basis (RGS 3) with overall mean 0.73 % dry weight basis; in HK 19 from 1.23 % dry weight basis (HG 2-30) to 2.28 % dry weight basis (GG 1) with overall mean 1.38 % dry weight basis; in BK 19 from 0.68 % dry weight basis (PNB) to 1.46 % dry weight basis (HG 563) with overall mean 0.83 % dry weight basis; in HS 20 from 1.01 % dry weight basis (HG 365) to 1.59 % dry weight basis (RGC 936) with overall mean 1.17 % dry weight basis; in BS 20 from 1.38 (M 83) to 2.20 % dry weight basis (RGC 1038) with overall mean 1.63 % dry weight basis; in HK 20 from 0.93 % dry weight basis (RGC 1055) to 1.72 % dry weight basis (HG 563) with overall mean 1.25 % dry weight basis; in BK 20 from 1.34 % dry weight basis (HG 6) to 1.81 % dry weight basis (HG 2-20) with overall mean 1.58 % dry weight basis(Table 4.2.23).

On the basis of overall performance, 2, 2, 25, 2, 11, 25, 15 and 25 (Number in each environment) genotypes exhibited higher silica content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. HG 870 (1.53 % dry weight basis) showed highest silica content in HS 19 followed by HG 75 (1.50 % dry weight basis), and X 10 (1.08 % dry weight basis); RGS 3 (1.23 % dry weight basis) in BS 19 followed by HG 563

Table 4.3.23: Mean performance of cluster bean genotypes under differentenvironments for silica content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	1.04	0.72	1.33	0.80	1.17	1.52	1.14	1.81	1.19
HG 884	0.61	0.62	1.64	0.74	1.07	1.55	1.32	1.60	1.14
HG 870	1.53	0.77	1.30	0.74	1.24	1.51	1.19	1.61	1.24
HG 563	0.61	1.21	1.34	1.46	1.58	1.56	1.72	1.56	1.38
HG 365	0.60	0.62	1.35	0.74	1.00	1.97	1.31	1.75	1.17
HG 3-52	0.62	0.99	1.28	0.75	1.05	1.63	1.19	1.56	1.13
HG 6	0.60	0.74	1.31	0.80	1.09	1.46	1.03	1.34	1.05
HVG 2-30	0.55	0.58	1.23	0.70	1.07	1.72	1.16	1.58	1.07
HG 100	0.67	0.69	1.92	0.71	1.16	1.82	1.20	1.51	1.21
FS 277	0.69	0.57	1.25	0.69	1.01	1.42	1.10	1.49	1.03
X-10	1.08	0.69	1.33	1.12	1.19	1.59	1.67	1.67	1.29
PNB	0.60	0.60	1.26	0.68	1.13	1.45	1.12	1.46	1.04
GG-1	0.60	0.60	2.28	0.78	1.21	1.88	1.22	1.55	1.27
GG-2	0.61	0.67	1.30	0.78	1.06	1.57	1.46	1.52	1.12
RGC 1017	1.00	0.98	1.34	0.73	1.17	1.50	1.15	1.56	1.18
RGC 1038	0.62	0.76	1.32	0.74	1.13	2.20	1.23	1.53	1.19
RGC 936	0.67	0.67	1.30	0.74	1.59	1.45	1.06	1.55	1.13
RGC 1055	0.61	0.74	1.26	0.74	1.04	1.40	0.93	1.77	1.06
RGC 1002	0.62	0.70	1.27	0.84	1.40	1.45	1.26	1.40	1.12
RGC 1003	0.65	0.59	1.32	0.72	1.05	1.48	1.29	1.44	1.07
RGC 1066	0.65	0.61	1.34	0.81	1.11	1.84	1.34	1.64	1.17
RGS 3	0.62	1.23	1.30	0.84	1.13	1.48	1.09	1.59	1.16
M-83	0.59	0.59	1.26	0.69	1.03	1.38	1.13	1.51	1.02
RGC 1033	0.62	0.70	1.33	1.10	1.18	1.86	1.37	1.65	1.23
HG 75	1.50	0.68	1.30	1.24	1.43	2.07	1.64	1.75	1.45
Over all Mean	**0.74**	**0.73**	**1.38**	**0.83**	**1.17**	**1.63**	**1.25**	**1.58**	**1.16**
C.D.	**0.06**	**0.06**	**0.05**	**0.03**	**0.05**	**0.16**	**0.11**	**0.07**	
C.V. at 5%	**5.19**	**4.61**	**2.28**	**2.15**	**2.61**	**5.99**	**5.30**	**2.84**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

(1.21 % dry weight basis) and RGC 1017 (0.98 % dry weight basis); GG 1 (2.28 % dry weight basis) in HK 19 followed HG 100 (1.92 % dry weight basis) and HG 884 (1.64 % dry weight basis); HG 563 (1.46 % dry weight basis) in BK 19 followed by HG 75 (1.24 % dry weight basis) and X 10 (1.12 % dry weight basis); RGC 936 (1.59 % dry weight basis) in HS 20 followed by HG 563 (1.58 % dry weight basis) and HG 75 (1.43 % dry weight basis); RGC 1038 (2.20 % dry weight basis) in BS 20 followed HG 75 (2.07 % dry weight basis) and HG 365 (1.97 % dry weight basis); HG 563 (1.72 % dry weight basis) in HK 20 followed by X 10 (1.67 % dry weight basis) and HG 75 (1.64 % dry weight basis); HG 2-20 (1.81 % dry weight basis) in BK 20 followed RGC 1055 (1.77 % dry weight basis) and Hg 365 and Hg 75 (1.75 % dry weight basis).

On the basis of overall mean across the environments HG 75 (1.45 % dry weight basis) had shown high silica content followed by HG 563 (1.38 % dry weight basis) and X 10 (1.29 % dry weight basis). Among the environments HK 19, HS 20, BS 20, HK 20 and BS 20 showed higher silica content than grand mean.

4.2.24 Neutral detergent fibre (NDF) content

NDF content in HS 19 ranged from 11.11% dry weight basis (HG 2-20) to 13.11% dry weight basis (RGS 3) with overall mean 12.27% dry weight basis; in BS 19 from 12.06 % dry weight basis (HVG 2-30) to 15.24% dry weight basis (RGC 936) with overall mean 13.61% dry weight basis; in HK 19 from 10.47% dry weight basis (FS 277) to 13.52 % dry weight basis (HG 884) with overall mean 11.47% dry weight basis; in BK 19 from 11.27 % dry weight basis (HVG 2-30) to 14.75 % dry weight basis (RGC 1003) with overall mean 12.69% dry weight basis; in HS 20 from 11.60 % dry weight basis (HVG 2-30) to 15.91 % dry weight basis (RGC 936) with overall mean 13.46% dry weight basis; in BS 20 from 11.48 (M 83) to 14.49% dry weight basis (HG 75) with overall mean 12.81% dry weight basis; in HK 20 from 10.87 % dry weight basis (M 83) to 13.55% dry weight basis (HG 75 and HG 365) with overall mean 12.20% dry weight basis; in BK 20 from 10.68% dry weight basis (PNB) to 13.97% dry weight basis (X 10) with overall mean 12.21% dry weight basis (Table 4.2.24).

On the basis of overall performance, 6, 19, 1, 11, 19, 15, 5 and 9(Number in each environment) genotypes exhibited higher NDF content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. RGS 3 (13.11 % dry weight basis) showed highest NDF content in HS 19 followed by X 10 (13.02 % dry weight basis) and HG 75 (13.02 % dry weight basis); RGC 936 (15.24 % dry weight basis) in BS 19 followed by HG 365 (15.20 % dry weight basis) and RGC 1017 (15.04% dry weight basis); HG 884 (13.52 % dry weight basis) in HK 19 followed X 10 (12.29 % dry weight basis) and HG 563 (12.36 % dry weight basis); RGC 1003 (14.75 % dry weight basis) in BK 19 followed by HG

75 (14.65 % dry weight basis) and RGC 1033 (14.15 % dry weight basis); RGC 936 (15.91 % dry weight basis) in HS 20 followed by HG 75 (15.38 % dry weight

Table 4.3.24: Mean performance of cluster bean genotypes under different environments for NDF content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	11.11	14.30	11.79	12.70	12.74	12.59	12.06	10.98	12.28
HG 884	12.06	12.62	13.52	12.59	13.04	13.31	12.51	11.28	12.62
HG 870	12.54	14.31	11.32	12.40	13.11	12.60	12.32	12.56	12.65
HG 563	12.22	14.69	12.26	13.50	15.07	13.18	11.91	11.67	13.06
HG 365	12.13	15.20	12.23	11.58	12.33	13.62	13.55	12.06	12.84
HG 3-52	11.83	14.33	11.49	12.52	12.79	12.40	12.24	13.01	12.58
HG 6	12.05	12.62	10.64	12.56	12.03	11.90	10.98	10.97	11.72
HVG 2-30	12.03	12.06	10.98	11.27	11.60	11.74	11.64	10.96	11.54
HG 100	12.29	12.55	11.65	11.92	14.12	13.61	12.50	13.43	12.76
FS 277	12.43	12.51	10.47	11.35	11.74	12.20	13.11	11.59	11.93
X-10	13.02	14.57	12.29	12.94	14.73	13.63	13.13	13.97	13.54
PNB	12.26	12.54	10.76	11.51	11.82	11.90	10.98	10.68	11.56
GG-1	12.05	12.58	11.70	12.65	11.99	12.61	12.47	13.30	12.42
GG-2	12.24	12.80	10.83	12.83	13.31	12.67	12.48	12.07	12.40
RGC 1017	12.74	15.04	12.07	12.18	14.74	12.32	12.24	13.37	13.09
RGC 1038	13.00	14.40	11.59	12.26	14.90	14.46	12.39	11.65	13.08
RGC 936	11.86	15.24	10.74	12.43	15.91	13.55	11.01	12.10	12.86
RGC 1055	11.64	12.93	10.92	11.63	12.98	12.01	11.43	10.71	11.78
RGC 1002	12.70	13.92	11.20	13.96	12.73	11.91	11.55	13.68	12.71
RGC 1003	12.36	13.83	11.57	14.75	13.85	12.05	12.11	12.15	12.83
RGC 1066	12.26	12.65	11.81	13.56	14.98	13.71	12.54	13.06	13.07
RGS 3	13.11	13.92	11.71	13.82	13.25	12.78	11.96	13.10	12.96
M-83	11.91	12.35	10.49	11.50	12.66	11.48	10.87	12.10	11.67
RGC 1033	11.96	13.72	11.05	14.15	14.76	13.56	13.52	11.59	13.04
HG 75	13.02	14.70	11.70	14.65	15.38	14.49	13.55	13.32	13.85
Over all Mean	**12.27**	**13.61**	**11.47**	**12.69**	**13.46**	**12.81**	**12.20**	**12.21**	**12.59**
C.D.	**0.79**	**0.52**	**0.54**	**0.33**	**0.44**	**0.33**	**0.34**	**0.34**	
C.V. at 5%	**3.92**	**2.30**	**2.88**	**1.59**	**2.00**	**1.59**	**1.68**	**1.67**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

basis) and HG 563 (15.07 % dry weight basis); HG 75 (14.49 % dry weight basis) in BS 20 followed RGC 1038 (14.46 % dry weight basis) and RGC 1066 (13.71 % dry weight basis); HG 365 and HG 75 (13.55 % dry weight basis) in HK 20 followed by RGC 1033 (13.52) and X 10 (13.13 % dry weight basis); X 10 (13.97 % dry weight basis) in BK 20 followed RGC 1002 (13.68 % dry weight basis) and HG 100 (13.43 % dry weight basis).

On the basis of overall mean across the environments HG 75 (13.85 % dry weight basis) had shown high NDF content followed by X 10 (13.54 % dry weight basis) and RGC 1017 (13.09 % dry weight basis) Among the environments BS 19, BK 19, HS 20 and BS 20 showed higher NDF content than grand mean.

4.3.25 Hemicellulose content

Hemicellulose content in HS 19 ranged from 1.79 % dry weight basis (HG 884) to 2.24% dry weight basis (RGC 1003) with overall mean 2.03% dry weight basis; in BS 19 from 1.38 % dry weight basis (RGC 1002) to 3.59% dry weight basis (X 10) with overall mean 2.53% dry weight basis; in HK 19 from 1.33 % dry weight basis (GG 2) to 2.37% dry weight basis (GG 1) with overall mean 2.00% dry weight basis; in BK 19 from 1.45 % dry weight basis (HG 365) to 2.67% dry weight basis (RGC 1066) with overall mean 1.92% dry weight basis; in HS 20 from 2.72 % dry weight basis (HG 6) to 3.81% dry weight basis (RGC 1017) with overall mean 3.37% dry weight basis; in BS 20 from 1.70% dry weight basis(RGC 1066) to 3.36% dry weight basis (HG 75) with overall mean 2.54% dry weight basis; in HK 20 from 0.97 % dry weight basis (HG 563) to 3.07% dry weight basis (FS 277) with overall mean 2.04 % dry weight basis; in BK 20 from 1.95 % dry weight basis (HG 2-20) to 2.13% dry weight basis (HG 3-52) with overall mean 2.02% dry weight basis(Table 4.2.25).

On the basis of overall performance, 9, 19, 2, 4, 25, 22, 3 and 0 (Number in each environment) genotypes exhibited higher hemicellulose content than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. RGC 1003 (2.24 % dry weight basis) showed highest hemicellulose content in HS 19 followed by HG 870 (2.21 % dry weight basis) and M 83 (2.18 % dry weight basis); X 10 (3.59 % dry weight basis) in BS 19 followed by RGS 3 (3.56 % dry weight basis) and RGC 936 (3.54 % dry weight basis); GG 1 (2.37 % dry weight basis) in HK 19 followed HG 75 (2.33 % dry weight basis) and HG 870 (2.28 % dry weight basis); RGC 1066 (2.67 % dry weight basis) in BK 19 followed by RGS 3 (2.40 % dry weight basis) and RGC 1033 (2.37 % dry weight basis); RGC 1017 (3.81 % dry weight basis) in HS 20 followed by HG 884 (3.70 % dry weight basis) and M 83 (3.68 % dry weight basis); HG 75 (3.36 % dry weight basis) in BS 20 followed HG 884 (3.10 % dry weight basis) and HG 2-20 (2.77 % dry weight basis); FS 277 (3.07 % dry weight basis) in HK 20 followed by RGS 3 (2.99 % dry weight basis) and RGC 1002 (2.74 % dry weight basis); HG 3-52 (2.13 % dry weight basis) in BK 20 followed HG 870 (2.07 % dry weight basis) and RGC 1038 (2.06 % dry weight basis).

Table 4.3.25: Mean performance of cluster bean genotypes under different environmentsfor hemicellulose content

Genotypes	HS 19	BS 19	HK19	BK 19	HS 20	BS 20	HK 20	BK 20	Over all Mean
HG 2-20	2.00	2.82	1.62	1.86	3.14	2.77	2.06	1.95	2.28
HG 884	1.79	2.52	2.13	1.91	3.70	3.10	2.07	2.02	2.41
HG 870	2.21	2.66	2.28	1.84	3.28	2.48	2.05	2.07	2.36
HG 563	2.14	1.92	2.09	1.81	3.43	2.40	0.97	2.05	2.10
HG 365	2.01	3.03	2.13	1.45	3.46	2.54	2.10	2.03	2.34
HG 3-52	1.91	1.82	2.13	1.86	3.37	2.33	1.99	2.13	2.19
HG 6	2.00	2.42	1.73	1.88	2.72	2.49	1.98	1.99	2.15
HVG 2-30	2.04	2.47	2.13	1.53	3.15	2.72	1.98	1.97	2.25
HG 100	1.97	2.46	2.12	2.02	2.81	2.60	2.10	2.02	2.26
FS 277	2.12	2.66	2.09	1.67	3.45	2.75	3.07	1.97	2.47
X-10	1.97	3.59	2.13	1.49	3.35	2.60	2.05	1.96	2.39
PNB	2.16	2.60	1.88	1.67	3.25	2.56	1.05	2.05	2.15
GG-1	2.03	2.40	2.37	1.95	3.55	2.47	2.08	1.98	2.35
GG-2	2.00	2.58	1.33	2.12	3.62	2.53	2.04	2.02	2.28
RGC 1017	2.01	2.63	2.18	1.76	3.81	2.46	2.06	2.03	2.37
RGC 1038	1.96	2.50	2.09	1.80	3.28	2.45	2.06	2.06	2.28
RGC 936	2.08	3.54	2.24	1.86	3.42	2.54	1.98	1.98	2.46
RGC 1055	1.83	1.44	1.91	1.70	3.44	2.53	1.98	2.06	2.11
RGC 1002	2.09	1.38	2.11	2.02	3.39	2.65	2.74	2.03	2.30
RGC 1003	2.24	1.61	1.67	2.35	3.38	2.45	2.28	2.06	2.26
RGC 1066	2.05	2.51	2.25	2.67	3.58	1.70	2.02	2.02	2.35
RGS 3	2.01	3.56	1.76	2.40	3.41	2.16	2.99	2.05	2.54
M-83	2.18	2.26	1.80	1.66	3.68	2.17	1.36	1.96	2.13
RGC 1033	2.07	3.07	1.55	2.37	3.29	2.56	1.99	2.06	2.37
HG 75	1.99	2.85	2.33	2.21	3.39	3.36	1.98	2.02	2.52
Over all Mean	**2.03**	**2.53**	**2.00**	**1.92**	**3.37**	**2.54**	**2.04**	**2.02**	**2.31**
C.D.	**0.22**	**0.61**	**0.28**	**0.33**	**0.35**	**0.38**	**0.32**	**0.07**	
C.V. at 5%	**6.58**	**14.69**	**8.34**	**10.31**	**6.30**	**9.13**	**9.38**	**2.10**	

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

On the basis of overall mean across the environments RGS 3 (2.54 % dry weight basis) had shown high hemicellulose content followed by HG 75 (2.52 % dry weight basis) and FS 277 (2.47 % dry weight basis). Among the environments BS 19, HS 20 and BS 20 showed higher hemicellulose content than grand mean.

4.3.26 Bacterial Leaf Blight (BLB) intensity

The data of Bacterial Leaf Blight (BLB) intensity was subjected to Angular transformation and the transformed values are presented in Table 4.3.16 in parenthesis. BLB intensity in HS 19 ranged from 26.05 % (30.67) (HG 75) to 40.25 % (39.57) (PNB) with overall mean 29.97% (33.14); in BS 19 from 30.00% (33.19) (HG 3-52) to 45.06% (42.15) (PNB) with overall mean 34.16% (35.71); in HK 19 from 35.43% (36.51) (HG 884) to 51.11% (45.62) (M 83) with overall mean 39.33%(38.81); in BK 19 from 38.64% (38.42) (HG 75) to 51.97% (46.11) (FS 277) with overall mean 42.58% (40.71); in HS 20 from 27.78% (31.79) (HG 75) to 42.34% (40.57) (PNB) with overall mean 32.40% (34.64); in BS 20 from 32.10% (34.48) (X 10) to 46.05% (42.71) (FS 277) with overall mean 36.69% (37.24); in HK 20 from 36.91% (37.39) (HG 870) to 51.11% (46.11) (M 83) with overall mean 40.72% (39.62); in BK 20 from 38.89% (38.56) (HG 870 and X 10) to 52.10% (46.18) (PNB) with overall mean 42.47% (40.64) (Table 4.2.26).

On the basis of overall performance, 24, 21, 6, 0, 21, 21, 2 and 0 (Number in each environment) genotypes exhibited lowest BLB intensity than grand mean in HS 19, BS 19, HK 19, BK 19, HS 20, BS 20, HK 19 and BK 19 respectively. HG 75 [26.05 % (30.67)] showed lowest BLB intensity in HS 19 followed by HG 870 [26.17 % (30.74)] and X 10 [26.79 % (31.15)]; HG 3-52 [30.00 % (33.19)] in BS 19 followed by RGC 936 [30.25% (33.35)] and HG 563 [30.74 % (33.65)]; HG 884 [35.43% (36.51)] in HK 19 followed HG 365 and X 10 [35.93 % (36.80)]; HG 75 [38.64 % (38.42)] in BK 19 followed by HG 563 [39.63% (38.99)] and RGC 1033 [39.75% (39.09)]; HG 75 [27.78% (31.79)] in HS 20 followed by HG 563 [28.40 % (32.18)] and RGC 1038 [28.64 % (32.33)]; X 10 [32.10 % (34.48)] in BS 20 followed RGC 1033 [32.71% (34.87)] and HG 75 [32.96% (35.02)]; HG 870 [36.91% (37.39)] in HK 20 followed by RGC 1033 [37.28% (37.61)] and HG 75 [37.53% (37.62)]; HG 870 and X 10 [38.89% (38.56)] in BK 20 followed HG 75 [39.26 % (38.78)] and RGC 1033 [39.38 % (38.85)].

On the basis of overall mean across the environments HG 75 [33.92 (35.55) had shown low BLB intensity followed by X 10 [34.45 (35.87)] and HG 563 [34.80 (36.09)]. Among the environments HS 19, BS 19, HS 20 and BS 20 showed significantly low BLB intensity than grand mean.

Table 4.3.26: Mean performance of cluster bean genotypes under different environments for bacterial leaf blight intensity (Transformed values in parenthesis)

Genotypes	**Hisar summer**	**Bawal summer**	**Hisar *kharif***	**Bawal *kharif***	**Hisar summer**	**Bawal summer**	**Hisar *kharif***	**Bawal *kharif***	**Over all Mean**
	Year 2019				**Year 2020**				
HG 2-20	27.04 (31.30)	31.97 (34.41)	37.41 (37.69)	40.62 (39.57)	30.74 (33.65)	35.68 (36.66)	38.77 (38.49)	39.88 (39.14)	40.62 (39.57)
HG 884	28.77 (32.41)	33.58 (35.39)	35.43 (36.51)	41.60 (40.14)	32.10 (34.49)	34.81 (36.14)	37.90 (37.98)	40.25 (39.59)	35.56 (36.55)
HG 870	26.17 (30.74)	31.60 (34.18)	38.03 (38.05)	41.85 (40.29)	31.11 (33.88)	35.31 (36.44)	36.91 (37.39)	38.89 (38.56)	34.98 (36.19)
HG 563	29.01 (32.56)	30.74 (33.65)	36.67 (37.25)	39.63 (38.99)	28.40 (32.18)	33.83 (35.54)	38.89 (38.56)	41.23 (39.93)	34.80 (36.09)
HG 365	30.12 (33.25)	32.47 (34.71)	35.93 (36.80)	41.97 (40.36)	33.21 (35.17)	33.45 (35.32)	38.15 (38.12)	39.63 (39.00)	35.62 (36.59)
HG 3-52	29.51 (32.88)	30.00 (33.19)	38.03 (38.05)	41.36 (40.00)	32.84 (34.94)	35.43 (36.51)	39.01 (38.63)	41.60 (40.15)	35.97 (36.80)
HG 6	33.21 (35.17)	33.58 (35.39)	38.89 (38.56)	41.11 (39.86)	33.08 (35.09)	37.29 (37.61)	38.27 (38.20)	42.22 (40.50)	37.21 (37.55)
HVG 2-30	35.43 (36.50)	40.00 (39.12)	46.42 (42.93)	49.14 (44.48)	38.03 (38.05)	44.20 (41.64)	48.77 (44.27)	48.77 (44.27)	43.85 (41.42)
HG 100	27.66 (31.70)	33.95 (35.62)	37.53 (37.76)	42.47 (40.65)	30.00 (33.18)	35.06 (36.92)	38.64 (38.41)	42.10 (40.32)	35.93 (36.76)
FS 277	37.04 (37.47)	43.21 (41.07)	48.03 (43.85)	51.97 (46.11)	39.63 (38.99)	46.05 (42.71)	50.86 (45.47)	51.48 (45.83)	46.03 (42.69)
X-10	26.79 (31.15)	33.33 (35.24)	35.93 (36.80)	39.88 (39.14)	29.38 (32.80)	32.10 (34.48)	39.26 (38.78)	38.89 (38.62)	34.45 (35.87)
PNB	40.25 (39.57)	45.06 (42.15)	48.27 (43.99)	51.23 (45.68)	42.34 (40.57)	45.31 (42.29)	50.00 (44.98)	52.10 (46.18)	46.82 (43.15)
GG-1	32.59 (34.79)	33.95 (35.62)	38.52 (38.34)	41.23 (39.93)	35.31 (36.44)	35.31 (36.43)	40.25 (39.36)	41.48 (40.07)	37.33 (37.63)
GG-2	29.63 (32.95)	33.46 (35.31)	37.53 (37.76)	41.11 (39.86)	31.60 (34.18)	35.06 (36.29)	38.89 (38.56)	41.97 (40.36)	36.16 (36.91)
RGC 1017	27.78 (31.78)	31.97 (34.41)	37.29 (37.62)	42.22 (40.50)	30.00 (33.18)	35.68 (36.66)	39.88 (39.14)	41.48 (40.07)	35.79 (36.67)
RGC 1038	28.77 (32.41)	31.60 (34.18)	37.78 (37.91)	41.97 (40.36)	28.64 (32.33)	35.31 (36.43)	39.26 (38.78)	41.97 (40.36)	35.66 (36.60)
RGC 936	27.41 (31.55)	30.25 (33.35)	39.26 (38.78)	41.73 (40.22)	29.26 (32.17)	36.79 (37.32)	38.64 (38.41)	41.85 (40.29)	35.65 (36.58)
RGC 1055	29.63 (32.96)	31.85 (34.34)	38.77 (38.49)	42.10 (40.43)	31.11 (33.88)	36.79 (37.32)	39.63 (39.90)	41.23 (39.93)	36.39 (37.05)
RGC 1002	28.64 (32.34)	33.09 (35.09)	38.40 (38.27)	40.00 (39.21)	32.22 (34.56)	36.91 (37.39)	40.00 (39.22)	42.59 (40.72)	36.48 (37.10)
RGC 1003	28.15 (32.01)	34.57 (35.99)	37.41 (37.69)	42.71 (40.79)	32.34 (34.63)	35.93 (36.81)	41.98 (40.36)	42.84 (40.86)	36.99 (37.40)
RGC 1066	27.78 (31.78)	33.58 (35.39)	37.04 (37.47)	41.11 (39.86)	29.26 (32.17)	34.32 (35.85)	39.51 (38.92)	40.12 (39.28)	35.34 (36.41)
RGS 3	28.15 (32.02)	33.33 (35.24)	37.66 (37.83)	40.37 (39.43)	30.12 (33.26)	36.55 (37.18)	38.64 (38.41)	40.37 (39.43)	35.65 (36.60)
M-83	34.94 (36.21)	43.09 (41.00)	51.11 (45.62)	48.64 (44.21)	40.86 (39.71)	44.32 (41.72)	51.11 (45.61)	50.25 (45.12)	45.54 (42.40)
RGC 1033	28.77 (32.42)	32.59 (34.79)	37.90 (37.98)	39.75 (39.09)	30.62 (33.57)	32.71 (34.87)	37.28 (37.61)	39.38 (38.85)	34.88 (36.15)
HG 75	26.05 (30.67)	31.11 (33.88)	38.03 (38.05)	38.64 (38.42)	27.78 (31.79)	32.96 (35.02)	37.53 (37.62)	39.26 (38.78)	33.92 (35.55)
Over all Mean	**29.97 (33.14)**	**34.16 (35.71)**	**39.33 (38.81)**	**42.58 (40.71)**	**32.40 (34.64)**	**36.69 (37.24)**	**40.72 (39.62)**	**42.47 (40.64)**	**37.29 (37.56)**
C.D.	**3.21 (2.01)**	**3.39 (2.05)**	**2.24 (1.32)**	**2.55 (1.48)**	**3.60 (2.11)**	**2.59 (1.54)**	**2.18 (1.48)**	**2.22 (1.30)**	
C.V. at 5%	**6.50 (3.63)**	**6.02 (3.48)**	**3.45 (2.06)**	**3.63 (2.21)**	**6.74 (3.87)**	**4.28 (2.15)**	**3.25 (2.21)**	**3.18 (1.94)**	

4.4 Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of mean for different quantitative characters based on pooled data of eight environments

The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of mean of various genotypes under study for different characters have been tabulated in table 4.4.1 and brief description for them is given here under following heads:

Plant height

For plant height both PCV (17.10) and GCV (17.08) were found moderate. Very high heritability (99.86%) with high genetic advance as per cent of mean (35.17%) was observed for this character which revealed the importance of additive gene action, and it could be exploited through simple selection procedure.

Days to 50% flowering

Low PCV (6.84) and GCV (6.76) were recorded for this character with. Very high heritability (97.66) and moderate genetic advance as percent of mean (13.77) was also observed for days to 50% flowering.

Days to maturity

Days to maturity had low PCV (8.28) and GCV (8.26) but had very high heritability (99.46) with moderate genetic advance as percent of mean (16.97).

Pods on main stem

High PCV (57.42) and GCV (57.39) were estimated for the pods on main stem. Very high heritability (99.9) along with very high genetic advance as percent of mean (118.16) was also observed for this character.

Pods per plant

Pods per plant had shown high PCV (29.1) and high GCV (29.08) with very high heritability (99.85) and genetic advance as percent of mean (59.86).

Pods per cluster

High PCV (29.95) and GCV (29.75) was observed for the pods per cluster. Very high heritability (98.66) with high genetic advance as percent of mean (60.88) was also observed for this character.

Seeds per pod

Low PCV (4.29) and low GCV (3.94) was observed for the seeds per pod along with high heritability (84.31) and low genetic advance as percent of mean (7.46).

Pod length

Pod length had shown moderate PCV (12.23) and GCV (12.16) with high heritability (98.96) and very high genetic advance as percent of mean (24.93).

Table 4.4.1: GCV, PCV, heritability and genetic advance as per cent of mean (GAM) for different quantitative characters based on pooled data of eight environments

	Heritability	GCV	PCV	G.A. % Mean
Plant Height	99.86	17.08	17.1	35.17
Days to 50% Flowering	97.66	6.76	6.84	13.77
Days to Maturity	99.46	8.26	8.28	16.97
Pod on main Stem (no.)	99.9	57.39	57.42	118.16
Pod per Plant (no.)	99.85	29.08	29.1	59.86
Pod per Cluster(no.)	98.66	29.75	29.95	60.88
Seed per Pod (no.)	84.31	3.94	4.29	7.46
Pod Length (cm)	98.96	12.16	12.23	24.93
Branches per Plant (no.)	99.03	43.98	44.2	90.16
100 seed weight (g)	94.44	7.32	7.53	14.66
Biomass per plot (kg)	98.64	18.3	18.43	37.45
Harvest Index (%)	95.79	15.41	15.74	31.06
Cluster per plant (no.)	99.39	29.87	29.97	61.35
Seed yield per Plot (Kg)	98.35	24.65	24.86	50.36
Gum Content (%)	97.94	11.15	11.27	22.74
Protein Content (%)	89.97	5.14	5.42	10.04
TSS (mg/g dry wt.)	91.03	4.31	4.52	8.47
Reducing Sugars (mg/g dry wt.)	91.26	6.6	6.91	12.99
Non-Reducing Sugars (mg/g dry wt.)	85.92	4.01	4.33	7.66
ADF (% dry wt. basis)	95.59	5.35	5.47	10.78
Lignin (% dry wt. basis)	85.52	5.5	5.95	10.48
Cellulose (% dry wt. basis)	92.84	5.7	5.92	11.31
Silica (% dry wt. basis)	96.34	9.06	9.23	18.31
NDF (% dry wt. basis)	97.18	4.85	4.91	9.84
Hemicellulose (% dry wt. basis)	70.79	5.01	5.95	8.68
BLB Disease Intensity (%)	97.52	10.13	10.26	20.62

G.A. % mean: Genetic advance as % of mean

Branches per plant

There was high PCV (44.20) and GCV (43.98) observed for this character and very heritability (99.03) along with genetic advance as percent of mean was also high (90.16).

100 seed weight

For 100 seed weight the PCV (7.53) and low GCV (7.32) observed were low; the heritability (94.44) was found very high and genetic advance as percent of mean (14.66) was observed moderate.

Biomass per plot

Biomass per plot had the moderate level of PCV (18.43) and GCV (18.30) but the very high heritability (98.64) along with the genetic advance as percent of mean was high (37.54).

Harvest index

The PCV (15.74) and GCV (15.41) were moderate but heritability (95.97) along with genetic advance as per cent of mean (31.06) were comparatively high.

Cluster per plant

There was high PCV (29.97) and GCV (29.87) observed for cluster per plant. The heritability (99.39) and genetic advance as percent of mean (61.35) was considerably high.

Seed yield per plot

For seed yield per plot the PCV (24.86) and GCV (24.65) were observed as high and the heritability (98.35) along with genetic advance as percent of mean (50.36) were high.

Gum content

Gum content had moderate range of PCV (11.27) and GCV (11.15), but heritability (97.94) was found high for this character along with the genetic advance as percent of mean (22.74).

Protein content

The protein content had very low PCV (5.42) and GCV (5.14) but high heritability (89.97) with moderate genetic advance as percent of mean (10.04).

Total soluble sugars

Total soluble sugars were found with low for PCV (4.52) and GCV (4.31) but as far as the heritability (91.03) is concerned it was found high along with low genetic advance as percent of mean (8.47).

Reducing sugars

Reducing sugars had low PCV (6.91) and GCV (6.60) but high heritability (91.26) and moderate genetic advance as percent of mean (12.99).

Non-reducing sugars

The PCV (4.33) and GCV (4.01) were observed low for the non-reducing sugars, but heritability (85.92) was high and genetic advance was moderate (7.66).

ADF content

The ADF content had low PCV (5.47) and GCV (5.35) but very high heritability (95.59) and moderate genetic advance (10.78).

Lignin content

The PCV (5.95) and GCV (5.50) were found low for lignin content and heritability was high (85.52) but genetic advance as percent of mean (10.48) was found moderate.

Cellulose content

Cellulose content had low PCV (5.92) and GCV (5.70) values but high heritability (92.84) with moderate genetic advance as percent of mean (11.31).

Silica Content

Silica content had low PCV (9.23) and GCV (9.06) but had high heritability (96.34) along with moderate genetic advance as percent of mean (18.31).

NDF content

The PCV (4.91) and GCV (4.85) values were observed as low for the NDF content, but heritability (97.18) was observed high with low genetic advance (9.84).

Hemicellulose content

The PCV (5.95) and GCV (5.01) values were low for the hemicellulose content, with high heritability (70.79) and low genetic advance (8.68).

BLB disease intensity

BLB intensity had moderate PCV (10.26) and GCV (10.13) but had high heritability (97.52) along with high genetic advance as percent of mean (20.62).

4.5 Phenotypic correlation coefficient analysis based on pooled data of eight environments

The correlation coefficients at phenotypic and genotypic levels among different quantitative characters were studied. These results have been presented in table 4.5.1 and 4.5.2. In almost all the cases, the magnitude of correlation coefficient at genotypic level was higher than their corresponding phenotypic correlation coefficient values. This indicates a good extent of strong inherent association between different characters.

4.5.1 Phenotypic correlation coefficient analysis for yield and component characters

Days to 50% flowering had positive and significant correlation with days to maturity (0.902), plant height (0.912), pods per cluster (0.773), pod length (0.606), but negative significant association with pods per plant (-0.662), branches per plant (-0.576), 100 seed weight (-0.551), biomass per plot (-0.265), harvest index (-0.758), cluster per plant (-0.664) and seed yield per plot (-0.675).

Table: 4.5.1. Phenotypic correlation coefficient analysis for yield and component characters

	PH	DFF	DM	PMS	PPP	PPC	SPP	PL	BPP	100 SW	BMPP	HI	CPP
PH													
D 50%	0.912^{**}												
DM	0.968^{**}	0.902^{**}											
PMS	0.253^{*}	0.033^{NS}	0.146^{NS}										
PPP	-0.481^{**}	-0.662^{**}	-0.553^{**}	0.244^{*}									
PPC	0.875^{**}	0.773^{**}	0.786^{**}	0.464^{**}	-0.424^{**}								
SPP	-0.038^{NS}	-0.196^{NS}	-0.156^{NS}	0.596^{**}	0.370^{**}	0.136^{NS}							
PL	0.544^{**}	0.606^{**}	0.543^{**}	0.039^{NS}	-0.536^{**}	0.537^{**}	0.274^{*}						
BPP	-0.562^{**}	-0.576^{**}	-0.564^{**}	-0.471^{**}	0.631^{**}	-0.709^{**}	-0.209^{NS}	-0.629^{**}					
100 SW	-0.379^{**}	-0.551^{**}	-0.467^{**}	0.322^{**}	0.807^{**}	-0.252^{*}	0.444^{**}	-0.384^{**}	0.411^{**}				
BMPP	-0.024^{NS}	-0.265^{*}	-0.100^{NS}	0.335^{**}	0.793^{**}	-0.010^{NS}	0.287^{*}	-0.372^{**}	0.371^{**}	0.632^{**}			
HI	-0.742^{**}	-0.758^{**}	-0.766^{**}	0.038^{NS}	0.642^{**}	-0.627^{**}	0.268^{*}	-0.428^{**}	0.502^{**}	0.578^{**}	0.080^{NS}		
CPP	-0.616^{**}	-0.731^{**}	-0.664^{**}	-0.022^{NS}	0.934^{**}	-0.595^{**}	0.272^{*}	-0.535^{**}	0.723^{**}	0.764^{**}	0.650^{**}	0.733^{**}	
SYPP	-0.502^{**}	-0.675^{**}	-0.572^{**}	0.242^{*}	0.973^{**}	-0.440^{**}	0.427^{**}	-0.477^{**}	0.582^{**}	0.828^{**}	0.749^{**}	0.702^{**}	0.950^{**}

Table: 4.5.2. Phenotypic correlation coefficient analysis for BLB intensity and quality characters

	GC	PC	TSS	RS	NRS	ADF	Lignin	CellC	Silica	NDF	HCellC
GC											
PC	-0.447^{**}										
TSS	-0.718^{**}	0.427^{**}									
RS	-0.610^{**}	0.442^{**}	0.849^{**}								
NRS	-0.710^{**}	0.401^{**}	0.989^{**}	0.763^{**}							
ADF	0.519^{**}	-0.417^{**}	-0.698^{**}	-0.744^{**}	-0.649^{**}						
Lignin	0.600^{**}	-0.356^{**}	-0.753^{**}	-0.746^{**}	-0.716^{**}	0.840^{**}					
CellC	0.489^{**}	-0.436^{**}	-0.655^{**}	-0.710^{**}	-0.606^{**}	0.969^{**}	0.727^{**}				
Silica	0.469^{**}	-0.492^{**}	-0.666^{**}	-0.730^{**}	-0.614^{**}	0.779^{**}	0.722^{**}	0.744^{**}			
NDF	0.478^{**}	-0.448^{**}	-0.669^{**}	-0.708^{**}	-0.624^{**}	0.977^{**}	0.841^{**}	0.940^{**}	0.772^{**}		
HCellC	0.031^{NS}	-0.308^{**}	-0.161^{NS}	-0.143^{NS}	-0.158^{NS}	0.308^{**}	0.349^{**}	0.270^{*}	0.288^{*}	0.502^{**}	
BLBI	-0.792^{**}	0.487^{**}	0.789^{**}	0.763^{**}	0.756^{**}	-0.780^{**}	-0.803^{**}	-0.727^{**}	-0.642^{**}	-0.759^{**}	-0.224^{NS}

Days to maturity had positive and significant association with plant height (0.968), days to 50% flowering (0.912), pods per cluster (0.786), pod length (0.543) but negatively and significantly correlated with pods per plant (-0.553), branches per plant (-0.564), 100 seed weight (-0.467), harvest index (-0.766), cluster per plant (-0.664) and seed yield per plant (-0.572).

Plant height showed positively correlated with days to maturity (0.968), days to 50% flowering (0.912), pods on main stem (0.253), pods per cluster (0.875), pod length (0.544) while, then negative significant correlation with pods per plant (-0.481), branches per plant (-0.562), 100 seed weight (-0.379), harvest index (-0.742), cluster per plant (-0.731) and seed yield per plant (-0.502).

Pods on main stem showed positive and significant correlation with plant height (0.253), pods per plant (0.244), pods per cluster (0.464), seeds per pod (0.596), 100seed weight (0.322), biomass per plot (0.335), seed yield per plot (0.242) but negatively significant correlation with branches per plant (-0.471) only.

Pods per plant showed positive and significant correlation with pods on main stem (0.244), seed per pod (0.370), branches per plant (0.631), 100 seed weight (0.807), biomass per plot (0.793), harvest index (0.642), cluster per plant (0.943) and seed yield per plot (0.973) but negative and significant correlation with plant height (-0.481), days to 50% flowering (-0.662), days to maturity (-0.553), pods per cluster (-0.424) and pod length (-0.536).

Pods per cluster wad found positively and significant correlated with plant height (0.875), days to 50% flowering (0.773), days to maturity (0.786), pods on main stem (0.464) and pod length (0.573) but were negatively significant correlated with pods per plant (-0.424), branches per plant (-0.709), 100 seed weight (-0.252), harvest index (-0.627), cluster per plant (-0.595) and seed yield per plot (-0.440).

Seed per pod showed positive and significant correlation with pods on main stem (0.596), pods per plant (0.370), pod length (0.274), 100 seed weight (0.444), biomass per plot (0.287), harvest index (0.268), cluster per plant (0.272) and seed yield per plot (0.427).

Pod length was found positively and significantly correlated with plant height (0.544), days to 50% flowering (0.606), days to maturity (0.543), pods per cluster (0.537) and seed per pod (0.274) but negatively and significantly correlated with pods per plant (-0.536), branches per plant (-0.629), 100 seed weight (-0.384), biomass per plot (-0.372), harvest index (-0.428), cluster per plant (-0.535) and seed yield per plot (-0.477).

Branches per plant was positively and significantly correlated with pod per plant (0.631), 100 seed weight (0.411), biomass per plot (0.371), harvest index (0.502), cluster per plant (0.723), seed yield per plot (0.582) and negatively and significantly correlated with plant height (-0.562), days to 50% flowering (-0.576), days to maturity (-0.564), pods on main stem (-0.471), pods per cluster (-0.709) and pod length (-0.629).

100 seed weight was positively and significantly correlated with pods on main stem (0.322), pod per plant (0.807), seed per pod (0.444), branches per plant (0.411), biomass per plot (0.632), harvest index (0.578), cluster per plant (0.764) and seed yield per plot (0.828) but negatively and significantly correlated with plant height (-0.379), days to 50% flowering (-0.551), days to maturity (-0.467), pods per cluster (-0.252) and pod length (-0.384).

Biomass per plot was positively and significantly correlated with pods on main stem (0.335), pod per plant (0.793), seed per pod (0.287), branches per plant (0.371), 100 seed weight (0.632), cluster per plant (0.650) and seed yield per plot (0.749) and negatively and significantly correlated with days to 50% flowering (-0.265) and pod length (-0.372).

Harvest index was positively and significantly correlated with pods per plant (0.642), seed per pod (0.268), branches per plant (0.502), 100 seed weight (0.578), cluster per plant (0.733), seed yield per plot (0.702) while, negatively and significantly correlated with plant height (-0.742), days to 50% flowering (-0.758), days to maturity (-0.766), pods per cluster (-0.627) and pod length (-0.428).

Cluster per plant was positively and significantly correlated with pods per plant (0.934), seeds per pod (0.272), branches per plant (0.723), 100 seed weight (0.764), biomass per plot (0.650), harvest index (0.733), seed yield per plot (0.702) and negatively correlated with plant height (-0.616), days to 50% flowering (-0.731), days to maturity (-0.664), pods per cluster (-0.595) and pod length (-0.535).

Seed yield per plot was found positively and significantly correlated with pods on main stem (0.242), pods per plant (0.973), seeds per pod (0.427), branches per plant (0.582), 100 seed weight (0.828), biomass per plot (0.749), harvest index (0.702), cluster per plant (0.950) but negatively and significantly correlated with plant height (-0.502), days to 50% flowering (-0.675), days to maturity (-0.572), pods per cluster (-0.440) and pod length (-0.477).

4.5.2 Phenotypic correlation coefficient analysis for bacterial leaf blight intensity and quality

Gum content was positively and significantly correlated with ADF content (0.519), lignin content (0.600), cellulose content (0.489), silica content (0.469), NDF content (0.478) but negatively and significantly correlated with protein content (-0.447), total soluble sugar content (-0.718) reducing sugar content (-0.610), non-reducing sugar content (-0.710) and BLB intensity (-0.792).

Protein content was positively and significantly correlated with total soluble sugar content (0.427), reducing sugar content (0.442), non-reducing sugar content (0.401), BLB intensity (0.487) but negatively and significantly correlated with gum content (-0.447), ADF content (-0.417), lignin content (-0.356), cellulose content (-0.436), silica content (-0.492), NDF content (-0.448) and hemicellulose content (-0.308).

Total soluble sugar content was positively and significantly correlated with protein content (0.427), reducing sugar content (0.849), non-reducing sugar content (0.989), BLB intensity (0.789) but negatively and significantly correlated with gum content (-0.718), ADF content (-0.698), lignin content (-0.753), cellulose content (-0.655), silica content (-0.666) and NDF content (-0.669).

Reducing sugar content was positively and significantly correlated with protein content (0.442), total soluble sugar content (0.849),non-reducing sugar content (0.763) and BLB intensity (0.763) but negatively and significantly correlated with gum content (-0.610), ADF content (-0.744), lignin content (-0.746), cellulose content (-0.710), silica content (-0.730) and NDF content (-0.708).

Non-reducing sugar content was positively and significantly correlated with protein content (0.401), total soluble sugar content (0.989), reducing sugar content (0.763), BLB intensity (0.756) but negatively and significantly correlated with gum content (-0.710), ADF content (-0.649), lignin content (-0.716), cellulose content (-0.606), silica content (-0.614) and NDF content (-0.624).

ADF content was positively and significantly correlated with gum content (0.519), lignin content (0.840), cellulose content (0.969), silica content (0.779), NDF content (0.977), hemicellulose content (0.308) but negatively and significantly correlated with protein content (-0.401), total soluble sugar content (-0.698), reducing sugar content (-0.744), non-reducing sugar content (-0.649) and BLB intensity (-0.780).

Lignin content was positively and significantly correlated with gum content (0.600),ADF content (0.840), cellulose content (0.727), silica content (0.722), NDF content (0.841) and hemicellulose content (0.349) but negatively and significantly correlated with protein content (-0.356), total soluble sugar content (-0.753), reducing sugar content (-0.746), non-reducing sugar content (-0.716) and BLB intensity (-0.803).

Cellulose content was positively and significantly correlated with gum content (0.489), ADF content (0.969), lignin content (0.727), silica content (0.744), NDF content (0.940), hemicellulose content (0.270) but negatively and significantly correlated with protein content (-0.436), total soluble sugar content (-0.655), reducing sugar content (-0.710), non-reducing sugar content (-0.606) and BLB intensity (-0.727).

Silica content was positively and significantly correlated with gum content (0.469), ADF content (0.779), lignin content (0.722), cellulose content (0.744), NDF content (0.772), hemicellulose content (0.288) but negatively and significantly correlated with protein content (-0.492), total soluble sugar content (-0.666), reducing sugar content (-0.730), non-reducing sugar content (-0.614) and BLB intensity (-0.642).

NDF content was positively and significantly correlated with gum content (0.478), ADF content (0.977), lignin content (0.841), cellulose content (0.940), silica content (0.772), hemicellulose content (0.502) but negatively and significantly correlated with protein content (-0.448), total soluble sugar content (-0.669), reducing sugar content (-0.708), non-reducing sugar content (-0.624) and BLB intensity (-0.759).

Hemicellulose content was positively and significantly correlated with ADF content (0.649), lignin content (0.716), cellulose content (0.606), silica content (0.614) and NDF content (0.624) but negatively and significantly correlated with protein content (-0.401) and BLB intensity (-0.756).

BLB intensity was positively and significantly correlated with protein content (0.487), total soluble sugar content (0.789), reducing sugar content (0.763), non-reducing sugar content (0.756), but negatively and significantly correlated with gum content (-0.792), ADF content (-0.780), lignin content (-0.803), cellulose content (-0.727), silica content (-0.642) and NDF content (-0.759).

4.6. Path coefficient analysis based on the pooled data of eight environments

To assess the real contribution of an individual character towards dependent characters correlation studies alone are not sufficient. Path coefficient provides a clear and more realistic picture of a complex situation that exists at correlation level. It measures the direct as well as indirect effect of one variable on the dependent variable through the other characters. The path coefficient analysis was done for yield and components and BLB intensity and quality characters. The results have been presented in Table 4.6.1 and 4.6.2. The low residual effect (0.056 and 0.087) indicated high contribution of independent characters to the dependent character *i.e.*, seed yield per plot and BLB intensity.

4.6.1 Path coefficient analysis for yield and component characters. (Residual: 0.0056)

	PH	DFF	DM	PMS	PPP	PPC	SPP	PL	BPP	100 SW	BMPP	HI	CPP	r_{gy}
PH	**0.044**	-0.103	0.014	0.098	0.024	-0.056	0.006	0.104	-0.050	-0.014	-0.001	0.032	-0.603	**-0.506****
DFF	0.040	**-0.110**	0.013	0.013	0.034	-0.050	0.030	0.117	-0.052	-0.020	-0.016	0.033	-0.721	**-0.691****
DM	0.042	-0.102	**0.014**	0.057	0.028	-0.05	0.022	0.104	-0.050	-0.017	-0.006	0.033	-0.651	**-0.578****
PMS	0.011	-0.004	0.002	**0.388**	-0.012	-0.03	-0.087	0.008	-0.042	0.012	0.019	-0.002	-0.022	**0.243***
PPP	-0.021	0.075	-0.008	0.094	**-0.051**	0.027	-0.054	-0.103	0.056	0.029	0.046	-0.028	0.915	**0.981****
PPC	0.039	-0.088	0.011	0.181	0.022	**-0.063**	-0.021	0.104	-0.063	-0.009	-0.001	0.027	-0.585	**-0.448****
SPP	-0.002	0.025	-0.002	0.253	-0.021	-0.01	**-0.133**	0.059	-0.020	0.017	0.018	-0.012	0.296	**0.469****
PL	0.024	-0.068	0.008	0.015	0.027	-0.034	-0.041	**0.191**	-0.056	-0.014	-0.022	0.018	-0.529	**-0.483****
BPP	-0.025	0.065	-0.008	-0.184	-0.032	0.045	0.030	-0.121	**0.088**	0.015	0.022	-0.022	0.713	**0.588****
100 SW	-0.017	0.064	-0.007	0.130	-0.042	0.016	-0.065	-0.076	0.037	**0.035**	0.038	-0.026	0.774	**0.860****
BMPP	-0.001	0.030	-0.001	0.130	-0.04	0.001	-0.042	-0.072	0.033	0.023	**0.058**	-0.004	0.638	**0.755****
HI	-0.032	0.084	-0.011	0.014	-0.032	0.039	-0.038	-0.081	0.044	0.020	0.005	**-0.044**	0.711	**0.707****
CPP	-0.027	0.082	-0.009	-0.009	-0.048	0.038	-0.040	-0.103	0.064	0.027	0.038	-0.032	**0.976**	**0.960****

r_{gy}: Genotypic correlation of component characters with seed yield per plot

4.6.1 Path coefficient analysis for bacterial leaf blight intensity and quality characters. (Residual: 0.0870)

	GC	PC	TSS	RS	NRS	ADF	Lignin	CellC	Silica	NDF	HCellC	r_{gd}
GC	**-0.458**	-0.043	3.213	-0.949	-2.204	0.273	-0.678	-0.402	0.126	0.323	-0.005	**-0.806****
PC	0.217	**0.09**	-2.032	0.733	1.322	-0.227	0.42	0.361	-0.133	-0.313	0.093	**0.531****
TSS	0.349	0.044	**-4.21**	1.376	2.82	-0.371	0.882	0.545	-0.182	-0.46	0.05	**0.838****
RS	0.295	0.045	-3.925	**1.477**	2.52	-0.399	0.837	0.605	-0.201	-0.49	0.042	**0.805****
NRS	0.356	0.042	-4.191	1.313	**2.835**	-0.354	0.873	0.515	-0.172	-0.44	0.051	**0.827****
ADF	-0.248	-0.041	3.1	-1.17	-1.989	**0.504**	-0.929	-0.776	0.208	0.647	-0.112	**-0.803****
Lignin	-0.302	-0.037	3.609	-1.201	-2.403	0.455	**-1.03**	-0.663	0.208	0.584	-0.102	**-0.881****
CellC	-0.235	-0.042	2.928	-1.139	-1.86	0.498	-0.869	**-0.785**	0.199	0.634	-0.098	**-0.768****
Silica	-0.219	-0.046	2.929	-1.135	-1.864	0.4	-0.815	-0.596	**0.262**	0.515	-0.091	**-0.659****
NDF	-0.225	-0.043	2.95	-1.101	-1.899	0.497	-0.916	-0.758	0.205	**0.657**	-0.149	**-0.781****
HCellC	-0.01	-0.033	0.828	-0.245	-0.568	0.223	-0.417	-0.306	0.094	0.387	**-0.252**	**-0.298**^{NS}

r_{gd}: Genotypic correlation of bacterial leaf blight with quality characters

4.6.1 Path coefficient analysis for yield and component characters based on pooled data of eight years

Direct effect

A perusal data of path coefficient analysis observed that cluster per plant (0.976) had highest direct and positive effect on seed yield per plant followed by pods on main stem (0.388), pod length (0.191), branches per plant (0.088), biomass per plot (0.058), plant height (0.044), 100 seed weight (0.035) and days to maturity (0.014). However, seeds per pod (-0.133), days to 50% flowering (-0.111), pods per cluster (-0.063), pods per plant (-0.051) and harvest index (-0.044) showed direct and negative effect on seed yield per plant.

Indirect effects

Days to maturity, pods on main stem, pods per plant, seeds per pod, pod length and harvest index had shown positive indirect effects whereas, days to 50% flowering, pods per cluster, branches per plant, 100 seed weight, biomass per plot and cluster per plant had negative indirect effect on seed yield through plant height.

Plant height, days to maturity, pods on main stem, pods per plant, seeds per pod, pod length and harvest index had shown positive indirect effects whereas, pods per cluster, branches per plant, 100 seed weight, biomass per plot and cluster per plant had negative indirect effect on seed yield through days to 50% flowering.

Plant height, pods on main stem, pods per plant, seeds per pod, pod length and harvest index had shown positive indirect effects whereas, days to 50% flowering, pods per cluster, branches per plant, 100 seed weight, biomass per plot and cluster per plant had negative indirect effect on seed yield through days to maturity.

Plant height, days to maturity, pod length,100-seed weight and biomass per plot had shown positive indirect effects whereas, days to 50% flowering, pods per plant, pods per cluster, seeds per pod, branches per plant, harvest index and cluster per plant had negative indirect effect on seed yield through pods on main stem.

Days to 50% flowering, pods on main stem, pods per cluster, branches per plant,100-seed weight and biomass per plot and cluster per plant plot had shown positive indirect effects whereas, plant height, days to maturity, seeds per pod, pod length, and harvest index had negative indirect effect on seed yield through pods per plant.

Plant height, days to maturity, pods on main stem, pods per plant, pod length and harvest index had shown positive indirect effects whereas, days to 50% flowering, seeds per pod, branches per plant, 100 seed weight, biomass per plot and cluster per plant had negative indirect effect on seed yield through pods per cluster.

Days to 50% flowering, pods on main stem, pod length, 100-seed weight, biomass per plot and clusters per plant had shown positive indirect effects whereas, plant height, days to maturity, pods per plant, pods per cluster, branches per plant and harvest index had negative indirect effect on seed yield through seeds per pod.

Plant height, days to maturity, pods on main stem, pods per plant and harvest index had shown positive indirect effects whereas, days to 50% flowering, pods per cluster, seeds per pod, branches per plant, 100 seed weight, branches per plant, and cluster per plant had negative indirect effect on seed yield through pod length.

Days to 50% flowering, pods per cluster, seeds per pod, branches per plant, 100 seed weight, biomass per plot and cluster per plant had shown positive indirect effects whereas, plant height, days to maturity, pods on main stem, pods per plant, pod length and harvest index had negative indirect effect on seed yield through branches per plant.

Days to 50% flowering, pods on main stem, pods per cluster, branches per plant, biomass per plot and cluster per plant had shown positive indirect effects whereas, plant height, days to maturity, pods per plant, seeds per pod, pod length and harvest index had negative indirect effect on seed yield through100 seed weight.

Days to 50% flowering, pods on main stem, pods per cluster, branches per plant,100 seed weight, and cluster per plant had shown positive indirect effects whereas, plant height, days to maturity, pods per plant, seeds per pod, pod length and harvest index had negative indirect effect on seed yield through biomass per plot.

Days to 50% flowering, pods on main stem, pods per cluster, branches per plant,100 seed weight, biomass per plot and cluster per plant had shown positive indirect effects whereas, plant height, days to maturity, pods per plant, seeds per pod and pod length had negative indirect effect on seed yield through harvest index.

Days to 50% flowering, pods per cluster, branches per plant,100 seed weight and biomass per plot had shown positive indirect effects whereas, plant height, days to maturity, pods on main stem, pods per plant, seeds per pod, pod length and harvest index had negative indirect effect on seed yield through cluster per plant.

4.6.2 Path coefficient analysis for bacterial leaf blight intensity and quality characters based on pooled data of eight environments

Direct effect

A perusal data of path coefficient analysis observed that non-reducing sugar content (2.835) had highest direct and positive effect on BLB intensity followed by reducing sugar content (1.477), NDF content (0.657), ADF content (0.504),silica content (0.262) and protein content (0.090). However, total soluble sugar content (-4.214), lignin content (-1.030), cellulose content (-0.785), gum content (-0.458) and hemicellulose content (-0.252) showed direct and negative effect on BLB intensity.

Indirect effect

BLB intensity was positively and indirectly effected by total soluble sugar content, ADF content, Silica content and NDF content but was negatively and indirectly effected by protein content, reducing sugar content, non-reducing sugar content, lignin content, cellulose content, and hemicellulose content through gum content.

Gum content, reducing sugar content, non-reducing sugar content, lignin content, cellulose content, and hemicellulose content had positive indirect effect *via* protein content on BLB intensity. There was negative indirect effect of total soluble sugar content, ADF content, Silica content and NDF content through protein content on BLB intensity.

Gum content, protein content, reducing sugar content, non-reducing sugar content, lignin content, cellulose content, and hemicellulose content showed negative indirect effects whereas, the three characters ADF content, Silica content and NDF content showed positive indirect effects on BLB intensity *via* total soluble sugars.

Gum content, protein content, non-reducing sugar content, lignin content, cellulose content, and hemicellulose content indicated positive indirect effects while, total soluble sugars, ADF content, Silica content and NDF content showed negative indirect effects on BLB intensity *via* reducing sugar content.

Gum content, protein content, reducing sugar content, lignin content, cellulose content, and hemicellulose content indicated positive indirect effects while, total soluble sugars, ADF content, Silica content and NDF content showed negative indirect effects on BLB intensity *via* non-reducing sugar content.

BLB intensity was positively and indirectly effected by total soluble sugar content, silica content and NDF content but was negatively and indirectly effected by gum content, protein content, reducing sugar content, non-reducing sugar content, lignin content, cellulose content, and hemicellulose content through ADF content.

BLB intensity was positively and indirectly effected by total soluble sugar content, ADF content, silica content and NDF content but was negatively and indirectly effected by gum content, protein content, reducing sugar content, non-reducing sugar content, cellulose content, and hemicellulose content through lignin content.

Total soluble sugar content, ADF content, silica content and NDF content showed positive indirect effect whereas, gum content, protein content, reducing sugar content, non-reducing sugar content, lignin content, and hemicellulose content had negative indirect effect on BLB intensity *via* cellulose content.

BLB intensity was positively and indirectly effected by total soluble sugar content, ADF content, and NDF content but was negatively and indirectly effected by gum content, protein content, reducing sugar content, non-reducing sugar content, lignin content, cellulose content, and hemicellulose content through silica content.

Total soluble sugar content, ADF content and Silica content showed positive indirect effect whereas, gum content, protein content, reducing sugar content, non-reducing sugar content, lignin content, cellulose content and hemicellulose content had negative indirect effect on BLB intensity *via* NDF content.

The characters *viz.,* total soluble sugar content, ADF content and silica content had shown positive indirect effect through hemicellulose content but gum content, protein content, reducing sugar content, non-reducing sugar content, lignin content and cellulose content had negative indirect effect on BLB intensity through hemicellulose content.

4.7 Stability analysis based on Eberhart and Russell's model, 1966

4.7.1 Pooled analysis of variance

The results of pooled analysis of variance on yield and component characters for stability as devised by Eberhart and Russell (1966) are presented in Table 4.7.1. The genotypes showed significant differences for all the characters except hemicellulose content when tested against pooled deviation revealed that the selected genotypes are rich in variation for various characters and may not be showing uniform performance in different environments. Environments showed highly significant differences for all the characters under study when tested against pooled deviation indicating that the environments were different from each other. Whereas, genotype x environment interaction components showed significant differences for the characters *i.e.,* pods per plant, pods per cluster, pod length, branches per plant, harvest index, total clusters, seed yield per plot and protein content when tested against pooled deviation, indicating wide differential behaviour of genotypes in changing environments. Mean sum of squares due to environments + (genotypes x environments) were highly significant for all the character studied except days to maturity and TSS content depicted the distinct nature of environments and genotype x environment interaction on phenotype expression. Significance of environment (linear) component for all the characters when tested against pooled deviation indicated that the genotypes responded linearly for all the characters under study. Mean squares for genotype x environments (linear) which is highly significant except days to 50% flowering, days to maturity,100 seed weight, except gum content (%), TSS, NRS, ADF and hemicellulose indicates that the variation in the performance of genotype is due to the regression of genotypes on environments and the performance is predictable in nature. On other hand high and significant, pooled deviations was found for most of the characters except number of seeds per pod and hemicellulose content indicated the performance of genotypes is entirely unpredictable in nature and mean sum of square for this character will be tested against pooled error.

Table 4.7.1: Pooled ANOVA over eight environments for different characters in cluster bean (Eberhart and Russell, 1966 model)

Source of Variation	D.F.	PH	DFF	DM	P MS	PPP	PPC	SPP	PL	BPP
Genotype	24	7629.470**	135.147**	1780.774**	14173.752**	32656.678**	63.682**	0.992**	11.958**	344.801**
Environment	7	205.114**	84.249**	96.619**	3007.346**	33967.313**	19.728**	2.293**	4.214**	36.612**
Gen. X Envion.	168	29.799	4.203	20.662	158.822	825.173**	1.195*	0.247	0.103*	2.259*
Env+Gen X Env	175	36.812*	7.405**	23.700	272.763**	2150.858**	1.936**	0.329**	0.268**	3.633**
Env (Linear)	1	1435.8**	589.746**	676.332**	21051.420**	237771.192**	138.099**	16.05**	29.496**	256.284**
Env X Gen(Lin)	24	39.011**	4.486	15.128	324.951**	3200.860**	2.997**	0.382*	0.27**	5.179**
Pooled Deviation	150	27.133**	3.99**	20.721**	125.889**	412.056**	0.859**	0.216	0.072**	1.701**
Pooled Error	384	5.02	0.859	2.109	3.295	10.164	0.272	0.193	0.034	1.13
Total	**199**	952.512**	22.811**	235.609**	1949.264**	5829.952**	9.383**	0.409	1.678**	44.779**

Source of Variation	D.F.	100 SW	BMPP	H.I.	CPP	SYPP	GC	PC	TSS	RS
Genotype	24	0.767**	4.339**	0.053**	2770.734**	0.715**	229.862**	30.493**	551.507**	27.871**
Environment	7	7.502**	19.812**	0.071**	1438.409**	1.326**	36.070**	29.145**	261.302*	68.996**
Gen. X Envion.	168	0.189	0.286	0.003**	77.881**	0.023**	3.228	7.221*	114.352	7.889
Env+Gen X Env	175	0.482**	1.067**	0.006**	132.303**	0.075**	4.542*	8.098**	120.23	10.333**
Env (Linear)	1	52.515**	138.687**	0.498**	10068.861**	9.282**	252.492**	204.018**	1829.112**	482.973**
Env X Gen(Lin)	24	0.164	0.598**	0.008**	273.513**	0.062**	1.662	15.960**	108.995	14.469**
Pooled Deviation	150	0.186**	0.225**	0.002**	43.465**	0.016**	3.350**	5.534**	110.635**	6.521**
Pooled Error	384	0.020	0.022	0.001	3.884	0.004	1.572	0.564	15.414	0.575
Total	**199**	0.516**	1.462**	0.011**	450.505**	0.153**	31.716	10.799	172.243	12.448

Source of Variation	D.F.	NRS	ADF	Lignin	CellC	Silica	NDF	HCellC	BLBI
Genotype	24	355.727**	7.397**	0.636**	4.385**	0.272**	9.032**	0.364	336.389**
Environment	7	212.981*	17.207**	0.906**	20.973**	9.852**	37.700**	18.392**	1553.179**
Gen. X Envion.	168	97.639	1.657	0.091	1.319	0.102	1.635	0.329	4.176
Env+Gen X Env	175	102.252	2.279**	0.124**	2.105**	0.492**	3.078**	1.052**	66.137**
Env (Linear)	1	1490.868**	120.450**	6.345*	146.811**	68.961**	263.901**	128.745**	10872.255**
Env X Gen(Lin)	24	82.741	1.791	0.153**	1.625*	0.153**	2.862**	0.204	7.321**
Pooled Deviation	150	96.117**	1.569**	0.078**	1.217**	0.090**	1.373**	0.336	3.506**
Pooled Error	384	15.733	0.082	0.024	0.099	0.003	0.085	0.045	2.972
Total	**199**	132.822	2.896	0.185	2.38	0.466	3.796	0.969	98.73

PH- Plant height, DFF- Days to 50% flowering, DM- Days to maturity, PMS- Pods on main stem, PPP- Pods per plant, PPC- Pods per cluster, SPP- Seeds per pod, PL- Pod length, BPP- Branches per plant, 100SW- 100 seed weight, BMPP- Biomass per plot, HI- Harvest index, CPP- Clusters per plant, SYPP- Seed yield per plot, GC- Gum content, PC- Protein content, TSS- Total soluble sugar, RS- Reducing sugar, NRS- Non-reducing sugar, ADF- Acid detergent fibre, Lignin- Lignin content, CellC- Cellulose content, Silica- Silica content, NDF- Neutral detergent fibre, HCellC- Hemicellulose content, BLBI- Bacterial leaf blight content

4.7.2 Stability parameters

4.7.2.1 Plant height

Mean value for plant height ranged from 65.50 cm (HG 6) to 163.62 cm (PNB) with an overall mean of 104.35cm. Among the genotypes tested, ten genotypes HG 884, HG 3-52, HG 100, X-10, GG-2, RGC 1017, RGC 1038, RGC 1055, RGC 1002 and RGS 3 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.2).

Considering the dwarf genotype as desirable, ten genotypes HG 884, HG 3-52, HG 100, X 10, GG 2, RGC 1017, RGC 1038, RGC 1055, RGC 1002 and RGS 3 recorded low mean value than overall mean, regression coefficient significantly equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable as dwarf genotypes for all the environments. None of the genotype recorded low mean value than overall mean, significant regression coefficient more than or less than unity (bi>1 or bi<1) and non-significant deviation from regression ($S^2di=0$). Therefore no genotype was found suitable as dwarf genotypes for better environment and for poor environment.

The genotypes *viz.* HG 2-20, HG 870, HG 563, HG 365, HG 6, HVG 2-30, FS 277, PNB, GG-1, RGC 936, RGC 1003, RGC 1066, M-83, RGC 1033 and HG 75 with significant deviations from regression exhibited unpredictable performance for plant height.

4.7.2.2 Days to flowering

Mean value for days to 50% flowering ranged from 31days (HG 6) to 42days (PNB) with an overall mean of 35 days. Among the genotypes tested, 12 genotypes HG 2-20, HG 870, HG 563, HG 3-52, X10, GG 2, RGC 1017, RGC 1038,RGC 1002, RGC 1003, RGC 1066 and RGC 1033 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.2).

Eleven genotypes, HG 2-20, HG 870, HG 563, HG 3-52, X 10, GG 2, RGC 1017, RGC 1038, RGC 1003, RGC 1066 and RGC 1033 recorded low or equal mean value than overall mean, regression coefficient significantly more than unity (bi=1)and non-significant deviation from regression ($S^2di=0$)were found suitable as early flowering for all the test environments. None of genotype recorded low mean value than overall mean, regression coefficient significantly more than unity (bi>1) and non-significant deviation from regression ($S^2di=0$) were found suitable for early flowering for better environment. Only one genotype RGC 1033 ($\mu = 34$, bi= 0.486**, $S^2di = -0.049$) recoded with low mean value than overall mean, regression coefficient significantly less than unity (bi<1) and non-significant deviation from regression ($S^2di=0$) were identified for early flowering for poor environment.

The genotypes *viz.* HG 884, HG 365, HG 6, HVG 2-30, HG 100, FS 277, PNB, GG-1, RGC 936, RGC 1055, RGS 3, M-83 and HG 75 with significant deviations from regression exhibited unpredictable performance.

Table: 4.7.2 Stability parameters for plant height and days to 50% flowering of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Plant Height			Days to 50% Flowering		
		Mean	**Bi**	**S^{2}di**	**Mean**	**bi**	**S^{2}di**
1	**HG 2-20**	99.94	0.943	8.192**	34	1.316	-0.002
2	**HG 884**	98.71	0.868	1.615	33	1.293	0.852**
3	**HG 870**	98.39	0.712	12.886**	33	1.284	0.05
4	**HG 563**	99.38	1.092	3.326**	34	1.213	0.041
5	**HG 365**	98.71	1.188	3.884**	33	1.068	0.751**
6	**HG 3-52**	99.75	1.156	-0.758	35	0.964	-0.061
7	**HG 6**	65.5	1.286	10.015**	31	1.811**	0.961**
8	**HVG 2-30**	111.28	0.613	7.987**	36	0.957	2.538**
9	**HG 100**	100.61	0.687	0.937	34	1.102	0.728**
10	**FS 277**	163.62	4.327**	52.654**	41	-0.296**	0.774**
11	**X-10**	98.68	0.795	-0.857	34	0.957	0.068
12	**PNB**	150.3	2.163**	52.937**	42	-0.037**	8.394**
13	**GG-1**	99.06	1.438	7.602**	34	1.149	0.389*
14	**GG-2**	99.45	1.07	-0.006	34	0.986	0.14
15	**RGC 1017**	99.76	0.629	-0.874	34	1.018	-0.062
16	**RGC 1038**	100.64	0.616	0.58	35	1.013	-0.171
17	**RGC 936**	99.64	0.681	1.907*	37	1.023	5.228**
18	**RGC 1055**	100.24	0.656	-1.397	35	1.255	0.773**
19	**RGC 1002**	100.69	0.559	-0.916	35	1.145	0.011
20	**RGC 1003**	100	0.559	2.173*	34	1.13	-0.109
21	**RGC 1066**	107	0.419	6.039**	34	1.234	-0.007
22	**RGS 3**	98.73	1.166	-0.368	35	1.463*	2.089**
23	**M-83**	107.62	1.197	9.274**	36	0.795	0.845**
24	**RGC 1033**	101.85	-0.217**	4.210**	34	0.486**	-0.049
25	**HG 75**	109.15	0.398*	3.218**	37	0.662	1.914**
	Over all Mean	**104.35**			**35**		

4.7.2.3 Days to maturity

Data on days to maturity ranged from 85days (HG 6) to 132days (FS 277) with an overall mean of 104 days. Among the genotypes tested, 12genotypes, HG 2-20, HG 884, HG 870, HG 563, HG 100, X 10, RGC 1017, RGC 1038, RGC 1055, RGC 1003, HG 75 and RGC 1002 exhibited non-significant deviations from regression (S^{2}di) as the genotypes are within the range of minimum deviation from regression and their performance can be predicted very well (Table 4.7.3).

Nine genotypes namely HG 2-20, HG 884, HG 870, HG 563, X 10, RGC 1038, RGC 1055, HG 75 and RGC 1002 recorded low mean value than overall mean, and non-significant deviation from unity (bi=1) as well as non-significant deviation from regression (S^2di=0)were found suitable for early maturity for all environment. None of the genotypes recorded low mean value than overall mean, regression coefficient significantly more than unity (bi>1) and non-significant deviation from regression (S^2di=0) and found suitable for early maturity for better environment. The genotypes namely HG 100, RGC 1017 and RGC 1003 with low mean value than overall mean, regression coefficient significantly less than unity (bi<1) and non-significant deviation from regression (S^2di=0)were identified for early maturity for poor environment.

The genotypes *viz.* HG 365, HG 3-52, HG 6, HVG 2-30, FS 277, PNB, GG-1, GG-2,RGC 936, RGC 1066, RGS 3, M-83 and RGC 1033 with significant deviations from regression exhibited unpredictable performance for days to maturity.

4.7.2.4 Pods on main stem

Mean value for number of pods on main stem ranged from 25.89 (RGC 936) to 148.67 (RGC 1066) with an overall mean of 42.34. Among the genotypes tested, only RGC 1002 exhibited non-significant deviations from regression (S^2di) as this genotype was within the range of minimum deviation from regression, its performance can be predicted very well (Table 4.3.3).

Among the genotypes tested, only RGC 1002 exhibited non-significant deviations from regression (S^2di) and average in response (bi=1), thus have performance over the environment but it was low in mean performance. No genotypes recorded high mean value than overall mean, regression coefficient significantly more than or less than unity and non-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment.

Twenty four genotypes *viz.* HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75 with significant deviations from regression exhibited unpredictable performance for pods on main stem.

4.7.2.5 Pods per plant

The data presented in table 4.7.4 revealed that the pods per plant ranged from 49.02 (PNB) to 176.05 (HG 2-20) with an overall mean of 126.81. All the genotypes tested exhibited significant deviations from regression (S^2di) therefore; their performance cannot be predicted very well.

Table: 4.7.3 Stability parameters for days to maturity and pods on main stem of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Days to Maturity			Pods on main stem		
		Mean	Bi	S^2di	Mean	bi	S^2di
1	**HG 2-20**	101	0.519	0.327	48.13	1.088	3.185**
2	**HG 884**	101	1.416	0.606	42.82	1.033	5.483**
3	**HG 870**	101	0.859	0.365	43.95	0.763**	15.755**
4	**HG 563**	101	1.158	0.243	45.97	1.209**	5.174**
5	**HG 365**	101	0.734	1.487**	43.07	0.949	6.267**
6	**HG 3-52**	102	0.586	1.057*	35.27	1.126*	10.305**
7	**HG 6**	85	1.219	4.506**	34	1.195**	13.545**
8	**HVG 2-30**	116	3.625**	1.36**	32.2	0.322**	41.687*
9	**HG 100**	102	0.413**	0.705	35.12	0.745**	1.967**
10	**FS 277**	132	1.254	10.044**	74.65	1.161*	111.643**
11	**X-10**	101	1.34	0.266	45.9	1.173**	5.381**
12	**PNB**	123	2.313**	39.812**	40.31	0.402**	55.716**
13	**GG-1**	102	1.297	3.918**	24.89	0.318**	44.900**
14	**GG-2**	103	0.954	1.779**	31.98	0.962	34.855**
15	**RGC 1017**	101	0.228**	0.765	37.05	1.297**	8.088**
16	**RGC 1038**	102	0.684	0.287	39.57	0.882	8.013**
17	**RGC 936**	102	0.52	1.204*	25.89	0.726**	24.319**
18	**RGC 1055**	102	0.752	0.067	37.1	1.230**	10.471**
19	**RGC 1002**	102	0.653	0.498	31.4	1.216	0.378
20	**RGC 1003**	102	0.431*	0.648	33.23	1.435**	22.519**
21	**RGC 1066**	102	1.233	1.001*	148.67	3.414**	513.372**
22	**RGS 3**	103	1.254	1.672**	33.28	0.453**	2.613**
23	**M-83**	105	-0.21**	80.451**	28.17	1.276**	16.023**
24	**RGC 1033**	103	0.432*	1.31*	38.98	0.701**	47.779**
25	**HG 75**	109	1.336	0.721	26.85	0.018**	12.174**
	Over all Mean	**104**			**42.34**		

4.7.2.6 Pods per cluster

Mean value for pods per cluster ranged from 4.22 (RGC 936) to 11.07 (FS 277) with an overall mean of 5.46. Among the genotypes tested, 12 genotypes HG 2-20, HG 884, HG 870, HG 563, HG 3-52, HG 6, HG 100, X-10, RGC 1038, RGC 936, RGC 1055 and RGS 3 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.4).

In present study, number of clusters per plant was found significantly and negatively associated with seed yield per plot. Therefore, considering less pod per cluster as desirable feature, the genotypes *viz.* HG 870, HG 563, HG 3-52, HG 6, HG 100, RGC 1038, RGC 936, RGS 3 and RGC 1055 recorded low mean value than overall mean, significant regression coefficient more equal to unity (bi=1) and non-significant deviation from regression (S^2di=0) were found well adapted to all the environment. No genotype recorded low mean value than overall mean, regression coefficient significantly more than unity (bi>1) and non-significant deviation from regression (S^2di=0) or found suitable for better environment. The genotypes namely HG 2-20, HG 884 and X-10 with low mean value than overall mean, regression coefficient significantly less than unity (bi<1) and non-significant deviation from regression (S^2di=0) were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 365, HVG 2-30, FS 277, PNB, GG-1, GG-2, RGC 1017, RGC 1002, RGC 1003, RGC 1066, M-83, RGC 1033 and HG 75with significant deviations from regression exhibited unpredictable performance for pods per cluster.

4.7.2.7 Pod length

Mean value for pod length ranged from 5.35 cm (GG-2) to 8.51 cm (PNB) with an overall mean of 5.79 cm. Among the genotypes tested, 16 genotypes *viz.*, HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 100, FS 277, GG-1, GG-2, RGC 1017, RGC 1055, RGC 1003, RGC 1066 and RGS 3 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.5).

Considering short pod as desirable phenotype, the genotypes *viz.* HG 2-20, HG 884, HG 563, HG 365, HG 3-52, HG 100, GG-1, RGC 1017, RGC 1066 and RGS 3 recorded low mean value, regression coefficient significantly equal to unity (bi=1) and non-significant deviation from regression (S^2di=0) were found suitable for all the environments. The genotypes *viz.* HG 870 and RGC 1055 recorded low mean value while, FS 277 recorded high mean value, significant regression coefficient more than unity (bi>1) and non-significant deviation from regression (S^2di=0) were found suitable for better environment as genotypes with shorter pods and with longer pods, respectively. The genotypes namely GG-2, RGC 1003 and RGC 1033 with low mean value than overall mean, regression coefficient significantly less than unity (bi<1) and non-significant deviation (S^2di=0) from regression were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 6, HVG 2-30, X-10, PNB, RGC 1038, RGC 936, RGC 1002, M-83 and HG 75 with significant deviations from regression exhibited unpredictable performance for pod length.

Table: 4.7.4 Stability parameters for pods per plant and pods per cluster of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Pods per plant			Pods per cluster		
		Mean	Bi	S^2di	Mean	bi	S^2di
1	**HG 2-20**	176.05	1.618**	15.519**	4.93	0.348**	-0.042
2	**HG 884**	164.54	1.619**	50.333**	4.73	0.239**	-0.041
3	**HG 870**	170.62	1.601**	19.913**	4.88	0.920	0.010
4	**HG 563**	175.7	1.896**	94.83**	5.28	0.647	-0.032
5	**HG 365**	165.88	1.600**	35.665**	4.48	0.067**	0.110*
6	**HG 3-52**	133.42	1.083*	16.581**	4.66	0.943	-0.0.13
7	**HG 6**	104.6	0.302**	108.007**	4.63	0.660	0.013
8	**HVG 2-30**	72.28	0.625**	54.828**	5.26	0.999	0.133*
9	**HG 100**	138.14	1.200**	25.682**	5.10	1.255	0.052
10	**FS 277**	79.58	0.167**	146.453**	11.07	2.791**	0.480**
11	**X-10**	166.45	1.482**	89.662**	5.05	0.535*	-0.065
12	**PNB**	49.02	0.128**	62.513**	9.73	0.331**	1.316**
13	**GG-1**	90.48	-0.030**	498.463**	4.30	1.505*	0.456**
14	**GG-2**	118.67	0.809**	218.762**	4.26	0.200**	0.138*
15	**RGC 1017**	145.64	1.584**	364.907**	5.17	1.089	0.161*
16	**RGC 1038**	152.88	1.402**	75.675**	5.21	1.408	0.025
17	**RGC 936**	105.03	0.999**	60.356**	4.22	0.796	-0.042
18	**RGC 1055**	144.00	1.356**	67.545**	4.84	0.647	0.010
19	**RGC 1002**	120.65	1.211**	142.972**	5.67	2.216**	0.263**
20	**RGC 1003**	119.87	1.103**	107.763**	5.52	2.403**	0.136*
21	**RGC 1066**	154.16	1.230**	128.051**	7.25	1.526*	0.708**
22	**RGS 3**	131.65	1.010**	71.354**	4.59	0.733	-0.062
23	**M-83**	72.75	0.434**	46.325**	6.09	2.003**	0.320**
24	**RGC 1033**	139.86	0.641**	482.875**	5.08	0.621	0.308**
25	**HG 75**	78.45	-0.069**	364.057**	4.55	0.118**	0.552**
	Over all Mean	**126.81**			**5.46**		

4.7.2.8 Seeds per pod

Mean value for seeds per pod was ranged from 8.10 (RGC 936) to 9.75 (RGC 1066) with an overall mean of 8.66. Among the genotypes tested, 17 genotypes HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, X-10, GG-1, GG-2, RGC 1038, RGC 1002, RGS 3, RGC 1033 and HG 75 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.5).

Table: 4.7.5 Stability parameters for pod length and seeds per pod of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Pod length			Seeds per pod		
		Mean	**Bi**	**S^2di**	**Mean**	**bi**	**S^2di**
1	**HG 2-20**	5.69	1.02	-0.007	9.04	0.875	0.069
2	**HG 884**	5.49	0.839	-0.001	8.86	0.876	-0.033
3	**HG 870**	5.86	1.658**	0.006	8.85	0.912	0.018
4	**HG 563**	5.57	0.672	0.002	8.83	1.306	0.014
5	**HG 365**	5.53	0.758	-0.001	8.65	1.011	-0.055
6	**HG 3-52**	5.55	0.735	-0.003	8.62	0.752	0.03
7	**HG 6**	5.38	0.922	0.062**	8.48	0.498	0.02
8	**HVG 2-30**	7.14	2.232**	0.024*	8.51	1.193	0.014
9	**HG 100**	5.46	0.779	-0.007	8.64	1.426	-0.048
10	**FS 277**	5.67	1.675**	-0.002	8.18	0.945	0.29**
11	**X-10**	5.54	0.862	0.024**	8.81	0.816	-0.023
12	**PNB**	8.51	0.851	0.068**	8.90	2.24**	0.607**
13	**GG-1**	5.43	0.756	-0.009	8.24	0.832	0.000
14	**GG-2**	5.35	0.385**	-0.002	8.48	0.999	-0.05
15	**RGC 1017**	5.66	1.305	0.001	8.85	2.589**	0.919**
16	**RGC 1038**	5.65	1.440**	0.019*	8.66	0.861	0.005
17	**RGC 936**	5.5	0.752	0.038**	8.1	0.643	0.147**
18	**RGC 1055**	5.71	1.504**	0.002	8.76	1.932**	0.222**
19	**RGC 1002**	5.58	0.829	0.029**	8.25	0.943	0.027
20	**RGC 1003**	5.36	0.177**	0.011	8.66	-0.126**	0.471**
21	**RGC 1066**	5.93	1.003	-0.007	9.75	2.509**	0.259**
22	**RGS 3**	5.47	0.833	0.010	8.39	0.926	0.024
23	**M-83**	6.83	1.803**	0.027**	9.13	-1.044**	0.898**
24	**RGC 1033**	5.59	0.556**	0.007	8.69	0.145**	-0.004
25	**HG 75**	5.37	0.652*	0.02*	8.27	0.939	-0.038
	Over all Mean	**5.79**			**8.66**		

The genotypes *viz.* HG 2-20, HG 884, HG 870, HG 563, HG 365, X-10, RGC 1033 and RGC 1038 were recorded high mean value, significant regression coefficient equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all the environment.

None of the genotype recorded high mean value than overall mean, regression coefficient significantly more than or less than unity and non-significant deviation from regression. Therefore, none the genotype was found specifically adapted for rich and poor environment. The genotypes *viz.* FS 277, PNB, RGC 1017, RGC 936, RGC 1055, RGC 1003, RGC 1066 and M-83 with significant deviations from regression exhibited unpredictable performance for seeds per pod.

4.7.2.9 Branches per plant

Mean value for branches per plant was ranged from 0.91 (RGC 1066) to 11.51 (RGC1038) with an overall mean of 8.61. Among the genotypes tested, 19 genotypes HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 6, HVG 2-30, FS 277, X-10, PNB, GG-1, GG-2, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1066, RGS 3, M-83 and RGC 1033 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.6).

The genotypes *viz.* HG 884, HG 870, HG 563, HG 365, GG-1, RGC 1038, RGC 936, RGC 1055, RGC 1002 and RGC 1033 were recorded high mean value, regression coefficient significantly equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all the environments.

The genotypes *viz.* HG 2-20, X-10, GG-2 and RGS 3 recorded high mean value than overall mean, significant regression coefficient more than unity (bi>1) and non-significant deviation from regression ($S^2di=0$) were found suitable for better environment. None of the genotypes was found with high mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 3-52, HG 100, RGC 1017, RGC 1003 and HG 75 with significant deviations from regression exhibited unpredictable performance for branches per plant.

4.7.2.10 100 seed weight

Mean value for 100 seed weight ranged from 2.18 g (HVG 2-30) to 2.73g (HG 3-52) with an overall mean of 2.42g. Among the genotypes tested, only one genotype HG 563 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, its performance can be predicted very well (Table 4.7.6).

The genotypes *viz.* HG 563 recorded high mean value, significant regression coefficient equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all tested environment. No genotypes recorded high mean value than overall mean, regression coefficient significantly more than or less than unity and non-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment.

The genotypes *viz.* HG 2-20, HG 884, HG 870, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75with significant deviations from regression exhibited unpredictable performance for 100 seed weight.

Table: 4.7.6 Stability parameters for branches per plant and 100 seed weight of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Branches per plant			100 seed weight		
		Mean	bi	S^2di	Mean	bi	S^2di
1	**HG 2-20**	11.23	1.876**	0.121	2.59	0.892	0.050**
2	**HG 884**	10.84	1.305	-0.222	2.55	1.08	0.044**
3	**HG 870**	10.71	0.928	-0.217	2.53	1.15	0.113**
4	**HG 563**	10.19	0.451	-0.062	2.59	0.813	-0.002
5	**HG 365**	10.6	0.957	0.209	2.53	0.997	0.042**
6	**HG 3-52**	10.67	2.003**	0.436*	2.73	0.369**	0.083**
7	**HG 6**	4.76	0.219*	0.047	2.45	0.966	0.064**
8	**HVG 2-30**	2.2	0.365	-0.14	2.17	1.210*	0.010*
9	**HG 100**	10.89	1.557	0.654*	2.48	0.612**	0.017**
10	**FS 277**	1.21	-0.115**	-0.182	2.24	0.903	0.034**
11	**X-10**	10.62	2.025**	0.282	2.64	0.670**	0.152**
12	**PNB**	1.02	-0.279**	-0.277	2.18	1.340**	0.096**
13	**GG-1**	11.07	1.395	0.412	2.29	1.244*	0.044**
14	**GG-2**	10.73	1.666*	0.06	2.33	1.121	0.036**
15	**RGC 1017**	11.13	1.656*	0.656*	2.59	0.867	0.050**
16	**RGC 1038**	11.51	0.753	-0.051	2.65	0.813	0.133**
17	**RGC 936**	10.74	1.45	0.147	2.21	1.013	0.022**
18	**RGC 1055**	10.42	0.666	-0.211	2.33	0.88	0.049**
19	**RGC 1002**	10.82	1.066	0.325	2.32	1.152	0.030**
20	**RGC 1003**	11.2	1.519	0.501*	2.33	1.460**	0.008*
21	**RGC 1066**	0.91	0.012**	-0.221	2.63	0.985	0.049**
22	**RGS 3**	10.87	1.666*	0.055	2.26	1.570**	0.028**
23	**M-83**	4.32	-0.259**	0.266	2.18	1.16	0.024**
24	**RGC 1033**	10.72	1.111	0.139	2.58	0.542**	0.141**
25	**HG 75**	5.75	1.008	2.035*	2.22	1.192	0.062**
	Over all Mean	**8.61**			**2.42**		

4.7.2.11 Biomass per plot

Mean value for biomass per plot ranged from 1.64 kg (PNB) to 3.07kg (HG 2-20) with an overall mean of 2.33kg. Among the genotypes tested, none of the genotype exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well (Table 4.7.7).

4.7.2.12 Harvest index

Mean value for harvest index was ranged from 15.06% (FS 277) to 36.00% (RGC 936) with an overall mean of 30.33%. Among the genotypes tested, 8 genotypes HG 884, HG 870, HG 3-52, HG 6, GG-2, RGC 1017, RGC 1038 and, RGC 1066 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.7).

Table: 4.7.7 Stability parameters for biomass per plot and harvest index of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Biomass per plant			Harvest index		
		Mean	Bi	S^2di	Mean	bi	S^2di
1	**HG 2-20**	3.07	1.514**	0.017**	32.57	1.319	0.0003*
2	**HG 884**	2.81	1.121	0.073**	31.95	1.139	0.0001
3	**HG 870**	2.88	1.206**	0.026**	31.29	0.787	0.0001
4	**HG 563**	2.90	1.313**	0.009**	32.66	1.104	0.0006**
5	**HG 365**	2.64	1.139*	0.033**	32.57	0.779	0.0003*
6	**HG 3-52**	2.31	1.232**	0.025**	33.26	1.502**	0.0000
7	**HG 6**	1.84	0.619**	0.088**	35.11	1.702**	0.0002
8	**HVG 2-30**	1.74	0.755**	0.045**	27.05	0.104**	0.0003*
9	**HG 100**	2.35	1.03	0.032**	31.87	0.846	0.0006**
10	**FS 277**	2.79	0.319**	0.201**	15.06	-0.130**	0.0003*
11	**X-10**	2.97	1.123	0.053**	31.49	1.124	0.0003*
12	**PNB**	1.64	0.422**	0.388**	24.95	1.023	0.0020**
13	**GG-1**	1.93	0.412**	0.014**	29.09	0.056**	0.0004**
14	**GG-2**	2.27	1.165**	0.071**	29.93	0.864	0.0002
15	**RGC 1017**	2.42	1.285**	0.025**	32.50	0.979	0.0002
16	**RGC 1038**	2.42	1.162**	0.026**	32.31	0.917	0.0000
17	**RGC 936**	2.20	1.298**	0.071**	23.59	-0.360**	0.0003*
18	**RGC 1055**	2.17	1.181**	0.005**	36.00	2.081**	0.0008**
19	**RGC 1002**	1.99	1.171**	0.017**	32.61	1.348*	0.0004**
20	**RGC 1003**	2.00	1.276**	0.032**	33.54	2.360**	0.0009**
21	**RGC 1066**	2.47	1.158*	0.022**	34.45	0.983	0.0002
22	**RGS 3**	2.34	1.032	0.047**	30.12	0.822	0.0003**
23	**M-83**	2.00	0.556**	0.224**	21.75	1.419*	0.0009**
24	**RGC 1033**	2.43	0.857*	0.031**	32.27	0.842	0.0006**
25	**HG 75**	1.68	0.654**	0.118**	32.00	1.393*	0.0004**
	Over all Mean	**2.33**			**30.33**		

The genotypes *viz.* HG 884, HG 870, HG 3-52, HG 6, RGC 1017, RGC 1038 and, RGC 1066 recorded high mean value, regression coefficient significantly equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all tested environment. No genotypes recorded high mean value than overall mean, regression coefficient significantly more than or less than unity and non-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment.

The genotypes *viz* HG 2-20, HG 563, HG 365, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, M-83, RGC 1033 and HG 75 with significant deviations from regression exhibited unpredictable performance for harvest index.

4.7.2.13 Clusters per plant

Mean value for cluster per plant was ranged from 13.41 (FS 277) to 52.78 (HG 2-20) with an overall mean of 35.93. Among the genotypes tested, four genotypes HG 6, HG 2-20, HG 884 and HG 563exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.8).

Three genotypes, HG 2-20, HG 884 and HG 563 recorded high mean value than overall mean, regression coefficient significantly more than unity (bi>1) and non-significant deviation from regression ($S^2di=0$) were found suitable for better environment. The genotype, HG 6 was found with mean value higher than over all mean, regression coefficient significantly equal to one and non-significant deviation from regression was found suitable for all the tested environments. But, no genotype with high mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 870, HG 365, HG 3-52, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75 with significant deviations from regression exhibited unpredictable performance for cluster per plant.

4.7.2.14 Seed yield per plot

Mean value for seed yield per plot ranged from 0.39kg (PNB) to 0.98kg (HG 2-20) with an overall mean of 0.70 kg. Among the genotypes tested, the genotypes RGC 1066, HG 2-20 and RGC 1055exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.8).

The genotypes *viz.* RGC 1066 recorded high mean value, regression coefficient significantly equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all tested environment. Two genotypes *viz.*, HG 2-20 and RGC 1055 recorded high mean value than overall mean, regression coefficient significantly more than unity (bi>1) and non-significant deviation from regression ($S^2di=0$) were found suitable for better environment. But, no genotype with high mean value than overall mean, significant regression coefficient less than unity (bi<1) and non-significant deviation from regression ($S^2di=0$) was identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1002, RGC 1003, RGS 3, M-83, RGC 1033 and HG 75 with significant deviations from regression exhibited unpredictable performance for seed yield per plot.

Table: 4.7.8 Stability parameters for clusters per plant and seed yield per plot of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Cluster per plant			Seed yield per plant		
		Mean	**Bi**	**S^2di**	**Mean**	**bi**	**S^2di**
1	**HG 2-20**	52.78	1.829**	-0.683	0.98	1.347**	0.0008
2	**HG 884**	47.64	1.513**	0.826	0.88	1.109	0.0042**
3	**HG 870**	46.86	0.938	10.849**	0.89	1.109	0.0019*
4	**HG 563**	50.57	2.218**	-0.542	0.93	1.469**	0.0021*
5	**HG 365**	46.06	1.510**	3.332**	0.85	1.337**	0.0044**
6	**HG 3-52**	38.38	1.285**	2.85**	0.75	1.313**	0.0021*
7	**HG 6**	34.82	0.973	-0.307	0.63	0.458**	0.0067**
8	**HVG 2-30**	20.65	0.143**	8.227**	0.47	0.512**	0.0041**
9	**HG 100**	37.79	1.508**	22.486**	0.74	1.007	0.0027**
10	**FS 277**	13.41	-0.292**	23.165**	0.42	0.305**	0.0028**
11	**X-10**	47.87	1.419**	11.774**	0.93	1.417**	0.0014*
12	**PNB**	15.37	-0.419**	43.956**	0.39	0.411**	0.0068**
13	**GG-1**	27.21	-0.780**	28.506**	0.56	0.447**	0.0031**
14	**GG-2**	34.88	1.335**	14.23**	0.67	1.059	0.0021*
15	**RGC 1017**	43.95	2.471**	16.909**	0.78	1.655**	0.0065**
16	**RGC 1038**	41.37	11.080	7.328**	0.77	1.172	0.0016*
17	**RGC 936**	26.88	1.472**	14.833**	0.52	1.158	0.0062**
18	**RGC 1055**	40.25	1.510**	2.827**	0.76	1.482**	0.0009
19	**RGC 1002**	33.74	1.392**	11.321**	0.64	1.331**	0.0014*
20	**RGC 1003**	35.06	1.536**	2.126*	0.64	1.291**	0.0025**
21	**RGC 1066**	32.61	0.023**	55.11**	0.84	1.171	0.0006
22	**RGS 3**	36.42	0.739**	14.647**	0.69	0.733**	0.0064**
23	**M-83**	20.91	0.211**	4.413**	0.44	0.492**	0.0168**
24	**RGC 1033**	42.8	0.776*	13.193**	0.77	0.705**	0.0025**
25	**HG 75**	29.97	0.871	18.467**	0.53	0.509**	0.0164**
	Over all Mean	**35.93**			**0.7**		

4.7.2.15 Gum content

Mean value for gum content ranged from 20.98 % (PNB) to 32.18 % (HG 3-52) with an overall mean of 27.65%. Among the genotypes tested, 17 genotypes HG 2-20, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, X-10, GG-1, RGC 1017, RGC 936, RGC 1002, RGC 1003, RGC 1066, RGC 1033 and HG 75 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.9).

The genotypes *viz.* HG 2-20, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X-10, GG-1, RGC 1066, RGC 1033 recorded high mean value, significant regression coefficient equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found well adapted for all tested environment. None of the genotype recorded high mean value than overall mean, significant regression coefficient more than unity (bi>1) and non-significant deviation from regression ($S^2di=0$) were found suitable for better environment. Likewise, no genotype with high mean value than overall mean, significant regression coefficient less than unity (bi<1) and non-significant deviation from regression ($S^2di=0$) were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 884, FS 277, PNB, GG-2, RGC 1038, RGC 1055, and M-83with significant deviations from regression exhibited unpredictable performance for gum content.

4.7.2.16 Protein content

Mean value for protein content was ranged from 19.32 (GG-1) to 23.94% (RGC 1055) with an overall mean of 21.54%. Among the genotypes tested, the genotypes RGC 1066 and RGC 1055 exhibited non-significant deviations from regression ($S^2di=0$) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.9).

None of genotype recorded high mean value, significant regression coefficient equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all tested environment. None of genotype recorded high mean value than overall mean, significant regression coefficient more than unity (bi>1) and non-significant deviation from regression ($S^2di=0$) were found suitable for better environment. But, only one genotype RGC 1066 with high mean value than overall mean, significant regression coefficient less than unity (bi<1) and non-significant deviation from regression ($S^2di=0$) were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1002, RGC 1003, , RGS 3, M-83, RGC 1033 and HG 75with significant deviations from regression exhibited unpredictable performance for protein content.

4.7.2.17 Total soluble sugar (TSS) content

Mean value for TSS content was ranged from 102.65 mg/g dry weight (HG 563) to 119.63 mg/g dry weight (FS 277) with an overall mean of 109.48 mg/g dry weight. Among the genotypes tested, three genotypes, HG 563, FS 277 and RGC 1038exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.10). Considering less TSS content as desirable phenotype, One genotype, RGC 1038 with low mean value than overall mean, significant regression coefficient less than unity (bi>1) and non-significant deviation from regression (S^2di=0) were identified as suitable genotypes for rich environment.

Table: 4.7.9 Stability parameters for gum content and protein content of cluster bean genotypes tested across the environments.

S. No.	**Genotypes**	**Gum content**			**Protein content**		
		Mean	**Bi**	**S^2di**	**Mean**	**bi**	**S^2di**
1	**HG 2-20**	31.05	1.19	0.126	21.57	1.354	0.346*
2	**HG 884**	30.46	1.42	0.645*	20.56	1.298	0.610**
3	**HG 870**	31.01	1.25	-0.036	20.91	1.351	0.979**
4	**HG 563**	29.66	1.12	-0.127	21.12	0.960	4.402**
5	**HG 365**	29.68	0.55	-0.19	21.96	3.199**	1.873**
6	**HG 3-52**	32.18	1.15	0.225	20.73	2.745**	0.449**
7	**HG 6**	27.95	1.21	0.013	22.49	-0.377**	2.367**
8	**HVG 2-30**	22.50	0.26	3.605	22.38	0.63	0.645**
9	**HG 100**	27.82	0.96	-0.062	20.65	-0.044**	0.536**
10	**FS 277**	23.17	1.67	1.004**	23.09	0.771	0.511**
11	**X-10**	30.63	1.01	-0.015	20.69	1.341	0.524**
12	**PNB**	20.98	-0.200**	0.929*	22.75	1.050	0.421**
13	**GG-1**	27.68	1.24	0.099	19.32	1.425	2.794**
14	**GG-2**	28.10	0.94	1.103**	19.99	3.539**	0.650**
15	**RGC 1017**	27.24	0.96	0.208	20.71	-2.553**	2.085**
16	**RGC 1038**	30.07	0.99	0.609*	22.2	1.726**	4.055**
17	**RGC 936**	24.22	1.44	2.478	21.37	-0.942**	2.567**
18	**RGC 1055**	29.2	0.89	1.706**	23.94	-0.068**	-0.047
19	**RGC 1002**	26.05	1.29	-0.351	22.11	1.509	0.492**
20	**RGC 1003**	25.53	1.31	0.338	22.76	0.703	0.299*
21	**RGC 1066**	31.14	0.96	0.384	21.08	0.283**	0.080
22	**RGS 3**	26.67	1.20	0.161	21.00	3.862**	5.671**
23	**M-83**	22.42	0.51	1.575**	22.89	0.850	0.235*
24	**RGC 1033**	28.92	1.16	0.435	20.01	0.619	6.848**
25	**HG 75**	26.83	0.56	-0.049	22.15	-0.231**	2.025**
	Over all Mean	**27.65**			**21.54**		

One genotype, HG 563 with low mean value than overall mean, significant regression coefficient less than unity (bi<1) and non-significant deviation from regression (S^2di=0) were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 2-20, HG 884, HG 870, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75 with significant deviations from regression exhibited unpredictable performance for TSS content.

4.7.2.18 Reducing sugar content

Mean value for reducing sugar content was ranged from 14.21 mg/g dry weight (HG 563) to 18.65 mg/g dry weight (FS 277) with an overall mean of 16.07 mg/g dry weight. Among the genotypes tested, only one genotype, HG 2-20 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.10).

Table: 4.7.10 Stability parameters for TSS content and reducing sugar content of cluster bean genotypes tested across the environments.

S. No.	Genotypes	TSS content			Reducing sugars content		
		Mean	bi	S^2di	Mean	bi	S^2di
1	**HG 2-20**	106.57	1.930*	8.184*	15.95	1.890**	0.154
2	**HG 884**	104.51	1.390	22.697**	15.21	0.541**	1.826**
3	**HG 870**	104.89	2.050*	9.498*	15.92	2.227**	2.967**
4	**HG 563**	102.65	-0.360**	2.705	14.21	-0.586**	1.721**
5	**HG 365**	105.80	3.180**	38.084**	14.7	-0.354**	1.469**
6	**HG 3-52**	108.17	-0.600**	55.995**	15.87	0.790	0.432**
7	**HG 6**	116.37	1.49	61.553**	17.73	2.173**	0.990**
8	**HVG 2-30**	115.06	-0.400**	41.700**	17.44	2.027**	2.636**
9	**HG 100**	107.34	2.030*	23.885**	15.96	0.464**	0.873**
10	**FS 277**	119.63	0.580	2.907	18.65	1.271	0.509**
11	**X-10**	107.21	0.740	43.621**	15.03	0.227**	2.934**
12	**PNB**	117.84	1.790	6.280*	17.93	1.386*	0.326**
13	**GG-1**	115.10	0.850	22.531**	16.28	1.215	1.413**
14	**GG-2**	107.11	-1.910**	60.546**	15.44	-0.587**	2.479**
15	**RGC 1017**	108.53	-0.540**	21.982**	16.02	0.915	0.323**
16	**RGC 1038**	108.01	2.020*	19.208	16.37	1.864**	0.430**
17	**RGC 936**	109.94	-0.320**	35.174**	16.40	0.580	2.491**
18	**RGC 1055**	107.90	2.270**	9.485*	15.92	1.364*	3.388**
19	**RGC 1002**	111.01	1.610	34.745**	16.54	2.233**	1.045**
20	**RGC 1003**	113.93	0.200	95.685**	16.19	1.052	4.972**
21	**RGC 1066**	106.82	0.860	43.742**	16.02	1.036	0.911**
22	**RGS 3**	109.51	2.630**	27.293**	16.09	0.849	6.190**
23	**M-83**	115.53	2.130*	53.510**	16.8	1.776**	2.781**
24	**RGC 1033**	103.36	0.620	24.398**	14.82	-0.327**	2.971**
25	**HG 75**	104.21	0.790	28.097**	14.38	0.975	3.316**
	Over all Mean	**109.48**			**16.07**		

Considering less reducing sugar content as desirable, none of the genotype recorded lower mean value than overall mean, significant regression coefficient equal to unity (bi=1) and non-significant deviation from regression (S^2di=0) was found suitable for all tested environment. Only one genotype, HG 2-20 recorded lower mean value than overall mean, significant regression coefficient more than unity (bi>1) and non-significant deviation from regression (S^2di=0) were found suitable for better environment. But, no genotype with lower mean value than overall mean, significant regression coefficient less than unity (bi<1) and non-significant deviation from regression (S^2di=0) was identified as suitable genotypes for poor environment.

The genotypes *viz* .HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75 with significant deviations from regression exhibited unpredictable performance for reducing sugar content.

4.7.2.19 Non-reducing sugar content

Mean value for non-reducing sugar content ranged from 88.44 mg/g dry weight (HG 563) to 100.98 mg/g dry weight (FS 277) with an overall mean of 93.41mg/g dry weight. Among the genotypes tested, the genotype, FS 277 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.11).

Considering less non-reducing sugar content as desirable, None of the genotype recorded lower mean value than overall mean, significant regression coefficient more than unity (bi>1) and non-significant deviation from regression (S^2di=0) were found suitable for better environment.

Likewise, none of the genotype with lower mean value than overall mean, significant regression coefficient less than unity (bi<1) and non-significant deviation from regression (S^2di=0) were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75with significant deviations from regression exhibited unpredictable performance for non-reducing sugar content.

4.7.2.20 Acid detergent fibre (ADF) content

Mean value for ADF content ranged from 9.29 % dry weight basis (HVG 2-30) to 11.33% dry weight basis (HG 75) with an overall mean of 10.29 % dry weight basis. Among the genotypes tested, none of the genotype exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well (Table 4.7.11).

4.7.2.21 Lignin content

Mean value for lignin content ranged from 2.54% dry weight basis (M-83) to 3.15% dry weight basis (HG 75) with an overall mean of 2.88 % dry weight basis. Among the genotypes tested, 10 genotypes, HG 2-20, RGC 1017, RGC 1066,PNB, HG 884, HG 365, HVG 2-30, M-83, X-10 and RGS 3 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.12).

Table: 4.7.11 Stability parameters for TSS content and reducing sugar content of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Non-reducing sugars content			ADF content		
		Mean	Bi	S^2di	Mean	bi	S^2di
1	HG 2-20	90.62	0.940	5.477**	10.01	1.033	0.492**
2	HG 884	89.30	1.560	13.667**	10.21	-0.369**	0.491**
3	HG 870	88.97	1.060	9.178**	10.29	1.438**	0.045*
4	HG 563	88.44	0.060	5.087**	10.96	1.545**	0.586**
5	HG 365	91.11	3.810**	27.480**	10.49	1.078	0.884**
6	HG 3-52	92.30	0.330	61.336**	10.39	1.772**	0.323**
7	HG 6	98.64	0.880	51.637**	9.57	1.086	0.170**
8	HVG 2-30	97.62	-0.980**	26.499**	9.29	0.584**	0.212**
9	HG 100	91.39	1.110	24.398**	10.50	-0.036**	0.516**
10	FS 277	100.98	0.900	1.753	9.45	0.879	0.407**
11	X-10	92.18	0.820	30.443**	11.14	0.446**	0.242**
12	PNB	99.91	1.270	8.619*	9.40	0.752	0.290**
13	GG-1	98.83	2.150*	22.292**	10.07	0.726*	0.714**
14	GG-2	91.67	-1.370**	60.554**	10.12	0.574**	0.059**
15	RGC 1017	92.50	-0.340**	19.629**	10.72	1.156	0.469**
16	RGC 1038	91.65	1.520	16.169**	10.81	1.097	0.800**
17	RGC 936	93.54	0.040	25.027**	10.40	1.545**	1.406**
18	RGC 1055	91.98	2.190*	6.672*	9.67	1.405**	0.274**
19	RGC 1002	94.47	0.150	18.185**	10.40	2.381**	1.000**
20	RGC 1003	97.74	0.660	71.702**	10.58	1.830**	0.484**
21	RGC 1066	90.80	1.680	45.004**	10.72	0.272**	0.659**
22	RGS 3	93.42	2.180*	40.481**	10.41	0.635**	0.621**
23	M-83	98.73	3.270**	42.443**	9.54	0.821	0.103**
24	RGC 1033	88.54	0.640	25.470**	10.67	0.846	0.781**
25	HG 75	89.83	0.470	10.666**	11.33	1.505**	0.363**
	Over all Mean	**93.41**			**10.29**		

Three genotypes, HG 2-20, RGC 1017 and RGC 1066 recorded high mean value, significant regression coefficient equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all tested environment. Four genotypes, HG 884 and HG 365 recorded high mean value than overall mean, significant regression coefficient more than unity (bi>1) and non-significant deviation from regression (S^2di=0) were found suitable for better environment. Likewise, only two genotypes, X-10 and RGS 3 with high mean value than overall mean, significant regression coefficient less than unity (bi<1) and non-significant deviation from regression (S^2di=0) were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 870, HG 563, HG 3-52, HG 6, HG 100, FS 277, GG-1, GG-2, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1033 and HG 75 with significant deviations from regression exhibited unpredictable performance for lignin content.

Table: 4.7.12 Stability parameters for lignin content and cellulose content of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Lignin content			Cellulose content		
		Mean	**Bi**	**S^2di**	**Mean**	**bi**	**S^2di**
1	**HG 2-20**	2.93	0.500	0.0056	7.22	0.821	0.285**
2	**HG 884**	2.91	1.754*	0.0004	7.28	-0.175**	0.360**
3	**HG 870**	2.91	1.369	0.0302**	7.43	1.279*	0.069**
4	**HG 563**	3.10	0.088**	0.0223**	7.93	1.538**	0.346**
5	**HG 365**	2.96	2.437**	0.0017	7.52	0.854	0.597**
6	**HG 3-52**	2.86	1.336	0.0102*	7.67	1.396**	0.323**
7	**HG 6**	2.77	0.827	0.0260**	6.76	1.031	0.106**
8	**HVG 2-30**	2.57	2.246**	0.0083	6.61	0.670*	0.060*
9	**HG 100**	2.87	1.279	0.0337**	7.62	0.425**	0.467**
10	**FS 277**	2.65	1.878**	0.0379**	6.75	0.874	0.159**
11	**X-10**	3.11	0.295*	0.0009	7.94	0.639**	0.269**
12	**PNB**	2.66	1.353	-0.0034	6.72	0.804	0.244**
13	**GG-1**	2.77	1.454	0.0288**	7.27	0.575**	0.470**
14	**GG-2**	2.80	0.951	0.0416**	7.30	0.605**	0.090**
15	**RGC 1017**	2.92	0.745	0.0074	7.84	1.097	0.385**
16	**RGC 1038**	2.99	0.783	0.0113*	7.71	1.113	0.683**
17	**RGC 936**	3.00	-0.614**	0.0285**	7.47	1.590**	0.816**
18	**RGC 1055**	2.87	1.058	0.0242**	6.82	1.140	0.242**
19	**RGC 1002**	2.83	0.864	0.0377**	7.51	2.113**	0.682**
20	**RGC 1003**	2.85	1.355	0.0530**	7.73	2.165**	0.504**
21	**RGC 1066**	2.97	0.569	0.0074	7.75	0.431**	0.613**
22	**RGS 3**	2.94	0.287*	0.0019	7.46	0.591**	0.548**
23	**M-83**	2.54	2.200**	0.0041	7.00	0.972	0.098**
24	**RGC 1033**	3.13	0.304*	0.0125*	7.57	0.962	0.725**
25	**HG 75**	3.15	-0.319**	0.0175**	8.19	1.491**	0.178**
	Over all Mean	**2.88**			**7.40**		

4.7.2.22 Cellulose content

Mean value for cellulose content ranged from 6.61% dry weight basis (HVG 2-30) to 8.19% dry weight basis (HG 75) with an overall mean of 7.40 % dry weight basis. Among the genotypes tested, none of genotype exhibited non-significant deviations from regression

(S^2di) as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well (Table 4.7.12).

4.7.2.23 Silica content

Mean value for silica content ranged from 1.02% dry weight basis (M-83) to 1.45 % dry weight basis (HG 75) with an overall mean of 1.16 % dry weight basis. Among the genotypes tested, none of the genotype exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well (Table 4.7.13).

Table: 4.7.13 Stability parameters for silica content and NDF content of cluster bean genotypes tested across the environments.

S. No.	Genotypes	Silica content			NDF content		
		Mean	**Bi**	**S^2di**	**Mean**	**bi**	**S^2di**
1	**HG 2-20**	1.19	0.902**	0.026**	12.28	1.161*	0.503**
2	**HG 884**	1.15	1.182**	0.015**	12.62	0.066**	0.566**
3	**HG 870**	1.24	0.583**	0.076**	12.65	1.066	0.124**
4	**HG 563**	1.38	0.598**	0.085**	13.06	1.600**	0.389**
5	**HG 365**	1.17	1.395**	0.012**	12.84	0.838	1.230**
6	**HG 3-52**	1.13	0.928*	0.017**	12.58	0.955	0.304**
7	**HG 6**	1.05	0.838**	0.005**	11.72	0.85	0.219**
8	**HVG 2-30**	1.07	1.212**	0.002**	11.54	0.358**	0.112**
9	**HG 100**	1.21	1.288**	0.043**	12.76	0.659**	0.601**
10	**FS 277**	1.03	0.962	0.001*	11.92	0.450**	0.633**
11	**X-10**	1.29	0.814**	0.036**	13.54	1.027	0.192**
12	**PNB**	1.04	0.998	0.001*	11.56	0.720**	0.232**
13	**GG-1**	1.27	1.468**	0.104**	12.42	0.123**	0.252**
14	**GG-2**	1.12	1.055	0.012**	12.4	0.914	0.126**
15	**RGC 1017**	1.18	0.708**	0.014**	13.09	1.325**	0.598**
16	**RGC 1038**	1.19	1.324**	0.041**	13.08	1.612**	0.513**
17	**RGC 936**	1.13	0.957	0.041**	12.86	2.534**	0.399**
18	**RGC 1055**	1.06	0.999	0.027**	11.78	1.080	0.097**
19	**RGC 1002**	1.12	0.875**	0.018**	12.71	0.850	0.924**
20	**RGC 1003**	1.07	1.001	0.004**	12.83	1.146	0.723**
21	**RGC 1066**	1.17	1.237**	0.004**	13.07	0.937	0.623**
22	**RGS 3**	1.16	0.714**	0.039**	12.96	0.845	0.284**
23	**M-83**	1.02	0.992	0.002**	11.67	0.820*	0.204**
24	**RGC 1033**	1.23	1.119**	0.020**	13.04	1.523**	0.679**
25	**HG 75**	1.45	0.850**	0.085**	13.85	1.539**	0.215**
	Over all Mean	**1.16**			**12.59**		

4.7.2.24 Neutral detergent fibre (NDF) content

Mean value for NDF content ranged from 11.54% dry weight basis(HVG 2-30) to 13.85% dry weight basis (HG 75) with an overall mean of 12.59 % dry weight basis. Among the genotypes tested, none of the genotype exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well (Table 4.7.13).

4.7.2.25 Hemicellulose content

Mean value for hemicellulose content ranged from 2.10% dry weight basis (HG 563) to 2.54 % dry weight basis (RGS 3) with an overall mean of 2.31 % dry weight basis. Among the genotypes tested, five genotypes HG 870, HG 100, GG-1, RGC 1038, RGC 1017 and HG 6 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.7.14).

Two genotypes, HG 870 and GG-1 recorded high mean value, regression coefficient significantly equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all tested environment. RGC 1038 was found stable but poorly adapted as it showed low mean than the overall mean. Only one genotype, RGC 1017 recorded high mean value than overall mean, significant regression coefficient more than unity (bi>1) and non-significant deviation from regression ($S^2di=0$) were found suitable for better environment. Likewise, only one genotype, HG 6 with high mean value than overall mean, significant regression coefficient less than unity (bi<1) and non-significant deviation from regression ($S^2di=0$) were identified as suitable genotypes for poor environment.

The genotypes *viz.* HG 2-20, HG 884, HG 563, HG 365, HG 3-52, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-2, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75 with significant deviations from regression exhibited unpredictable performance for hemicellulose content.

4.7.2.26 Bacterial leaf blight intensity

Mean value for bacterial leaf blight intensity, ranged from 33.35% (HG 75) to 46.24% (PNB) with an overall mean of 36.79%. Among the genotypes tested, 23 genotypes, HG 2-20, HG 884, HG 870, HG 563, , HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, RGC 1033 and HG 75 exhibited non-significant deviations from regression (S^2di) as the genotypes are within the range of minimum deviation from regression, their performance can be predicted very well (Table 4.3.14).

Out of 25 genotypes, 17 genotypes, HG 2-20, HG 884, HG 870, HG 563, HG 3-52, HG 100, X-10, GG-2, RGC 1017, RGC 1038, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, RGC 1033 and HG 75 recorded low mean value than overall mean, significant regression coefficient equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all tested environment with less susceptibility against bacterial leaf blight while, HVG 2-30, FS 277 and PNB were found stable but highly susceptible in all the environments. Only one genotype, RGC 936 recorded low mean value than overall mean, significant regression coefficient more than unity (bi>1) and non-significant deviation from regression ($S^2di=0$) were found suitable for better environment with leas BLB intensity. Likewise, only two genotypes, HG 6 and GG-1withlow mean value than overall mean, significant regression coefficient less than unity (bi<1) and non-significant deviation from regression ($S^2di=0$) were identified as suitable genotypes for poor environment with least BLB intensity.

The genotypes *viz.* HG 365 and M-83 with significant deviations from regression exhibited unpredictable performance for bacterial leaf blight intensity.

Table: 4.7.14 Stability parameters for hemicellulose content and bacterial leaf blight intensity of cluster bean genotypes tested across the environments.

S. No.	**Genotypes**	**Hemi cellulose**			**BLB intensity**		
		Mean	**Bi**	**S^2di**	**Mean**	**bi**	**S^2di**
1	**HG 2-20**	2.28	1.019	0.042**	34.88	1.015	-0.448
2	**HG 884**	2.41	1.288**	0.032**	35.17	0.884	0.2
3	**HG 870**	2.36	0.884	0.002	34.78	1.073	0.452
4	**HG 563**	2.10	1.086	0.190**	34.17	1.019	0.24
5	**HG 365**	2.35	1.197*	0.055**	35.03	0.808*	1.422*
6	**HG 3-52**	2.19	0.874	0.062**	35.53	0.98	1.011
7	**HG 6**	2.15	0.648**	0.004	37.08	0.761**	-0.094
8	**HVG 2-30**	2.25	0.959	0.023*	43.27	1.09	-0.404
9	**HG 100**	2.26	0.606**	-0.003	35.48	1.137	-0.417
10	**FS 277**	2.47	0.971	0.148**	45.43	1.154	-0.496
11	**X-10**	2.39	1.224*	0.181**	33.55	0.954	0.62
12	**PNB**	2.15	1.141	0.129**	46.24	0.887	-0.41
13	**GG-1**	2.35	1.016	0.014	36.71	0.688**	0.413
14	**GG-2**	2.28	1.237*	0.062**	35.68	0.945	-0.671
15	**RGC 1017**	2.37	1.279**	0.001	35.26	1.127	-0.701
16	**RGC 1038**	2.28	0.939	-0.01	35.17	1.147	-0.18
17	**RGC 936**	2.46	1.139	0.129**	35.42	1.226**	0.747
18	**RGC 1055**	2.11	0.997	0.151**	36.03	1.019	-0.217
19	**RGC 1002**	2.30	0.714**	0.272**	36.1	0.972	0.118
20	**RGC 1003**	2.26	0.752**	0.174**	36.24	1.067	-0.091
21	**RGC 1066**	2.35	0.799*	0.200**	34.69	1.021	-0.328
22	**RGS 3**	2.54	0.89	0.307**	35.39	0.97	-0.068
23	**M-83**	2.13	1.295**	0.070**	44.69	1.092	3.563**
24	**RGC 1033**	2.37	0.995	0.098**	34.31	0.885	0.192
25	**HG 75**	2.52	1.051	0.090**	33.35	1.078	-0.005
	Over all Mean	**2.31**			**36.79**		

4.7.3 Environmental indices

Environment index reveals the suitability of an environment at a particular location. Breeze (1969) pointed out that the estimates of environment index can provide the basis for identifying the favourable environment for the expression of maximum potential of the genotype.

Based on the positive values of environment indices conclude the favourable environment for genotypes. Environmental indices of all characters studies are presented in the table 4.7.15.The environment, HS 19 was found to be most favourable production environment for most of the characters *viz.*, days to 50% flowering, pods on main stem, pods per plant, pods per cluster, seeds per pod, pod length, biomass per plant, clusters per plant, seed yield per plot, gum content, TSS content and non-reducing sugar content. Whereas, BK 19 was found to be the most unfavourable for days to maturity, pods on main stem, pods per plant, pods per cluster, seeds per pod, pod length, branches per plant, biomass per plant, clusters per plant, seed yield per plot, gum content, non-reducing sugar content and hemicellulose content.

Table 4.7.15: Environmental indices for yield, its component, quality characters and bacterial leaf blight intensity across the environments in cluster bean

Characters	HS 19	BS 19	HK 19	BK 19	HS 20	BS 20	HK 20	BK 20	Mean
PH	-0.14	1.20	2.58	-1.47	-0.17	-2.55	1.32	-0.77	**104.35**
DFF	2.44	-0.64	-0.30	-0.59	0.25	0.12	-0.94	-0.35	**35.00**
DM	-0.55	0.58	0.91	-2.03	1.59	-0.52	0.59	-0.57	**104.00**
PMS	7.50	5.94	5.59	-10.16	2.69	-2.96	-3.31	-5.28	**42.34**
PPP	27.84	-1.26	10.23	-30.89	21.50	-0.54	2.54	-29.43	**126.81**
PPC	0.67	0.36	0.49	-0.95	0.03	-0.14	-0.20	-0.26	**5.46**
SPP	0.42	-0.03	-0.13	-0.43	0.25	0.20	0.10	-0.38	**8.67**
PL	0.24	0.14	0.10	-0.39	0.15	0.07	0.03	-0.35	**5.79**
BPP	0.66	0.48	0.02	-1.25	0.91	-0.44	0.01	-0.39	**8.61**
100 SW	0.27	-0.33	0.04	0.47	0.31	-0.27	-0.17	-0.33	**2.42**
BMPP	0.75	-0.62	0.07	-0.62	0.67	-0.02	-0.02	-0.22	**2.32**
HI	0.00	0.06	0.01	0.02	-0.03	-0.03	-0.03	0.01	**0.30**
CPP	7.55	-0.54	4.14	-5.31	1.72	-2.64	-0.28	-4.65	**35.93**
SYPP	0.25	-0.11	0.04	-0.16	0.12	-0.08	-0.01	-0.05	**0.70**
GC	1.10	0.74	-0.64	-0.78	-0.14	-0.68	0.36	0.05	**27.65**
PC	-0.15	0.17	0.01	-0.24	-0.11	0.53	-1.18	0.96	**21.54**
TSS	2.61	1.75	-0.74	-1.95	-1.12	-0.01	1.83	-2.36	**109.48**
RS	-0.07	-0.50	0.07	-0.17	-1.28	1.10	1.64	-0.78	**16.07**
NRS	2.68	2.25	-0.81	-1.78	0.16	-1.12	0.19	-1.57	**93.41**
ADF	-0.05	0.80	-0.82	0.49	-0.20	-0.01	-0.12	-0.09	**10.29**
Lignin	0.01	0.01	0.14	-0.12	-0.20	0.09	0.06	0.01	**2.88**
CellC	-0.06	0.79	-0.96	0.60	0.00	-0.09	-0.18	-0.10	**7.40**
Silica	-0.42	-0.43	0.21	-0.34	0.01	0.47	0.09	0.41	**1.16**
NDF	-0.32	1.02	-1.12	0.10	0.87	0.22	-0.39	-0.38	**12.59**
HCellC	-0.27	0.23	-0.31	-0.39	1.07	0.23	-0.27	-0.29	**2.31**
BLBI	-6.81	-2.63	2.55	5.79	-4.39	-0.10	-0.10	5.69	**36.79**

Characters:

PH- Plant height, DFF- Days to 50% flowering, DM- Days to maturity, PMS- Pods on main stem, PPP- Pods per plant, PPC- Pods per cluster, SPP- Seeds per pod, PL- Pod length, BPP- Branches per plant, 100SW- 100 seed weight, BMPP- Biomass per plot, HI- Harvest index, CPP- Clusters per plant, SYPP- Seed yield per plot, GC- Gum content, PC- Protein content, TSS- Total soluble sugar, RS- Reducing sugar, NRS- Non-reducing sugar, ADF- Acid detergent fibre, Lignin- Lignin content, CellC- Cellulose content, Silica- Silica content, NDF- Neutral detergent fibre, HCellC- Hemicellulose content, BLBI- Bacterial leaf blight content

Environments:

HS 19- Hisar summer 2019, BS 19- Bawal summer 2019, HK 19- Hisar *kharif* 2019, BK 19- Bawal *kharif* 2019, HS 20- Hisar summer 2020, BS 20- Bawal summer 2020, HK 20- Hisar *kharif* 2020, BK 20- Bawal *kharif* 2020

4.8 Stability analysis based on AMMI model (Gauch and Zobel, 1997)

4.8.1 Pooled analysis of variance

The combined analysis (Table 4.8.1) of variance showed that mean sum of squares due to genotypes and environments were significant for all the characters. This indicated the presence of variability among the genotypes and environments. The Genotype x Environment interaction (GEI) was significant for all the 26 characters. The AMMI analysis of variance (Table 4.8.1) for seed yield per plot across the environments showed that 30.57 % of the total variation was attributed to genotypic effects, 56.48 % to environmental effects and 12.94 % to genotype × environment interaction effects. The presence of GEI was clearly demonstrated by the AMMI model, indicating the substantial differences in genotypic response across the environments. The G x E interaction was portioned among the first three interaction principal component axis (IPCA), as they were 61.82 %, 14.24 % and 11.48 % respectively; and the cumulative variance was about 87.55 % for PCAI, PCAII and PCA III. This implies that the interaction of the 25 cluster bean genotypes with eight environments was predicted by the first three components of genotypes and environments. For the remaining characters the various components of ANOVA *viz.*, genotypic effect, environment effect, G x E effect and PCA axis were clearly demonstrated in Table 4.8.1.

4.8.2 Stability parameters

4.8.2.1 Plant height

AMMI 1 biplot display:

Genotypes or environments that appear on a perpendicular line of a graph had similar mean yields and those that fall almost on a horizontal line had similar interactions (Crossa *et al.*, 1990 a & b). Genotypes or environments on the right side of the midpoint of the perpendicular line have higher mean value those on the left side. As a result, the plant height of genotypes including, HG 6, HG 870, X-10, HG 884, HG 365, RGS 3, GG-1, HG 563, GG-2, RGC 936, HG 3-52, RGC 1017, HG 2-20, RGC 1003, RGC 1055, HG 100, RGC 1038, RGC 1002 and RGC 1033was recorded less than the overall mean and negative genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 1066, M-83, HG 75, HVG 2-30, PNB and FS 277 were found tall and with positive genotypic index were adapted to unfavourable environments. Considering the dwarf stature as desirable, the environments lying on the left side are favourable environments and those lying on right side are unfavourable. Therefore, environments HS 19, BK 19, HS 20, BS 20 and BK 20 were present on the left hand side of the midpoint of the main effect axis with negative environmental index, seemed to be rich environments, while BS 19, HK 20 and HK 19 with positive environmental index were generally poor environments (Figure 4.8.1 (a)).

Table 4.8.1: AMMI analysis for various characters in cluster bean across different environments

Source of Variation	DF	PH	% Explained	DFF	% Explained	DM	% Explained
Genotype	**7**	205.114**	0.76	84.249**	12.99	96.619**	1.44
Environment	**24**	7629.497**	96.60	135.147**	71.45	1780.774**	91.15
Gen. X Envion.	**168**	29.799**	2.64	4.203**	15.56	20.662**	7.40
PCA I	**30**	64.494**	38.65	9.669**	41.08	77.936**	67.36
PCA II	**28**	59.173**	33.10	7.522**	29.83	14.403**	11.62
PCA III	**26**	22.283**	11.57	3.161**	11.64	10.727**	8.03
Pooled Error	**400**	5.088	0.00	0.865	0.00	2.22	0.00

Source of Variation	DF	PMS	% Explained	PPP	% Explained	PPC	% Explained
Genotype	**7**	3007.346**	5.43	33967.313**	20.49	19.728**	7.40
Environment	**24**	14173.752**	87.69	32656.678**	67.56	63.682**	81.85
Gen. X Envion.	**168**	158.822**	6.88	825.173**	11.95	1.195**	10.75
PCA I	**30**	577.493**	64.93	2983.466**	64.56	2.901**	43.35
PCA II	**28**	135.814**	14.25	860.307**	17.38	1.734**	24.19
PCA III	**26**	106.622**	10.39	383.201**	7.19	1.145**	14.83
Pooled Error	**400**	3.354	0.00	10.09	0.00	0.304	0.00

Source of Variation	DF	SPP	% Explained	PL	% Explained	BPP	% Explained
Genotype	**7**	6.878**	19.72	4.214**	8.84	36.612**	2.88
Environment	**24**	2.976**	29.26	11.958**	85.97	344.801**	92.86
Gen. X Envion.	**168**	0.741**	51.02	0.103**	5.19	2.259**	4.26
PCA I	**30**	1.391**	33.52	0.271**	46.93	5.124**	40.51
PCA II	**28**	1.187**	26.69	0.155**	25.12	3.458**	25.51
PCA III	**26**	0.737**	15.39	0.074**	11.05	1.893*	12.97
Pooled Error	**400**	0.194	0.00	0.033	0.00	1.105	0.00

PH- Plant height, DFF- Days to 50% flowering, DM- Days to maturity, PMS- Pods on main stem, PPP- Pods per plant, PPC- Pods per cluster,

SPP- Seeds per pod, PL- Pod length, BPP- Branches per plant,

Source of Variation	**DF**	**100 SW**	**% Explained**	**BMPP**	**% Explained**	**H.I.**	**% Explained**
Genotype	**7**	7.502**	51.12	19.812**	47.68	0.071**	22.43
Environment	**24**	0.767**	17.91	4.339**	35.80	0.052**	56.65
Gen. X Envion.	**168**	0.189**	30.97	0.286**	16.53	0.003**	20.92
PCA I	**30**	0.393**	37.08	0.907**	56.57	0.009**	56.01
PCA II	**28**	0.314**	27.65	0.330**	19.19	0.003**	19.64
PCA III	**26**	0.189**	15.46	0.168**	9.08	0.002**	11.36
Pooled Error	**400**	0.021	0.00	0.022	0.00	0.001	0.00

Source of Variation	**DF**	**CPP**	**% Explained**	**SYPP**	**% Explained**	**GC**	**% Explained**
Genotype	**7**	1438.409**	11.23	1.326**	30.57	36.070**	4.00
Environment	**24**	2770.734**	74.17	0.714**	56.49	229.862**	87.41
Gen. X Envion.	**168**	77.881**	14.59	0.023**	12.94	3.228**	8.59
PCA I	**30**	273.713**	62.76	0.081**	61.82	6.634**	36.70
PCA II	**28**	68.047**	14.56	0.020**	14.24	4.835**	24.96
PCA III	**26**	51.895**	10.31	0.017**	11.49	2.642*	12.67
Pooled Error	**400**	3.984	0.00	0.003	0.00	1.655	0.00

Source of Variation	**DF**	**PC**	**% Explained**	**TSS**	**% Explained**	**RS**	**% Explained**
Genotype	**7**	29.145**	9.49	261.302**	5.34	68.996**	19.50
Environment	**24**	30.493**	34.05	551.507**	38.62	27.871**	27.00
Gen. X Envion.	**168**	7.221**	56.45	114.352**	56.05	7.889**	53.50
PCA I	**30**	15.965**	39.48	194.520**	30.38	20.305**	45.96
PCA II	**28**	9.162**	21.14	160.014**	23.32	8.416**	17.78
PCA III	**26**	9.026**	19.34	111.327**	15.07	6.748**	13.24
Pooled Error	**400**	0.564	0.00	15.588	0.00	0.561	0.00

100SW- 100 seed weight, BMPP- Biomass per plot, HI- Harvest index, CPP- Clusters per plant, SYPP- Seed yield per plot, GC- Gum content, PC- Protein content, TSS- Total soluble sugar, RS- Reducing sugar

Source of Variation	DF	NRS	% Explained	ADF	% Explained	Lignin	% Explained
Genotype	**7**	212.981**	5.64	17.207**	20.90	0.906**	17.19
Environment	**24**	355.727**	32.30	7.397**	30.81	0.636**	41.34
Gen. X Envion.	**168**	97.639**	62.06	1.657**	48.29	0.091**	41.47
PCA I	**30**	171.486**	31.36	2.668**	28.76	0.177**	34.59
PCA II	**28**	149.461**	25.51	2.435**	24.50	0.121**	22.09
PCA III	**26**	110.509**	17.52	2.226**	20.79	0.099**	16.88
Pooled Error	**400**	15.871	0.00	0.089	0.00	0.025	0.00

Source of Variation	DF	CellC	% Explained	Silica	% Explained	NDF	% Explained
Genotype	**7**	20.973**	31.00	9.852**	74.42	37.700**	34.94
Environment	**24**	4.385**	22.22	0.272**	7.03	9.032**	28.70
Gen. X Envion.	**168**	1.319**	46.79	0.102**	18.55	1.635**	36.37
PCA I	**30**	2.057**	27.85	0.193**	33.76	2.818**	30.77
PCA II	**28**	2.012**	25.42	0.143**	23.25	2.066**	21.06
PCA III	**26**	1.872**	21.97	0.120**	18.08	1.756**	16.62
Pooled Error	**400**	0.103	0.00	0.003	0.00	0.092	0.00

Source of Variation	DF	HCellC	% Explained	BLB I	% Explained
Genotype	**7**	18.392**	66.77	1553.179**	55.34
Environment	**24**	0.364**	4.53	336.389**	41.09
Gen. X Envion.	**168**	0.329**	28.70	4.176**	3.57
PCA I	**30**	0.732**	39.71	9.464**	40.46
PCA II	**28**	0.479**	24.24	5.295*	21.13
PCA III	**26**	0.335**	15.74	4.307	15.96
Pooled Error	**400**	0.044	0.00	3.08	0.00

NRS- Non-reducing sugar, ADF- Acid detergent fibre, Lignin- Lignin content, CellC- Cellulose content, Silica- Silica content, NDF- Neutral detergent fibre, HCellC- Hemicellulose content, BLBI- Bacterial leaf blight content

Genotypes or environments with large IPCA1 scores, either positive or negative had large interactions whereas, genotypes or environments with IPCA1 score of zero or nearly zero had smaller interactions (Crossa *et al.*,1990 a & b). The genotypes with large interactions are specifically adapted to particular environment. The HS 20, BS 20, HK 19, HS 19 and BS 19 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HK 19 and BS 19 were found to have above overall mean. Therefore, these environments were not suitable by keeping in view the importance of dwarf stature as desirable. Similarly, the genotypes HG 3-52, HG 884, RGC 1033, RGS 3, RGC 1017, RGC 1055, RGC 1002, GG-2, GG-1, RGC 1038, HG 870, HG 6, HG 563, RGC 936, HG 365 and HG 2-20 had near zero score on the first IPCA1indicating that these genotypes were less influenced by the environments and are stable genotypes. All of these, genotypes registered below overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to dwarf stature of genotype at that particular environment.

AMMI 2 biplot between IPAC1 vs. IPAC2:

In AMMI 2 biplot, the environmental scores are joined to the origin by side lines. Environments with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction. The environment BS 20 had short spokes and it did not exert strong interactive forces while HS 19, BS 19, HK 19, BK 19, HS 20, HK 20 and BK 20 with long spokes were more differentiating environments. The genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction. In the present study, the genotypes, HG 884, HG 3-52, HG 100, X 10, GG 1, GG 2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGS 3 and RGC 1033 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 20, HG 870, HG 365, HG 563, HG 6, HVG 2-30, FS 277, PNB, RGC 1003, RGC 1066, M 83 and HG 75 found more responsive since they were away from the origin (Figure 4.8.1(b)).Genotypes and environments that fall in the same sectors interact positively; negatively if they fall in opposite sectors. If they fall into adjacent sectors, interaction is somewhat more complex. The best genotypes with respect to HS 20, BS 20 and HK 20 were HG 2-20, HG 870, HG 563, HG 365, RGC 1033 and RGC 1066 with respect to HK 19, BS 19 and HS 19 were HG 100 and FS 277; with respect to BK 20 and BK 19 were HG 884, HG 6, HVG 2-30, X 10, RGC 936, RGC 1055 and RGS 3. On other hand, genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their better adaptation to that particular environment. In this case, the best adapted genotypes for BS 20 was RGC 1033.

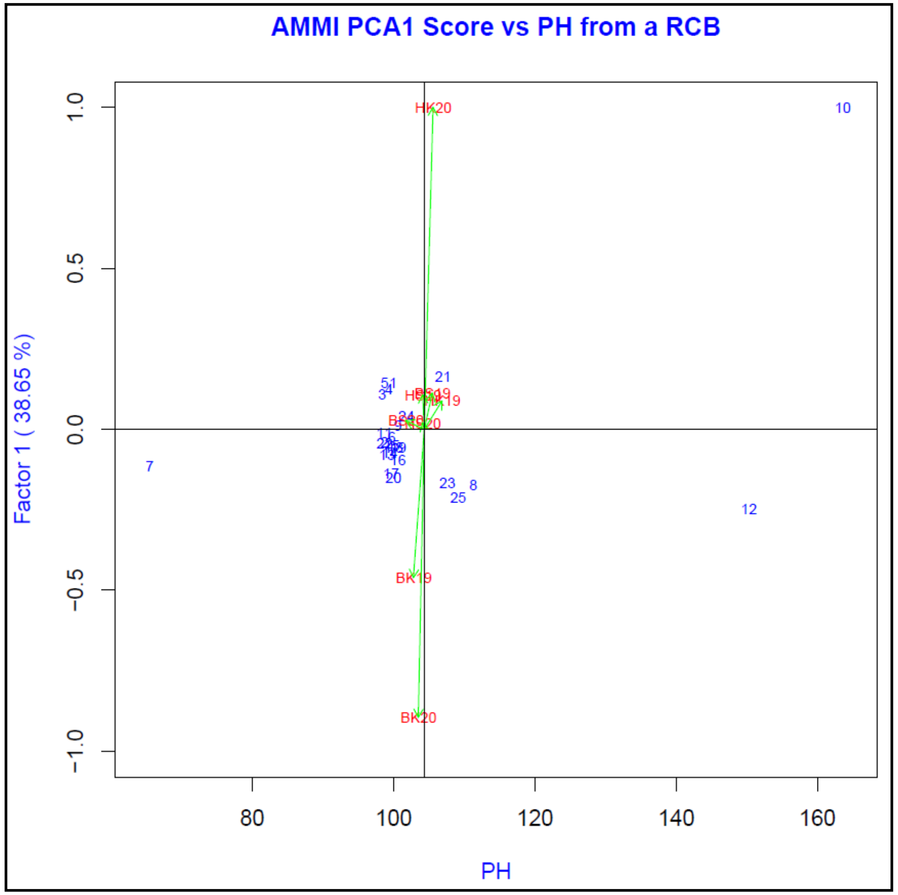

Figure 4.8.1 (a): AMMI 1 biplot for plant height of 25 cluster bean genotypes and eight environments using genotypic and environmental scores

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

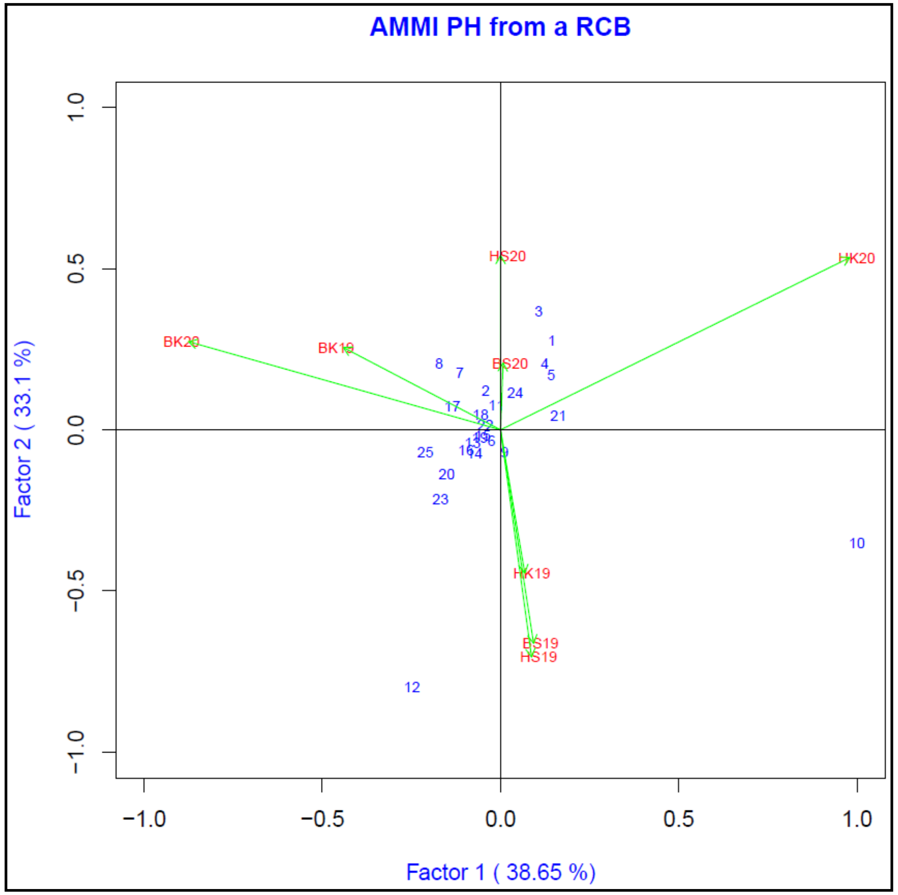

Figure 4.8.1 (b): AMMI 2 biplot for plant height showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

4.8.2.2 Days to flowering

AMMI 1 biplot display:

The genotypes namely, HG 6, HG 884, HG 870, HG 365, RGC 1033, RGC 1003, RGC 1066, GG-2, GG-1, HG 2-20, HG 563, RGC 1017, X-10, HG 100, RGS 3, RGC 1038, HG 3-52 and RGC 1055 had number of days to flowering less than the overall mean and negative genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 1002, HVG 2-30, M-83, RGC 936, HG 75, FS 277 and PNB were generally late in flowering and with positive genotypic index were adapted to unfavourable environments.

Considering the early flowering as desirable, the environments lying on the left side are favourable environments and those lying on right side are unfavourable. Therefore, environments HK 20, BS 19, BK 19, BK 20 and HK 19 were present on the left hand side of the midpoint of the main effect axis with negative environmental index, seemed to be rich environments, while BS 20, HS 20 and HS 19with positive environmental index were generally poor environments (Figure 4.8.2 (a)).The environments BK 19 and HS 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HS 20 was found to have above overall mean. Therefore, this environment was not suitable by keeping in view the importance of early flowering as desirable. Similarly, the genotypes X-10, RGC 1038, HG 884, HG 365, RGC 1002, RGC 1033, RGC 1055, RGS 3, HG 100, HG 3-52, HG 563, RGC 1066, RGC 1017, GG-2, HG 2-20, HG 870, M-83, RGC 1003 and GG-1had near zero score on the first IPCA1indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 884, HG 870, HG 365, RGC 1033, RGC 1003, RGC 1066, GG-2, GG-1, HG 2-20, HG 563, RGC 1017, X-10, HG 100, RGS 3, RGC 1038, HG 3-52 and RGC 1055registered below overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to early flowering of genotype at that particular environment. Genotypes, M 83 and RGC 936 were identified as specifically adapted to the HS 20 and HS 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 20 and HK 20 had short spokes and they do not exert strong interactive forces while BK 19, BK 20, BS 19, HK 19, HS 19 and HS 20 with long spokes were more differentiating environments. In the present study, the genotypes, RGC 1017, RGC 1066, HG 563, RGC 1002, RGC 1038, X-10, HG 3-52, GG-1, GG-2, RGC 1003 and RGC 1033 were close to the origin and hence they were non sensitive to environmental interactive forces whereas RGC 936, HG 6, HVG 2-30, HG 2-20, HG 365, HG 884, RGC 1055, RGS 3, HG 100, HG 870, M-83, HG 75, FS 277 and PNB found more responsive since they were away from the origin (Figure 4.8.2 (b)). The best genotypes with respect to BK 19 and HS 19 were HG 3-52, FS 277, X 10, PNB and M 83; with respect to BS 19, HK 19 and HK 20 were HG 870, HG 100, RGC 1055, RGS 3 and HG 75; with respect to BK 20 and BS 20 were HG 6, HVG 2-30, GG 2, RGC 1038, RGC 936, RGC 1002, RGC 1003, RGC 1066 and RGC 1033; and with respect to HS 19 were HG 2-20, HG 884, HG 563, HG 365, GG 1 and RGC 1017. In this case, the best adapted genotypes for BS 20 was HG 6; for BK 20wasRGC 936; for BS 19 was RGS 3; for HK 19 and HK 20wasHG 75; for BK 19 and HS 20 was M 83.

4.8.2.3 Days to maturity

AMMI 1 biplot display:

The genotypes namely, HG 6, HG 365, HG 563, X-10, HG 884, RGC 1017, HG 870, HG 2-20, RGC 1003, RGC 1066, RGC 1002, HG 100, RGC 1038, GG-1, HG 3-52, RGC 936, RGC 1055, RGS 3, GG-2 and RGC 1033 had number of days to maturity less than the overall mean and negative genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, M-83, HG 75, HVG 2-30, PNB and FS 277 were generally late in maturity and with positive genotypic index were adapted to unfavourable environments. Considering the early maturity as desirable, the environments lying on the left side are favourable environments and those lying on right side are unfavourable. Therefore, environments BK 19, BK 20, HS 19 and BS 20were present on the left hand side of the midpoint of the main effect axis with negative environmental index, seemed to be rich environments, while BS 19, HK 20, HK 19 and HS 20with positive environmental index were generally poor environments (Figure 4.8.3 (a)). The environments BK 19, BS 20, HS 20 and HK 19 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HS 20and HK 19were found to have above overall mean. Therefore, these environments were not suitable by keeping in view the importance of early maturity as desirable. Similarly, the genotypes RGC 1003, RGC 936, GG-2, RGC 1017, RGC 1002, HG 365, X-10, RGC 1066, RGC 1055, HG 100, RGC 1038, HG 3-52, HG 563, RGC 1033, HG 2-20, GG-1, HG 884, HG 870, HG 75, RGS 3, HG 6 and FS 277 had near zero score on the first IPCA1indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, RGC 1003, RGC 936, GG-2, RGC 1017, RGC 1002, HG 365, X-10, RGC 1066, RGC 1055, HG 100, RGC 1038, HG 3-52, HG 563, RGC 1033, HG 2-20, GG-1, HG 884, HG 870, RGS 3 and HG 6 registered below overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments.

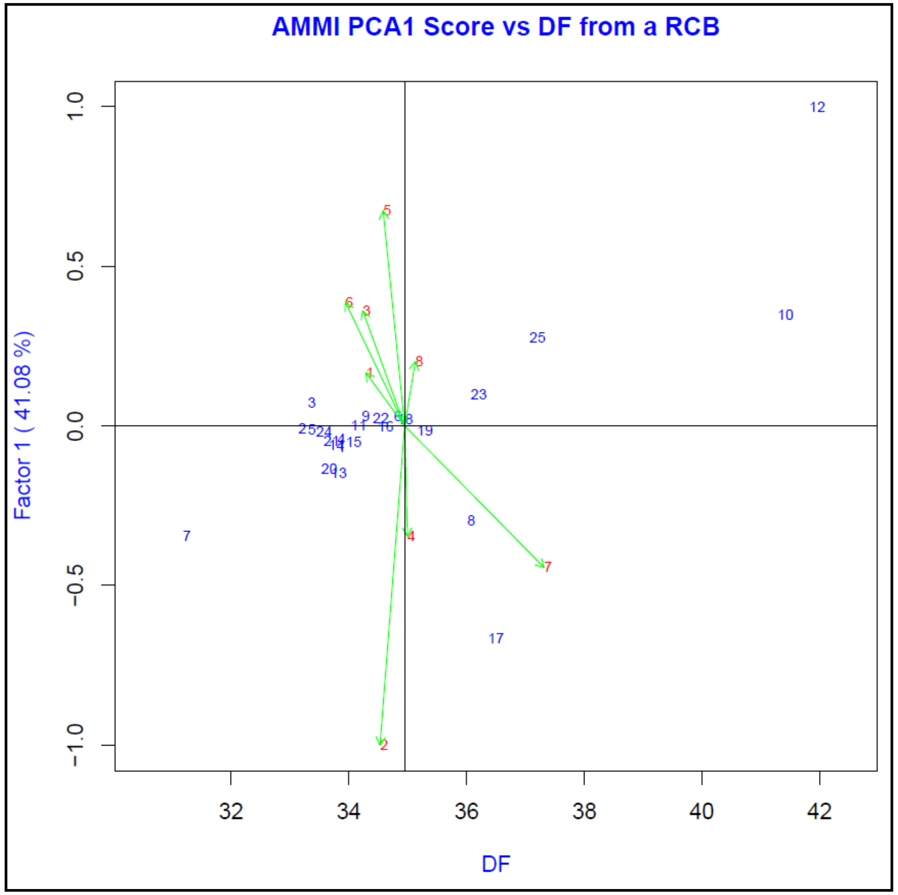

Figure 4.8.2 (a): AMMI 1 biplot for days to 50% flowering of 25 cluster bean genotypes and eight environments using genotypic and environmental scores.

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

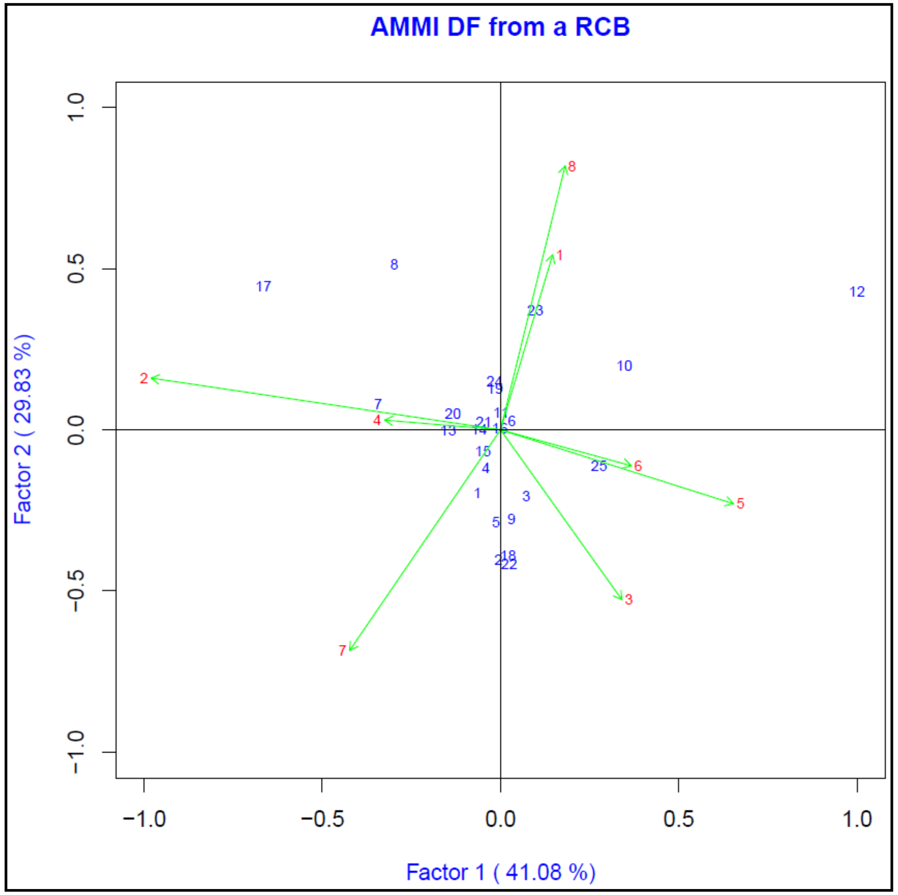

Figure 4.8.2 (b): **AMMI 2 biplot for days to 50% showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to early maturity of genotype at that particular environment. Genotype, HG 75 identified as specifically adapted to the HK 19, HK 20 and HS 20and these environments were considered as the favourable environments for HG 75.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BK 19, HS 19, HS 20, HK 20 and BS 19had short spokes and they do not exert strong interactive forces while BK 20, BS 20 and HK 19with long spokes were more differentiating environments. In the present study, the genotypes, HG 884, HG 870, HG 563, HG 365, HG 3-52, X-10, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3 and HG 75 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HVG 2-30, HG 6, HG 100, FS 277, PNB, GG-1, M-83 and RGC 1033 found more responsive since they were away from the origin (Figure 4.8.3 (b)). The best genotypes with respect to BK 19, HK 19 and HS 20 were HG 2-20, HG 563, HG 3-52, HG 6, GG 1 and RGC 1033; with respect to HS 19, BS 19 and HK 20 were HG 884, HG 870, HVG 2-30, FS 277, PNB, RGS 3 and HG 75; with respect to BS 20 were HG 365, HG 100, X 10, GG 2, RGC 1017, RGC 1055, RGC 1002 and RGC 1066; and with respect to BK 20 were RGC 1038, RGC 936 and M 83. In this case, the best adapted genotypes for HS 19 was HG 6; for BS 19 were PNB; for HK 19 and HK 20were HVG 2-30 and FS 277: for BK 20wasM 83.

4.8.2.4 Pods on main stem

AMMI 1 biplot display:

The genotypes namely, RGC 1066, FS 277, HG 2-20, HG 563, X-10, HG 870, HG 365 and HG 884 had pods on main stem more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 1038, RGC 1033, RGC 1055, RGC 1017, HG 3-52, HG 100, HG 6, RGS 3, RGC 1003, HVG 2-30, GG-2, RGC 1002, M-83, HG 75, RGC 936 and GG-1 were generally with less pod bearing on main stem and with negative genotypic index were adapted to unfavourable environments. Considering the high pod bearing on main stem as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments PNB, HS 19, BS 19, HK 19 and HS 20were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BS 20, HK 20, BK 20 and BK 19withnegative environmental index were generally poor environments (Figure 4.8.4 (a)). The environments HK 20, HK 19 and BS 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HK 20 and HK 19 were found to have below overall mean.

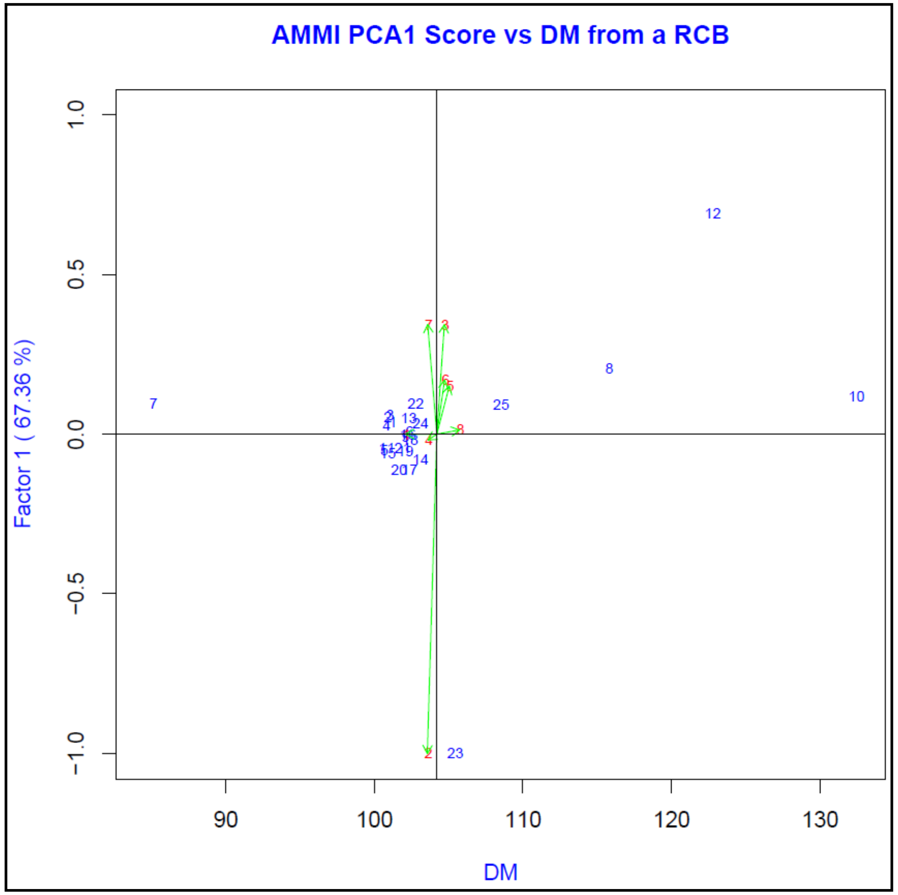

Figure 4.8.3 (a): **AMMI 1 biplot for days to maturity of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

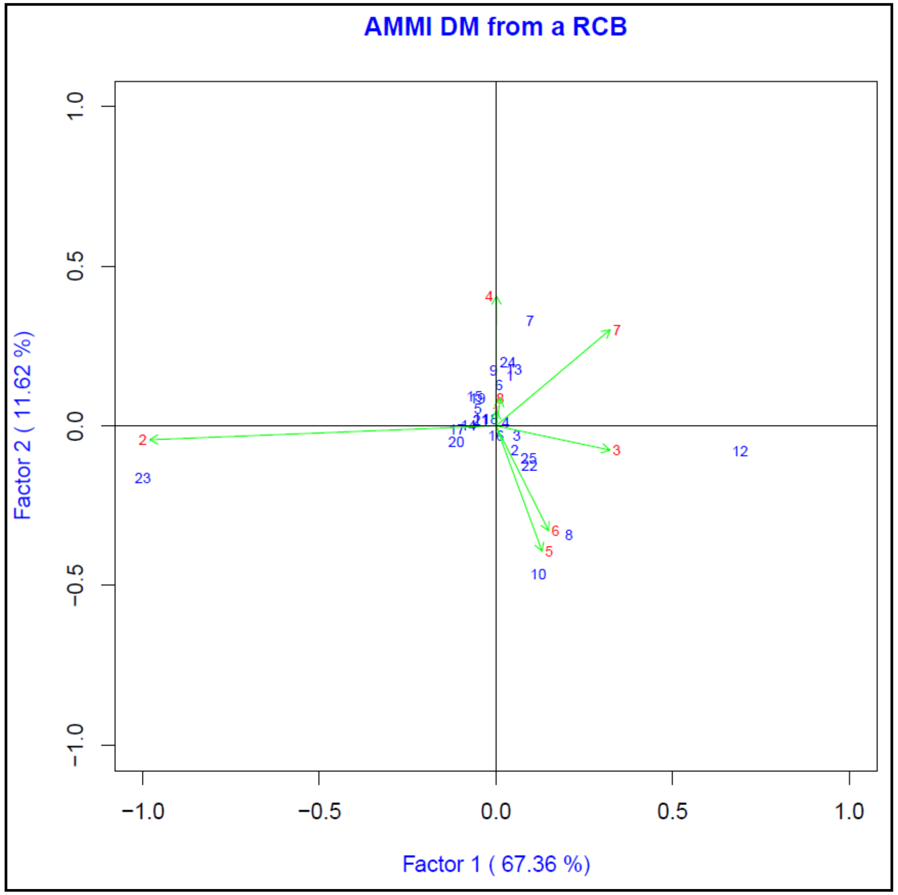

Figure 4.8.3 (b): **AMMI 2 biplot for days to maturity showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Therefore, these environments were not suitable by keeping in view the importance of high pod bearing on main stem as desirable. Similarly, the genotypes X-10, PNB, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, M-83, RGC 1033 and HG 75 had near zero score on the first IPCA1indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 2-20, HG 884, HG 870, HG 563, HG 365 and X-10registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to high pod bearing on main stem of genotype at that particular environment. Genotypes, HG 870, HG 365 and HG 884; HG 6 and RGC 1033 were identified as specifically adapted to the BS 19 and HK 19; HK 20and BS 20 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 20 and HK 20 had short spokes and they do not exert strong interactive forces while BK 19, BK 20, BS 19, HK 19, HS 19 and HS 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X-10, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, M-83 and RGC 1033 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HVG 2-30, FS 277, PNB, GG-1, RGC 1066, RGS 3 and HG 75 found more responsive since they were away from the origin (Figure 4.8.4 (b)). The best genotypes with respect to BS 19, BS 20 and HK 19 were HG 2-20, HG 884, HG 870, HG 365, FS 277, GG-1, GG-2, RGC 1055 and RGC 1002; with respect to BK 19 and BK 20were HVG 2-30, HG 100, RGC 936, RGS 3, RGC 1033 and HG 75; with respect to HS 19were HG 563, HG 3-52, X-10, RGC 1017, RGC 1003, RGC 1066 and M-83; and with respect to HK 20 and HS 20 were HG 6, PNB and RGC 1038. In this case, the best adapted genotypes for BS 19 and HK 19 was FS 277; for BK 19 and BK 20 were HG 75 and for HS 19was RGC 1066.

4.8.2.5 Pods per plant

AMMI 1 biplot display:

The genotypes namely, HG 2-20, HG 563, HG 870, X-10, HG 365, HG 884, RGC 1066, RGC 1038, RGC 1017, RGC 1055, RGC 1033, HG 100, HG 3-52 and RGS 3 had pods per plant more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 1002, RGC 1003, GG-2, RGC 936, HG 6, GG-1, FS 277, HG 75, M-83, HVG 2-30 and PNB were generally with fewer pods and with negative genotypic index were adapted to unfavourable environments.

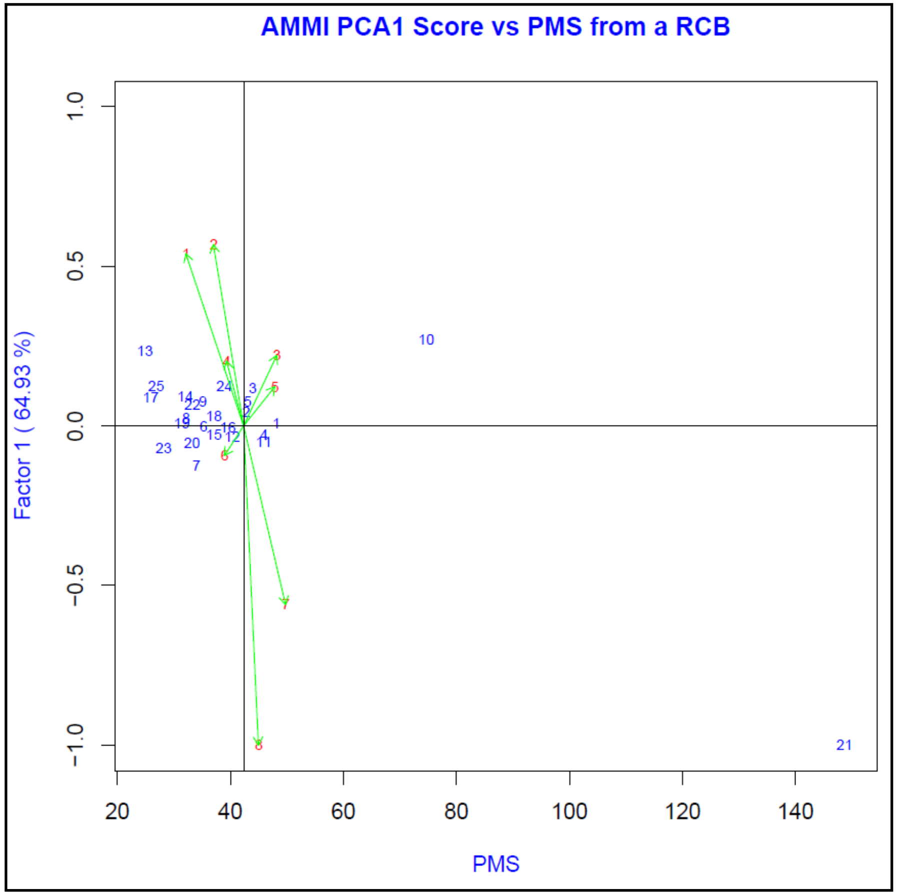

Figure 4.8.4 (a): **AMMI 1 biplot for pods on main stem of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

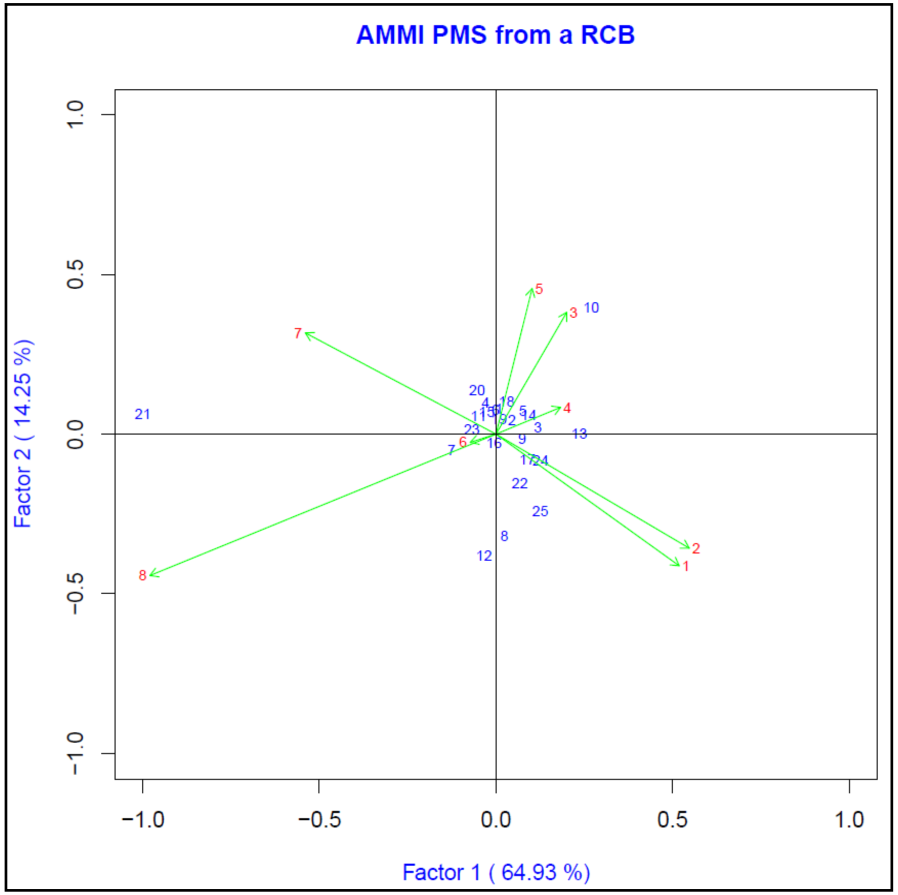

Figure 4.8.4 (b): **AMMI 2 biplot for pods on main stem showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Considering the high pod bearing as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments BK 19, BK 20, BS 19 and BS 20were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BK 19, BK 20, BS 19 and BS 20with negative environmental index were generally poor environments (Figure 4.8.5 (a)). The environments BS 19, HK 19 and HK 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But BS 19was found to have below overall mean. Therefore, these environments were not suitable by keeping in view the importance of high pod bearing as desirable. Similarly, the genotypes RGC 936, RGS 3, HG 3-52, HG 100 and RGC 1003 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 100, HG 3-52 and RGS 3 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to high pod bearing of genotype at that particular environment. Genotypes, GG 2; HG 6;HG 100 and RGC 1055;RGC 1017 and HG 563 were identified as specifically adapted to the BS 19 and BS 20; BK 19 and BK 20; HK 19; HS 20andHS 19respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 19 and HK 20 had short spokes and they do not exert strong interactive forces while BK 19, BK 20, BS 20, HK 19, HS 19 and HS 20with long spokes were more differentiating environments. In the present study, the genotypes, HG 100 and RGC 936 were close to the origin and hence they were non sensitive to environmental interactive forces whereas, HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75were found more responsive since they were away from the origin (Figure 4.8.5 (b)). The best genotypes with respect HK 20 were GG 2, RGC 936, RGC 1033 and HG 75; with respect to BK 19, BK 20, BS 19 and BS 20 were HG 6, HVG 2-30, FS 277, PNB, GG 1 and M 83; with respect to HK 19 and HS 20 were HG 2-20, HG 884, HG 100, X 10, RGC 1038, RGC 1055 and RGC 1066; and with respect to HS 19 were HG 870, HG 563, HG 365, HG 3-52 and RGS 3. In this case, the best adapted genotypes for HK 20 was GG 2; for BS 19 and BS 20 was HVG 2-30: for BK 19 and BK 20 were HG 884, M 83 and FS 277: for HS 19 were RGC 1017; for HK 19 were RGC 1038 and RGC 1066 and for HS 20 was X 10.

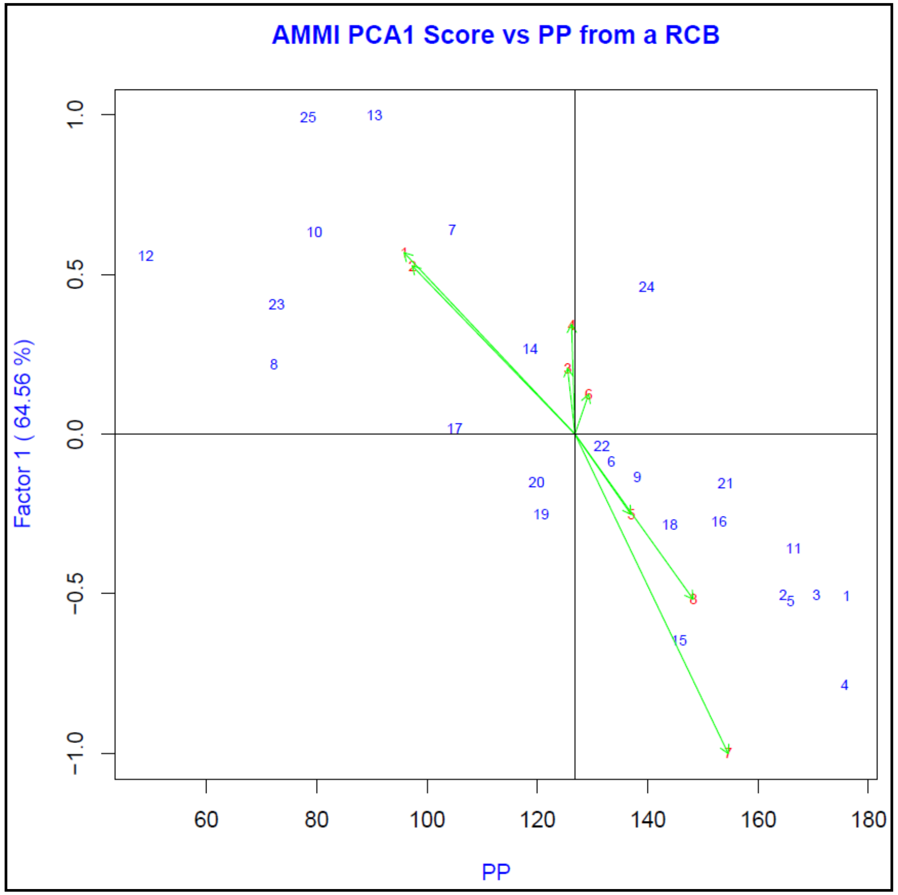

Figure 4.8.5 (a): **AMMI 1 biplot for pods per plant of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

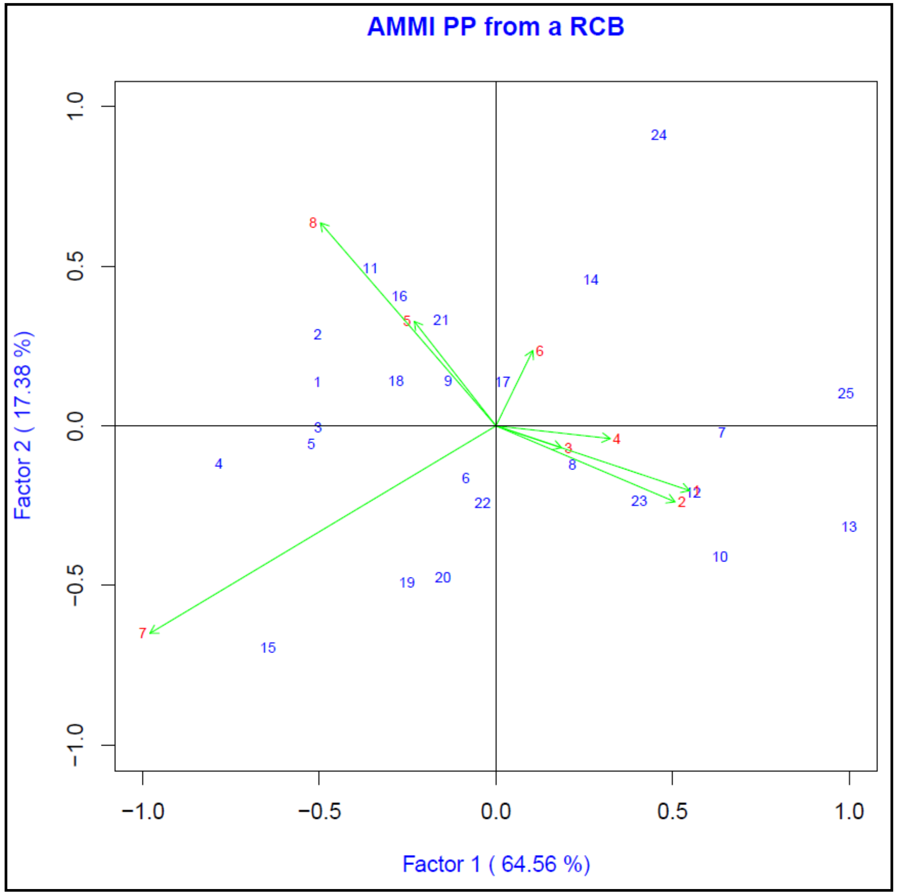

Figure 4.8.5 (b): **AMMI 2 biplot for pods per plant showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

4.8.2.6 Pods per cluster

AMMI 1 biplot display:

The genotypes namely, RGC 936, GG-2, GG-1, HG 365, HG 75, RGS 3, HG 6, HG 3-52, HG 884, RGC 1055, HG 870, HG 2-20, X-10, RGC 1033, HG 100, RGC 1017, RGC 1038, HVG 2-30 and HG 563 had pods per cluster less than the overall mean and negative genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 1003, RGC 1002, M-83, RGC 1066, PNB and FS 277 were generally late in maturity and with positive genotypic index were adapted to unfavourable environments. Considering the fewer pods per cluster as desirable, the environments lying on the left side are favourable environments and those lying on right side are unfavourable. Therefore, environments BK 19, BK 20, BS 20 and HK 20 were present on the left hand side of the midpoint of the main effect axis with negative environmental index, seemed to be rich environments, while BS 19, HK 19, HS 19 and HS 20 with positive environmental index were generally poor environments (Figure 4.8.6. (a)). The environments BK 20, BS 20 and HK 19 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HK 19 was found to have above overall mean. Therefore, this environment was not suitable by keeping in view the importance of fewer pods per cluster as desirable. Similarly, the genotypes HG 870, HG 3-52, HVG 2-30, HG 100, RGC 1017, RGC 936, RGC 1055 and RGS 3 had near zero score on the first IPCA1indicating that these genotypes were less influenced by the environments and are stable genotypes. All of these genotypes registered below overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to fewer pod per cluster of genotype at that particular environment. Genotypes, HG 365 and GG 2; M 83 and RGC 1002 and RGC 1003 were identified as specifically adapted to the HK 20; BS 19andHS 20; HS 19respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environment, HK 19 had short spokes and it does not exert strong interactive forces while BK 19, BK 20, BS 19, BS 20, HK 20, HS 19 and HS 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 3-52, RGC 1017, RGC 936, RGS 3 and HG 100 were close to the origin and hence they were non sensitive to environmental interactive forces whereas, HG 6, HVG 2-30, FS 277, X-10, PNB, GG-1, GG-2, RGC 1038, RGC 1055, RGC 1002, RGC 1003, RGC 1066, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.6 (b)).

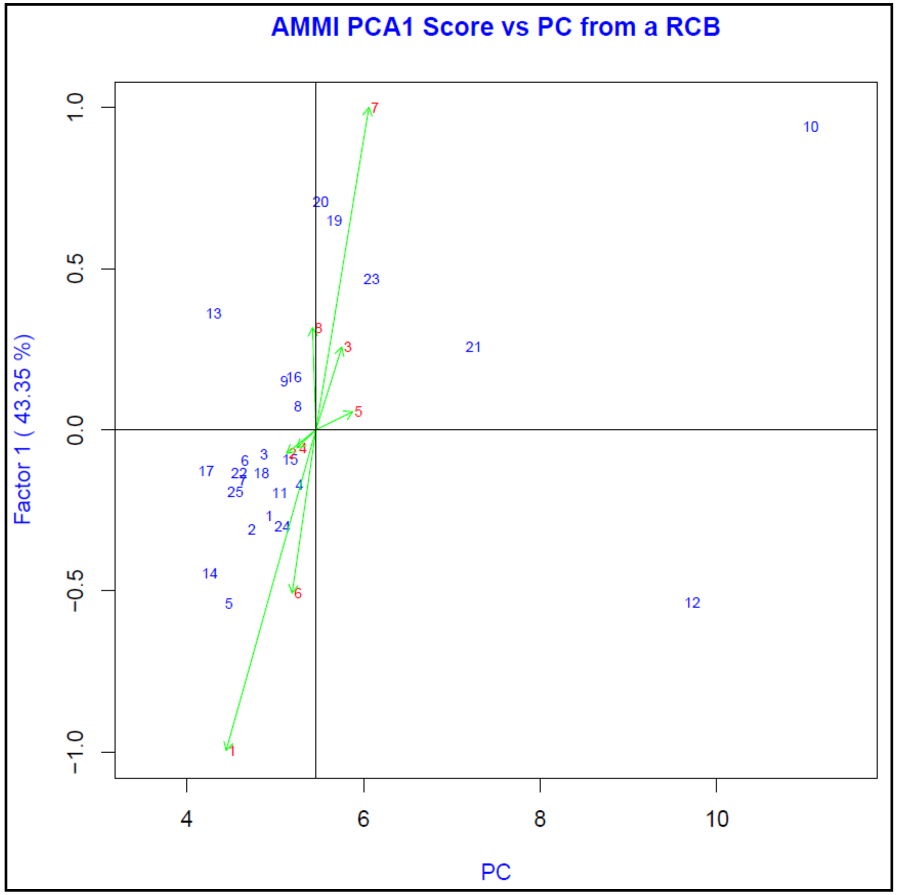

Figure 4.8.6 (a): **AMMI 1 biplot for pods per cluster of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

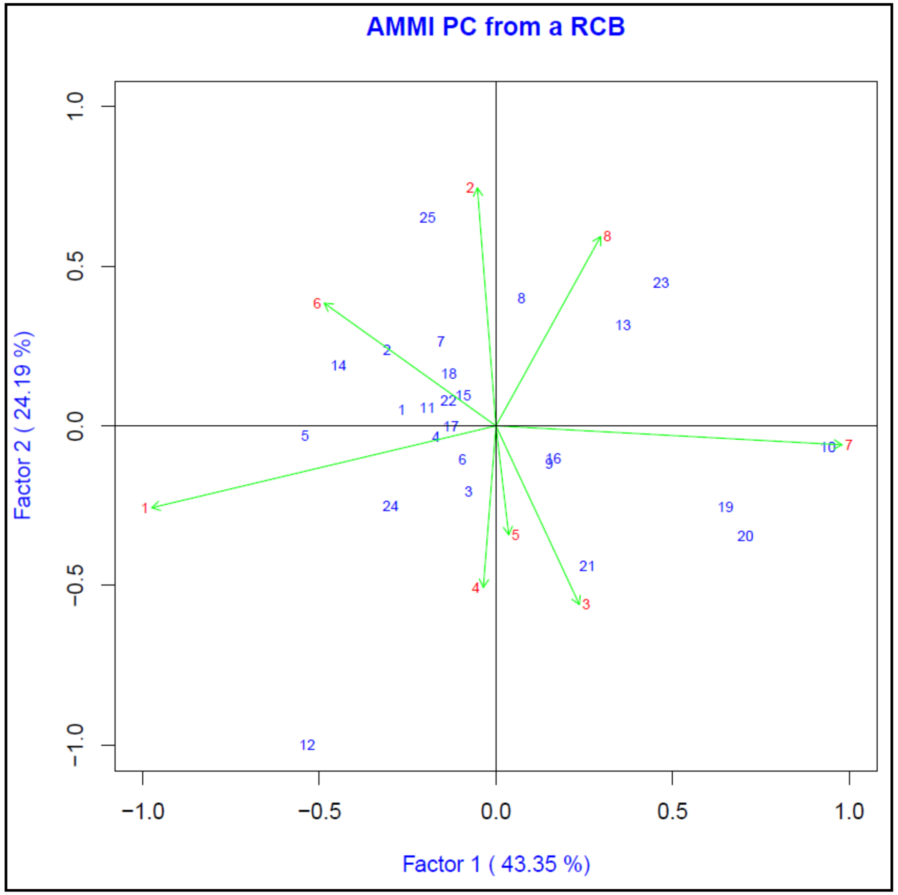

Figure 4.8.6 (b): **AMMI 2 biplot for pods per cluster showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

The best genotypes with respect to HS 20 were HVG 2-30, GG 1 and M 83; with respect to BS 19, HK 19 and HS 19were HG 100, FS 277, RGC 1038, RGC 1002, RGC 1003 and RGC 1066; with respect to BK 20 and HK 20 were HG 2-20, HG 884, HG 6, X 10, GG 2, RGC 1017, RGC 1055, RGS 3 and HG 75; and with respect to BK 19 and BS 20 were HG 870, HG 563, HG 365, HG 3-52, PNB, RGC 936 and RGC 1033. In this case, the best adapted genotypes for BK 20 was HG 75; for HK 20 were HG 884 and GG 2; for BS 19 was RGC 1066; for HS 19wasFS 277 and for HS 20 were GG1 and M 83.

4.8.2.7 Seeds per pod

AMMI 1 biplot display:

The genotypes namely, RGC 1066, M-83, HG 2-20, PNB, HG 884, RGC 1017, HG 870, HG 563, X-10, RGC 1055, RGC 1033 and RGC 1003 had seeds per pod more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 1038, HG 365, HG 100, HG 3-52, HVG 2-30, GG-2, HG 6, RGS 3, HG 75, RGC 1002, GG-1, FS 277 and RGC 936 were generally with less seeds per pod and with negative genotypic index were adapted to unfavourable environments. Considering the high seeds per pod as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments BK 19, BK 20, BS 19 and HK 19were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BS 20, HK 20, HS 19 and HS 20 with negative environmental index were generally poor environments (Figure 4.8.7 (a)). The environments BS 20 and HS 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. Similarly, the genotypes HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, X-10, GG-1, GG-2, RGC 1038, RGC 936, RGC 1002, RGS 3, RGC 1033 and HG 75 had near zero score on the first IPCA1indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 2-20, HG 884, HG 870, HG 563, X 10 and RGC 1033 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to high seed per pod of genotype at that particular environment. Genotypes, RGC 1017; RGC 1003 and FS 277 were identified as specifically adapted to the HS 19; HK 20 and BK 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environment, BS 20had short spokes and it did not exert strong interactive forces while BK 19, BK 20, BS 19, HK 19, HK 20, HS 19 and HS 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X-10, GG-1, GG-2, RGC 1038, RGS 3 and HG 75 were close to the origin and hence they were non sensitive to environmental interactive forces whereas FS 277, PNB, RGC 1017, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, M-83 and RGC 1033 found more responsive since they were away from the origin (Figure 4.8.7 (b)). The best genotypes with respect to BS 20 and HS 20 were HG 563, HG 100, GG 2 and RGC 1066; with respect to HK 19 and HS 19were HG 870, HG 365, RGC 1017, RGC 936, RGC 1055 and RGC 1002; with respect to BK 20 and HK 20 were HG 2-20, HG 3-52, HVG 2-30, FS 277, X 10, PNB, RGC 1038, RGC 1003, RGS 3 and HG 75; and with respect to BK 19 and BS 19 were HG 884, HG 6, GG 1, M 83 and RGC 1033. In this case, the best adapted genotypes for HK 19was RGC 1055; for HS 19 was RGC 1017: for HS 20was RGC 1066: for HK 20 was PNB and for BK 19 and BS 19 was M 83.

4.8.2.8 Pod length

AMMI 1 biplot display:

The genotypes namely, GG-2, RGC 1003, HG 75, HG 6, GG-1, HG 100, RGS 3, HG 884, RGC 936, HG 365, X-10, HG 3-52, HG 563, RGC 1002, RGC 1033, RGC 1038, RGC 1017, FS 277, HG 2-20 and RGC 1055 had pod length less than the overall mean and negative genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, HG 870, RGC 1066, M-83, HVG 2-30 and PNB were generally with shorter pods and with positive genotypic index were adapted to unfavourable environments. Considering the shorter pods as desirable, the environments lying on the left side are favourable environments and those lying on right side are unfavourable. Therefore, environments BK 19 and BK 20 were present on the left hand side of the midpoint of the main effect axis with negative environmental index, seemed to be rich environments, while BS 19, BS 20, HK 19, HK 20, HS 19 and HS 20 with positive environmental index were generally poor environments (Figure 4.8.8 (a)). The environments BS 20 and HK 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But both of these environments were found to have above overall mean. Therefore, these environments were not suitable by keeping in view the importance of shorter pods as desirable. Similarly, the genotypes HG 2-20, HG 100, GG-1, RGC 1002 and RGC 1066 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 2-20, HG 100, GG-1 and RGC 1002 registered below overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments.

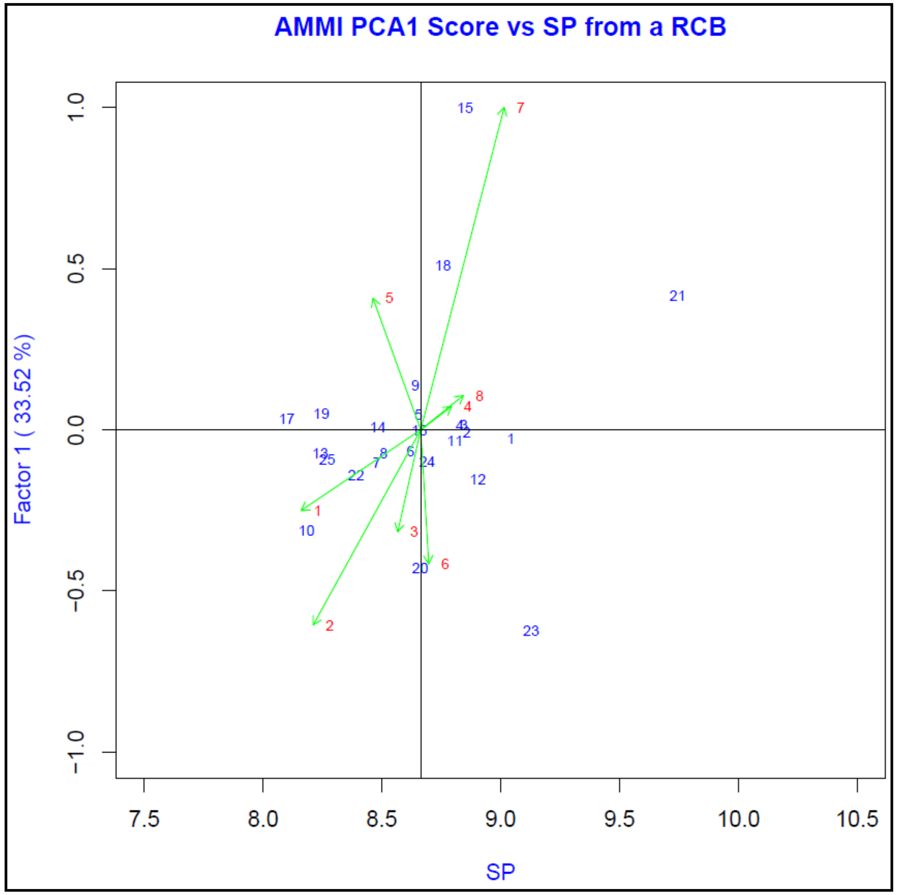

Figure 4.8.7 (a): AMMI 1 biplot for seeds per pod of 25 cluster bean genotypes and eight environments using genotypic and environmental scores

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

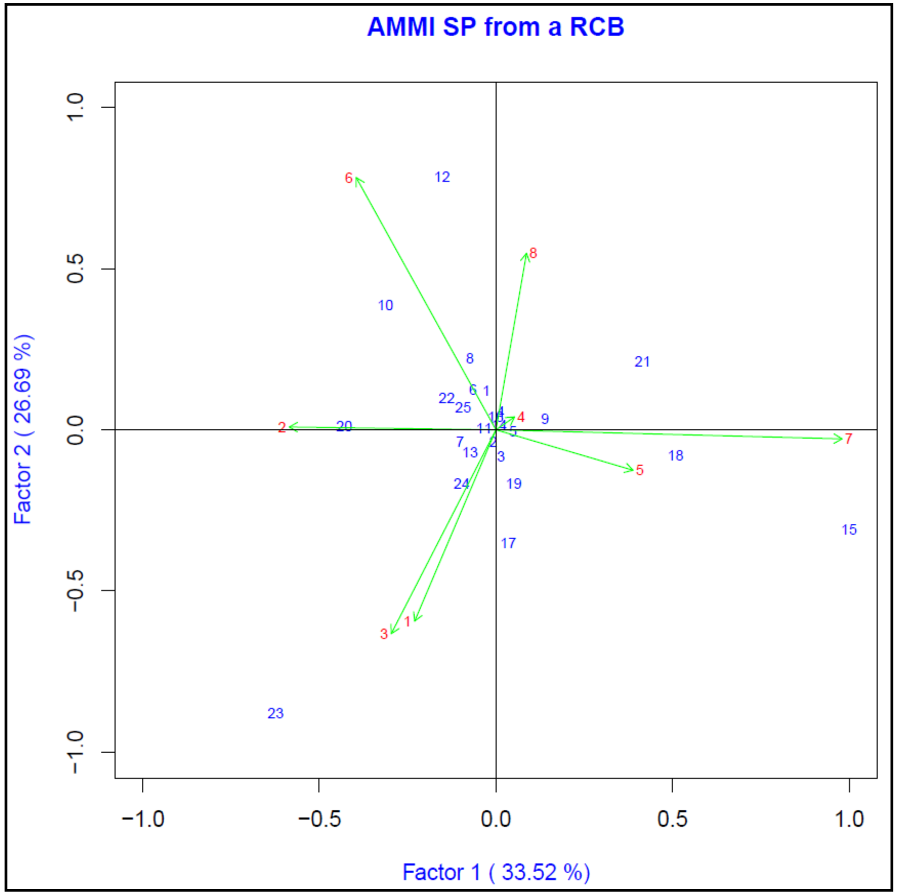

Figure 4.8.7 (b): **AMMI 2 biplot for seeds per pod showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to shorter pods of genotype at that particular environment. Genotypes, GG 2, HG 75 ad HG 6; RGC 1002; HG 2-20 and X 10; and HG 870 were identified as specifically adapted to the BK 19; BK 20; HS 19; BS 19 and BS 20 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 20 and HK 20 had short spokes and they do not exert strong interactive forces while BK 19, BK 20, BS 19, HK 19, HS 19 and HK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 2-20, HG 100, GG 1 and RGC 1066 were close to the origin and hence they were non sensitive to environmental interactive forces whereas, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, FS 277, X-10, PNB, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.8 (b)). The best genotypes with respect to BK 19 and BK 20 were GG 1, RGC 936, RGC 1002, RGC 1003, RGS 3 and HG 75; with respect to BS 20, HK 19 and HK 20were HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X 10, GG 2 and RGC 1033; with respect to HS 19 were PNB, RGC 1017, RGC 1038, RGC 1055, RGC 1066 and M 83; and with respect to BS 19 and HS 20 were HG 870, HVG 2-30 and FS 277. In this case, the best adapted genotypes for HK 19 was X 10; RGS 3 for BK 19 and for BS 19 were HG 870 and FS 277.

4.8.2.9 Branches per plant

AMMI 1 biplot display:

The genotypes namely, RGC 1038, HG 2-20, RGC 1003, RGC 1017, GG-1, HG 100, RGS 3, HG 884, RGC 1002, RGC 936, GG-2, RGC 1033, HG 870, HG 3-52, X-10, HG 365, RGC 1055 and HG 563 had branches per plant more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, HG 75, HG 6, M-83, HVG 2-30, FS 277, PNB and RGC 1066 were generally with fewer branches per plant and with negative genotypic index were adapted to unfavourable environments. Considering the highly branched genotypes as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments BS 19, HK 19, HK 20, HS 19 and HS 20were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BK 19, BK 20 and BS 20with negative environmental index were generally poor environments (Figure 4.8.9. (a)). The environment HK 19had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments.

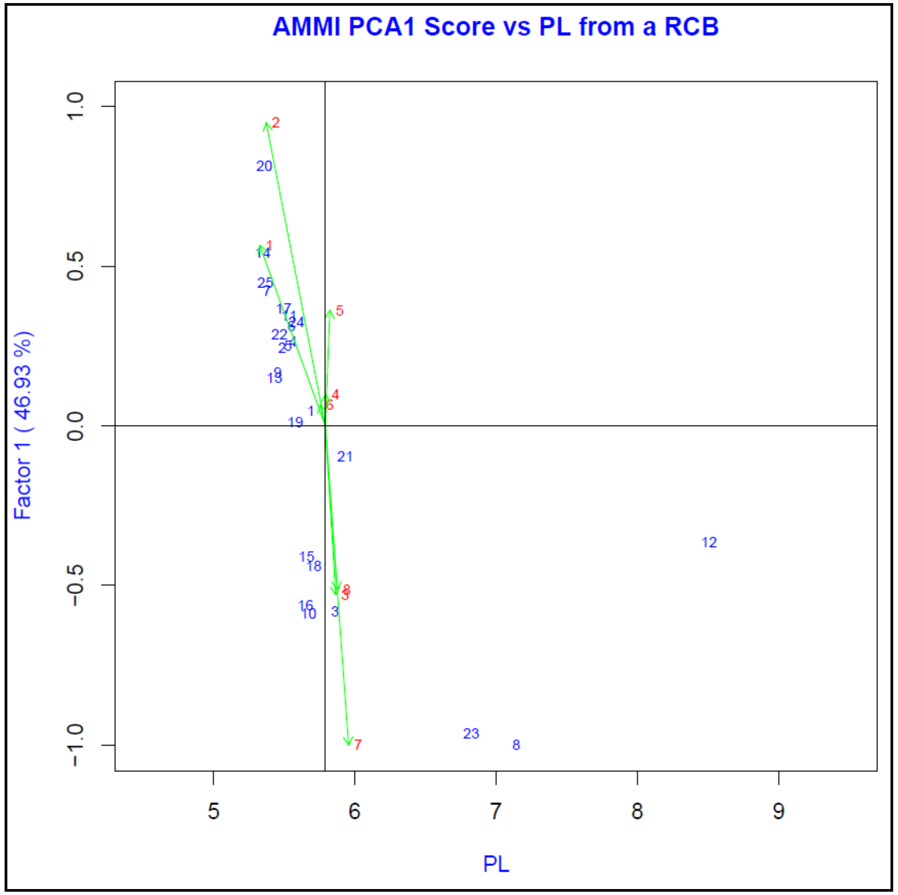

Figure 4.8.8 (a): **AMMI 1 biplot for pod length of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

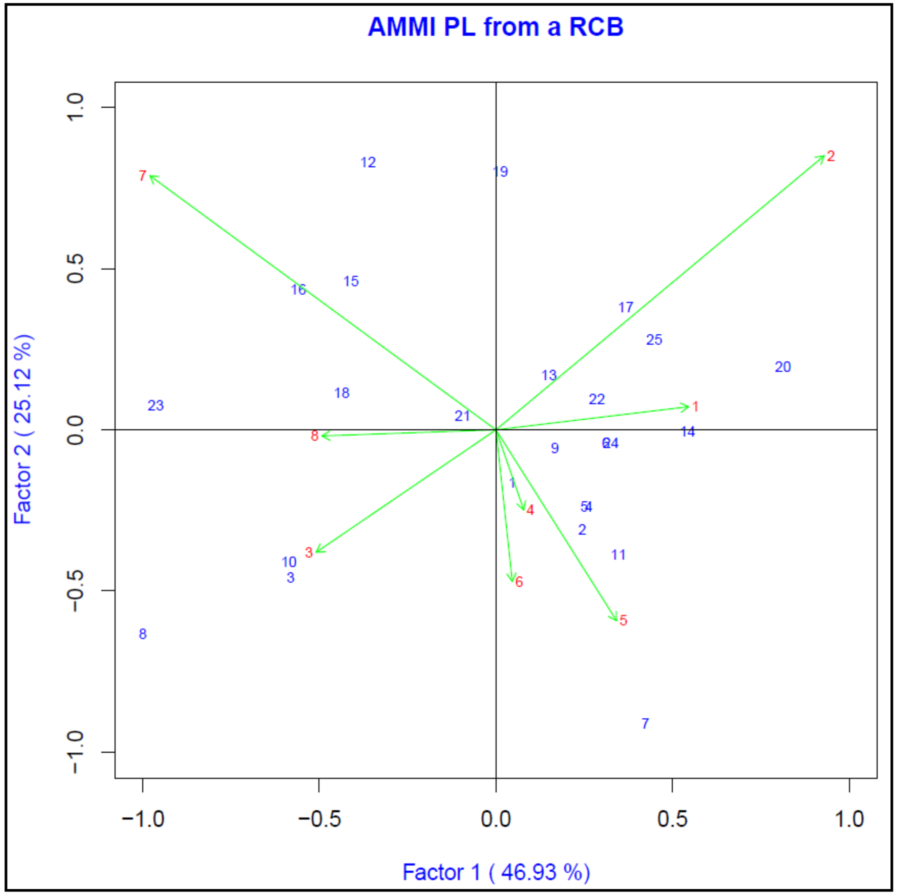

Figure 4.8.8 (b): **AMMI 2 biplot for pod length showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Similarly, the genotypes HG 870, HG 365, RGC 1002, RGC 1003, RGC 1033 and HG 75 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 870, HG 365, RGC 1002, RGC 1003 and RGC 1033 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to highly branched genotype at that particular environment. Genotypes, X 10 and HG 3-52; HG 100 and GG 2 were identified as specifically adapted to the BS 19 and HS 19; HS 20 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 20 and HK 19 had short spokes and they do not exert strong interactive forces while, BK 19, BK 20, BS 19, HK 20, HS 19 and HS 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 884, HG 870, RGC 1038, RGC 1055 and RGC 936 were close to the origin and hence they were non sensitive to environmental interactive forces whereas, HG 2-20, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.9 (b)).The best genotypes with respect to BK 20 and BS 20 were HG 870, HG 563, HG 6, PNB, RGC 1038 and M 83; with respect to BK 19 were HVG 2-30, FS 277, RGC 1055, RGC 1002, RGC 1066, RGC 1033 and HG 75; with respect to BS 19, HK 19 and HK 20 were HG 365, HG 3-52, X 10, GG 1, GG 2, RGC 1017 and RGC 936; and with respect to HS 19 and HS 20 were HG 2-20, HG 884, HG 100, RGC 1003 and RGS 3. In this case, the best adapted genotypes for BS 20 was HG 563; for BK 20 was M 83; for HS 20 was RGC 1003; for HK 19 was HG 365 and for HK 20 was GG 1.

4.8.2.10 100 seed weight

AMMI 1 biplot display:

The genotypes namely, HG 3-52, RGC 1038, X-10, RGC 1066, RGC 1017, HG 563, HG 2-20, RGC 1033, HG 884, HG 870, HG 365, HG 100 and HG 6 had 100 seed weight more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 1003, GG-2, RGC 1055, RGC 1002, GG-1, RGS 3, FS 277, HG 75, RGC 936, M-83, PNB and HVG 2-30 were generally with less 100 seed weight and with negative genotypic index were adapted to unfavourable environments. Considering the bold seeded genotypes as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable.

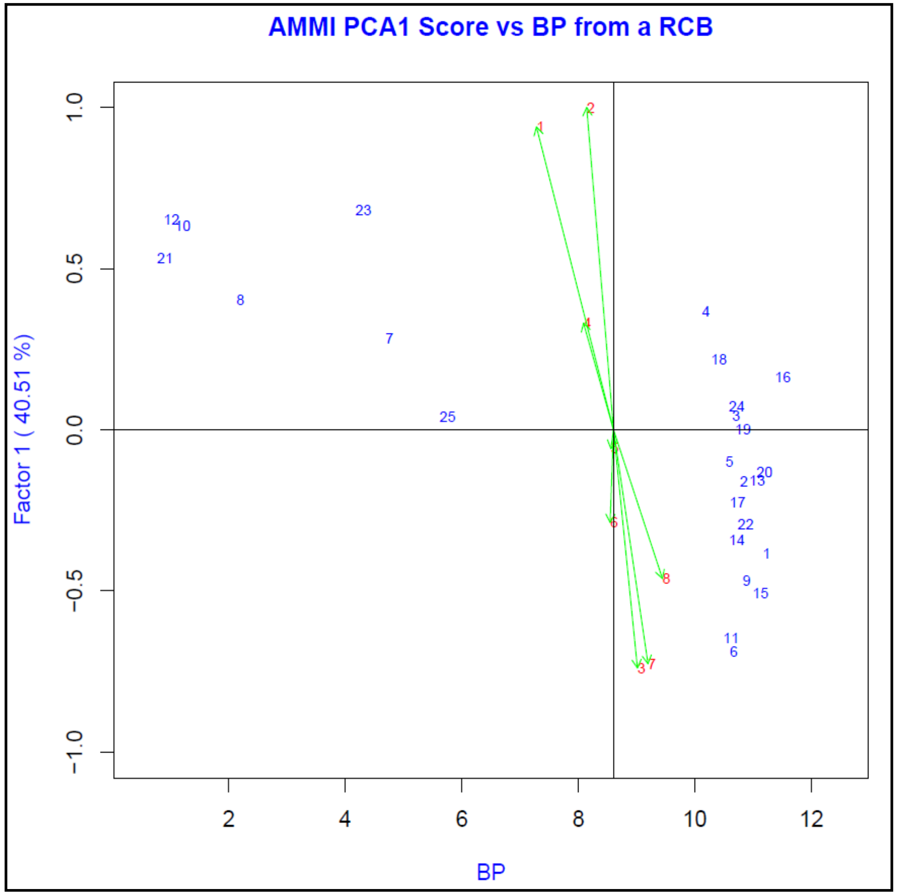

Figure 4.8.9 (a): **AMMI 1 biplot for branches per plant of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

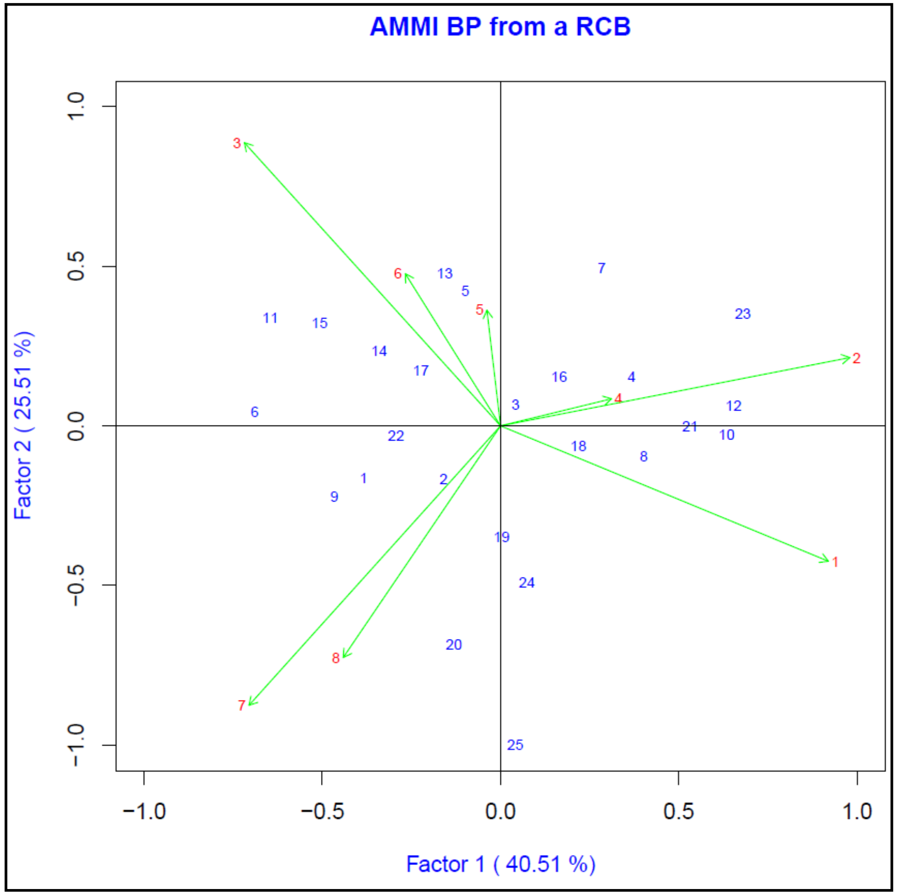

Figure 4.8.9 (b): **AMMI 2 biplot for branches per plant showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Therefore, environments BK 19, HK 19, HS 19 and HS 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BK 20, BS 19, BS 20 and HK 20 with negative environmental index were generally poor environments (Figure 4.8.10 (a)). The environments BS 20, HK 19 and HS 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But BS 20 was found to have below overall mean. Therefore, these environments were not suitable by keeping in view the importance of bold seeded genotypes as desirable. Similarly, the genotypes HG 563, HVG 2-30, GG-1, GG-2, RGC 1055, RGC 1003 and RGS 3 had near zero score on the first IPCA1indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, only HG 563 registered above overall mean along with the IPCA1 score close to zero, HG 563 adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to bold seeded genotype at that particular environment. Genotypes, RGC 1017; HG 2-20, HG 884 and HG 365; M 83; RGC 936, FS 277 and HG 75; and PNB were identified as specifically adapted to the HS 20; HS 19; BS 20; HK 20; and BS 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 20, HK 19 and HS 20 had short spokes and they do not exert strong interactive forces while BK 19, BK 20, BS 19, HK 20 and HS 19 with long spokes were more differentiating environments. In the present study, the genotypes, HG 563, HVG 2-30 and RGS 3 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 870, HG 365, HG 3-52, HG 6, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.10 (b)). The best genotypes with respect to BS 19 and HS 20 were HG 3-52, HG 100, RGC 1017, RGC 1038, RGC 936 and RGC 1066; with respect to BK 19, BS 20, HK 19 and HK 20 were HG 6, FS 277, PNB, GG 1, GG 2, RGC 1002, RGC 1003, RGS 3, M 83 and HG 75; and with respect to BK 20 and HS 19 were HG 2-20, HG 884, HG 870, HG 563, HG 365 and X 10. In this case, the best adapted genotypes for BS 19 was HG 3-52 and RGC 1038; for BS 20 and HK 19 was RGS 3; for BK 19 were GG 2, RGC 1002, RGC 1003, and M 83: for HK 20 were HG 75; for HS 19 was HG 2-20; and for BK 20 was HG 870.

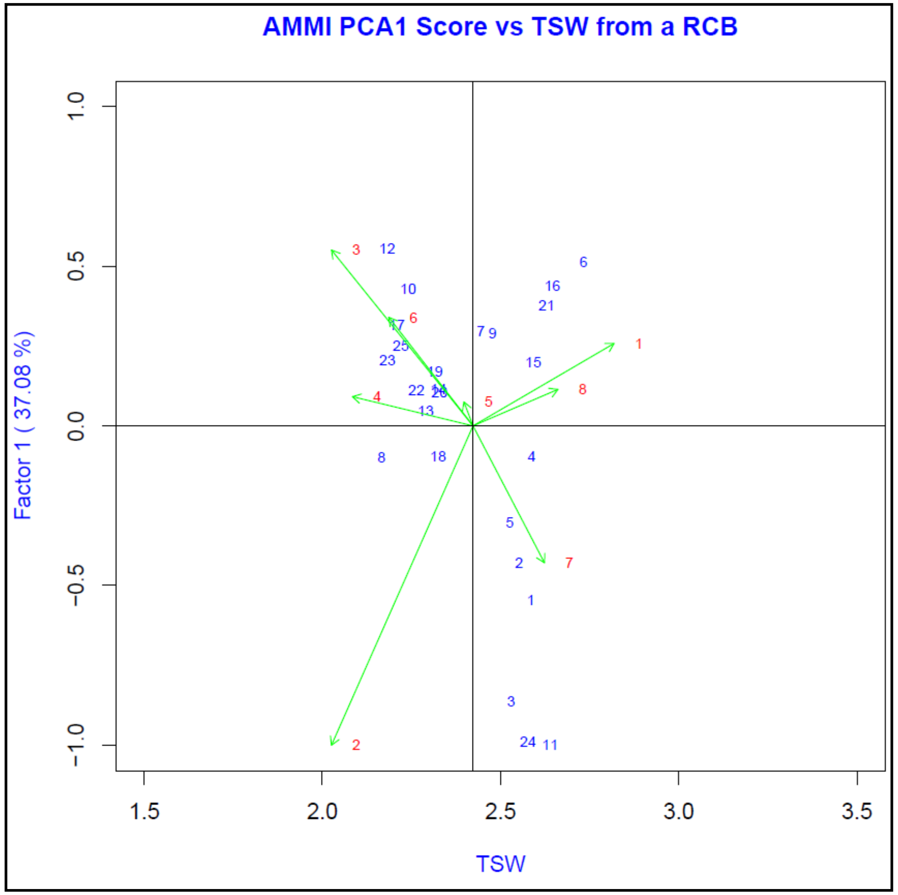

Figure 4.8.10 (a): **AMMI 1 biplot for 100 seed weight of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

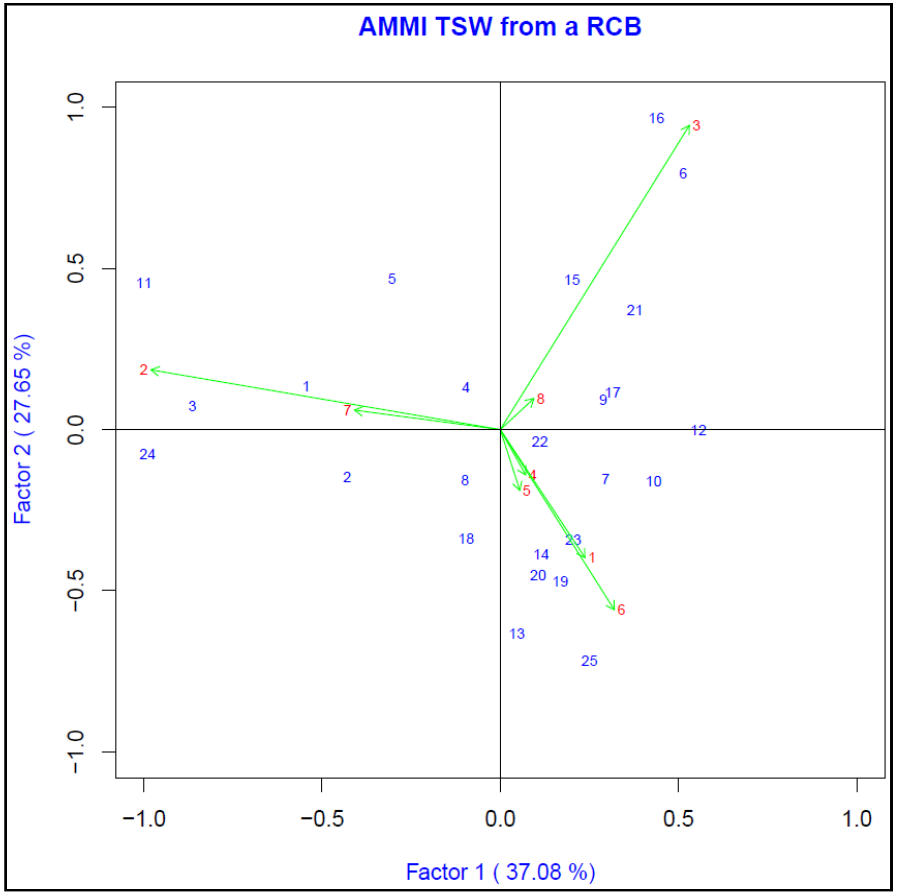

Figure 4.8.10 (b): AMMI 2 biplot for 100 seed weight showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

4.8.2.11 Biomass per plot

AMMI 1 biplot display:

The genotypes namely, HG 2-20, X-10, HG 563, HG 870, HG 884, FS 277, HG 365, RGC 1066, RGC 1033, RGC 1038, RGC 1017, HG 100 and RGS 3 had biomass per plot more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, HG 3-52, GG-2, RGC 936, RGC 1055, M-83, RGC 1003, RGC 1002, GG-1, HG 6, HVG 2-30, HG 75 and PNB were generally with less biomass per plot and with negative genotypic index were adapted to unfavourable environments. Considering the high biomass as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments HS 19, HK 19, HS 20 and HK 20were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BS 19, BK 20, BK 19 and BK 20 with negative environmental index were generally poor environments (Figure 4.10.11 (a)).The environments BS 19, BS 20 and HK 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But BS 20 and HK 20 were found to have below overall mean. Therefore, these environments were not suitable by keeping in view the importance of high biomass as desirable. Similarly, the genotypes HG 100, X-10, RGC 1038, RGC 1055, RGC 1066, RGS 3 and RGC 1033 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 100, X-10, RGC 1038, RGC 1066, RGS 3 and RGC 1033 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with high biomass per plot at that particular environment. Genotypes, HG 6 and HG 75; GG 1 and M 83; RGC 1055; HG 3-52 and GG 2; RGS 3were identified as specifically adapted to the BK 19; BK 20; BS 20; HK 19 and HK 20 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 19 and HS 20 had short spokes and they do not exert strong interactive forces while BK 19, BK 20, BS 20, HK 19, HK 20 and HS 19 with long spokes were more differentiating environments. In the present study, the genotypes, X-10, RGC 1038, RGC 1055, RGC 1066, RGS 3, HG 563 and HG 3-52 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 870, HG 365, HG 6, HVG 2-30, HG 100, FS 277, PNB, GG-1, GG-2, RGC 1017, RGC 936, RGC 1002, GC 1003, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.10.11 (b)).

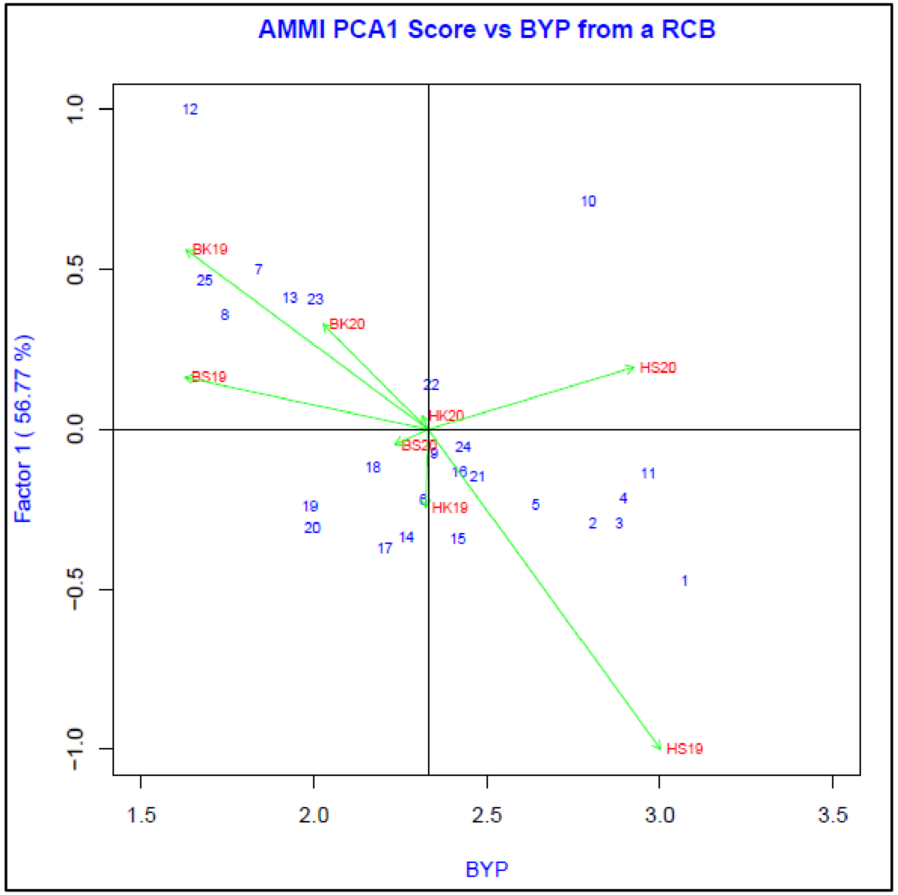

Figure 4.8.11 (a): **AMMI 1 biplot for biomass per plot of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

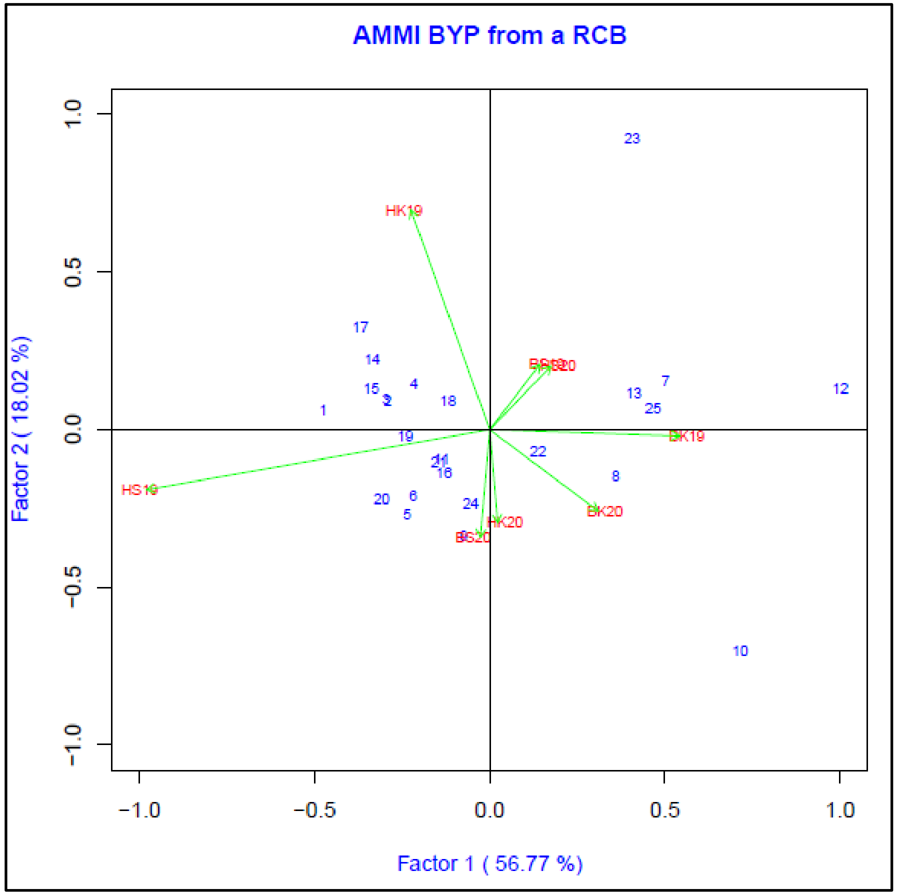

Figure 4.8.11 (b): AMMI 2 biplot for biomass per plot showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

The best genotypes with respect to BS 19 and HS 20 were HG 6, PNB, GG 1, M 83 and HG 75; with respect to BK 19, HK 20 and BK 20 were HVG 2-30, RGS 3 and FS 277; with respect to HK 19 were HG 2-20, HG 884, HG 870, HG 563, GG 2, RGC 1017, RGC 936 and RGC 1055; and with respect to HS 19 and BS 20 were HG 365, HG 3-52, HG 10, X 10, RGC 1038, RGC 1002, RGC 1003, RGC 1066 and RGC 1033. In this case, the best adapted genotypes for BK 20 was HVG 2-30; and for BS 20 were HG 100 and RGC 1033.

4.8.2.12 Harvest index

AMMI 1 biplot display:

The genotypes namely, RGC 1055, HG 6, RGC 1066, RGC 1003, HG 3-52, RGC 1002, HG 2-20, HG 563, HG 365, RGC 1017, RGC 1038, RGC 1033, HG 75, HG 100, HG 884, X-10, HG 870 and RGS 3 had harvest index more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, GG-2, GG-1, HVG 2-30, PNB, RGC 936, M-83 and FS 277were generally with low harvest index and with negative genotypic index were adapted to unfavourable environments. Considering the high harvest index as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments BK 19, BK 20, BS 19, HK 19 and HS 19 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BS 20, HK 20 and HS 20 with negative environmental index were generally poor environments (Figure 4.8.12 (a)). The environments HS 19, BK 19, HK 20 and BK 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HK 20 was found to have harvest index below overall mean. Therefore, this environment was not suitable by keeping in view the importance of high biomass as desirable. Similarly, the genotypes HG 2-20, HG 884, HG 870, HG 563, X-10, PNB, GG-2, RGC 1017, RGC 1038, RGC 1066, RGS 3 and RGC 1033had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 2-20, HG 884, HG 870, HG 563, X-10, RGC 1017, RGC 1038, RGC 1066, RGS 3 and RGC 1033 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with high harvest index at that particular environment. Genotypes, RGC 1055 and RGC 1003; HG 2-20 and X 10; GG 2; HG 870, FS 277, RGC 1038, RGS 3 and RGC 1033 were identified as specifically adapted to the BS 19; HS 19; BS 20, HK 20 and HS 20; and BK 19, BK 20 and HS 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 20, HK 19 and HS 20 had short spokes and they do not exert strong interactive forces while HS 19, BS 19, BK 19, HK 20 and BK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 563, X-10, GG-2, RGC 1017, RGC 1066 and RGC 1038 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 870, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, PNB, GG-1, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.12 (b)). The best genotypes with respect to BS 19 were HG 2-20, HG 884, HG 563, HG 3-52, RGC 1003 and RGC 1066; with respect to HS 19 were HG 6, X-10, PNB, RGC 1055, RGC 1002, M-83 and HG 75; with respect to BK 19, HS 20, BS 20 and BK 20 were HG 870, HG 365, HG 100, FS 277, GG-2, RGC 1017, RGC 1038, RGC 936, RGS 3 and RGC 1033; and with respect to HK 19 and HK 20 were HVG 2-30, FS 277 and GG-1. In this case, the best adapted genotypes for BS 19 was RGC 1003; for BK 19 and BK 20 were RGS 3 and RGC 1033: and for BS 20 and HS 20 was GG 2.

4.8.2.13 Cluster per plant

AMMI 1 biplot display:

The genotypes namely, HG 2-20, HG 563, X-10, HG 884, HG 870, HG 365, RGC 1017, RGC 1033, RGC 1038, RGC 1055, HG 3-52, HG 100 and RGS 3 had clusters per plant more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 1003, GG-2, HG 6, RGC 1002, RGC 1066, HG 75, GG-1, RGC 936, M-83, HVG 2-30, PNB and FS 277 were generally with less clusters per plant and with negative genotypic index were adapted to unfavourable environments. Considering the high number of clusters per plant as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments HK 19, HS 19 and HS 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BK 19, BK 20, BS 19, BS 20 and HK 20withnegative environmental index were generally poor environments (Figure 4.8.13 (a)). The environments BS 19 and BS 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But BS 19 and BS 20were found to have below overall mean. Therefore, these environments were not suitable by keeping in view the importance of high number of clusters per plant as desirable. Similarly, the genotypes HG 870, HG 3-52, HG 6, HG 100, RGC 1038, RGS 3 and RGC 1033 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes.

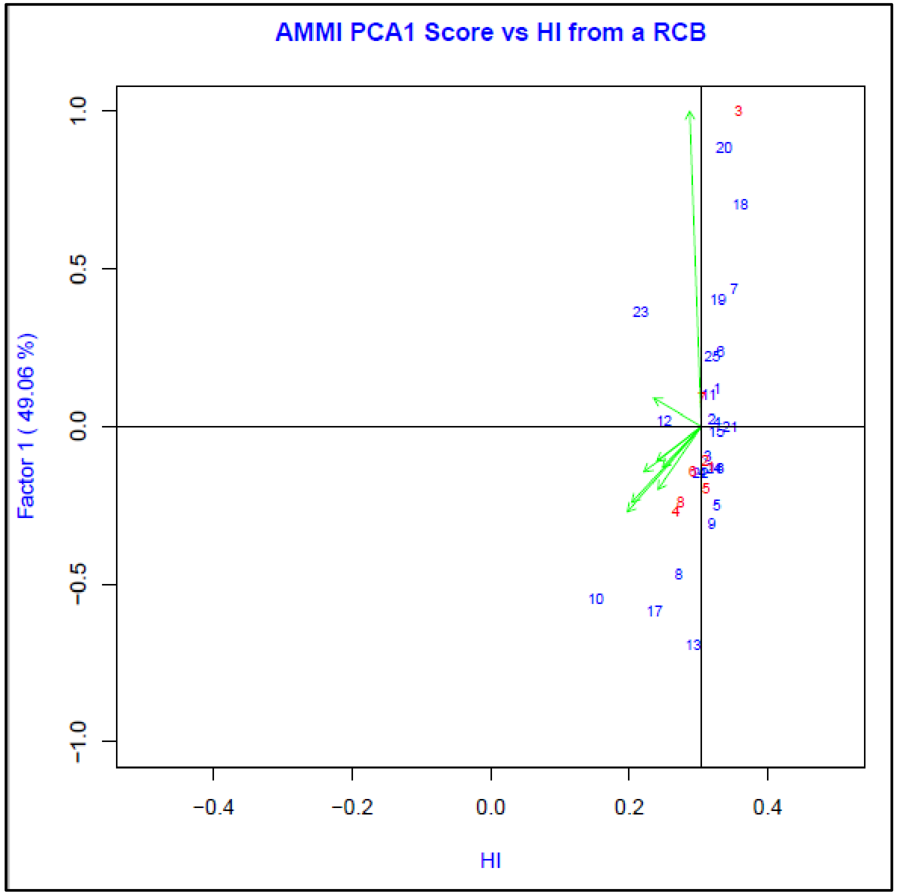

Figure 4.8.12 (a): **AMMI 1 biplot for harvest index of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

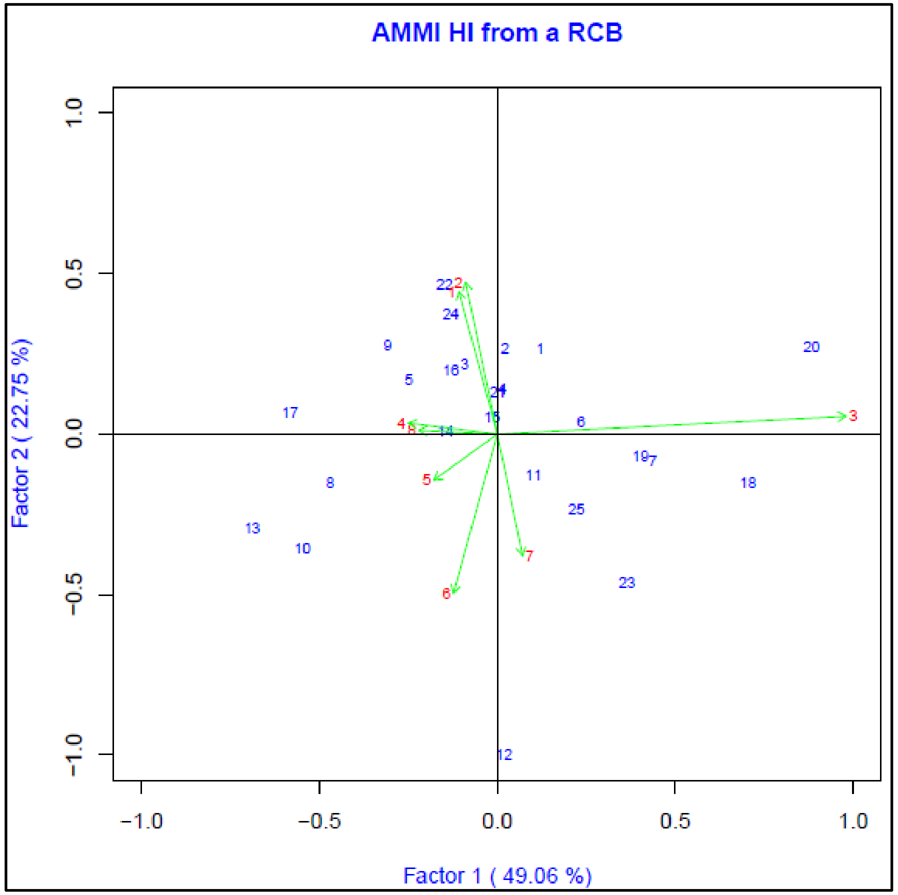

Figure 4.8.12 (b): **AMMI 2 biplot for harvest index showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Out of these, HG 870, HG 3-52, HG 100, RGC 1038, RGS 3 and RGC 1033 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with high number of clusters per plant at that particular environment. Genotypes, RGC 1055; RGC 1017; and HG 75 were identified as specifically adapted to the HK 19; HS 19; BK 19 and BK 20 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environment, BS 20 had short spokes and did not exert strong interactive forces while BK 19, BK 20, BS 19, HK 19, HK 20, HS 19 and HS 20 with longs pokes were more differentiating environments. In the present study, the genotypes, HG 6 and RGS 3 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.13 (b)). The best genotypes with respect to BK 20 and BS 20 were HG 6, HVG 2-30, GG 1, M 83 and RGC 1033; with respect to BK 19, HK 20 and HS 20 were FS 277, PNB and RGC 1066; with respect to BS 19 were HG 884, HG 870, HG 365, HG 6, HVG 2-30, X 10, GG 2, RGC 936 and RGC 1055; and with respect to HK 19 and HS 19 were HG 2-20, HG 563, HG 3-52, HG 100, RGC 1017, RGC 1038 and RGC 1002. In this case, the best adapted genotypes for BK 20 were HVG 2-30 and M 83; for BS 19wasHG 6: for BK 19 and HK 20 was HG 75: for HK 19 were HG 2-20 and HG 563; for HS 19was RGC 1017; and for BS 19 was HG 870.

4.8.2.14 Seed yield per plot

AMMI 1 biplot display:

The genotypes namely, HG 2-20, HG 563, X-10, HG 870, HG 884, HG 365, RGC 1066, RGC 1017, RGC 1033, RGC 1038, RGC 1055, HG 3-52 and HG 100 had seed yield per plot more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGS 3, GG-2, RGC 1003, RGC 1002, HG 6, GG-1, HG 75, RGC 936, HVG 2-30, M-83, FS 277 and PNB were generally with low seed yield per plot and with negative genotypic index were adapted to unfavourable environments. Considering the high seed yield per plot as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable.

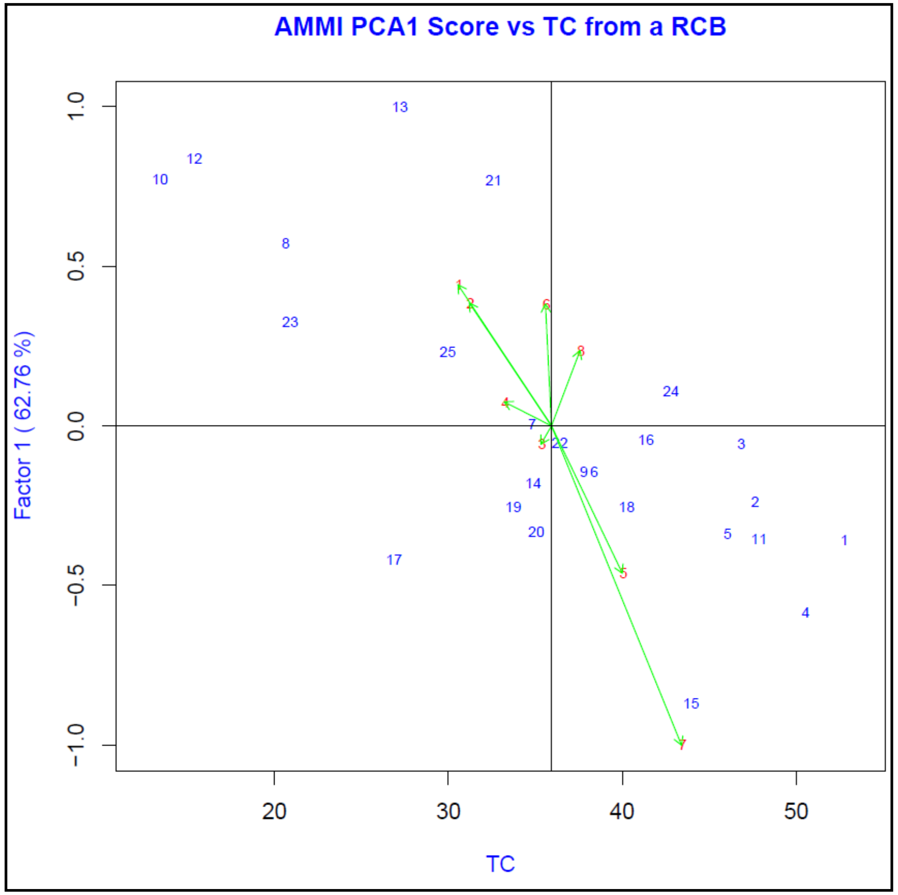

Figure 4.8.13 (a): AMMI 1 biplot for clusters per plant of 25 cluster bean genotypes and eight environments using genotypic and environmental scores

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

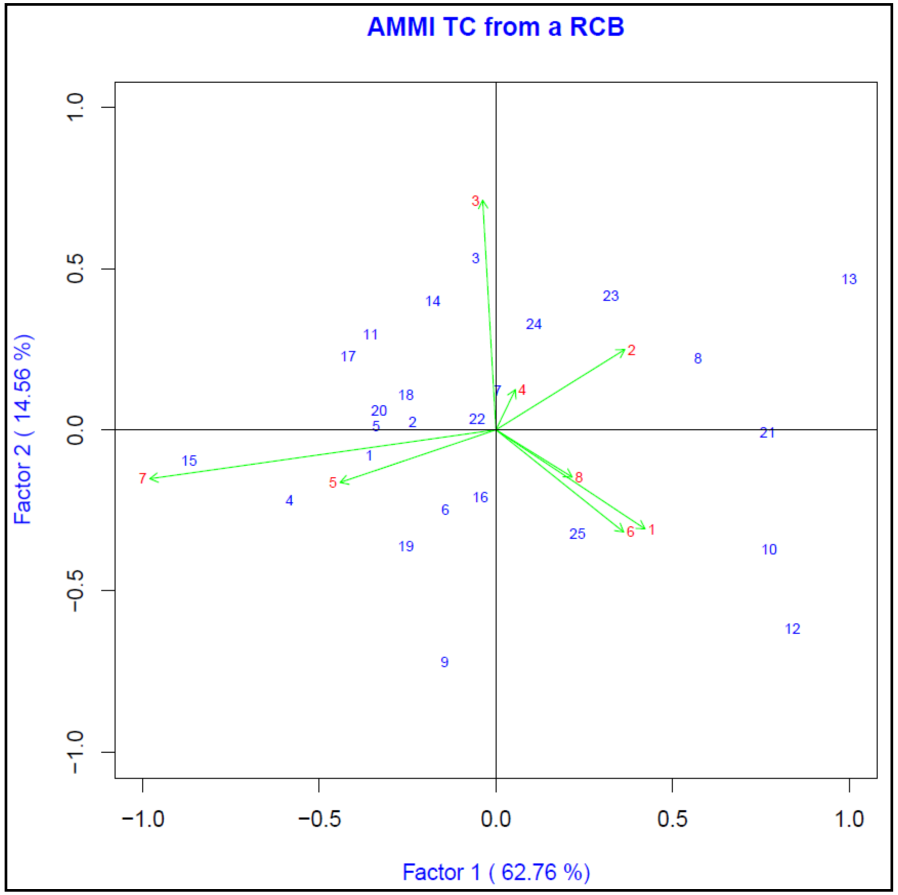

Figure 4.8.13 (b): **AMMI 2 biplot for clusters per plant showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Therefore, environments HK 19, HS 19 and HS 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BK 19, BK 20, BS 19, BS 20 and HK 20withnegative environmental index were generally poor environments (Figure 4.8.14 (a)). The environments 19, HK 19, HS 20, BS 20 and BK 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But BS 19, BS 20 and BK 20 were found to have below overall mean. Therefore, these environments were not suitable by keeping in view the importance of high seed yield per plot as desirable. Similarly, the genotypes HG 100, GG-2, RGC 936, RGC 1038, RGC 1066 and HG 870 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 100, RGC 1038, RGC 1066 and HG 870 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with high seed yield per plot at that particular environment. Genotypes, RGS 3 and RGC 1033 were identified as specifically adapted to the HK 20 and HS 20 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BK 19, BS 20, HS 20 and HK 20 had short spokes and they do not exert strong interactive forces while HS 19, BS 19, HK 19 and BK 20 with long spokes were more differentiating environments. In the present study, the genotypes, RGC 936, HG 870, RGC 1038 and HG 884 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75found more responsive since they were away from the origin (Figure 4.8.14 (b)). The best genotypes with respect to BS 19 and HK 19 were HG 6, GG 2, M 83 and HG 75; with respect to BK 19, HS 20, BS 20, HK 20 and BK 20 were HVG 2-30, HG 100, FS 277, PNB, GG 1, RGS 3 and RGC 1033; and with respect to HS 19 were HG 563, HG 365, X 10, HG 3-52, RGC 1038 and RGC 1066. In this case, the best adapted genotypes for HK 19 and BS 19 was GG 2; for HK 20 were RGS 3 and RGC 1033; and for BS 20 and BK 20 was HG 100.

4.8.2.15 Gum content

AMMI 1 biplot display:

The genotypes namely, HG 3-52, RGC 1066, HG 2-20, HG 870, X-10, HG 884, RGC 1038, HG 365, HG 563, RGC 1055, RGC 1033, GG-2, HG 6, HG 100 and GG-1 had gum content more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments.

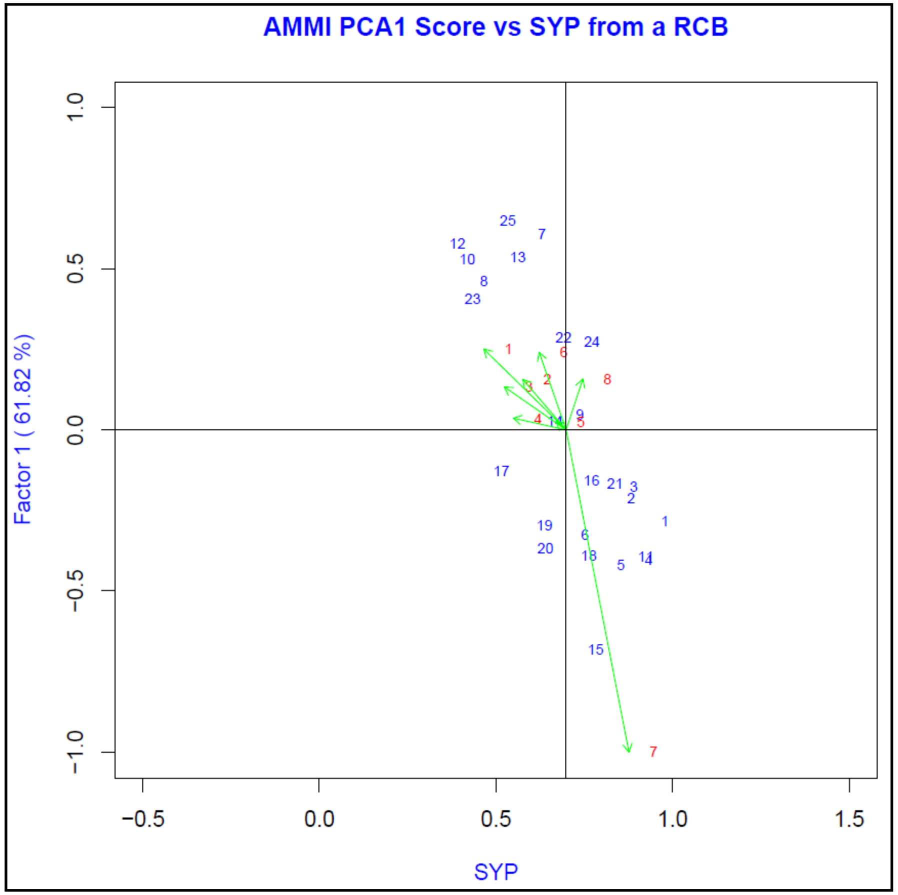

Figure 4.8.14 (a): **AMMI 1 biplot for seed yield per plot of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

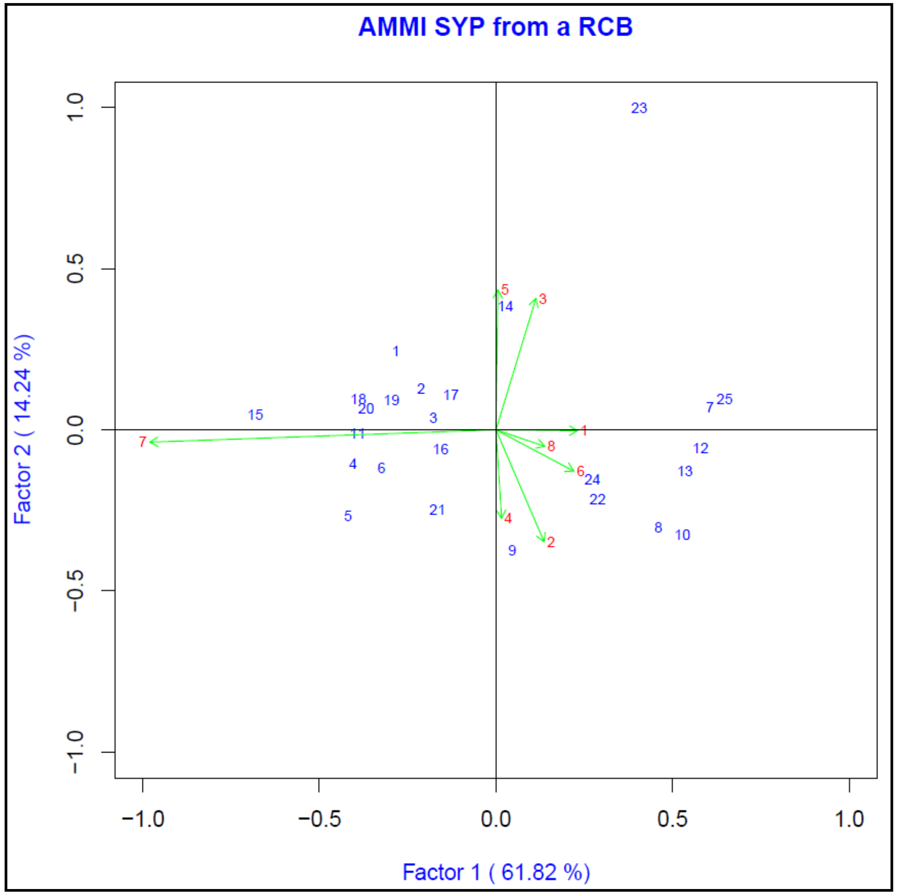

Figure 4.8.14 (b): AMMI 2 biplot for seed yield per plot showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

In contrast, the genotypes, RGC 1017, HG 75, RGS 3, RGC 1002, RGC 1003, RGC 936, FS 277, HVG 2-30, M-83 and PNB were found with low gum content and with negative genotypic index were adapted to unfavourable environments. Considering the high gum content as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments HS 19, BS 19, HK 20 and BK 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while HK 19, BK 19, HS 20 and BS 20 with negative environmental index were generally poor environments (Figure 4.8.15 (a)). The environments HS 20, BS 20 and HK 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HS 20 and BS 20 were found to have below overall mean. Therefore, these environments were not suitable by keeping in view the importance of high gum content as desirable. Similarly, the genotypes HG 870, HG 365, HG 100, X-10, GG-1, RGC 1017, RGC 1002, RGC 1066, RGC 1033 and HG 75 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 870, HG 365, HG 100, X-10, GG-1, RGC 1066 and RGC 1033registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with gum content at that particular environment. Genotypes, RGC 1055 and RGC 1017 were identified as specifically adapted to the HS 19 and HS 20 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, HS 20, BS 20 and HK 20 had short spokes and they do not exert strong interactive forces while HS 19, BS 19, HK 19, BK 19 and BK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 870, HG 365, X-10, GG-1, RGC 1002 and HG 75 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, PNB, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1003, RGC 1066, RGS 3, M-83 and RGC 1033 found more responsive since they were away from the origin (Figure 4.8.15 (b)). The best genotypes with respect to HS 20 were HG 100, FS 277, GG 1, GG 2, RGC 1002, RGC 1003, RGC 1066, RGS 3, M 83 and RGC 1033; with respect to HS 19, BK 19 and BS 20 were HVG 2-30, X 10, PNB and RGC 1017; with respect to HS 19 and HK 19 were HG 884, HG 6, RGC 936 and HG 75; and with respect to HK 20 and BK 20 were HG 2-20, HG 870, HG 563, HG 365, HG 3-52, RGC 1038 and RGC 1038. In this case, the best adapted genotypes for HS 20 were HG 75 and GG 1; for BS 20was RGC 1017; and for HG 20 was HG 3-52.

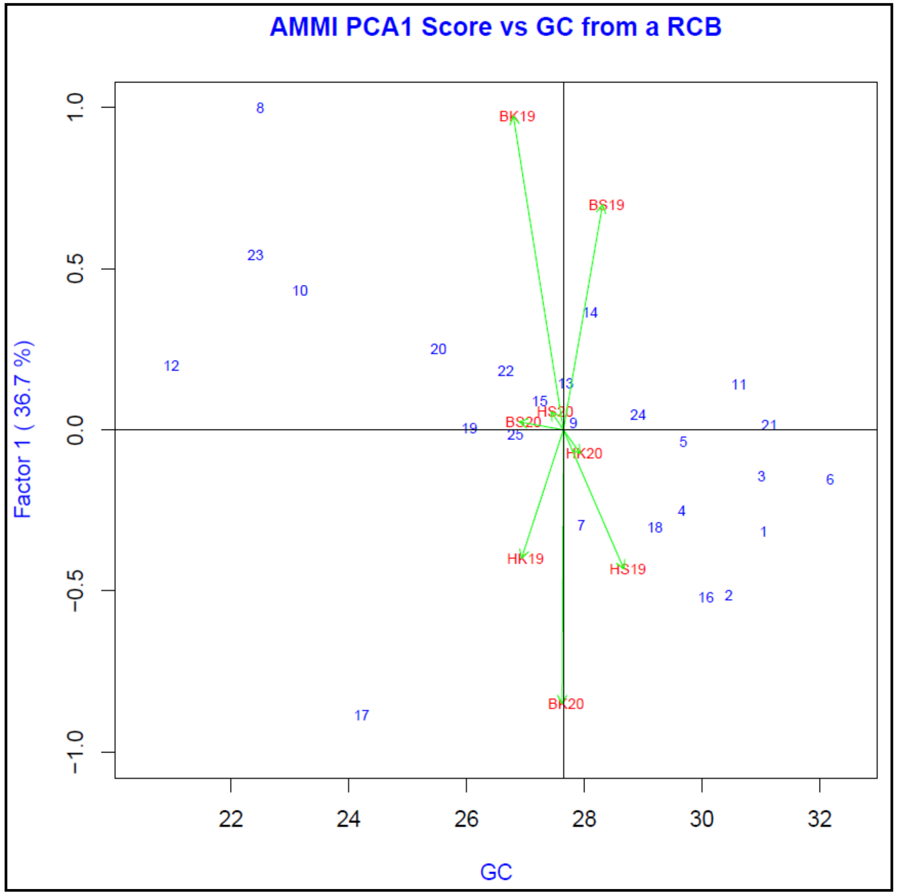

Figure 4.8.15 (a): **AMMI 1 biplot for gum content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

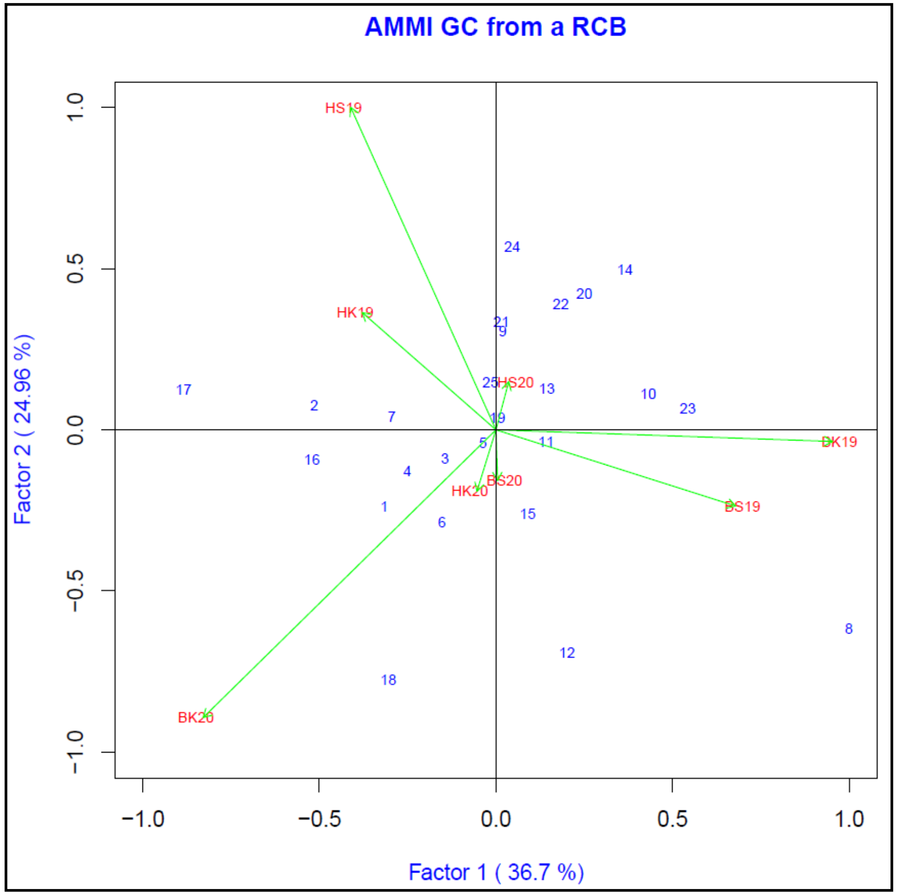

Figure 4.8.15 (b): **AMMI 2 biplot for gum content showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

4.8.2.16 Protein content

AMMI 1 biplot display:

The genotypes namely, RGC 1055, FS 277, M-83, RGC 1003, PNB, HG 6, HVG 2-30, RGC 1038, HG 75, RGC 1002, HG 365 and HG 2-20had protein content more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 936, HG 563, RGC 1066, RGS 3, HG 870, HG 3-52, RGC 1017, X-10, HG 100, HG 884, RGC 1033, GG-2 and GG-1 were generally with low gum content and with negative genotypic index were adapted to unfavourable environments. Considering the high protein content as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments BS 19, HK 19, BS 20 and BK 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while HS 19, BK 19, HS 20 and HK 20 with negative environmental index were generally poor environments (Figure 4.8.16 (a)). The environments HK 19, BK 19 and BS 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But BK 19 and BS 20 were found to have below overall mean. Therefore, these environments were not suitable by keeping in view the importance of high protein content as desirable. Similarly, the genotypes HG 2-20, HG 884, HG 6, HVG 2-30, FS 277, X-10, PNB, GG-1, RGC 1038, RGC 1002, RGC 1003, RGC 1066 and M-83 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 2-20, HG 6, HVG 2-30, FS 277, PNB, GG-1, RGC 1038, RGC 1002, RGC 1003 and M-83 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with protein content at that particular environment. Genotypes, RGC 1002; HG 365; HG 3-52; RGC 1066; and RGC 1017 were identified as specifically adapted to the BS 20; BK 20; HS 20; BK 19 and HK 20 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, HK 19, BK 19 and BS 20 had short spokes and they do not exert strong interactive forces while HS 19, BS 19, HS 20, HK 20 and BK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 2-20, HG 884, FS 277, X-10, GG 1, M 83, RGC 1066 and PNB were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, RGC 1033 and HG 75found more responsive since they were away from the origin (Figure 4.8.16 (b)).

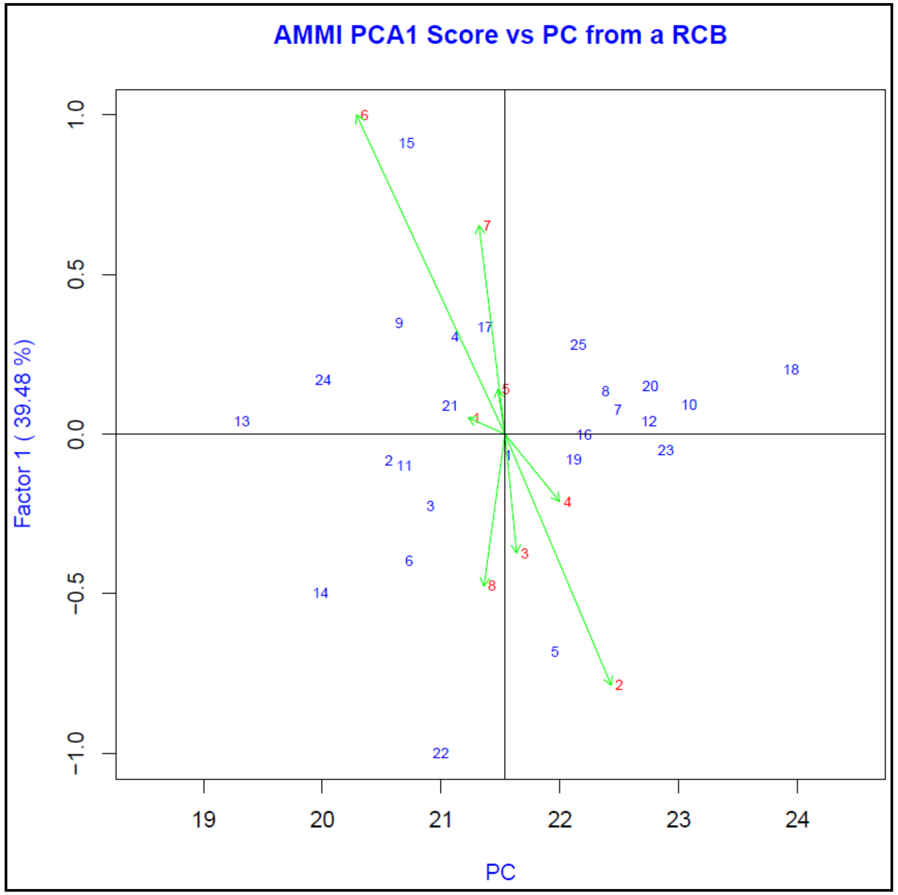

Figure 4.8.16 (a): **AMMI 1 biplot for protein content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

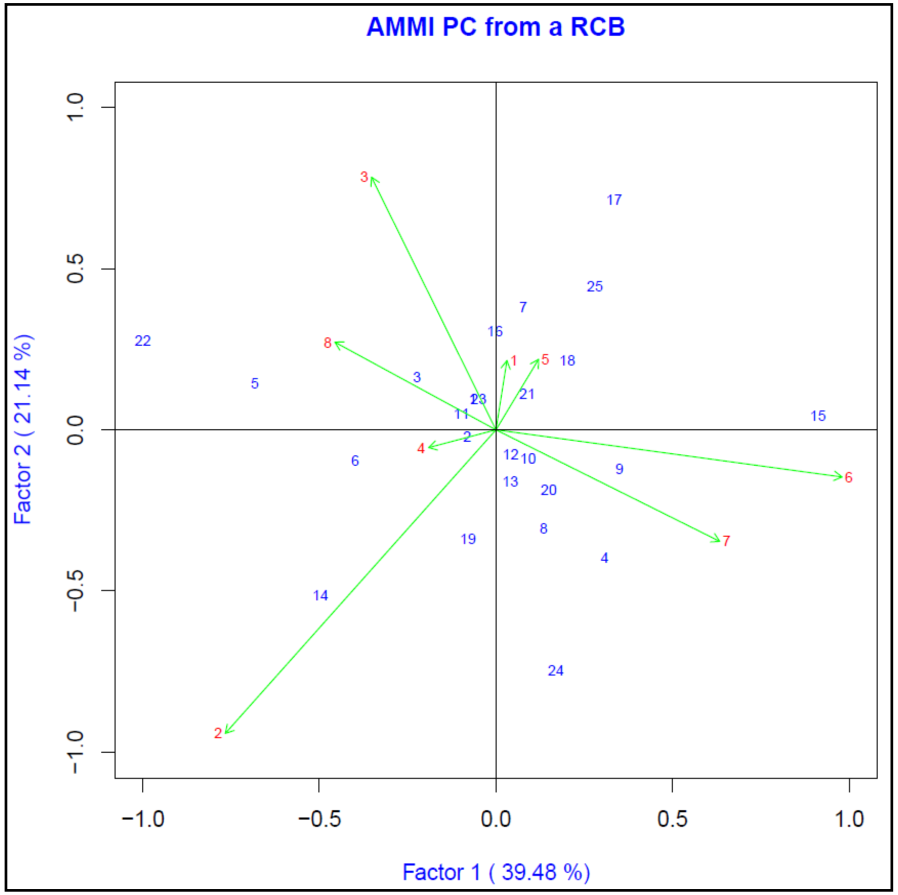

Figure 4.8.16 (b): **AMMI 2 biplot for protein content showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

The best genotypes with respect to HK 19 and BK 19 were HG 6, RGC 1017, RGC 936, RGC 1055, RGC 1066 and HG 75; with respect to HS 19 and HK 20 were HG 563, PNB, GG 1, RGC 1003 and RGC 1033; with respect to BS 19 and HS 20 were HG 2-20, HG 870, HG 365, X 10, RGC 1038, RGS 3 and M 83; and with respect to BS 20 and BK 20 were HG 884, HG 3-52, GG 2 and RGC 1002. In this case, the best adapted genotypes for BK 19 and BK 19 were HG 6, RGC 1055 and RGC 1066; and for BS 20 were HG 563 and HG 3-52.

4.8.2.17 Total soluble sugar (TSS) content

AMMI 1 biplot display:

The genotypes namely, HG 563, RGC 1033, HG 75, HG 884, HG 870, HG 365, HG 2-20, RGC 1066, GG-2, X-10, HG 100, GC 1055, RGC 1038, HG 3-52 and RGC 1017 had TSS content less than the overall mean and negative genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGS 3, RGC 936, RGC 1002, RGC 1003, HVG 2-30, GG-1, M-83, HG 6, PNB and FS 277 were generally with high TSS content and with positive genotypic index were adapted to unfavourable environments. Considering the genotypes with low TSS content as desirable, the environments lying on the left side are favourable environments and those lying on right side are unfavourable. Therefore, environments HK 19, BK 19, HS 20, BS 20 and BK 20 were present on the left hand side of the midpoint of the main effect axis with negative environmental index, seemed to be rich environments, while HS 19, BS 19 and HK 20 with positive environmental index were generally poor environments (Figure 4.8.17 (a)). The environments BS 19, HK 19 and BK 19 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But BS 19 was found to have TSS content above overall mean. Therefore, these environments were not suitable by keeping in view the importance of genotypes with low TSS content as desirable. Similarly, the genotypes HG 2-20, HG 884, HVG 2-30, RGS 3, FS 277, RGC 936 and PNB had near zero score on the first IPCA1indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 2-20 and HG 884 registered below overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to low TSS content of genotype at that particular environment. Genotypes, X 10; HG 3-52, HG 100 and RGC 1017 were identified as specifically adapted to the BS 19; BK 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 19, HK 19 and HK 20 had relatively shorter spokes than rest of the environments and they do not exert strong interactive forces while HS 19, BK 19, HS 20, BS 20 and BK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 2-20, HG 884, HG 563, FS 277 and GG-1 were relatively close to the origin than other genotypes and hence they were non sensitive to environmental interactive forces whereas HG 870, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, X-10, PNB, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.17 (b)). The best genotypes with respect to BS 20 were HG 2-20, HG 870, HG 100, RGC 936, RGC 1002 and HG 75; with respect to BK 19 and HS 20 were HG 884, HG 563, HG 3-52, FS 277, X 10, GG 1, RGC 1017, RGC 1066 and RGC 1033; with respect to HS 19, HK 19 and HK 20 were HG 365, HG 6, PNB, RGC 1038, RGC 1055, RGS 3 and M 83; and with respect to BS 19 and BK 20 were HVG 2-30 and GG 2. In this case, the best adapted genotypes for BS 20 was HG 75; for BK 19 was RGC 1017; for BS 19 was HVG 2-30; for BK 20 was RGC 1003; for HK 20 were RGC 1038 and RGC 1055; and for HK 19 was PNB.

4.8.2.18 Reducing sugar content

AMMI 1 biplot display:

The genotypes namely, HG 563, HG 75, HG 365, RGC 1033, X-10, HG 884, GG-2, HG 3-52, HG 870, RGC 1055, HG 2-20, HG 100, RGC 1017 and RGC 1066 had reducing sugar content less than the overall mean and negative genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGS 3, RGC 1003, GG-1, RGC 1038, RGC 936, RGC 1002, M-83, HVG 2-30, HG 6, PNB and FS 277 were generally with high reducing sugar content and with positive genotypic index were adapted to unfavourable environments. Considering the genotypes with low reducing sugar content as desirable, the environments lying on the left side are favourable environments and those lying on right side are unfavourable. Therefore, environments HS 19, BS 19, BK 19, HS 20 and BK 20 were present on the left hand side of the midpoint of the main effect axis with negative environmental index, seemed to be rich environments while, HK 19, BS 20 and HK 20 with positive environmental index were generally poor environments (Figure 4.8.18 (a)). The environmentsBS19, HK19, BK19 and BK20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HK 19 was found to have above overall mean. Therefore, environment HK 19 was not suitable by keeping in view the importance of genotypes with low reducing sugar content as desirable. Similarly, the genotypes HG 3-52, RGC 1017 and RGC 1066 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. All of these, genotypes registered below overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to low reducing sugar content of genotype at that particular environment.

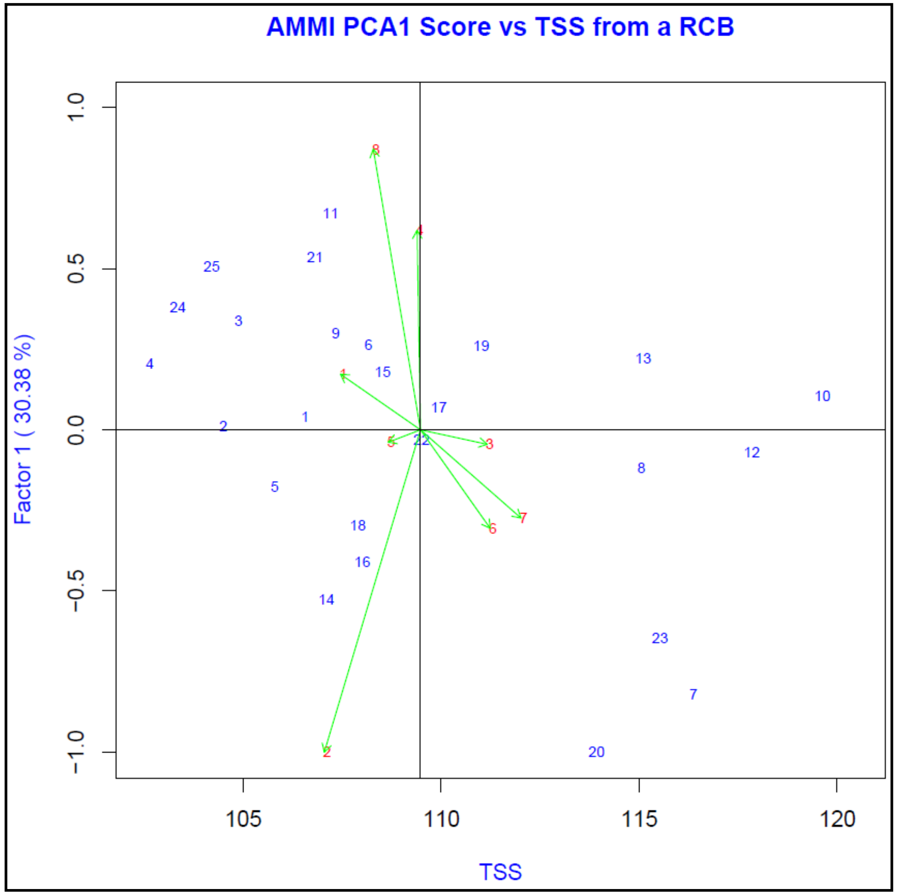

Figure 4.8.17 (a): AMMI 1 biplot for TSS content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

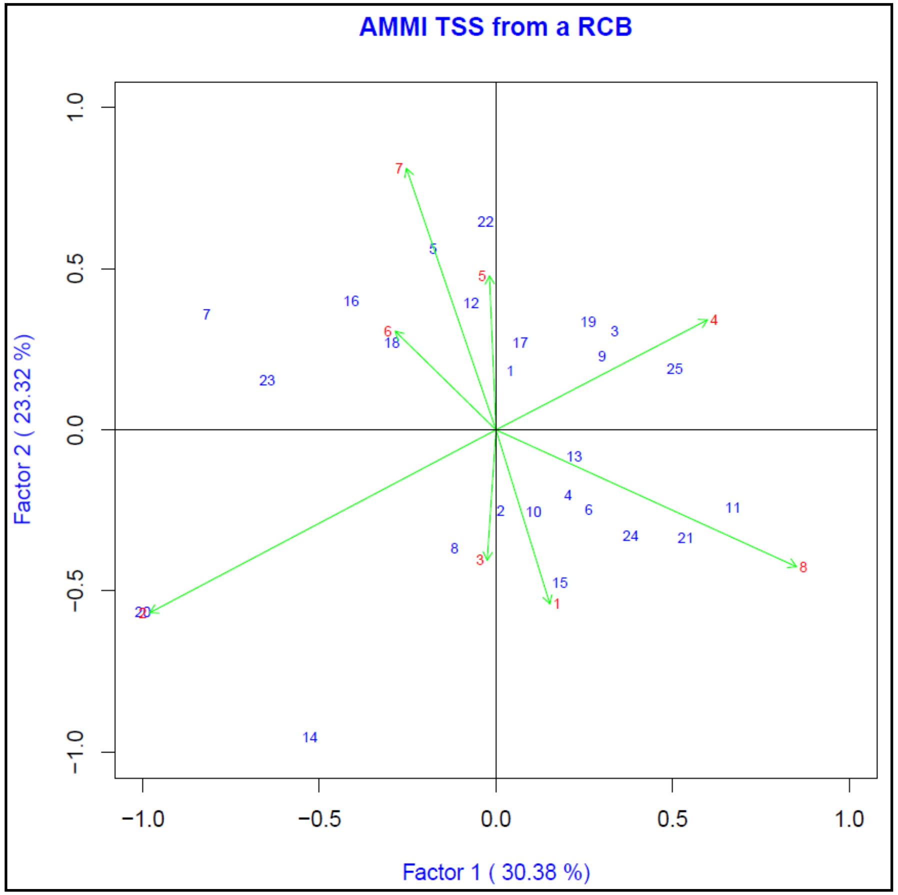

Figure 4.8.17 (b): **AMMI 2 biplot for TSS content showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Genotypes, HG 100 and RGC 1066; HG 884; HG 3-52 and RGC 1017 were identified as specifically adapted to the HS 19; BS 19; BK 19respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BS 19 and BK 20 had short spokes and they do not exert strong interactive forces while HS 19, HK 19, BK 19, HS 20, BS 20 and HK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 3-52, X-10, RGC 1017 and RGC 1066 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 6, HVG 2-30, HG 100, FS 277, PNB, GG-1, GG-2, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003,RGS 3, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.18 (b)). The best genotypes with respect to HS 19, BK 19 and BK 20 were HG 563, HG 365, HG 3-52, GG 2, RGC 936, RGC 1066 and RGC 1033; with respect to BS 19, HS 20 and BS 20 were HG 884, HG 100, X 10, RGC 1017 and HG 75; with respect to HK 19 were HG 870, HVG 2-30, RGC 1003 and M 83; and with respect to HK 20 were HG 2-20, HG 6, FS 277, PNB, GG 1, RGC 1002 and RGS 3. In this case, the best adapted genotype for HS 19 was RGC 1066; for BK 20 was HG 3-52; for BS 19 were HG 884 and RGC 1017; and for BS 20 were HG 100 and HG 75.

4.8.2.19 Non-Reducing sugar content

AMMI 1 biplot display:

The genotypes namely, HG 563, RGC 1033, HG 870, HG 884, HG 75, HG 2-20, RGC 1066, HG 365, HG 100, RGC 1038, GG-2, RGC 1055, X-10, HG 3-52 and RGC 1017 had non-reducing sugar content less than the overall mean and negative genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGS 3, RGC 936, RGC 1002, HVG 2-30, RGC 1003, HG 6, M-83, GG-1, PNB and FS 277 were generally with high non-reducing sugar content and with positive genotypic index were adapted to unfavourable environments. Considering the genotypes with low non-reducing sugar content as desirable, the environments lying on the left side are favourable environments and those lying on right side are unfavourable. Therefore, environments HK 19, BK 19, BS 20 and BK 20 were present on the left hand side of the midpoint of the main effect axis with negative environmental index, seemed to be rich environments, while HS 19, BS 19, HS 20 and HK 20 with positive environmental index were generally poor environments (Figure 4.8.19 (a)). The environments 20and HK 19 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HK 20was found to have above overall mean. Therefore, this environment was not suitable by keeping in view the importance of genotypes with low non-reducing sugar content as desirable.

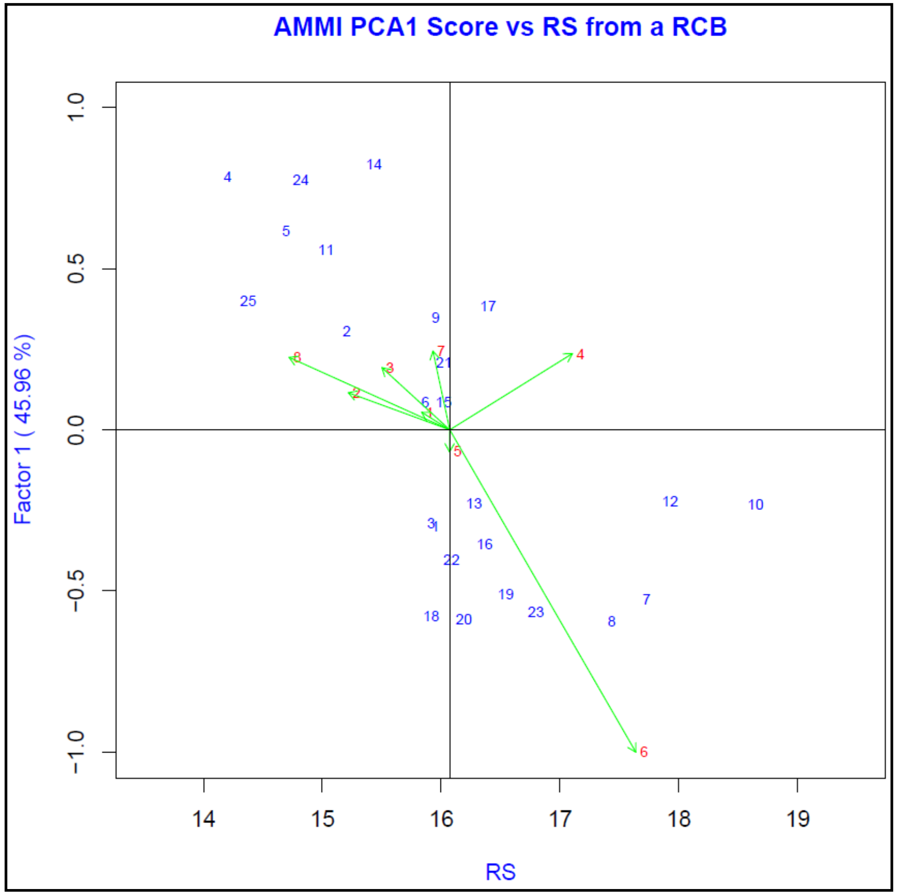

Figure 4.8.18 (a): **AMMI 1 biplot for reducing sugar content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

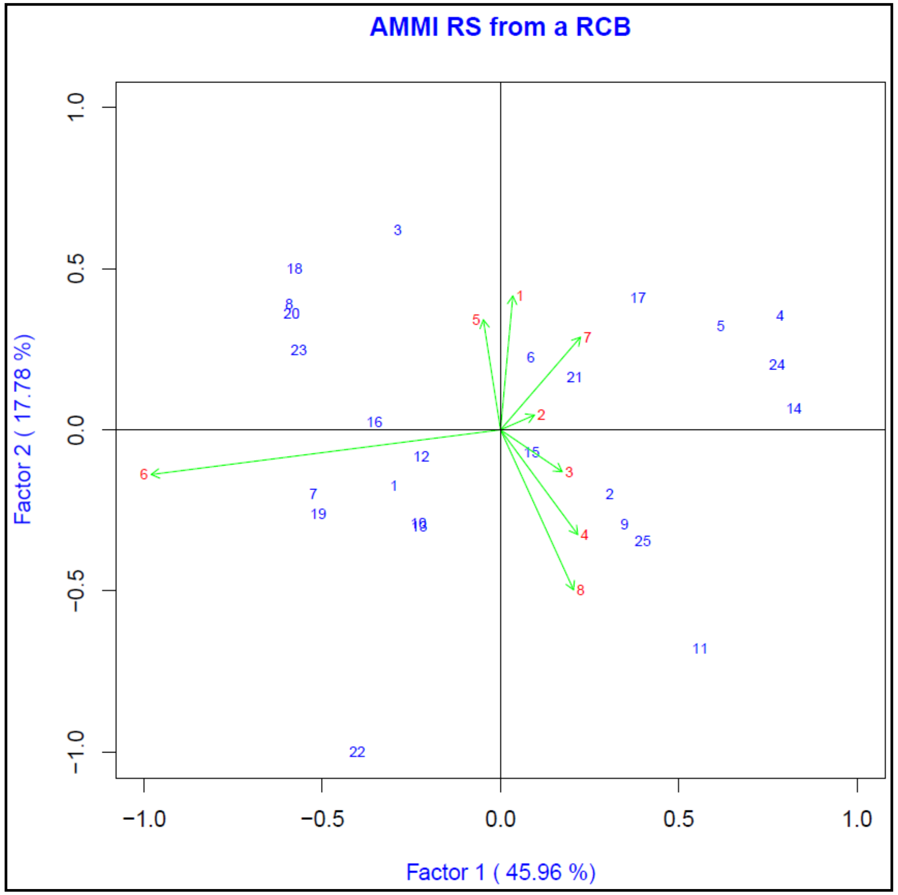

Figure 4.8.18 (b): **AMMI 2 biplot for reducing sugar content showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Similarly, the genotypes HG 2-20, HG 884, HG 100, GG-1 and GG-2 had near zero score on the first IPCA1indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 2-20, HG 884, HG 100 and GG-2 registered below overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to low non-reducing sugar content of genotype at that particular environment. Genotypes, RGC 1002; GG 2; RGC 936; RGC 1038; RGC 1055; HG 3-52 and X 10; and HKR 06-487 were identified as specifically adapted to the BS 19; BS 20; HK 20; BK 20; HK 19; BK 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environment, HK 20 had short spoke and do not exert strong interactive forces while HS 19, BS 19, HK 19, BK 19, HS 20, BS 20 and BK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 2-20, HG 884, HG 100, FS 277, and GG-1 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, X-10, PNB, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.19 (b)). The best genotypes with respect to BS 19 and BK 19 were HG 884, HVG 2-30, FS 277, GG 2, RGC 1017 and RGC 1033; with respect to HS 20 and BS 20 were HG 2-20, HG 870, HG 563, HG 3-52, HG 100, X 10, GG 1, RGC 1002, RGC 1066 and HG 75; with respect to HK 20 and BK 20 were HG 6, RGC 1003 and M 83; and with respect to HS 19 and HK 19 were HG 365, PNB, RGC 1038, RGC 936, RGC 1055 and RGS 3. In this case, the best adapted genotypes for BS 19 was HG 884; for BK 19 were HVG 2-30 and RGC 1017: for BS 20wereHG 870, RGC 1002 and HG 75 for HK 19 were PNB and RGC 936; and for BK 20 was RGC 1003.

4.8.2.20 Acid detergent fibre (ADF) content

AMMI 1 biplot display:

The genotypes namely, HG 75, X-10, HG 563, RGC 1038, RGC 1066, RGC 1017, RGC 1033, RGC 1003, HG 100, HG 365, RGS 3, RGC 1002, RGC 936, HG 3-52 and HG 870 had ADF content more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, HG 884, GG-2, GG-1, HG 2-20, RGC 1055, HG 6, M-83, FS 277, PNB and HVG 2-30 were generally with low ADF content and with negative genotypic index were adapted to unfavourable environments. Considering the high ADF content as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable.

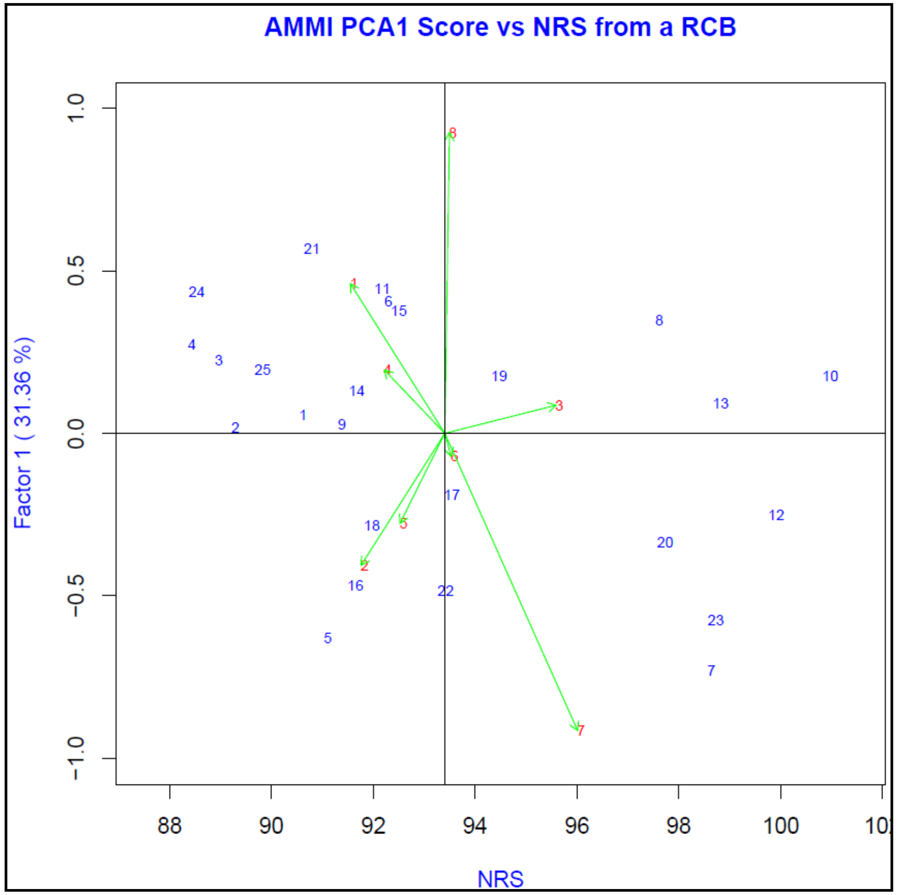

Figure 4.8.19 (a): **AMMI 1 biplot for non-reducing sugar content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

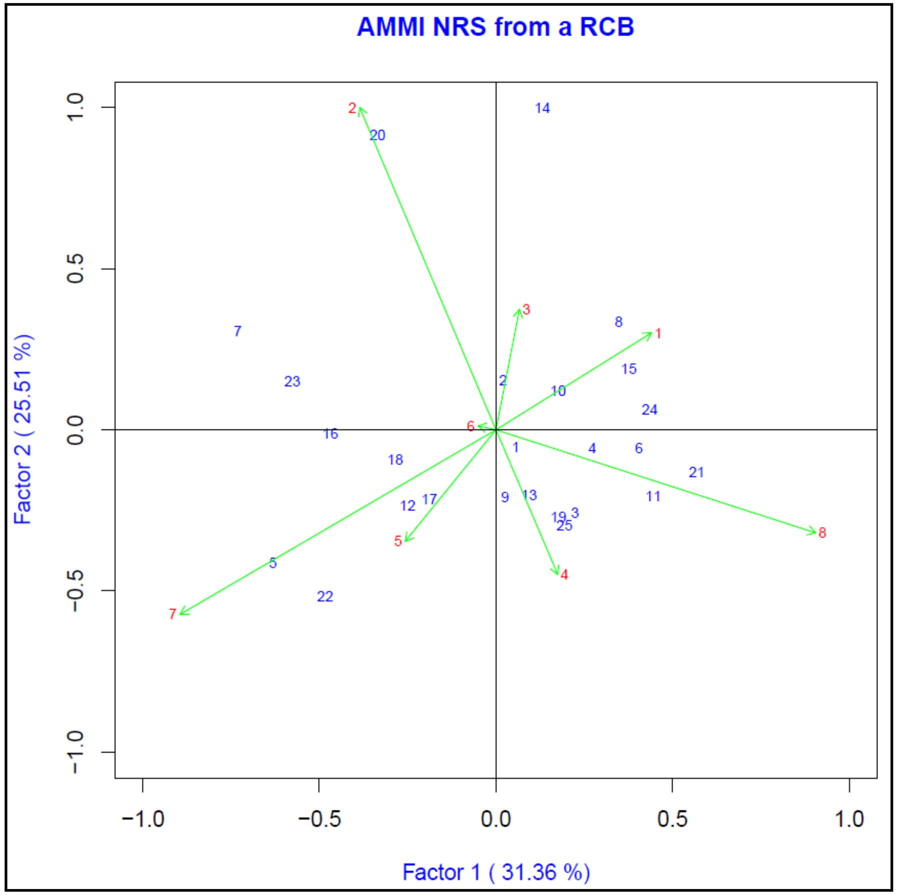

Figure 4.8.19 (b): **AMMI 2 biplot for non-reducing sugar content showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Therefore, environments BS 19 and BK 19 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while HS 19, HK 19, HS 20, BS 20, HK 20 and BK 20 with negative environmental index were generally poor environments (Figure 4.8.20 (a)). The environments BS 19 and BK 19 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. Similarly, the genotypes HG 2-20, HG 870, HG 6, X 10, GG 2, RGC 1017, RGC 1055 and RGC 1003 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 870, X 10, RGC 1017 and RGC 1003 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with ADF content at that particular environment. Genotypes, GG 2; RGC 1003; HG 884; FS 277, HVG 2-30 and PNB were identified as specifically adapted to the HK 20; BK 19; BK 20 and HS 19; HK 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BK 19, BK 20 and HS 19 had short spokes and they do not exert strong interactive forces while BS 19, HK 19, HS 20, BS 20 and HK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 870, HG 6, RGS 3 and M-83 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 563, HG 365, HG 3-52, HVG 2-30, HG 100, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.20 (b)). The best genotypes with respect to BS 20 were HG 100, X 10, RGC 1038, RGC 1066 and RGC 1033; with respect to HS 20 were HG 563, RGC 1017, RGC 936, RGC 1055 and HG 75;with respect to HS 19, HK 19, HK 20 and BK 20 were HG 884, HG 365, HVG 2-30, FS 277, PNB, GG 1, GG 2, RGS 3 and M 83; and with respect to BS 19 and BK 19 were HG 2-20, HG 870, HG 3-52, HG 6, RGC 1002 and RGC 1003. In this case, the best adapted genotypes for HK 20 was GG 2; for BK 19 were HG 2-20 and HG 870; for BS 20 was HG 100; for HK 19 was HG 365; for HS 19 were HVG 2-30 and PNB; and for BK 20were RGS 3 and M 83.

4.8.2.21 Lignin content

AMMI 1 biplot display:

The genotypes namely, HG 75, RGC 1033, X-10, HG 563, RGC 936, RGC 1038, RGC 1066, HG 365, RGS 3, HG 2-20, RGC 1017 and HG 870, HG 884 had lignin content more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments.

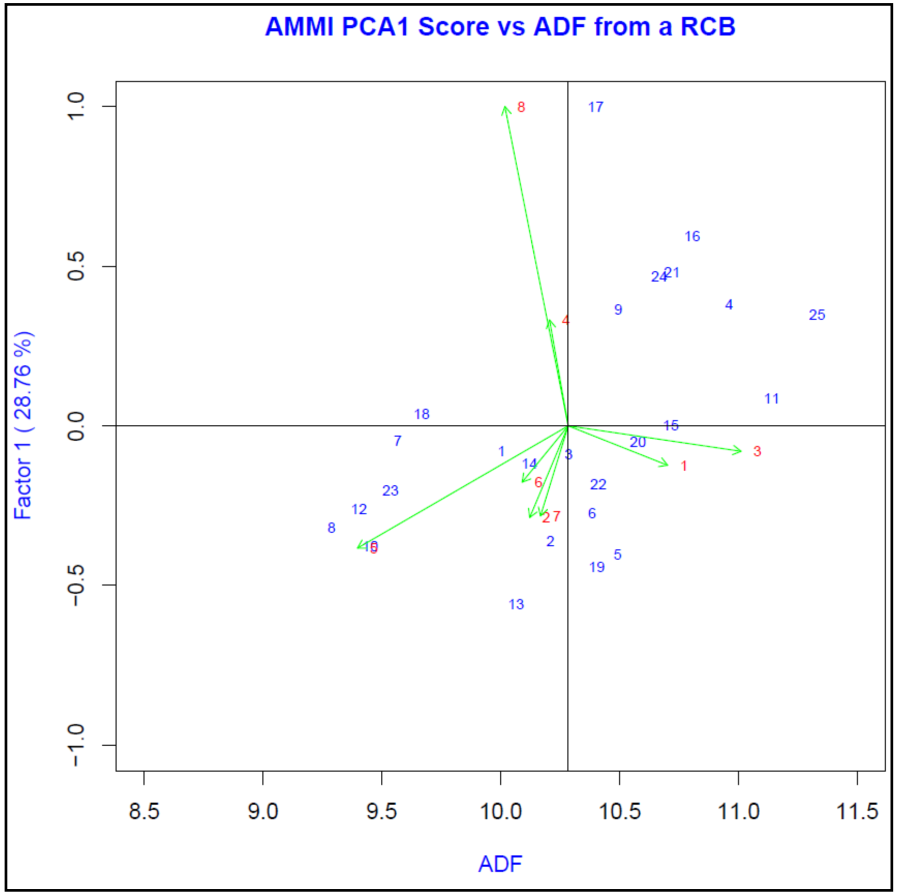

Figure 4.8.20 (a): **AMMI 1 biplot for ADF content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

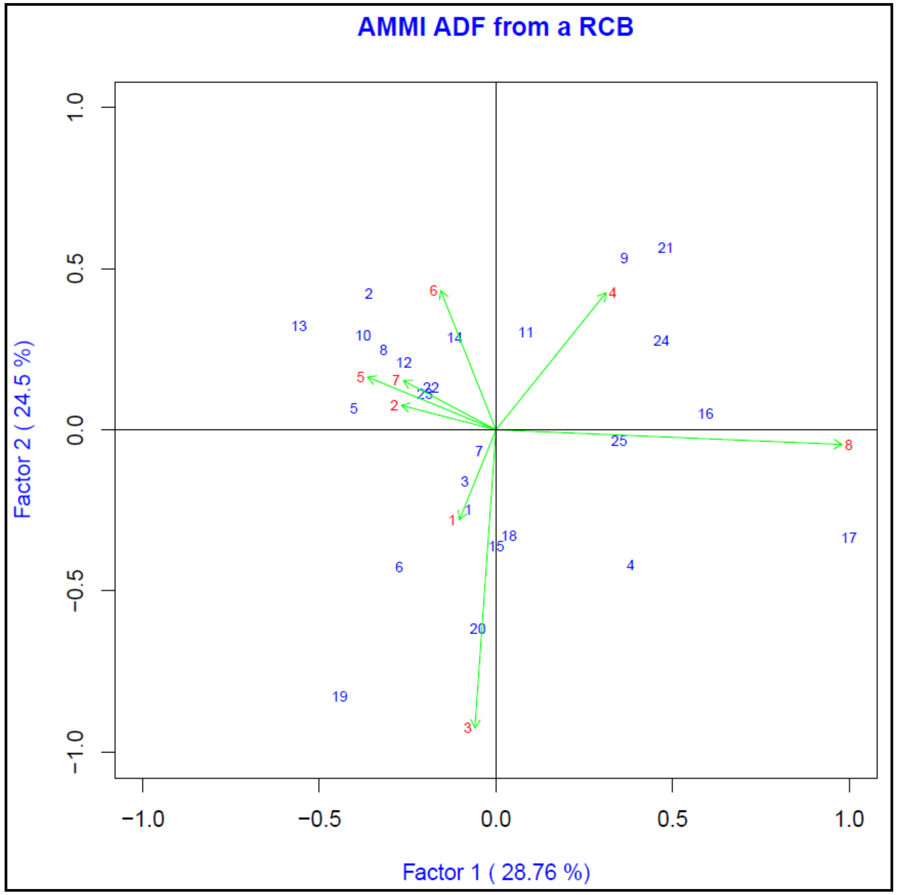

Figure 4.8.20 (b): **AMMI 2 biplot for ADF content showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

In contrast, genotypes, HG 100, RGC 1055, HG 3-52, RGC 1003, RGC 1002, GG-2, HG 6, GG-1, PNB, FS 277, HVG 2-30 and M-83 were generally with low lignin content and with negative genotypic index were adapted to unfavourable environments. Considering the high lignin content as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments HS 19, BS 19, HK 19, BS 20, HK 20 and BK 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while BK 19 and HS 19with negative environmental index were generally poor environments (Figure 4.8.21 (a)). The environments HS 19, BS 19, BK 19, BS 20 and HK 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But BK 19 was found to have lignin content below overall mean. Therefore, these environments were not suitable by keeping in view the importance of high lignin content as desirable. Similarly, the genotypes HG 870, HG 3-52, HG 100, PNB, RGC 1055, HG 2-20 and RGC 1033 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 870, HG 2-20 and RGC 1033 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with lignin content at that particular environment. Genotypes, HG 884; PNB; HG 6; and GG 2 were identified as specifically adapted to the HK 19; BK 19, BK 20; BS 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, HS 19 and BS 20 had short spokes and they do not exert strong interactive forces while BS 19, HK 19, BK 19, HS 20, HK 20 and BK 20 with long spokes were more differentiating environments. In the present study, the genotypes, PNB and RGC 1066 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, HG 100, FS 277, X-10, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.21 (b)). The best genotypes with respect to HS 20 were HG 563, HG 100, X 10, RGC 1038, RGC 936, RGC 1033 and HG 75; with respect to BS 19 were HG 2-20, HG 870, GG 2, RGC 1017, RGC 1055, RGC 1066 and RGS 3; with respect to HS 19, BS 20, HK 20 and BK 20 were HG 884, HVG 2-30, FS 277, PNB, RGC 1003 and M 83; and with respect to HK 19 and BK 19 were HG 365, HG 3-52, HG 6, GG 1 and RGC 1002. In this case, the best adapted genotypes for HS 20 was RGC 936; for BS 19 was RGC 1055; for BK 19 was HG 3-52: for BK 20 was HG 884; and for BS 20 was PNB.

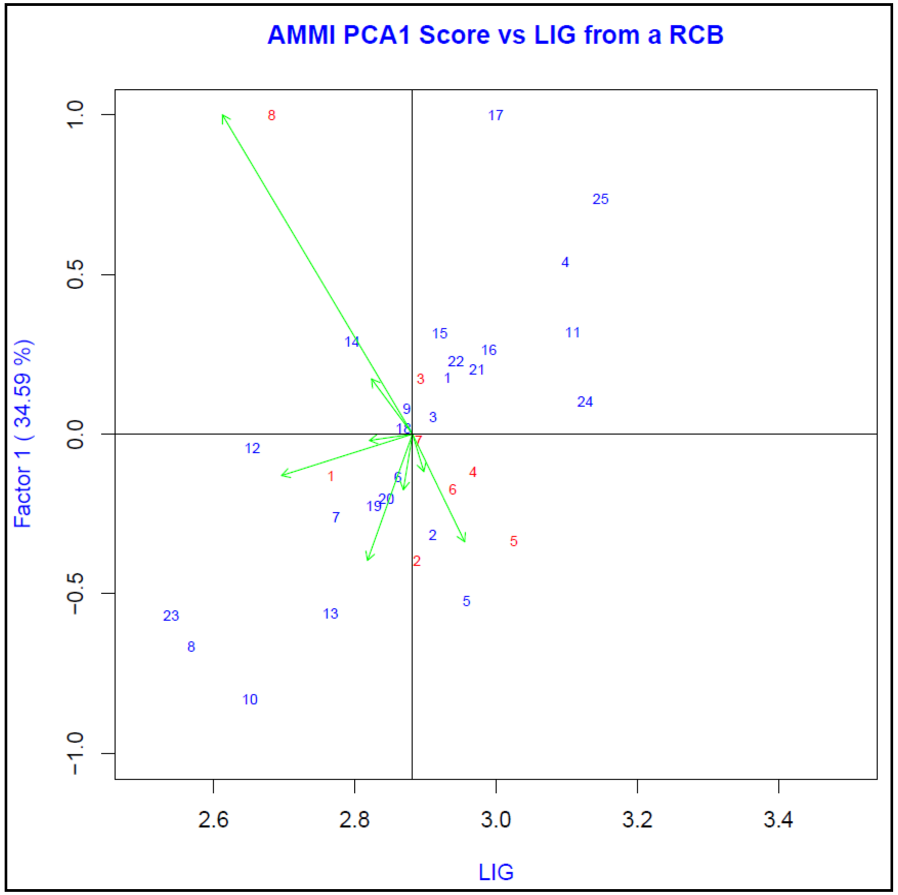

Figure 4.8.21 (a): **AMMI 1 biplot for lignin content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

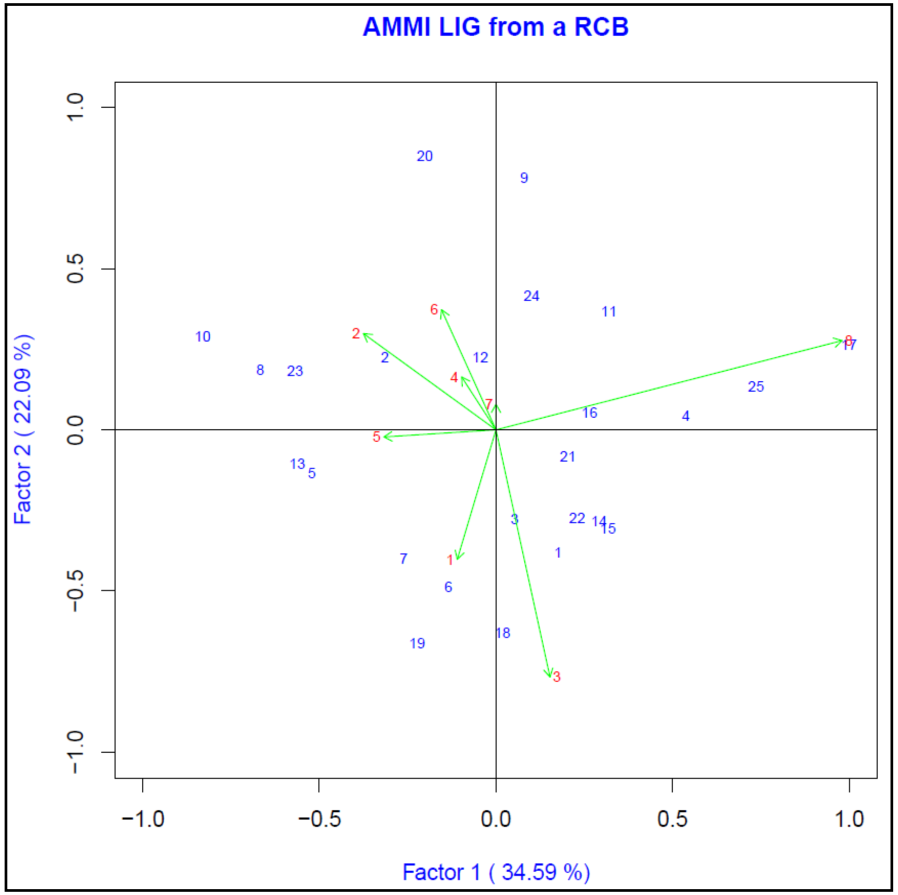

Figure 4.8.21 (b): **AMMI 2 biplot for lignin content showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

4.8.2.22 Cellulose content

AMMI 1 biplot display:

The genotypes namely, HG 75, X-10, HG 563, RGC 1017, RGC 1066, RGC 1003, RGC 1038, HG 3-52, HG 100, RGC 1033, HG 365, RGC 1002, RGC 936, RGS 3 and HG 870 had cellulose content more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, GG-2, HG 884, GG-1, HG 2-20, M-83, RGC 1055, HG 6, FS 277, PNB and HVG 2-30 were generally with low cellulose content and with negative genotypic index were adapted to unfavourable environments. Considering the high cellulose content as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments BS 19, BK 19 and HS 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while HS 19, HK 19, BS 20, HK 20 and BK 20 with negative environmental index were generally poor environments (Figure 4.8.22 (a)). The environments HS 19, BS 19, BK 19 and BS 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HS 19 and BS 20 were found to have below overall mean. Therefore, these environments were not suitable by keeping in view the importance of high cellulose content as desirable. Similarly, the genotypes HVG 2-30, FS 277, RGC 936 and HG 75 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, RGC 936 and HG 75 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with cellulose content at that particular environment. Genotypes, GG 1 and HVG 2-30 were identified as specifically adapted to the BK 20 and HK 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, HS 19 and HK 19 had short spokes and they do not exert strong interactive forces while BS 19, BK 19, HS 20, BS 20, HK 20 and BK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HVG 2-30, FS 277 and HG 75 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83 and RGC 1033found more responsive since they were away from the origin (Figure 4.8.22 (b)).

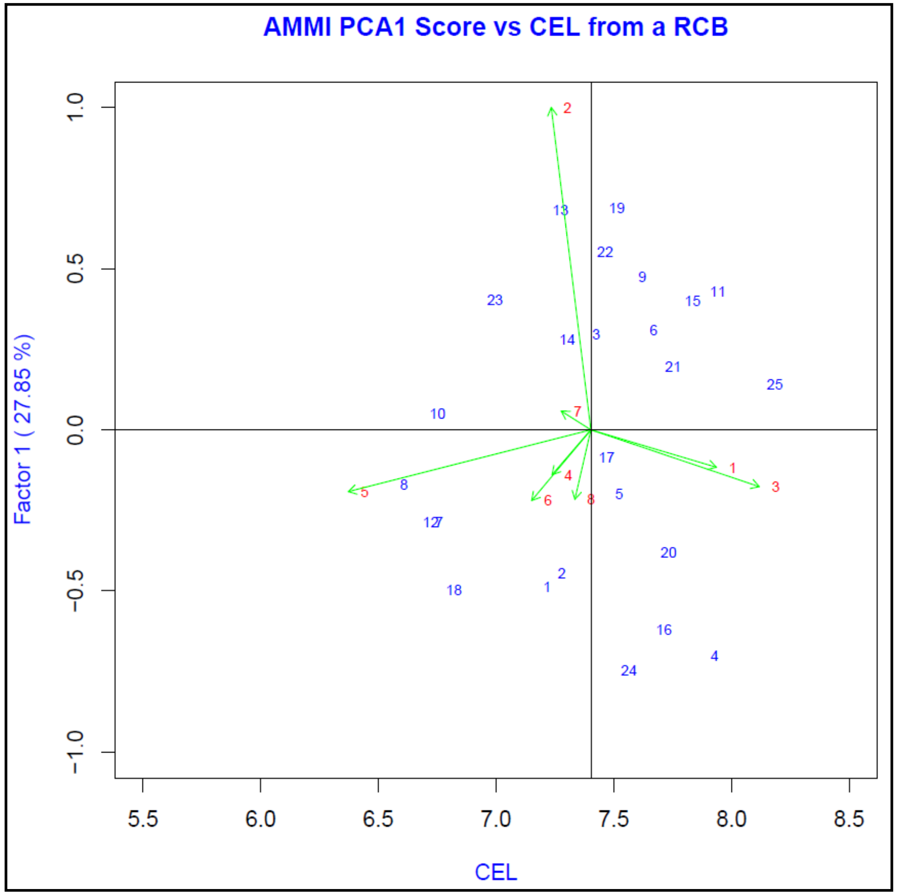

Figure 4.8.22 (a): **AMMI 1 biplot for cellulose content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

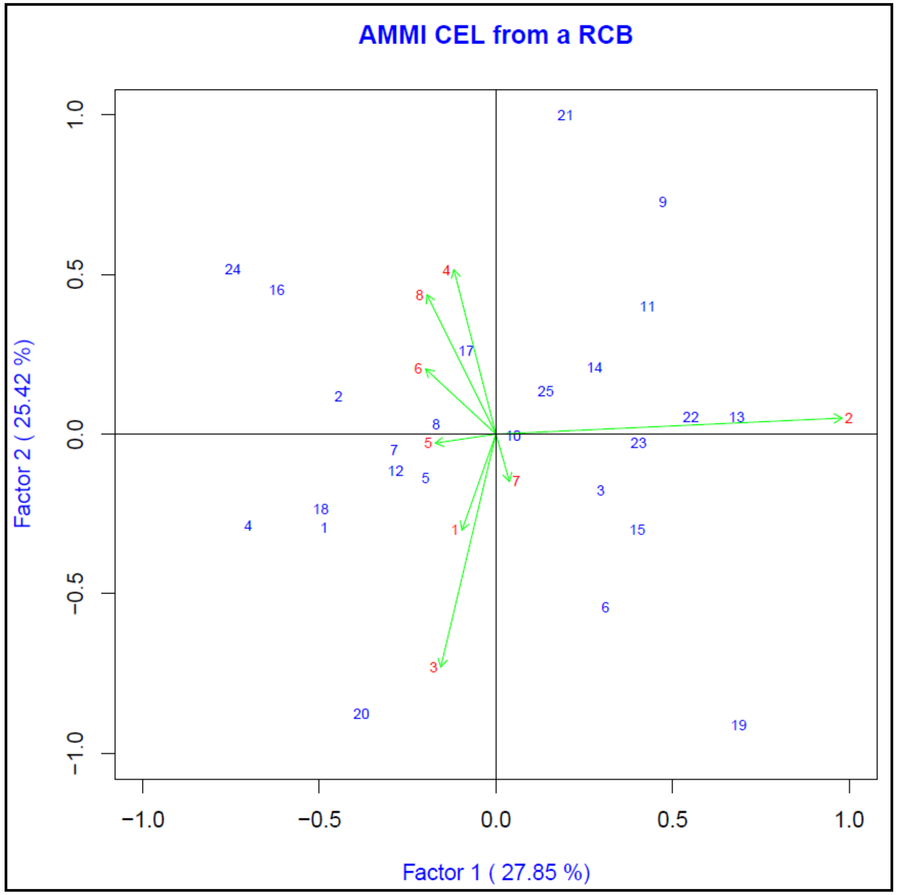

Figure 4.8.22 (b): AMMI 2 biplot for cellulose content showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

The best genotypes with respect to BK 20 were HG 100, X 10, GG 1, GG 2, RGC 1066, RGS 3 and HG 75; with respect to HS 19 were HG 870, HG 3-52, FS 277, RGC 1017, RGC 1002 and M 83; with respect to BS 19, HK 19 and BK 19 were HG 2-20, HG 563, HG 365, HG 6, PNB and RGC 1055; and with respect to HS 20, BS 20 and HK 20 were HG 884, HVG 2-30, RGC 1038, RGC 936 and RGC 1033.

In this case, the best adapted genotypes for HK 20 was RGC 936; for BK 19wasHG 365: for BS 19 was RGC 1003; and for HK 19 were HG 6 and PNB.

4.8.2.23 Silica content

AMMI 1 biplot display:

The genotypes namely, HG 75, HG 563, X-10, GG-1, HG 870, RGC 1033, HG 100, HG 2-20, RGC 1038, RGC 1017, HG 365, RGC 1066 and RGS 3 had silica content more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, HG 884, HG 3-52, RGC 936, GG-2, RGC 1002, HVG 2-30, RGC 1003, RGC 1055, HG 6, PNB, FS 277 and M-83 were generally with low silica content and with negative genotypic index were adapted to unfavourable environments. Considering the high silica content as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments HK 19, HS 20, BS 20, HK 20 and BK 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while HS 19, BS 19 and BK 19with negative environmental index were generally poor environments (Figure 4.8.23 (a)). The environments HS 20 and HK 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. Similarly, the genotypes HG 3-52, HG 6, HVG 2-30, FS 277, PNB, GG-2, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83 and RGC 1033 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, RGC 1066, RGS 3 and RGC 1033registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with silica content at that particular environment. Genotypes, RGC 936 and RGC 1002; RGS 3; GG 1 were identified as specifically adapted to the BS 19; HK 20; HK 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, HS 20, HK 20 and BK 20 had short spokes and they do not exert strong interactive forces while HS 19, BS 19, HK 19, BK 19 and BS 20 with long spokes were more differentiating environments.

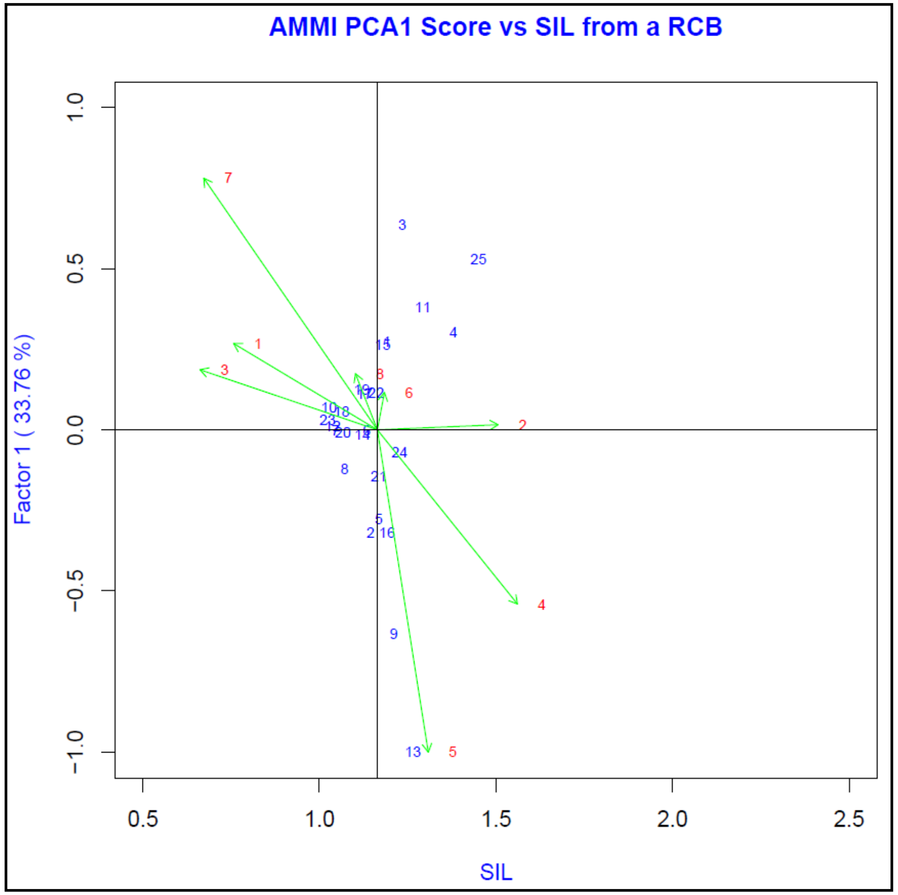

Figure 4.8.23 (a): **AMMI 1 biplot for silica content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

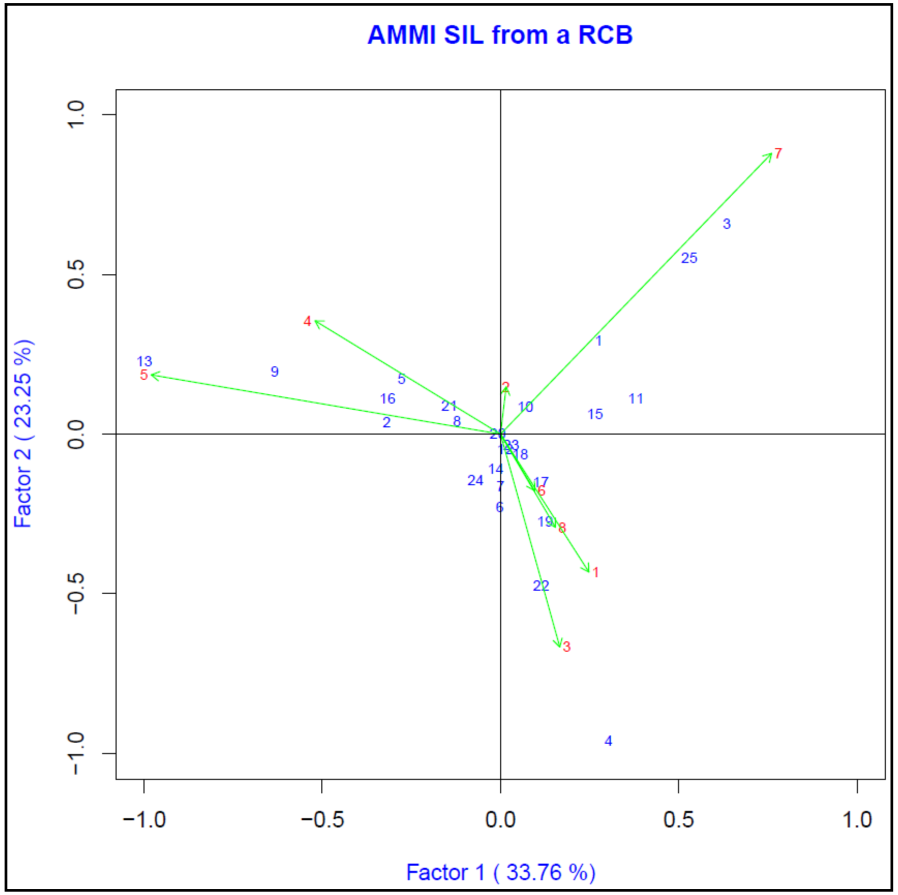

Figure 4.8.23 (b): **AMMI 2 biplot for silica content showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

In the present study, the genotypes, HG 6, HVG 2-30, FS 277, PNB, GG-2, RGC 936, RGC 1055, RGC 1003, RGC 1066, M 83 and RGC 1033 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 3-52, HG 100, X-10, GG-1, RGC 1017, RGC 1038, RGC 1002, RGS 3 and HG 75 found more responsive since they were away from the origin (Figure 4.8.23 (b)). The best genotypes with respect to HS 19 and BK 20 were HG 2-20, HG 870, FS 277, X 10, RGC 1017 and HG 75; with respect to BS 19, BK 19, HS 20 and HK 20 were HG 563, PNB, RGC 936, RGC 1055, RGC 1002, RGS 3 and M 83; and with respect to HK 19 and BS 20 were HG 884, HG 365, HVG 2-30, HG 100, GG 1, RGC 1038, RGC 1003 and RGC 1066. In this case, the best adapted genotypes for BK 20 was FS 277; for HS 19 was HG 870: for HK 20 was RGC 936: for HS 20 was RGC 1002; for BS 19 was RGS 3; for HK 19 was GG 1; and for BS 20 was HG 100.

4.8.2.24 Neutral detergent fibre (NDF) content

AMMI 1 biplot display:

The genotypes namely, HG 75, X-10, RGC 1017, RGC 1038, RGC 1066, HG 563, RGC 1033, RGS 3, RGC 936, HG 365, RGC 1003, HG 100, RGC 1002, HG 870 and HG 884 had NDF content more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, HG 3-52, GG-1, GG-2, HG 2-20, FS 277, RGC 1055, HG 6, M-83, PNB and HVG 2-30 were generally with low NDF content and with negative genotypic index were adapted to unfavourable environments. Considering the high NDF content as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments BS 19, BK 19, HS 20 and BS 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments, while HS 19, HK 19, HK 20 and BK 20 with negative environmental index were generally poor environments (Figure 4.8.24 (a)). The environments BK 19 and BS 19had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. Similarly, the genotypes HG 2-20, HG 870, HG 6, HG 100, X-10, GG-2, RGC 1055, RGC 1003 and M-83 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 870, HG 100, X-10 and RGC 1003 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments.

Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with NDF content at that particular environment. Genotypes, RGC 1003; HG 75; HVG 2-30 and PNB; FS 277 and GG 1 identified as specifically adapted to the BK 19 and BK 20; HK 20; HK 19;

BK 20, HK 20 and HS 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, HS 19 and BS 19 had relatively short spokes than other environments and they do not exert strong interactive forces while HK 19, BK 19, HS 20, BK 20, HK 20 and BK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 870, HG 6, HG 100, X-10, GG-2, HG 3-52 and PNB were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 884, HG 563, HG 365, HVG 2-30, FS 277, GG-1, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.24 (b)). The best genotypes with respect to HS 19 and BK 20 were HG 3-52, HG 6, GG 1, GG 2, RGC 1002, RGS 3 and M 83; with respect to HK 19 and HK 20 were HG 884, HG 870, HG 365, HVG 2-30, HG 100, FS 277 and PNB; with respect to BK 19 and HS 20 were X 10, RGC 1017, RGC 1003, RGC 1066, RGC 1033 and HG 75; and with respect to BS 19 and BS 20 were HG 2-20, HG 563, RGC 1038, RGC 936 and RGC 1055. The best genotypes for BK 20 was HG 100; for HS 19 was HG 3-52; for HK 19 was HG 884; for HK 20 was FS 277; for BK 19 was RGC 1003; for BS 20 was HG 2-20 and for BS 19 was RGC 1038.

4.8.2.25 Hemicellulose content

AMMI 1 biplot display:

The genotypes namely, RGS 3, HG 75, FS 277, RGC 936, HG 884, X-10, RGC 1033, RGC 1017, HG 870, GG-1, RGC 1066 and HG 365 had hemicellulose content more than the overall mean and positive genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, RGC 1002, GG-2, HG 2-20, RGC 1038, HG 100, RGC 1003, HVG 2-30, HG 3-52, PNB, HG 6, M-83, RGC 1055 and HG 563were generally with low hemicellulose content and with negative genotypic index were adapted to unfavourable environments. Considering the high hemicellulose content as desirable, the environments lying on the right side are favourable environments and those lying on left side are unfavourable. Therefore, environments BS 19, HS 20 and BS 20 were present on the right hand side of the midpoint of the main effect axis with positive environmental index, seemed to be rich environments while, HS 19, HK 19, BK 19, HK 20 and BK 20 with negative environmental index were generally poor environments (Figure 4.8.25 (a)).The environments HS 19, HK 19, BS 20 and HK 20 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But HS 19, HK 19 and HK 20 were found to have below overall mean. Therefore, these environments were not suitable by keeping in view the importance of high hemicellulose content as desirable.

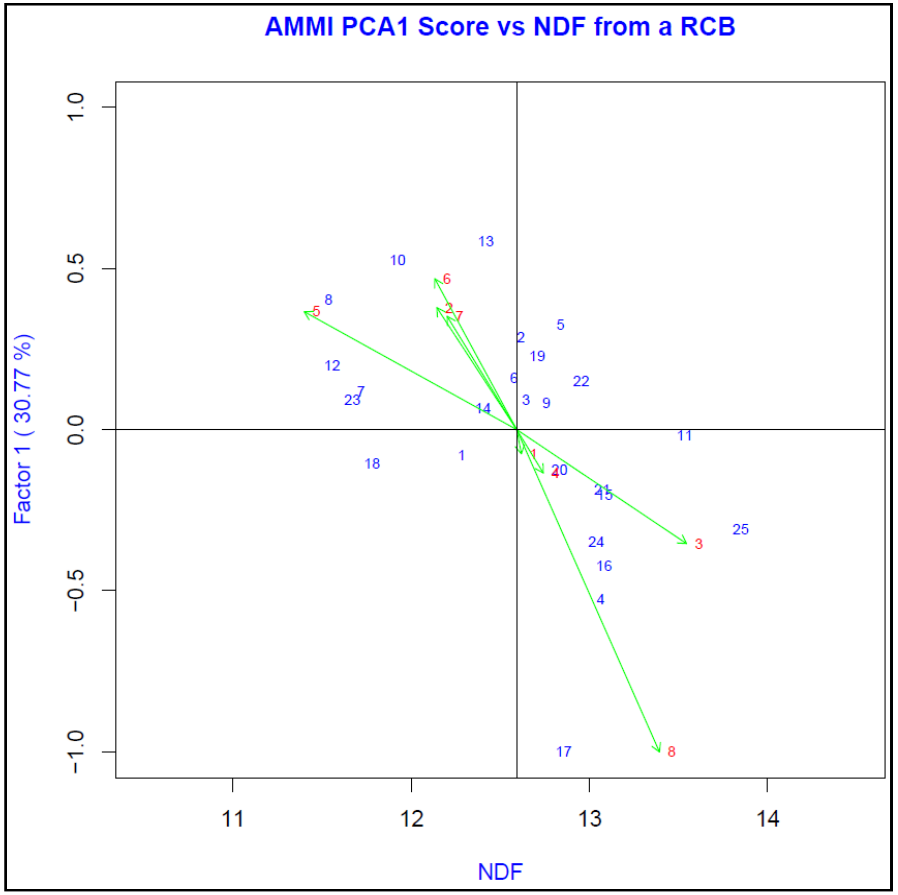

Figure 4.8.24 (a): **AMMI 1 biplot for NDF content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores**

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

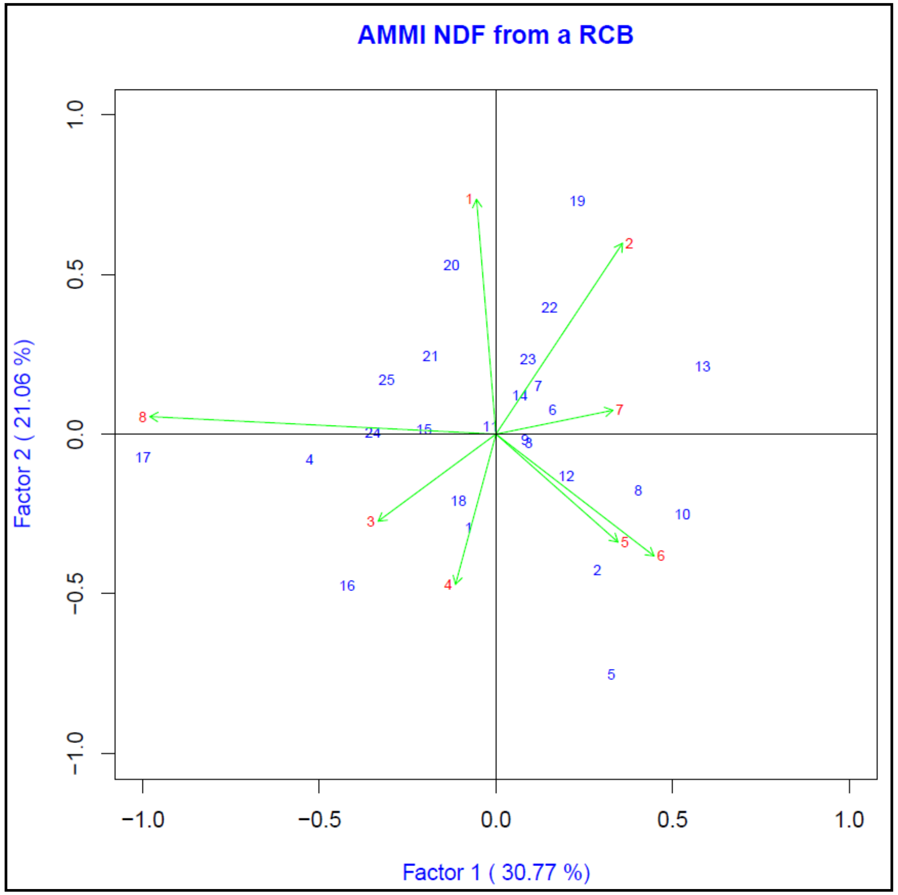

Figure 4.8.24 (b): AMMI 2 biplot for NDF content is showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments.

Code	**Genotypes**	**Code**	**Genotypes**
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

Similarly, the genotypes HG 884, HG 870, HG 6, HVG 2-30, HG 100, FS 277, GG-2, RGC 1017, RGC 1038, RGC 1066, M-83 and HG 75 had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. Out of these, HG 884, HG 870, FS 277, RGC 1017, RGC 1066 and HG 75 registered above overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to genotype with hemicellulose content at that particular environment. Genotypes, HG 884, GG 1 and RGC 1066; M 83; X 10 were identified as specifically adapted to the BS 20; HK 20; BS 19 respectively and these environments were considered as the favourable environments for these genotypes.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, HS 19, HK 19, BK 19, HS 20, BS 20 and BK 20 had short spokes and they do not exert strong interactive forces while BS 19 and HK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 884, HG 870, HVG 2-30, HG 100, RGC 1017, RGC 1038, RGC 1066 and GG-1 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 2-20, HG 563, HG 365, HG 3-52, HG 6, FS 277, X-10, PNB, GG-2, RGC 936, RGC 1055, RGC 1002, RGC 1003, RGS 3, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.25 (b)). The best genotypes with respect to BK 19 and HK 20 were HG 100, RGC 1002, RGC 1003 and RGC 1066; with respect to HS 19, HK 19, BK 20, HS 20 and BS 20 were HG 884, HG 563, HG 3-52, GG 1, RGC 1055 and M 83; and with respect to BS 19 were HG 870, HG 365, HVG 2-30, X 10, PNB, RGC 1017, RGC 936 and HG 75. In this case, the best adapted genotypes for BK 19 was RGC 1002; for BS 20, BK 20, HS 19, HS 20 were HG 884 and GG 1 and for BS 19 was X 10.

4.8.2.26 Bacterial leaf blight intensity

AMMI 1 biplot display:

The genotypes namely, HG 75, X-10, HG 563, RGC 1033, HG 870, HG 2-20, RGC 1066, HG 884, HG 365, RGC 936, RGS 3, RGC 1038, RGC 1017, HG 100, HG 3-52, GG-2, RGC 1055, RGC 1002, RGC 1003 and HG 6had bacterial leaf blight intensity less than the overall mean and negative genotypic index indicating that genotypes are adapted to favourable environments. In contrast, genotypes, GG-1, HVG 2-30, M-83, FS 277 and PNB were generally with low bacterial leaf blight intensity and with positive genotypic index were adapted to unfavourable environments. Considering the genotypes with low bacterial leaf blight intensity as desirable, the environments lying on the left side are favourable environments and those lying on right side are unfavourable. Therefore, environments HS 19, BS 19, HS 20 and BS 20 were present on the left hand side of the midpoint of the main effect axis with negative environmental index, seemed to be rich environments, while HK 19, BK 19, HK 20 and BK 20 with positive environmental index were generally poor environments (Figure 4.8.26 (a)).

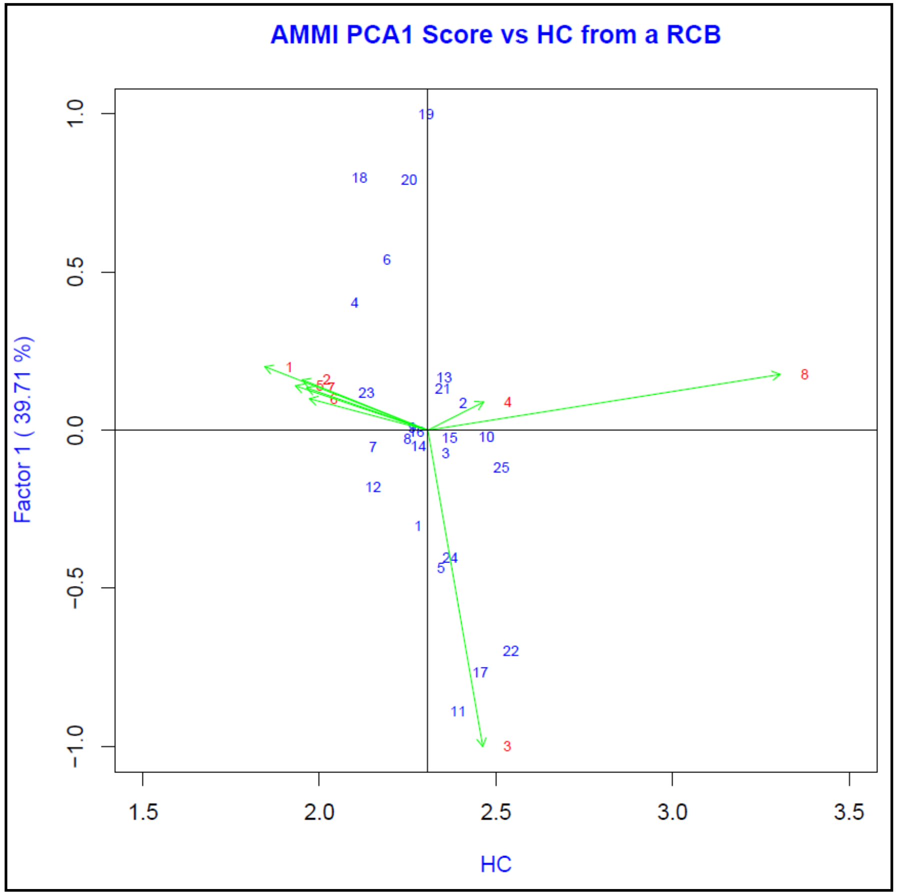

Figure 4.8.25 (a): AMMI 1 biplot for hemicellulose content of 25 cluster bean genotypes and eight environments using genotypic and environmental scores.

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

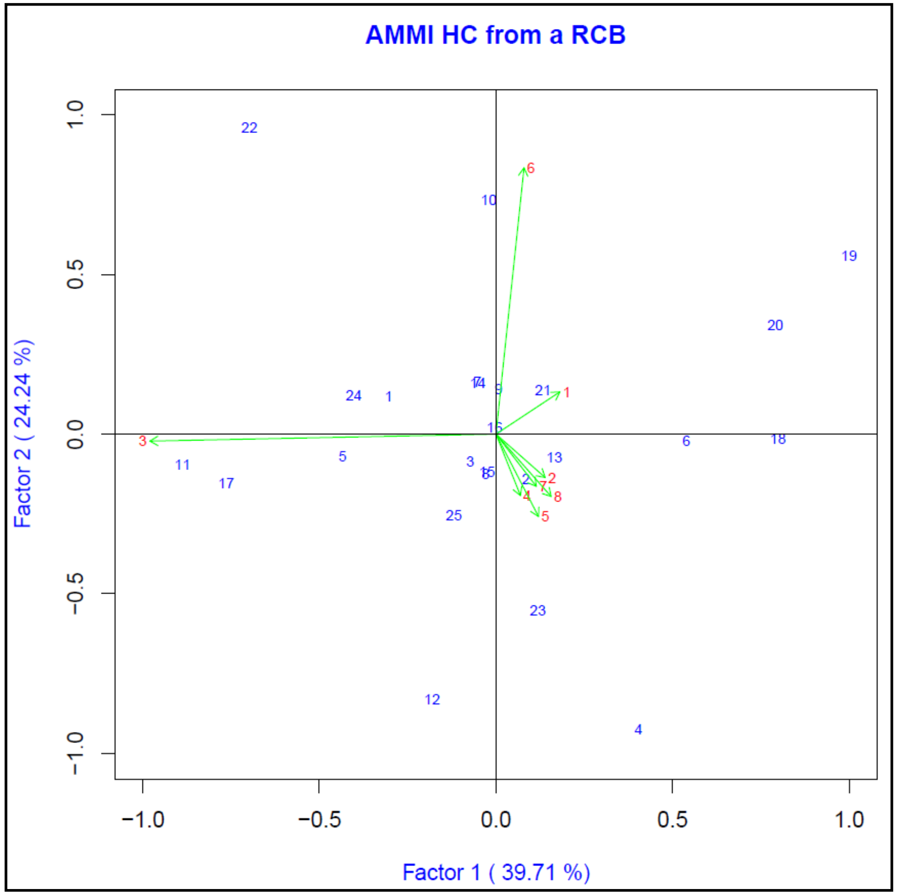

Figure 4.8.25 (b): AMMI 2 biplot for hemicellulose content is showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments.

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

The environment BK 19 and BS 19 had IPC1 scores are near to zero and hence had small interaction effects and considered as stable indicating that all the genotypes performed well in these environments. But BK 19 was found to have bacterial leaf blight intensity above overall mean. Therefore, this environment was not suitable by keeping in view the importance of genotypes with low bacterial leaf blight intensity as desirable. Similarly, the genotypes HG 870, HG 563, X-10, RGC 1055, RGC 1002 and RGS 3had near zero score on the first IPCA1 indicating that these genotypes were less influenced by the environments and are stable genotypes. All of these genotypes, registered below overall mean along with the IPCA1 score close to zero, they were adjudged as the stable genotype and had general adaptation to all the environments. Similar signs of IPCA 1 score for both genotype and environment implies positive interaction and if different, their interaction is negative and thus it attributes to low bacterial leaf blight intensity of genotype at that particular environment. Genotypes, RGC 1017 and RGC 1038 were identified as specifically adapted to the BS 20 and this environment was considered as the favourable environment for this genotype.

AMMI 2 biplot between IPAC1 vs. IPAC2:

The environments, BK 19 and BK 20 had short spokes and they do not exert strong interactive forces while HS 19, BS 19, HK 19, HS 20, BS 20 and HK 20 with long spokes were more differentiating environments. In the present study, the genotypes, HG 2-20, HG 870, HG 100, RGC 1002 and RGS 3 were close to the origin and hence they were non sensitive to environmental interactive forces whereas HG 884, HG 563, HG 365, HG 3-52, HG 6, HVG 2-30, FS 277, X-10, PNB, GG-1, GG-2, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1003, RGC 1066, M-83, RGC 1033 and HG 75 found more responsive since they were away from the origin (Figure 4.8.26 (b)). The best genotypes with respect to BS 19 and HS 20 were HG 884, HG 365, PNB, GG 1, GG 2 and RGC 1033; with respect to HS 19 were HG 3-52 and HG 6;with respect to HK 20 were HG 100, FS 277, X 10, RGC 1003, RGC 1066, M 83 and HG 75;and with respect to HK 19, BK 19, BK 20 and BS 20 were HG 2-20, HG 870, HG 563, HVG 2-30, RGC 1017, RGC 1038, RGC 936, RGC 1055, RGC 1002 and RGS 3.In this case, the best adapted genotypes for BK 19 was HG ; for BS 20 was RGC 936: for HK 19 was HVG 2-30; for BK 20 was RGC 1017; for BS 19 was X 10; for HS 20 were HG 365 and GG 1; and for HS 19 was HG 6.

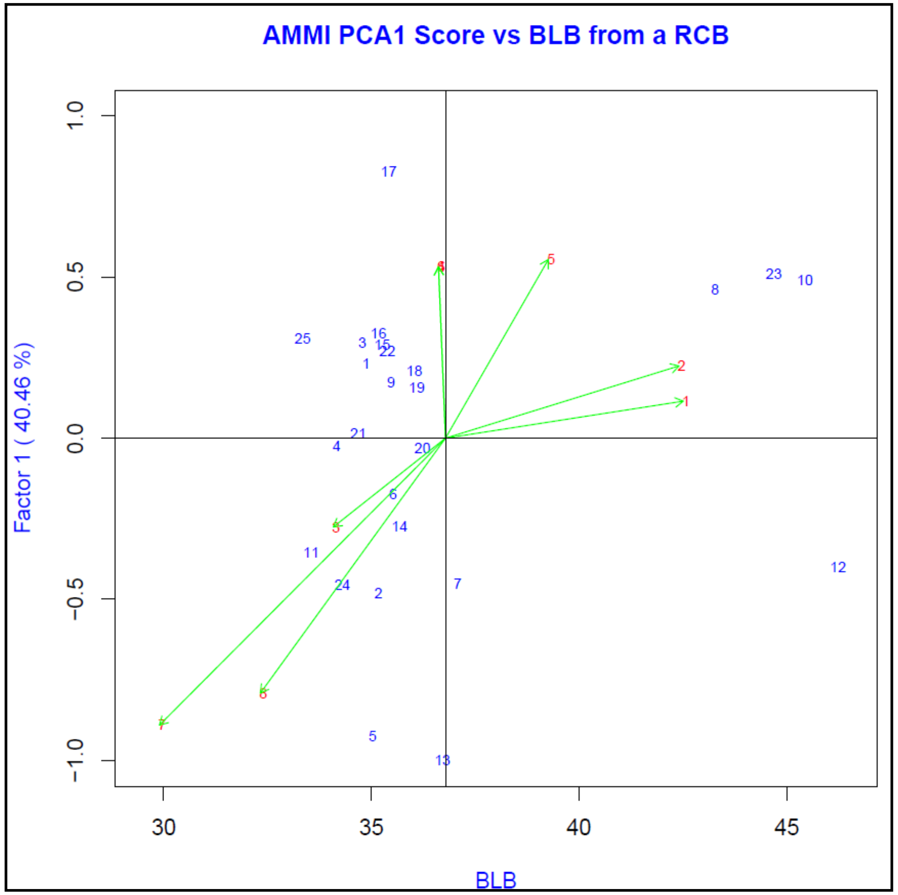

Figure 4.8.26 (a): AMMI 1 biplot for bacterial leaf blight intensity of 25 cluster bean genotypes and eight environments using genotypic and environmental scores.

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

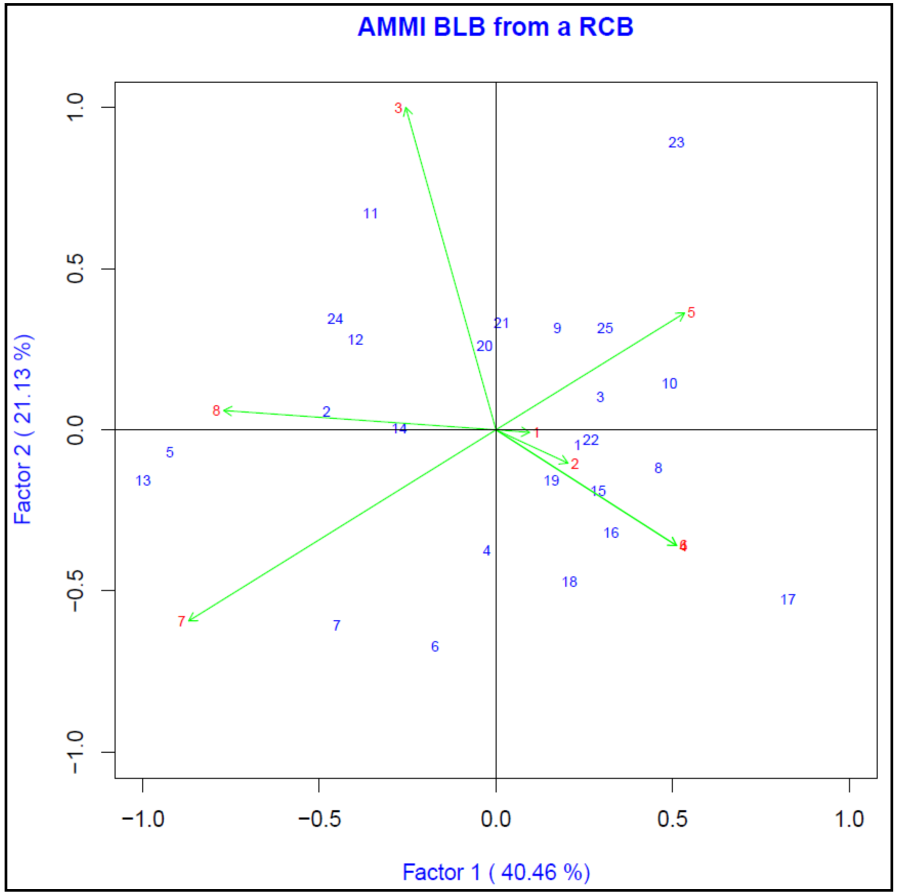

Figure 4.8.26 (b): AMMI 2 biplot for bacterial leaf blight intensity showing the interaction of IPCA 2 against IPCA 1 scores of 25 cluster bean genotypes in eight environments

Code	Genotypes	Code	Genotypes
G1	HG 2-20	G14	GG-2
G2	HG 884	G15	RGC 1017
G3	HG 870	G16	RGC 1038
G4	HG 563	G17	RGC 936
G5	HG 365	G18	RGC 1055
G6	HG 3-52	G19	RGC 1002
G7	HG 6	G20	RGC 1003
G8	HVG 2-30	G21	RGC 1066
G9	HG 100	G22	RGS 3
G10	FS 277	G23	M-83
G11	X-10	G24	RGC 1033
G12	PNB	G25	HG 75
G13	GG-1		
Code	**Environment**	**Code**	**Environment**
E1	Bawal *Kharif* 2019	E5	Hisar *Kharif* 2019
E2	Bawal *Kharif* 2020	E6	Hisar *Kharif* 2020
E3	Bawal Summer 2019	E7	Hisar Summer 2019
E4	Bawal Summer 2020	E8	Hisar Summer 2020

4.9. Molecular diversity analysis using SSR markers

4.9.1. Estimation of Polymorphic Information Content and Allelic diversity

In the present study, 25 cluster bean genotypes which include cultivated varieties of different states were genotyped using EST-SSRs. The list of genotypes and SSR markers used in the present investigation is summarized in tables 3.1 and 3.6 of chapter 3, respectively. In the present study a total of 102 SSRs were used for diversity analysis, out of which 55 SSRs were amplified and only 23 markers were showed polymorphism among 25 cluster bean genotypes used in the study (figure 4.9.1 to 4.9.3). The polymorphic markers were subjected to further analysis. Marker's profile acquired on agarose gel was scored manually by taking binary numbers 1 or 0 for the presence or absence of amplified PCR product. Molecular weights of individual amplicons were estimated using 100 bp DNA ladder. In this way, a binary data matrix was generated, which was used for subsequent analysis. Polymorphic Information Content value (PIC value), which indicates the discriminatory power by measuring allele diversity at a locus, was determined for each SSR marker across the genotypes and it was varied between 0.07 for marker CTN01 to 0.66 for markers CTN08 with an average of 0.406 per locus (table 4.9.1)**.**

4.9.2. Estimation of genetic relationship among the Cluster bean genotypes

Genetic similarity coefficients were computed for each pair of the 25 cluster bean genotypes from the SSR data matrix using Jaccard's similarity coefficient (Jaccard, 1908). The SIMQUAL (SM) module of Software *NTSYS-pc,2.02e* (Rohlf, 1992) was utilized to generate a similarity matrix based on Jaccard's similarity coefficient given in table 4.9.3. The similarity coefficient among the genotypes ranged from 0.45 to 0.95 with a mean value of 0.65. The highest genetic similarity value was found between genotypes RGC 936 and RGC1003. On the other hand, the lowest genetic similarity was found between HG 884, GG 1, M 83, GG 2, RGC 1007, HG-2-20 and HG 365. This suggests significant genetic divergence among the cultivars under study.

4.9.3. Clustering of Cluster bean genotypes The clustering of 25 cluster bean genotypes was carried out based on a genetic similarity matrix by employing an un-weighted pair group method with arithmetic average (UPGMA) algorithm following SAHN (sequential, agglomerative, hierarchical and non-overlapping) clustering module. The dendrogram is acquired using the Plot Tree function in *NTSYS-pc ver. 2.02* software (Rohlf, 2000). The reliability of the cluster analysis was assessed using online procedure which was carried out with DendroUPGMA computer program**.**

In the present study, clustering patterns obtained from the dendrogram clearly resolved the 25 genotypes into five distinct clusters (table 4.9.2; figure 4.9.4). The mean of the similarity matrix data (0.65) was taken as the dendrogram's cut-off line position. Cluster II was the largest cluster having 18 genotypes, followed by Cluster V (3 genotypes), Cluster I (2 genotypes), Cluster III and Cluster IV (1 genotype). Most of the important cultivated varieties such as RGC 1038, HG 3-52, HVG 2-30, HG 563, RGC 936 and HG 75 etc. are grouped together in Cluster II. These results indicated that important cultivars of cluster bean have a high level of genetic similarity and have a narrow genetic base.

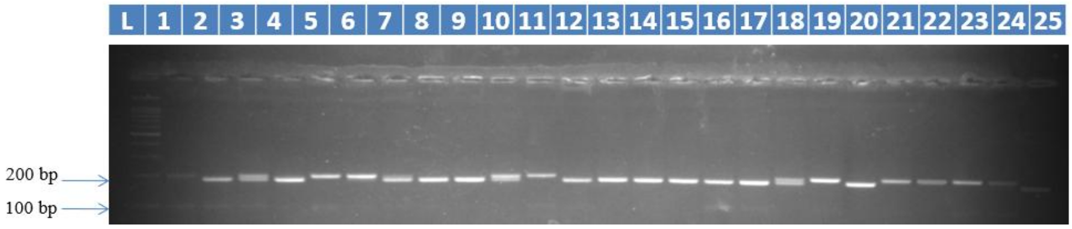

Fig.4.9.1: Amplification profile of marker CTN06 showing polymorphism between cluster bean genotypes

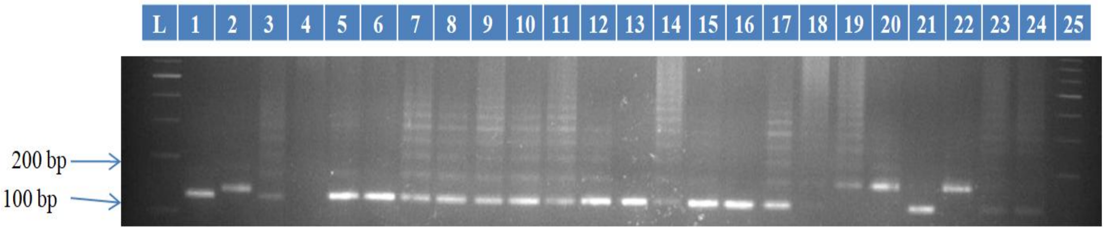

Fig. 4.9.2: Amplification profile of marker GDR 2 showing polymorphism between cluster bean genotypes

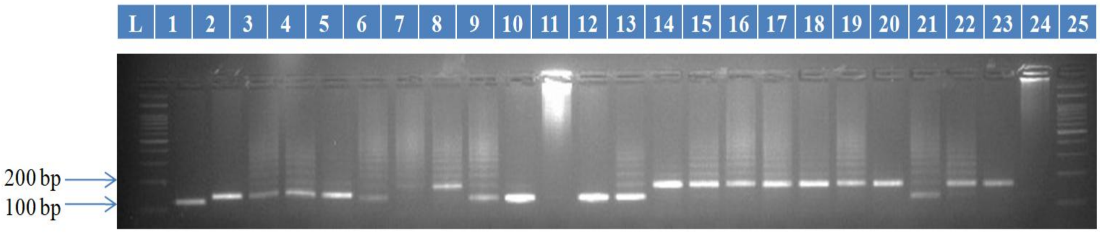

Fig. 4.9.3: Amplification profile of marker GDR 10 showing polymorphism between cluster bean genotypes

Table 4.9.1: Polymorphism features of twenty-three polymorphic SSR markers

S. No.	Marker	Product size (bp)	Allele Count	PIC	S. No.	Marker	Product size (bp)	Allele Count	PIC
1	GDR 1	245-300	2	0.374	13	CTN14	280-320	2	0.215
2	GDR 2	150-180	3	0.536	14	CTN16	400-450	2	0.375
3	GDR 4	275-310	3	0.588	15	CTN17	350-550	2	0.269
4	GDR 6	275-300	2	0.320	16	CTN23	145-155	2	0.269
5	GDR 9	365-400	3	0.524	17	CTN24	230-280	2	0.320
6	GDR 10	150-180	3	0.571	18	CTN35	260-270	2	0.311
7	GDR 11	250-275	2	0.461	19	CTN37	230-240	4	0.651
8	CTN01	130-150	2	0.074	20	CT223	255-280	2	0.346
9	CTN05	350-520	2	0.322	21	CT224	210-245	2	0.211
10	CTN06	185-210	2	0.370	22	CT225	245-260	2	0.375
11	CTN08	120-210	4	0.667	23	CT230	175-280	4	0.633
12	CTN09	250-300	4	0.577					

Table 4.9.2: Clustering pattern of Cluster bean genotypes obtained by using SSR markers

Cluster	Number of genotypes	Genotypes
Cluster-I	2	HG 2-20 and HG 365
Cluster-II	18	HG 870, HG 6, RGC 1038, HG 3-52, PNB, HVG 2-30, X 10, HG 100, RGC 1002, HG 563, RGC 936, RGC 1003, RGS 3, RGC 1055, FS 277, RGC 1066, RGC 1033 and HG 75
Cluster-III	1	RGC 1017
Cluster-IV	1	GG 1
Cluster-V	3	HG 884, GG 2 and M 83

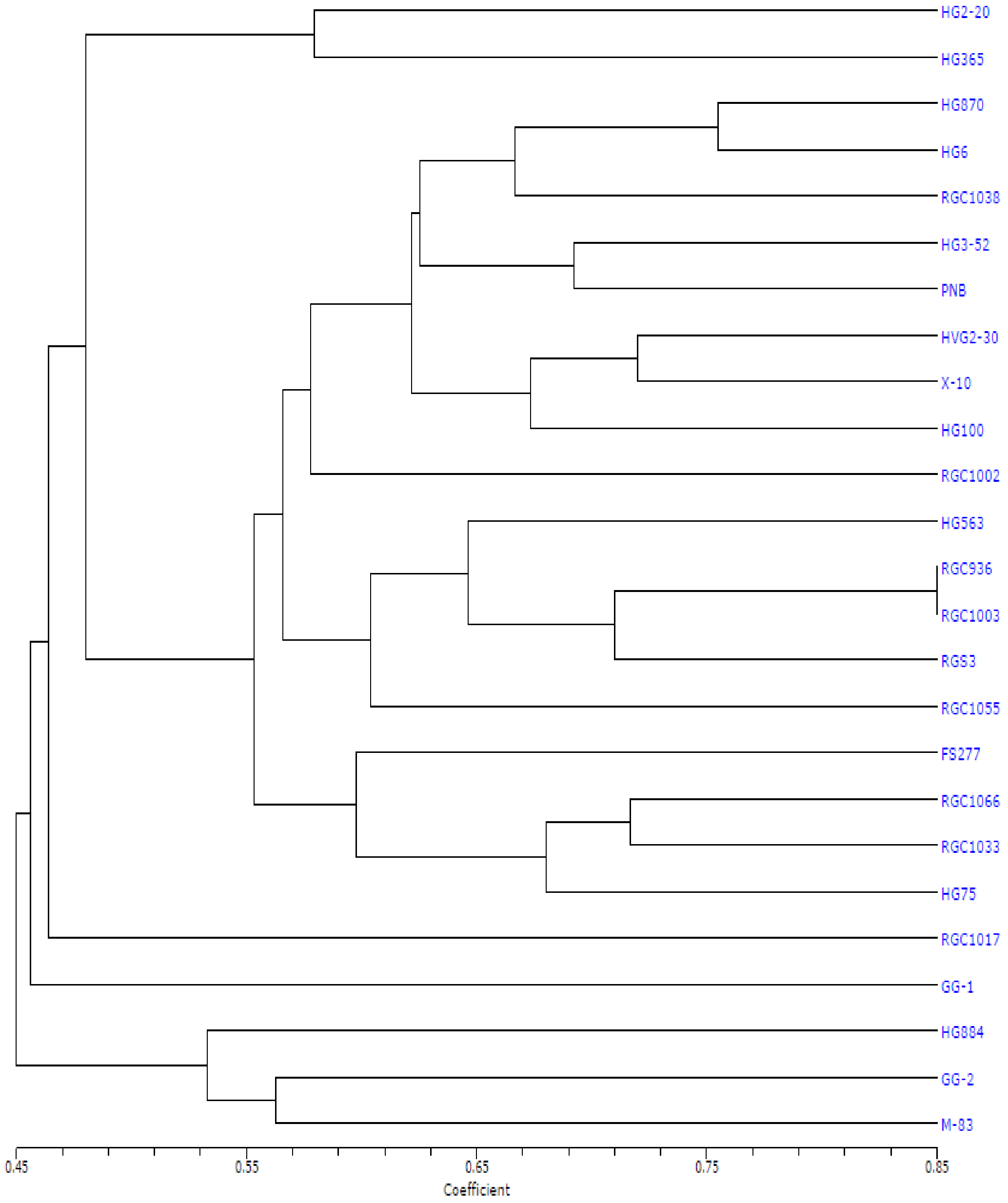

Fig. 4.9.4: Dendrogram of cluster bean genotypes based on the SSR marker data set using UPGMA based on Jaccard's similarity coefficient

Table 4.9.3: Jaccard's Similarity coefficient between pairs of cluster bean genotypes

Genotypes	HG2-20	HG884	HG870	HG563	HG365	HG3-52	HG6	HVG2-30	HG100	FS277	X-10	PNB	GG-1	GG-2	RGC1017	RGC1038	RGC936	RGC1055	RGC1002	RGC1003	RGC1066	RGS3	M-83	RGC1033	HG75
HG2-20	1.000																								
HG884	0.289	1.000																							
HG870	0.563	0.447	1.000																						
HG563	0.471	0.410	0.556	1.000																					
HG365	0.581	0.350	0.486	0.571	1.000																				
HG3-52	0.457	0.474	0.629	0.500	0.556	1.000																			
HG6	0.444	0.500	0.758	0.568	0.500	0.553	1.000																		
HVG2-30	0.410	0.500	0.605	0.649	0.500	0.632	0.750	1.000																	
HG100	0.359	0.611	0.595	0.553	0.526	0.622	0.649	0.684	1.000																
FS277	0.586	0.308	0.529	0.576	0.457	0.472	0.543	0.500	0.410	1.000															
X-10	0.417	0.436	0.583	0.541	0.514	0.657	0.639	0.722	0.667	0.514	1.000														
PNB	0.350	0.513	0.667	0.579	0.595	0.694	0.676	0.667	0.658	0.400	0.525	1.000													
GG-1	0.324	0.385	0.571	0.410	0.421	0.400	0.629	0.538	0.526	0.342	0.436	0.553	1.000												
GG-2	0.308	0.556	0.462	0.462	0.556	0.415	0.553	0.512	0.579	0.325	0.381	0.649	0.514	1.000											
RGC1017	0.421	0.439	0.395	0.463	0.513	0.419	0.442	0.512	0.537	0.366	0.419	0.422	0.439	0.386	1.000										
RGC1038	0.395	0.450	0.595	0.595	0.568	0.579	0.743	0.641	0.590	0.618	0.538	0.658	0.568	0.500	0.537	1.000									
RGC936	0.410	0.500	0.564	0.649	0.579	0.632	0.615	0.650	0.641	0.583	0.590	0.667	0.463	0.512	0.548	0.730	1.000								
RGC1055	0.350	0.475	0.500	0.579	0.553	0.488	0.476	0.548	0.432	0.436	0.488	0.600	0.405	0.525	0.422	0.500	0.667	1.000							
RGC1002	0.378	0.474	0.541	0.583	0.474	0.568	0.553	0.590	0.667	0.514	0.611	0.525	0.436	0.381	0.452	0.579	0.590	0.452	1.000						
RGC1003	0.486	0.541	0.611	0.657	0.541	0.639	0.579	0.615	0.605	0.588	0.595	0.632	0.425	0.405	0.476	0.605	0.853	0.676	0.639	1.000					
RGC1066	0.500	0.400	0.541	0.583	0.556	0.611	0.553	0.590	0.500	0.559	0.568	0.488	0.400	0.349	0.525	0.667	0.590	0.488	0.568	0.595	1.000				
RGS3	0.472	0.415	0.513	0.639	0.450	0.500	0.488	0.561	0.550	0.571	0.538	0.465	0.349	0.395	0.615	0.550	0.730	0.500	0.538	0.694	0.667	1.000			
M-83	0.385	0.513	0.463	0.364	0.439	0.488	0.442	0.444	0.432	0.366	0.452	0.488	0.341	0.564	0.488	0.500	0.512	0.488	0.386	0.442	0.525	0.575	1.000		
RGC1033	0.500	0.359	0.688	0.588	0.472	0.571	0.600	0.513	0.500	0.613	0.528	0.526	0.472	0.375	0.381	0.629	0.513	0.415	0.528	0.514	0.719	0.541	0.487	1.000	
HG75	0.389	0.447	0.556	0.556	0.486	0.583	0.611	0.564	0.553	0.625	0.629	0.500	0.486	0.425	0.429	0.639	0.649	0.463	0.629	0.611	0.676	0.595	0.538	0.688	1.000

CHAPTER-V

DISCUSSION

The results of the present in previous chapter have been described under following categories.

5.1 Characterization of cluster bean genotypes based on morphological characters

5.2 Analysis of variance (ANOVA) for individual environment

5.3 Mean performance and range across the environments for different quantitative characters

5.4 Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV),heritability and genetic advance as per cent of mean for different quantitative characters

5.5 Phenotypic correlation coefficient analysis

- 5.5.1 Phenotypic correlation coefficient analysis for yield and component characters
- 5.5.2 Phenotypic correlation coefficient analysis for bacterial leaf blight intensity and quality characters

5.6. Path coefficient analysis

- 5.6.1 Path coefficient analysis for yield and component characters and BLB intensity and quality characters

5.7 Stability analysis based on Eberhart and Russell‘s model, 1966 and AMMI Model, 1997

- 5.7.1 Pooled analysis of variance
- 5.7.2 Stability parameters

5.8 Molecular diversity analysis using SSR markers

5.1 Characterization of cluster bean genotypes based on morphological characters

Plant morphology for characterization has been in practised since a long time. Taxonomical classification of plants done by Linnaeus was also based on morphological characterization. Plant morphology studies are being used for both varietal purity testing and also varietal identification. Majority of the breeding programs use a core set of parents with similar pedigrees and characteristics to combine desirable characters like yield, quality and disease resistance*etc*. This results in close ties of consanguinity of varieties and therefore, offspring heritable variation lingers in the inbreeding level (Nie *et al*., 2016).This increases the difficulty of phenotype screening of varieties and varietal infringement. Therefore, germplasm characterization, evaluation and quantification of genetic diversity is indispensable for expedient use of plant genetic resources (Zada *et al.* 2013). Plant morphological characters have been used for classification in recent years by Deepashree *et al.* (2021), Manivannan *et al.* (2016) and Umesha *et al.* (2015) in cluster bean.

In the present study, morphological characterization in 25 cluster bean genotypes is presented in Figure (4.1) and Tables (4.1) in the previous chapter, was done on the basis of eight qualitative characters *viz.*, plant growth habit, leaf pubescence, leaf margin, leaf colour, flower colour, pod pubescence, seed colour and seed shape. However, two characters namely, position of first trifoliate leaf and first cluster from bottom were found inconsistent within the replication for each genotype in each environment. Therefore, the characterization of genotypes on the basis of these two characters could not be done.

In plant growth habit, three genotypes each with unbranched and sparsely branched row habit and remaining 19 genotypes were branched. Considering leaf pubescence, the genotypes were found either pubescent or glabrous. Out of 25 genotypes 22 were found pubescent while, three namely, HVG 2-30, PNB and M 83 were found with glabrous leaves. Leaf margin were of two types *i.e.,* serrated and smooth. 17 genotypes were with serrated leaf margin and smooth leaf margin was found in eight genotypes. Leaf colour, was classified into two categories *i.e.*, dark green and light green. The largest group showed dark green type having 21 genotypes while; four genotypes namely, HVG 2-30, PNB, RGC 197, HG 75 and M 83 were having light green leaves.

In flower colour, two types of flower colours were observed *i.e.* pink and white. The pink coloured flowers were found in 20 genotypes while, five genotypes namely, HVG 2-30, GG 2, RGC 936, HG 75 and M 83 were observed with white coloured flowers. Thegenotypes were found with either pubescent pods or with glabrous pods. Out of 25 genotypes 21 were found pubescent while, four genotypes namely, HVG 2-30, FS 277, PNB and M 83were found glabrous pods. The genotypes with glabrous pods were also found with glabrous leaves. These genotypes are vegetable type as the fresh and green pods of these genotypes are used as vegetable. Lack of pubescence on pods makes these genotypes best suited for such purpose.

Great variability have been observed under present study for seed colour in cluster bean as the genotypes were grouped into five categories *i.e*., Pale yellow pink, moderate orange, medium grey, light grey and light greenish grey as per the Lilac colour groups by Royal Horticultural Society colour chart. The seed colour of four genotypes each was found pale yellow pink and medium grey, moderate orange was in three genotypes, nine genotypes had light grey coloured seed and light greenish grey seed colour was found in five genotypes. For seed, the genotypes were grouped into two categories *i.e*. square and flat & round. Out of 25 genotypes 21 genotypes were found with square shaped seed while, four genotypes namely, HVG 2-30, GG 2, AG 112, PNB and M 83 had flat & square seed shape. It is suggested that all the characters studied could be utilized to establish distinctness among the existing along with the newly developed genotypes. Similar results were found by Kumar *etal.* (2013) for flower colour, leaf pubescence, plant growth habit and leaf margin; Umesha *et al.* (2015) for flower colour, pod pubescence and seed shape and Manivannan *et al.* (2016) for most of the characters in cluster bean. Similar results were also found by Oo *et al.* (2022), Arya *et al.* (2021) and Olasupo *et al.* (2016) in cowpea and Kalaiyarasi and Padmavathi (2021), Mounika *et al.* (2020) and Kaur *et al.* (2017) in *Vigna radiata*. These outcomes will be helpful in DUS (Distinctness, Uniformity and Stability) testing which is essential for the grant of protection of new plant variety under Plant Variety & Farmers' Rights (PVP&FR) act, 2011.

5.2Analysis of variance (ANOVA) for individual environment

The mean sum of squares for all the studied characters *viz.*, plant height, days to 50% flowering, days to maturity, pods on main stem, pod per cluster, cluster per plant, pod per plants, seed per pod, pod length, branches per plant, 100 seed weight, biomass per plot, harvest index, seed yield per plot, gum content , protein content, total soluble sugar content, reducing sugar content, non-reducing sugar content, cellulose content, hemicellulose content, NDF content, ADF content, silica content, lignin content and bacterial leaf blight intensity over the environments has been showed in previous chapter in table 4.2 showed significant differences among the genotypes. These results clearly indicate that the cluster bean genotypes used for present study had sufficient variability to give valid estimate for further studies for different characters. It suggests that selection of superior genotypes can be fruitful in developing and release of new varieties for different ecologies. Similar findings were also reported by Deepashree *et al.* (2021), Kumar *et al.* (2019), Muthuselvi *et al.* (2018), Patel *et al.* (2018) and Sivia *et al.* (2017).

5.3 Mean performance and range across the environment for phenological, growth, quality, bacterial leaf blight intensity, yield and its component characters

5.3.1. Phenological characters

Days to 50% flowering and Days to maturity

All the genotypes flowered late during summer seasons of both the years but for maturity no clear pattern was shown. The summer seasons received less rains than the *kharif* seasons. During the water stress the plants tends to shorten their growth period by drought escape mechanism. Drought escape is achieved successfully when phonological development is matched with the shorter periods of soil moisture availability in the growing season and terminal drought stress (Farooq *et al.* 2022). This reduction in vegetative phase of the crop cycle is considered as an adaptive mechanism which allows the crop to complete its life cycle before the onset of drought period. Secondly, the late flowering genotypes are the one with late maturity, large leaves with bold seeds. This indicates that the resources are more allocated for plant growth and extra photosynthates are available for seed production. The large-sized leaf will eventually accumulate more carbon, which ultimately results setting of bold seed in the pod Sharma *et al.* (2021). The negative correlation is also observed between flowering time and pods per plant by Sharma *et al.* 2021 and in present study. This also reveals that the late flowering genotypes are generally poor yielders. HG 6 had shown earlier flowering and maturity across the environments followed by HG 884 for flowering and HG 2-20 for maturity while, PNB was late in flowering and FS 277 late in maturity. Similarly, large leaved genotypes namely, FS 277, HVG 2-30, M 83 and PNB flowered and matured late than their short leaved counterpart genotypes. Reddy *et al.* (2018), Muthuselvi *et al.* (2018) and Rathore *et al.* (2018) obtained similar results for days to 50% flowering and days to maturity. Singh *et al.* (2022), Panchta *et al.* (2017), Panchta *et al.* (2016) and Vir and Singh (2015) also observed early flowering during summer season in cluster bean.

5.3.2. Plant growth characters

Plant height and Branches per plant

All the genotypes recorded maximum plant height under BS 19, HK 19, and HK 20. HG 6 was found to be dwarf followed by HG 870 while, FS 277 was found tallest across the environments. The plant height under HS 19, BK 19, HS 20, BS 20 and BK 20 was recorded more than the rest of the environments. This may be due to lower competition for water and nutrients. Under water deficit conditions, plant growth is reduced either due to reduction in cytokinin transport from roots to shoots or due to increased amount of abscisic acid in leaves which reduces the flexibility of cells wall and therefore reduces the growth (Mujtaba and Alam, 2002). Higher plant heights were also reported by Panchta *et al.* (2017), Panchta *et al.* (2016) and Vir and Singh (2015) during *kharif* season which is less water deficit environment than the summer season.

On the basis of overall mean across the environments, RGC 1038 was adjudged as highly branched followed by HG 2-20 while, RGC 1066 was observed as unbranched. Among the environments least branching was observed in BK 19 and BK 20 showed significantly maximum number of branches per plant than grand mean. In cluster bean it is a common phenomenon that on main stem at leaf axil either branch or cluster will form. Increase in branch increases the yield as the branched genotypes bears small but more clusters. On the other hand the unbranched genotypes bears more cluster on main stem instead of branches Dadheech *et al.* (2020) and Sharma *et al.* (2021).

The results yielded for plant height and branches per plant were in agreement to the findings of Patel *et al.* 2022, Sharma *et al.* (2021), Reddy *et al.* (2018), Muthuselvi *et al.* (2018), Rathore*et al.* (2018), Kumar*et al.* (2017) and Jukanti *et al.* 2015 in cluster bean.

5.3.3. Yield and component characters

Pod and Seed characters

The genotypes bear high number of pod on main stem during summer season except for HK 19 as compared to *Kharif* seasons. RGC 1066 was found with highest number of pods on main stem followed by FS 277 while, GG 1 was found with least number of pods on main stem.Similarly, highest number of pods per plant was observed in HG 563 followed by HG 870 and high number of pods per plant was observed in all environments except BK 19 and BS 20.The present outcome of the study validates the phenomenon discussed in previous section that, the genotypes with unbranched nature bears more pods on main stem while, highly branched genotype possess pods per plant into several small clusters.

Pod per cluster were found minimum in RGC 936 followed by GG 2 while, maximum pods per cluster were found in FS 277. Least number of pods per cluster was found in *Kharif* environments except HK 19 than the corresponding summer seasons. Similarly, the genotype HG 2-20, followed by HG 563 and environments HS 19, HK 19 and HS 20 were found with highest number of clusters per plant. The genotype, GG 2 was found with shortest pods followed by RGC 1003. The environments BK 19 and BK 20 yielded shortest pods among all environments studied. The shorter pod length was restricted to the high yielding released varieties. The physiological constraint in the form of photosynthetic assimilates leads to the evolution of harmonization characters like clusters per plant, cluster length and pods per cluster (Dadheech *et al.* 2020). Consequently, unbranched genotypes have more pods per cluster, long clusters and less number of cluster per plant. On other hand highly branched genotypes possesses less pods per cluster, short clusters and high number of clusters per plant. Similar results for pod characters were obtained by Patel *et al.* 2022, Teja *et al.* 2022, Jilen *et al.* 2022, Muthuselvi *et al.* (2018),Khalid *et al.* (2017), Kumar *et al.* (2017), Umesha *et al.* 2015, Jukanti *et al.* 2015 and Vir and Singh (2015).

Highest number of seeds per pod across the environments was observed in RGC 1066 followed by RGC 1033. Among the environments, HS 19, HS 20, BS 20 and HK 20 showed highest number seeds per pod than grand mean. Similarly, HG 3-52 showed highest 100 seed weight followed by RGC 1038 while, the environments HS 19, HK 19, BK 19 and HS 20 showed highest 100 seed weight than grand mean. Highest seed yield per plot across the environments was observed with HG 2-20 followed by HG 563. Among the environments,HS 19, HK 19 and HS 20 showed highest seed yield per plot than grand mean. Branched genotypes with more clusters were found high yielding in present study. The genotype RGC 1066 was also among the top yielders due to its moderately long pods and more number of seeds per pod. Branches in unbranched genotypes must have been compensated with high number of pods on main stem. The linkage between clusters on main stem, pod length and number of seeds per pod was also reported by Sharma *et al.*(2021). The genotypes with high gum content group were also found high yielding as gum is major storage polysaccharide in cluster bean seed accounting up to 26-35% of seed dry weight Chaudhary *et al.* (2019). The results obtained for seed characters and seed yield per plot are in accordance with the findings of Kumari *et al.* (2022), Vishnoi *et al.*(2021), Khalid *et al.* (2017), Panchta *et al.* (2017), Wankahde *et al.* (2017), Panchta *et al.* (2016),Muthuselvi *et al.* (2018), Vir and Singh (2015).

Biomass and Harvest index

Highest biomass per plot was observed for HG 2-20 followed by X 10. Among the environments HS 19, HK 19, HS 20 and HK 20 showed significantly highest biomass per plot than grand mean. Similarly, highest harvest index was recorded with RGC 1055 followed by HG 6 and RGC 1066. The environments HS 19, BS 19, HK 19, BK 19 and BK 20 showed highest harvest index than grand mean. Higher biomass accumulation and harvest index often associated with higher seed yield but some workers reported contradictory results (Asefa, 2019). Present findings for biomass per plant and harvest index in cluster bean are in agreement with the findings of Vishnoi *et al.* 2021, Muthuselvi *et al.* (2018), Solanki *et al.* 2017, Singla *et al.* 2016, Jukanti *et al.* 2015.

5.3.4. Quality characters

Gum and Protein content

HG 3-52 exhibited highest gum content followed by RGC 1066 and HG 2-20. Among the environments high gum content than grand mean was observed in HS 19, BS 19, HK 20 and BK 20. Similarly, highest protein content across the environments was found in RGC 1055followed by FS 277 and M 83.Among the environments BS 19, HK 19, BS 20 and BK 20 showed high protein content than grand mean. Galactomannan gum biosynthesis involves differential regulation of several genes among the genotypes. In gum rich genotypes, up regulation of two core enzymes, ManS (Mannan Synthase) (involved in assembling the mannan backbone during galactomannan synthesis) and GMGT (Galactomannan Galactosyltransferase) is observed by Rajaprakasam *et al.* (2021). The results of gum and protein content are in agreement with the results obtained by Teja *et al.* (2022), Gresta *et al.* (2018), Reddy *et al.* (2017), Reddy *et al.* (2018), Wadhwa & Joshi (2017) and Wankahde *et al.* (2017).

5.3.16. Non-structural carbohydrates

HG 563 was found with highest TSS, reducing sugar and non-reducing sugar content followed by RGC 1033 for TSS and reducing sugar content and HG 75 for non-reducing sugar content. Among the environments HK 19, BK 19, HS 20, BS 20 and BK 20showed least TSS and non-reducing sugar content than grand mean while, HS 19, BS 19, BK 19, HS 20 and BK 20 showed least reducing sugar content than grand mean. During infections the apoplasm of cell wall is the battlefield for pathogens to compete host cell for resources mainly sugars for colonization (Naseem *et al.* 2017). There is prominent role of sugar metabolism, transport and signalling in plant-pathogen interactions as they are the source of energy for both plant and pathogen. Concentration of sugars in the host is the outcome of the efficiency of pathogen to hijack sugar transport system and on the other hand the efficiency of host to retrieve the lost sugars (Liu *et al.* 2022). Theresults obtained are in confirmation with the outcome of the study done by Lata *et al.* 2016 in cluster bean dry leaves. Similar studies were conducted by Gahlot *et al.* 2022 and Sharma*et al.* 2020 in cluster bean, Mahesh *et al.* 2019 in Dolichos bean and Sharma *et al.* 2012 for estimating non-structural carbohydrates using fresh sample.

5.3.17. Structural carbohydrates

HG 75 exhibited high ADF, NDF, lignin, cellulose and silica content followed by X 10 for ADF, NDF and cellulose while, RGC 1033 for lignin and HG 563 for silica content. Among the environments BS 19, BK 19 and HS 20 showed higher ADF, lignin and cellulose content than grand mean. Similarly, environments HK 19, HS 20, BS 20, HK 20 and BS 20 showed higher silica content than grand mean. BS 19, BK 19, HS 20 and BS 20 showed higher NDF content than grand mean and BS 19, HS 20 and BS 20 showed higher hemicellulose content than grand mean. Among the array of defence structural carbohydrates plays a vital role in plant defence mechanism. Most of the plant cell wall is based on network of cellulose micro-fibrils cross-linked hemicellulose. Secondary cell wall is reinforced by lignin. Apart from this whenever cell wall integrity is disturbed it serves as a signal for defence mechanism and plant may release other reinforcement polymers e.g. callose, phenolic compounds and toxic substances. Abo Omar *et al.*(2021), Amasaib *et al.* (2016), Lata *et al.* (2016), Salama and Nawar (2016) and Wadhwa *et al.* (2013) conducted similar studies in cluster bean which yielded similar results to estimate structural carbohydrates.

5.3.18. Bacterial leaf blight (BLB) intensity

Across the environments HG 75 was found least susceptible against bacterial leaf blight followed by X 10. Among the environments HS 19, BS 19, HS 20 and BS 20 showed low BLB intensity than grand mean. Gahlot *et al.*(2022) for bacterial leaf blight, Yadav *et al.*(2020) for *Fusarium* Wilt and Sharma *et al.* (2019) for *Alternaria* blight and found similar results. PNB was found with maximum lesion size of bacterial leaf blight in the study conducted by Lata *et al.* (2016).

5.4 Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean (GAM) for different quantitative characters based on pooled data of eight environments

In the present study, the magnitudes of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the characters, indicating that these variations were not mainly governed by genotypic factors and there was considerable influence of environment. There was less difference between PCV and GCV for most of the characters studied except number of seeds per pod. Presence of substantial PCV and GCV for pods on main stem, pods per plant, pods per cluster, branches per plant, cluster per plant and seed yield per plant indicated considerable variations for characters studied and thus there is good scope for further improvement by genetic manipulation. In quality characters also the magnitude of PCV in higher than the GCV, indicating environmental influence on them. There was less difference between PCV and GCV for most of the quality characters. Moderate values of PCV and GCV were observed for gum content and BLB disease intensity. Whereas, substantial GCV and high PCV values were not found for any of the quality character under study.

These findings were in conformity with the results of Panchta *et al*. (2017), Gresta *et al.* (2017), Rathore *et al.* (2018), and Khalid *et al.* (2017) for number of pods per plant, plant height and seed yield. Likewise, similar findings were also reported by Reddy et al. (2018) for plant height; by Kumar *et al.* (2015) Sivia *et al.*(2018) and Pathak *et al*. (2015)for seed yield and number of pods per plant; by Girish *et al.* (2012), Khalid *et al.* (2017), and Ansari *et al.* (2017)for pods per plant and plant height; by Kumar *et al.* (2015) and Morris *et al.*(2010) for seed yield, plant height and number of clusters per plant.

The moderate values of PCV and GCV were observed for plant height, pod length, biomass per plot and harvest index. Whereas, moderate GCV and high PCV values were not found for any character under study. The similar findings of moderate PCV and GCV values have been reported by Sivia *et al.* (2016), Jitender *et al.* (2014), Kumar *et al.* (2015) and Panchta *et al*. (2017) for pod length, and biomass; Vishnoi *et al.* (2017), Reddy *et al.* (2018), Rathore *et al*. (2018), Panchta *et al*. (2017), and Deepashree *et al.* (2021),Sultan *et al.* (2012), Pathak *et al.* (2015), Pathak *et al.* (2011a), Jukanti *et al.* (2015), Saini *et al*. (2010) and Panchta *et al*. (2017) for harvest index and biomass. A low PCV and GCV estimates were recorded for days to 50% flowering, days to maturity, seeds per pod and 100 seed weight. Similar results were earlier reported by Kumar *et al.* (2015), Grestav *et al.* (2018), Ansari *et al.* (2017), Bhatt *et al.* (2015), Muthusselvi *et al.* (2018), Rathore (2018), Pathak *et al.* (2015), Girish*et al.* (2012).

Heritability (broad sense) were observed very high for the characters *viz.*, plant height, days to 50% flowering, days to maturity, pods on main stem, pods per plant, pods per cluster, seed per pod, pod length, branches per plant, 100 seed weight, biomass per plot, harvest index, cluster per plant and seed yield per plot. These characters could be directly improved through selection because of less influence of environment. But only heritability could not be considered for the selection of elite genotypes in breeding programme because it includes both additive and non-additive gene effects. Heritability (broad sense) were observed high for almost all the quality characters under study *viz.*, gum content, protein content, total soluble sugars, reducing sugars, non-reducing sugars, ADF content, Lignin content, cellulose content, silica content, NDF content and BLB disease intensity. These characters could be directly improved through selection because of less influence of environment. But only heritability could not be considered for the selection of elite genotypes in breeding programme because it includes both additive and non-additive gene effects.

High values of GCV along with high heritability were observed in characters *viz.*, pods on main stem, pods per plant, pods per cluster, branches per plant, clusters per plant and seed yield per plot, indicating that there is scope for improvement of these characters by selection. Genetic advance as per cent of mean were observed high in plant height, pods on main stem, pods per plant, pods per cluster, pods length, branches per plant, 100 seed weight, biomass per plot and harvest index while, moderate GAM were observed in days to 50% flowering, days to maturity and 100 seed weight, indicating that these characters could be improved and exploited through selection. High values of GCV along with high heritability were not observed in any of the characters, indicating that there is no scope for improvement of these characters by selection. Genetic advance as per cent of mean (GAM) were observed high in gum content and BLB disease intensity while, moderate GAM were observed in protein content, reducing sugar content, ADF content, lignin content, cellulose content and silica content indicating that these characters could be improved and exploited through selection.

High heritability coupled with high genetic advance as per cent of mean for the characters suggests that there was predominant additive variation and hence characters could be improved through direct selection.

The results of present investigation were in accordance with the findings of Jitender *et al.* (2014), Vishnoi *et al.* (2017), Manivannan *et al.* (2016) and Muthusselvi *et al.* (2017, 2018).The concurrent results were also supported by Sultan *et al.* (2012), Kumar *et al.* (2015, 2013,2014), Wei-Xin *et al.* (2009), Girish *et al.* (2012), Khalid *et al.* (2017), Gresta *et al.* (2017, 2018) for seed yield, pods per plant, pods on main stem and plant height; by Sivia *et al.* (2016) for clusters per plant, pods per plant and days to 50% flowering; by Panchta *et al.* (2019) and Rathore *et al.* (2018) for pods per plant; by Gretsa *et al.* (2018) and Panchta *et al.* (2020)for days to 50% flowering; by Saini *et al*. (2010) and Panchta *et al.* (2020) for days to maturity; by Kumar *et al.* (2015) and Jukanti *et al*. (2017) for plant height, days to 50%

flowering and pods per plant; by Sivia *et al.* (2016) and Gresta *et al*. (2018) for plant height; by Khalid *et al.* (2017) for number of clusters per plant.

High coefficient of phenotypic and genotypic variation and high heritability along with high GAM were observed in pods on main stem, pods per plant, pods per cluster, seeds on pod and branches per plant indicating these characters could be improved through direct selection for high-yielding cluster bean breeding. Moderate coefficient of phenotypic and genotypic variation and high heritability along with high GAM were observed in gum content, and BLB disease intensity. The selection for gum content while, selection against BLB intensity would result into high-yielding cluster bean varieties with high gum content.These findings were similarly substantiated by Panchta *et al.* (2017). These results were thereby earlier reported by Pawan *et al.* (2016), Abraham *et al.* (2017), Goudar *et al.* (2017) and Teja *et al.* (2022) for pods per plant and plant height; by Panchta *et al.* (2016) for plant height and seed yield; by Panchta *et al.* (2016) and Kumar *et al.* (2020) for seed yield and pods per plant; by Sultan *et al.* (2012) for clusters per plant; by Wankhade *et al.* (2016) for plant height.

High estimates of heritability accompanied with low GAM, low GCV and PCV were observed in days to 50% flowering, days to maturity, seeds per pods, TSS content, non-reducing sugar content, NDF content, hemi-cellulose content and 100 seed weight confirmed as earlier reported by Mahla *et al.* (2006), Pathak *et al*. (2011) and Deepashree *et al.*(2020), indicating non-additive gene effects and selection for such character may not be rewarding.

5.5 Phenotypic correlation coefficient analysis

5.5.1 Phenotypic correlation coefficient analysis for yield and component characters

Correlation coefficient studies provide an idea to find out degree of relationship between two or more quantitative characters. Seed yield is a compound character, which is influenced by environment and associated by genotypic factors and various components to yield performance. Kumar *et al.* (2015) and Santosha *et al.* (2017) indicated that correlation analysis helps the breeder to work out the selection strategy effectively for seed yield which is associated with many component characters and is regulated by many genes, which is highly complex.

In the present study, a perusal of data on correlation coefficient at phenotypic level is shown in Table 4.5.1 in previous chapter. Similarly, a perusal of data on correlation coefficient at phenotypic level is shown in Table 4.5.2 in previous chapter. The correlation coefficients for 14 yield and component and 12 quality and pathological characters in 25 cluster bean genotypes were investigated to find out the relationship among them. Findings were in similar trend with Vishnoi *et al.* (2017), Teja *et al.* (2022), Abraham *et al.* (2017), Panchta *et al.* (2017), Goudar *et al.* (2017), Kumar *et al.* (2020) and Wankhade *et al.* (2016).

Plant height showed positively and significantly correlated with days to maturity, days to 50% flowering, pods on main stem, pods per cluster and pod length. Days to 50% flowering had positive and significant correlation with days to maturity plant height, pods per cluster and pod length but Days to maturity had positive and significant association with plant height, days to 50% flowering, pods per cluster, pod length. It was in concurrence with result as reported by Panchta *et al.* (2017), Goudar *et al.* (2017) and sivia *et al.* (2016) for plant height.

Pods on main stem was positively and significantly associated with plant height, pods per plant, pods per cluster, seeds per pod, 100 seed weight, biomass per plot, seed yield per plot. Pods per plant showed positive and significant correlation with pods on main stem, seed per pod, branches per plant, 100 seed weight, biomass per plot, harvest index, cluster per plant and seed yield per plot. Pods per cluster wad found positively and significant correlated with plant height, days to 50% flowering, days to maturity, pods on main stem and pod length. Seed per pod showed positive and significant correlation with pods on main stem, pods per plant, pod length, 100 seed weight, biomass per plot, harvest index, cluster per plant and seed yield per plot. Pod length was found positively and significantly correlated with plant height, days to 50% flowering, days to maturity, pods per cluster, seed per pod, 100 seed weight, biomass per plot, harvest index, cluster per plant and seed yield per plot. Branches per plant was positively and significantly correlated with pod per plant, 100 seed weight, biomass per plot, harvest index, cluster per plant, seed yield per plot.100 seed weight was positively and significantly correlated with pods on main stem, pod per plant), seed per pod, branches per plant, biomass per plot, harvest index, cluster per plant, seed yield per plot. Cluster per plant was positively and significantly correlated with pods per plant, seeds per pod, branches per plant, 100 seed weight, biomass per plot, harvest index, seed yield per plot. Biomass per plot was positively and significantly correlated with pods on main stem), pod per plant, seed per pod, branches per plant, 100 seed weight, cluster per plant, seed yield per plot. Harvest index was positively and significantly correlated with pods per plant, seed per pod, branches per plant, 100 seed weight, cluster per plant, seed yield per plot.

Similar findings either one or more than one character have been earlier supported by Kumar *et al*. (2020), Sivia *et. al.* (2016), Mannivannan *et al.* (2016), Jitender *et al.* (2014), Khalid *et al.* (2017), Vishnoi *et al.* (2017), Gretsa *et al.* (2017, 2018), Lekshamannan *et al.* (2016),Abraham *et al*. (2017), Bhatt *et al.* (2015), Santosha *et al.* (2017), Teja *et al*. (2022), Wankhade *et al.* (2016) and Deepashree *et al*. (2022).

Seed yield per plot, 100 seed weight and cluster per plant showed negative significant association with plant height, days to maturity, pods per cluster and pod length. Negative significant correlation was observed for 100-seed weight with similar result has been reported by Goudar *et al.* (2017) and Deepashree *et. al.* (2020). Seed yield per plant was positively and significantly associated with pods on main stem, pods per plant, seed per pod, branches per plant, 100 seed weight, biomass per plot, harvest index, cluster per plant, indicating simultaneous selection based on these characters would be effective for seed yield. These results have supported either one or more than one character indicated as earlier reported by Kumar *et al*. (2016), Sivia *et. al.* (2016), Reddy *et al.* (2018), Gretsa *et al.* (2017), Santosha *et al.* (2017), Panchta *et al*. (2017), Kumar *et al.* (2020) and Deepashree *et al*. (2021).

BLB intensity was positively and significantly correlated with protein content, total soluble sugar content, reducing sugar content, non-reducing sugar content.

Gum content was positively and significantly correlated with ADF content, lignin content, cellulose content, silica content, NDF content. Protein content was positively and significantly correlated with total soluble sugar content, reducing sugar content, non-reducing sugar content and BLB intensity.

Total soluble sugar content was positively and significantly correlated with protein content, reducing sugar content, non-reducing sugar content, BLB intensity. Reducing sugar content was positively and significantly correlated with protein content, total soluble sugar content, non-reducing sugar content, BLB intensity. Non-reducing sugar content was positively and significantly correlated with protein content, total soluble sugar content (0.989), reducing sugar content and BLB intensity.

ADF content was positively and significantly correlated with gum content, lignin content, cellulose content, silica content, NDF content and hemicellulose content.

Lignin content was positively and significantly correlated with gum content, ADF content, cellulose content, silica content, NDF content, hemicellulose content. Cellulose content was positively and significantly correlated with gum content, ADF content, lignin content, silica content, NDF content, hemicellulose content. Silica content was positively and significantly correlated with gum content, ADF content, lignin content, cellulose content, NDF content, hemicellulose content. NDF content was positively and significantly correlated with gum content, ADF content, lignin content, cellulose content, silica content and hemicellulose content.

Hemicellulose content was positively and significantly correlated with ADF content, lignin content, cellulose content, silica content and NDF content.

BLB intensity negatively and significantly correlated with gum content, ADF content, lignin content, cellulose content, silica content and NDF content. Gum content, protein content, TSS content, reducing sugars and non-reducing sugars showed negative and significant correlation with ADF content, lignin content, cellulose content, silica content and NDF content.

5.6. Path coefficient analysis

5.6.1 Path coefficient analysis for yield and component characters and BLB intensity and quality characters

Path analysis is a powerful measure to estimate the contribution of direct and indirect effects of various independent characters on a dependent character *i.e.*, seed yield per plot. In the present investigation, direct and indirect effects of various quantitative characters on seed yield per plant are presented in Table 4.6.1. The high direct effect of number of clusters per plant, pods on main stem, pod length, branches per plant, biomass per plot, plant height, 100 seed weight and days to maturity on seed yield per plant indicated that these are important components of seed yield. Thus, direct selection for high seed yield per plant based on these characters would be effective. The result of these characters agrees with the previous reports by Tsegaye *et al.* (2018) and Bamji *et al*. (2020). Similar findings were earlier supported by Manisha *et al*. (2018), Mayuri Sahu (2019) and Snehal *et al*. (2021) for 100 seed weight; by Manggoel *et al* (2012) for seeds per pod; by Lal *et al* (2017).

However, seeds per pod, days to 50% flowering, pods per cluster, pods per plant and harvest index showed direct and negative effect on seed yield per plant, indicating simultaneous selection against of these characters would be benificial for seed yield improvement. Pods per cluster hSeveral earlier workers were similarly reported by Kumar *et al*. (2016, 2020), Panchta *et al.* (2017), Bhatt *et al.* (2015), Muthuselvi *et al*. (2017, 2018) and Khalid *et al*. (2017) for clusters per plant; by Jukanti *et al*. (2015), Kumar et al. (2020) and Panchta *et al*. (2017) for days to 50% flowering; by Abraham *et. al.* (2019) for pod length.

The present study revealed that characters *viz.,* clusters per plant, pods on main stem, pod length, branches per plant, biomass per plot, plant height, 100 seed weight and days to maturity would be selected as important ones towards seed yield for cluster bean improvement programme. The value of residual effect in path analysis was found to be 0.0056, showing maximum effect of the characters on seed yield per plant under study.

In the present investigation, direct and indirect effects of various characters on seed yield per plant are presented in Table 4.6.2. The high direct effect of non-reducing sugars, reducing sugar content, NDF content, ADF content, silica content and protein content on BLB disease intensity indicated that these are important components of seed yield. Thus, direct selection against BLB disease intensity based on these characters would be effective.

However, total soluble sugar content, lignin content, cellulose content, gum content and hemicellulose content showed direct and negative effect on BLB intensity. The present study revealed that characters *viz.,* non-reducing sugars, reducing sugar content, NDF content, ADF content, silica content and protein content would be selected as important ones towards BLB disease intensity for cluster bean improvement programme. The value of residual effect in path analysis was found to be 0.087, showing maximum effect of the characters on BLB disease intensity under study.

5.7 Stability analysis based on Eberhart and Russell's, 1966 and AMMI model, 1997

5.7.1 Pooled analysis of variance

a) Based on Eberhart and Russell's model, 1966

The results of pooled analysis of variance for stability as devised by Eberhart and Russell (1966) presented in table 4.7.1 in previous chapter showed that genotypes different for all the charactersexcept hemicellulose, environments for all the characters and genotype x environment interaction were significant for the characters namely, number of pods per plant, number of pods per cluster, pod length, number of branches per plant, harvest index, total clusters, protein content and seed yield per plot indicating that genotypes are rich in variation for various characters, micro environments created through different cultivation seasons were different from each other and genotype x environment interaction components showed wide differential behaviour of genotypes under changing environments.Mean sum of squares due to environments + (genotypes x environments) were highly significant for all the characters studied except dry matter and TSS content depicted the distinct nature of environments and genotype x environment interaction on phenotype expression and significance of environment (linear) component for all the characters indicated that the genotypes responded linearly for most of the characters under study. Significance for mean squares for genotype x environments (linear) for all characters except days to 50% flowering 100 seed weight, gum content (%), TSS, NRS, ADF and hemicellulose indicates variation in the performance of genotype is due to the regression of genotypes on environments. The significance of pooled deviations for all the characters except seeds per pod and hemicellulose content depicts that the performance of genotypes is entirely unpredictable in nature. These result corroborates with the findings of Teja *et al.* (2022), Arunkumar *et al.* (2017), Wankhade *et al.* (2017),Kumar *et al.* (2016),Jain and Patel (2012),Pathak *et al.* (2010) in cluster bean; Borude *et al.* (2021), Nitesh *et al.* (2021) and Kachanur *et al.* (2017) in mung bean; Manivannan *et al.* (2019) and Singh *et al.* (2018) in cowpea for different components of analysis of variance and characters.

b) Based on AMMI model, 1997

The results of pooled analysis of variance for stability as given by Gauch and Zobel, 1997 presented in table 4.8.1 in previous chapter showed that genotypes, environments and genotype x environment interaction were significantly different for all the characters when tested against pooled deviation.This suggests that genotypes are rich in variation for various characters, micro environments created through different cropping seasons were different from each other and genotype x environment interaction components showed wide differential behaviour of genotypes over the changing environments. Similar findings were also reported by Sharma *et al.* (2022) and Benakanahalli *et al.*(2021) in cluster bean; Samyuktha *et al.* (2020) and Baraki *et al.* (2020) in mung bean; Jeberson *et al.* (2020) in urd bean; Kindie *et al.* (2021) and Kuruma *et al.* (2019)in cowpea; Arya *et al.* (2022) in Faba bean.

5.7.2 Stability parameters

Plant height

The present study revealed that HK 19 most favourable environment for plant height as indicated by environmental index, whereas BS 20 resulted in dwarfness.

Considering the dwarf genotype as desirable, ten genotypes HG 884, HG 3-52, HG 100, X 10, GG 2, RGC 1017, RGC 1038, RGC 1055, RGC 1002 and RGS 3 recorded low mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable as dwarf genotypes for all the environments.No genotypes recorded low mean value than overall mean, significant regression coefficient more than and less than unity with non-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment as dwarf genotype.

In cluster bean for plant height using Eberhart and Russell's model, Teja *et al.*(2022) identified genotype IC-140777 with general adaptability, eight genotypes with specific adaptability for unfavourable while, IC-9077-P1, IC-10323, IC-28287 and IC-200696 for favourable environment as tall genotypes in cluster bean. Wankhade *et al.* (2017) identified genotypes IC-415163, IC-421825, IC-421832and IC-369861 with general adaptability, eight genotypes with specific adaptability for unfavourable while, 11 genotypes for favourable environment as tall genotypes in cluster bean. Jain and Patel (2012) adjudged genotypes GAUG-0416, GAUG-0308, GAUG-0004 and GAUG-0309 with general adaptability, genotype GAUG-501 with specific adaptability for unfavourable while, genotypes GG-2 and GAUG-0522for favourable environment as tall genotypes.

Genotypes HG 3-52, HG 884, RGC 1033, RGS 3, RGC 1017, RGC 1055, RGC 1002, GG-2, GG-1, RGC 1038, HG 870, HG 6, HG 563, RGC 936, HG 365 and HG 2-20 were found near the origin in AMMI biplot this indicates the less interaction of these genotypes with environments. Therefore, these genotypes can be recommended for their general cultivation over the environments. Similarly, the environments, HS 20, BS 20 and HS 19 were found suitable for the cultivation of all the genotypes included in the study.

Days to 50% flowering

The environment, HS 19 was found most favourable environment for days to 50% floweringas indicated by environmental index, whereas HK 20 resulted in earliness in flowering.

Eleven genotypes, HG 2-20, HG 870, HG 563, HG 3-52, X 10, GG 2, RGC 1017, RGC 1038, RGC 1003, RGC 1066 and RGC 1033 recorded low or equal mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable as early flowering for all the test environments.None of genotyperecorded low mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for early flowering for better environment. Only one genotype RGC 1033 recoded with low mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified for early flowering for poor environment.

Using Eberhart and Russell's model, Wankhade *et al.* (2017) reported 6 genotypes with specific adaptability for poorwhile, 15 genotypes for rich environment and genotypes IC-248087, IC-415159 and RGC-936 with general adaptability early flowering in cluster bean. Similarly, Jain and Patel (2012) reported genotypes GG-2, GAUG-0004, GAUG-0503, GAUG-0512 and GAUG-0513with specific adaptability for poor while, genotypes GAUG-0308, GAUG-0309 GG-1 and GAUG-0501for rich environment and genotypes GAUG-0522 and GAUG-0524 with general adaptability early flowering in cluster bean.

AMMI analysis showed that genotypes HG 884, HG 870, HG 365, RGC 1033, RGC 1003, RGC 1066, GG-2, GG-1, HG 2-20, HG 563, RGC 1017, X-10, HG 100, RGS 3, RGC 1038, HG 3-52 and RGC 1055 were stable and early flowering across the environments and had general adaptation. The environmentBK 19 was found favourable environments for all the genotypes. In Rice, Harikesh *et al.* (2021) reported Improved Pusa Basmati 1, HKR 98-476 and HKR 08-417 as stable genotypes for days to 50% flowering while, Jain*et al.* (2018) reported various genotypes for suitable different production systems for days to 50% flowering using AMMI model.

Days to maturity

The environment, HS 20 was found most favourable environment for days to maturityas indicated by environmental index, whereas BK 19 resulted in earliness in maturity.

Nine genotypes namely HG 2-20, HG 884, HG 870, HG 563, X 10, RGC 1038, RGC 1055, HG 75 and RGC 1002 recorded low mean value than overall mean, and non-significant deviation from unity as well as non-significant deviation from regression were found suitable for early maturity for all environment.None of the genotypes recorded low mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression and found suitable for early maturity for better environment. The genotypes namely HG 100, RGC 1017 and RGC 1003 with low mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified for early maturity for poor environment.

In cluster bean using Eberhart and Russell's model, Teja *et al.* (2022) identified genotype IC-10323 with general adaptability, while, genotypes, IC-13365, IC-200680, IC-140777 and IC-200715 with specific adaptability for unfavourable and IC-9233-P3, IC-140774, IC-200679 and IC-200696 for favourable environment with early maturity.Similarly, Jain and Patel(2012) reported genotypes GAUG-0309, GAUG-0416, GAUG-0513 and GAUG-0522 with general adaptability, while, genotype, GAUG-0503 with specific adaptability for unfavourable and GAUG-0512 for favourable environment.

For days to maturity, RGC 1003, RGC 936, GG-2, RGC 1017, RGC 1002, HG 365, X-10, RGC 1066, RGC 1055, HG 100, RGC 1038, HG 3-52, HG 563, RGC 1033, HG 2-20, GG-1, HG 884, HG 870, RGS 3 and HG 6 were identified as the stable and early genotypes having general adaptation across the environments. Similarly, BK 19 and BS 20 were found stable environment indicating that all the genotypes performed better under these environments.In Rice, while using AMMI model Harikesh *et al.* (2021) reported Improved Pusa Basmati 1, HKR 98-476 and HKR 08-417 as stable genotypes for days to maturity.

Pods on main stem

The environment, HS 19 was found most favourable environment for pods on main stem as indicated by environmental index, whereas BK19 resulted in less number of pods on main stem. Among the genotypes tested, only RGC 1002 exhibited non-significant deviations from regression and average in response, thus have performance over the environment but it was low in mean performance. No genotypes recorded high mean value than overall mean, significant regression coefficient more than unity and less than with non-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment.

In Cluster bean using Eberhart and Russell's model, Dadheech *et al.* (2022) reported genotypes, RGC 1066 for rich environment high number of clusters on main stem in cluster bean.

The genotypes, HG 2-20, HG 884, HG 870, HG 563, HG 365 and X-10 adjudged as the stable, with high number of pods per plant genotypes and having general adaptation across the environments. Similarly, the environment, BS 20 was found stable environment indicating that all the genotypes performed better under these environments.

Pods per plant

The environment, HS19 was found most favourable environment for pods per plantas indicated by environmental index, whereas BK19 resulted in less number of pods per plant. All the genotypes testedexhibited significant deviations from regression therefore; their performance cannot be predicted very well.

In Cluster bean using Eberhart and Russell's model, Teja *et al.* (2022) reported genotype, IC-140777with specific adaptability for poorwhile, IC-9229-P3 and IC-140774for rich environment andgenotypes IC-39989, IC-103295 and IC-200696with general adaptability with high number of pods per plant in cluster bean. Wankhade *et al.* (2017) reported genotypes, IC-421837, PLG-85 and IC-421798 with specific adaptability for poor while, 10 genotypes for rich environment and genotypes IC-421815 and IC-373480 with general adaptability with high number of pods per plant.Jain and Patel (2012) reported genotypes, GAUG-0004, GAUG-0503 and GAUG-0524 with specific adaptability for poorwhile, genotypes GAUG-0308, GAUG-0309 andGAUG-0312for rich environment and genotype GAUG-0411 with general adaptability with high number of pods per plant.Singh *et al.* (2018) reported genotype, C-1013 and C-1126with specific adaptability for favourable and genotypes C-967, C-1085 and C-1127 with specific adaptability with high mean for unfavourable in cowpea.

AMMI analysis revealed that the genotypes, HG 100, HG 3-52 and RGS 3 were stable, with high pod bearing per plant across the environments and had general adaptation. Among the environments, HK 19 and HK 20 were found favourable environments for all the genotypes. Thangavel *et al.* (2011) reported mung bean genotypes G 34, G 22 and G 12 with high number of pods per plant with stable phenotype using AMMI model.

Pods per cluster

The environment, HS 19 was found most favourable environment for pods per clusteras indicated by environmental index, whereas BK19 resulted in less number of pods per cluster.

In present study, significant and negative association was found between pods per cluster and seed yield per plot. Pods per cluster and clusters per plant were also found negatively and significantly associated. Clusters per plant also showed indirect negative effect on seed yield per plot *via* pods per cluster.Therefore, considering less pod per cluster as desirable feature, the genotypes *viz.* HG 870, HG 563, HG 3-52, HG 6, HG 100, RGC 1038, RGC 936, RGS 3 and RGC 1055 recorded low mean value than overall mean, significant regression coefficient more equal to unity and non-significant deviation from regression were found well adapted to all the environment. No genotype recorded low mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression or found suitable for better environment. The genotypes namely HG 2-20, HG 884 and X-10 with low mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

Using Eberhart and Russell's model, Kumar *et al.* (2012) reported genotypes RU 8708 and HG 157 with general adaptability with high number of pods per cluster in black gram. Similarly, Singh *et al.* (2014) reported genotypes DMC 17and P Baishakhi with high general adaptability for pods per cluster with high mean in mung bean.

AMMI biplot analysis identified HG 870, HG 3-52, HVG 2-30, HG 100, RGC 1017, RGC 936, RGC 1055 and RGS 3 non sensitive to environmental interactive forces and found with least number of pods per cluster. These genotypes were found stable across the environments whereas BK 20 and BS 20 were found stable and favourable environments.

Seeds per pod

The environment, HS19 was found most favourable environment for seeds per podas indicated by environmental index, whereas BK19 resulted in less seeds per pod.

The genotypes *viz.* HG 2-20, HG 884, HG 870, HG 563, HG 365, X-10, RGC 1033 and RGC 1038 were recorded high mean value, significant regression coefficient equal to unity (bi=1) and non-significant deviation from regression ($S^2di=0$) were found suitable for all the environment.

No genotypes recorded high mean value than overall mean, significant regression coefficient more than unity and less than with non-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment.

Using Eberhart and Russell's model, Wankhade *et al.* (2017) reported genotypes IC-415102, IC-369789 and IC-373427 with general adaptability, 13 genotypeswell adapted for richwhile, 11 genotypes were found well adapted for poor environments with high number of seeds per pod in cluster bean. Similarly, El-Shainey *et al.* (2014) reported Dokii 331, IT93K2045-20 and Black Crowder genotypeswith specific adaptability for poor and IT91K118-20, IT82C-16 and Blackeye Crowder with specific adaptability rich environment while, genotypes IT93K2045-20, Dokii331, Cram7 and Black Crowder with general adaptation with high number of seeds per pod in cowpea.

Genotypes, HG 2-20, HG 884, HG 870, HG 563, X 10 and RGC 1033 were found with high number of seeds per pod and were found near the origin in AMMI biplot indicating less interaction with environments. So these genotypes can be recommended for their general cultivation over the environments. Similarly the environments, BS 20 and HS 20 were found suitable for the cultivation of all the genotypes included in the study. The genotypes of pigeon pea AL-1491, H-97-24 and ICPL-88034 were found stable for seeds per pod by Singh *et al.* (2018) while conducting the study on stability using AMMI model.

Pod length

The environment, HS19was found most favourable environment for pod length as indicated by environmental index, whereas BK19 resulted in shorter pods.

Considering short pod as desirable phenotype, the genotypes *viz.* HG 2-20, HG 884, HG 563, HG 365, HG 3-52, HG 100, GG-1, RGC 1017, RGC 1066 and RGS 3 recorded low mean value, significant regression coefficient equal to unity and non-significant deviation from regression were found suitable for all the environments. The genotypes *viz.* HG 870 and RGC 1055 recorded low mean value while, FS 277 recorded high mean value, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for better environment as genotypes with shorter pods and with longer pods, respectively. The genotypes namely GG-2, RGC 1003 and RGC 1033 with low mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

Using Eberhart and Russell's model, Teja *et al.* (2022) reported genotypes, IC-28283, IC-28287 and IC-177844 suitable for rich while, IC-39989, IC-103295 and IC-200696 for all environments with long pods in cluster bean. Similarly, El-Shainey *et al.* (2014) reported IT91K118-20, Sudany and Kaha 1 genotypes with specific adaptability for poor environment while, IT93K2045-20, Black Crowder, Azmerly and IT81D-889 genotypes with general adaptation with long pods in cowpea.

According to AMMI, genotypes HG 2-20, HG 100, GG-1 and RGC 1002 registered below overall mean along with the IPCA1 score close to zero were found as stable genotype and had general adaptation to all the environments but none of the environments was found as stable *i.e.*, with small interaction effects for pod length. In a study conducted by Singh *et al.* (2018) in pigeon pea the genotypes H-82-1, WREG28, TT-302 and ICPL-99004 were found stable for pod length.

Branches per plant

The environment, HS20 was found most favourable environment for braches per plantas indicated by environmental index, whereas BK19 resulted in less number of branches per plant.

The genotypes *viz.* HG 884, HG 870, HG 563, HG 365, GG-1, RGC 1038, RGC 936, RGC 1055, RGC 1002 and RGC 1033 were recorded high mean value, significant regression coefficient equal to unity and non-significant deviation from regression were found suitable for all the environments.The genotypes *viz.*HG 2-20, X-10, GG-2 and RGS 3 recorded high mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for better environment. None of the genotypes was identified as suitable genotypes for poor environment.

Using Eberhart and Russell’s model for number of branches per plant, Wankhade*et al.* (2017) reported 9 genotypes with specific adaptability for poorwhile, 19 genotypes for rich environment and genotypes IC-373427, IC-369861 and IC-369868 with general adaptability with high number of branches per plant. Similarly, Kumar*et al.* (2012) reported genotypes COBG 683 and LBG 623 general adaptability with high number of branches in black gram. Patel *et al.* (2014) reported parents CMSGT0307A, GTH1 and five hybrids with general adaptability while, parents GTR 0525, GTR 0524and two hybrids for better environment with high number of branches per plant in pigeon pea. Singh *et al.* (2018) reported genotypes, C-113 C-738, C-951 and C-1085 with specific adaptability for favourable and genotypes C-863 and C-1089 with specific adaptability with high mean for unfavourable in cowpea.

Genotypes HG 870, HG 365, RGC 1002, RGC 1003 and RGC 1033 were found as highly branched and stable genotype as they were placed near the origin of the AMMI biplot indicating little interaction of these genotypes with environments. Environment HK 19 was found stable and high yielding environments.Singh *et al.* (2018) used AMMI model in pigeon pea and reported genotypes AL-1491 and Phule T-8020 as best genotypes for this character.

100 seed weight

The environment, BK 19was found most favourable environment for bold seed indicated by environmental index, whereas BS 19 and BK 20 resulted in less 100 seed weight.

The genotypes *viz.* HG 563 recorded high mean value, significant regression coefficient equal to unity and non-significant deviation from regression was found suitable for all tested environment.No genotypes recorded high mean value than overall mean, significant regression coefficient more than unity and less than with non-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment.

Using Eberhart and Russell's model, Wankhade*et al.* (2017) reported 12 genotypes well adapted for rich while, 5 genotypes namely, IC-421801, IC-421821, RGC-936, IC-402296 and IC-373480 well adapted for poor environments with bold seeds in cluster bean. Similarly, El-Shainey *et al.* (2014) reported genotypes Azmerly, IT81D-889, Black eye Crowder and Black Crowder genotypes with specific adaptability for poor and genotypes, Dokii 331, IT91K118-20, IT82C-16 andIT85F2205,Blackeye Crowder with specific adaptability for rich environment respectively while, two genotypes with general adaptation with bold seeds in cowpea.

Genotype HG 563 adjudged as stable genotype with bold seeds as it was placed near the origin of the AMMI biplot indicating little interaction of this genotype with environments. EnvironmentsHK 19 and HS 20were found stable and high yielding environments. A study using AMMI model was also conducted by Shimray *et al.* (2022) for 100 seed weight in mung bean and identified IG5986, IG5982, ILC6025 and ICCV14307 as stable genotypes.Singh *et al.* (2018) reported WRGE-31 and Phule T-8020 as stable genotypes for 100 seed weight in pigeon pea.

Biomass per plot

The environment, HS 19was found most favourable environment for high biomass per plotas indicated by environmental index, whereas BS 19 and BK 19 resulted in less biomass accumulation.

Among the genotypes tested, none of the genotype exhibited non-significant deviations from regression as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well.

Using Eberhart and Russell's model, Patel*et al.* (2014) reported nine parents and five hybrids with high general adaptability and two hybrids with specific adaptability for favourable environment for biological yield in pigeon pea. Similarly, Singh*et al.* (2014) reported genotypes Meha and DM 05-74-11 with high general adaptability for biological yield with high mean in mung bean.

For biomass per plant, HG 100, X-10, RGC 1038, RGC 1066, RGS 3 and RGC 1033 showed small interaction with environments, so these genotypes were considered as stable genotypes across the environments. Environment BS 19 was found stable and high yielding environments for the character. Satasiya and Pual (2022) in linseed reported KL 241 and KL 263 as stable genotypes for harvest index and seed yield.

Harvest index

The environment, BS 19was found most favourable environment for high harvest indexas indicated by environmental index, whereas HS 20, BS 20 and HK 20 resulted in less harvest index.

The genotypes *viz.* HG 884, HG 870, HG 3-52, HG 6, RGC 1017, RGC 1038 and, RGC 1066 recorded high mean value, significant regression coefficient equal to unity (bi=1) and non-significant deviation from regression were found suitable for all tested environment. No genotypes recorded high mean value than overall mean, significant regression coefficient more than unity and less than with non-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment.

Using Eberhart and Russell's model, Patel *et al.* (2014) reported parent 0544 CMSGT0307 and one hybrid well adapted for poor environments for harvest index in pigeon pea while, parent AGTR well adapted for poor and eight hybrids for rich environment for harvest index in pigeon pea. Similarly, Singh *et al.* (2014) reported genotypes DMS 01-34-2, TMB 37 and DM 05-74-11 with high general adaptability for harvest index with high mean in mung bean.Desai *et al.* (2016) reported genotypes, GG-1, GJG-3 and Dahod yellow with general adaptability for harvest index in chickpea.

AMMI biplot located the genotypes HG 2-20, HG 884, HG 870, HG 563, X-10, RGC 1017, RGC 1038, RGC 1066, RGS 3 and RGC 1033 near the origin of and represented them generally adapted genotypes with high harvest index. HS 19, BK 19 and BK 20 were found suitable for the cultivation of all the genotypes. Satasiya and Pual (2022) in linseed reported KL 263 and Surabhi as stable genotypes for harvest index and seed yield.

Clusters per plant

The environment, HS 19was found most favourable environment for high number of clusters per plantas indicated by environmental index, whereas BK 19 resulted in low number of clusters per plant.

Three genotypes, HG 2-20, HG 884 and HG 563 recorded high mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for better environment. But, no genotype with high mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

Using Eberhart and Russell's model, Kumar *et al.* (2012) reported genotypes RU 8709, RU 8708 and LBG 623 with general adaptability with high number of clusters per plant in black gram.Similarly, Singh *et al.* (2014) reported genotypes NDM 9-18, DMS 01-34-2, DM 05-74-11, P 1131, IPM 99-394 and P Baishakhi with high general adaptability for number of clusters per plant with high mean in mung bean.Singh *et al.* (2018) reported genotype, C-1133 with specific adaptability for favourable and genotypes,IC-219640, C-

1085, C-1126 and C-1127 with specific adaptability with high mean for unfavourable in for number of cluster per plant in cowpea.

According to AMMI biplot analysis, the genotypes HG 870, HG 3-52, HG 100, RGC 1038, RGS 3 and RGC 1033 were found stable and high yielding whereas, none of the environment was found favourable for this character. Thangavel *et al.* (2011) reported mung bean genotypes G 34 and G 12 with high number of cluster per plant and environment of llavampatti with stable phenotype using AMMI model.

Seed yield per plot

The environment, HS 19was found most favourable environment for high seed yield per plotas indicated by environmental index, whereas BK 19 resulted in low seed yield per plot.

The genotypes *viz.* RGC 1066 recorded high mean value, significant regression coefficient equal to unity and non-significant deviation from regression were found suitable for all tested environment. Two genotypes *viz.,* HG 2-20 and RGC 1055 recorded high mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for better environment. But, no genotype with high mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

Using Eberhart and Russell's model in cluster bean for seed yield, Arunkumar *et al.* (2017) adjudged genotypes, RG-936-1-5-1 and HG 884 with general adaptability, genotypesHG-563, RGC-986 and HG 365specifically adapted to rich while, genotype Gourishankar-9for poor environments.Similarly, Wankhade *et al.* (2017) reported five genotypes with general adaptability,11genotypes specifically adapted to rich while, genotypeIC-421816, IC-421831 and IC-421837 for poor environments. Jain and Patel (2012) reported genotypes GAUG-0309 and GAUG-0411with general adaptability,genotypes GAUG-416, GG-2 and GAUG-0522 specifically adapted to rich while, genotypeGAUG-0524, GAUG-0503, GAUG-0501, GAUG-0308 and GAUG-0309for poor environments. Desai *et al.* (2016) reported genotypes, IC-269273 and IC-269295, GG-1, GJG-3 and Dahod Yellow with general adaptability for seed yield in chickpea. Singh *et al.* (2018) reported genotypes, C-797, C-1085 and C-1109 with specific adaptability for favourable and genotypes C-863 and C-956 with specific adaptability for unfavourable for seed yield in cowpea.

AMMI biplot located the genotypes HG 100, GG-2, RGC 936, RGC 1038, RGC 1066 and HG 870 near the origin of and represented them generally adapted genotypes with high seed yield per plot. The environments, HK 19 and HS 20 were found suitable for the cultivation of all the genotypes.In cluster bean,Sharma *et al.*(2022)conducted study on stability analysis using AMMI model and reported GAUG 1507 as stable genotype and

Vijapur location was found favourable while, Benakanahalli *et al.*(2021)in cluster bean reported IC 415106, IC 420320 and IC 402301 as stable genotypes. In cowpea, Ddamulira *et al.* (2015) and found C1J as stable genotype while, Serere location among all the locations studied of Uganda was found favourable.In mung bean, The genotype SML 668 was found most stable genotypes by Baraki *et al.*(2020) while, the genotypes V2802BG, HG 22, and EC 396098 were found stable for all the environments studied by Samyuktha *et al.*(2020). The genotypes VBG 12-034, IPU 13-3 and COBG 13-04 were found stable with wider adaptability for grain yield by Jeberson *et al.*(2020) in urd bean. In pigeon pea, Rao *et al.*(2020) found genotype WRG-327 as stable genotype while, Singh *et al.*(2018) found genotypes GT-101, H-97-24, UPAS-120 and ICPL-85010 stable genotypes for seed yield.

Gum content

The environment, HS 19was found most favourable environment for high gum contentas indicated by environmental index, whereas BK 19 resulted in low gum content.

The genotypes *viz.* HG 2-20, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X-10, GG-1, RGC 1066, RGC 1033 recorded high mean value, significant regression coefficient equal to unity and non-significant deviation from regression were found well adapted for all tested environment. No genotypes recorded high mean value than overall mean, significant regression coefficient more than unity and less than with non-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment.

Using Eberhart and Russell’s model in cluster bean for gum content, Teja *et al.* (2022) suggested genotypes, IC-103295 and IC-140791 with general adaptability, genotype IC-200715 specifically adapted to rich while, genotypes IC-34344 andIC-140774 for poor environments with high gum. Wankhade *et al.* (2017) suggested genotypes, IC-421830 and IC-421840 with general adaptability, five genotypes specifically adapted to rich and 12 genotypes for poor environments with high gum content.

HG 870, HG 365, HG 100, X-10, GG-1, RGC 1066 and RGC 1033 among the genotypes and HK 20 among the environments were found stable and with high overall mean for gum content on the basis of AMMI biplot analysis for this character. IC 415106, IC 420320 and IC 402301 were adjudged as stable genotypes for gum content by Benakanahalli *et al.*(2021) using AMMI model.

Protein content

The environment, BK 20 was found most favourable environment for high protein contentas indicated by environmental index, whereas HK 20 resulted in low protein content.

None of genotype recorded high mean value, significant regression coefficient equal to unity and non-significant deviation from regression was found suitable for all tested environment. None of genotyperecorded high mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for better environment. But, only one genotype RGC 1066 with high mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

Using Eberhart and Russell’s model in cluster bean for protein content, Teja *et al.* (2022) suggested genotypes, IC-10333, IC-28286, IC-103295and IC-200715 with general adaptability, genotypes IC-9233-P3, C-10323, IC-13365 and IC-140777 specifically adaptedtorichwith high protein content.Wankhade *et al.* (2017) suggested genotype, IC-421830 with general adaptability, 16 genotypes specifically adapted to poor and three genotypes namely IC-421816, IC-421821 and IC-369868 specifically adapted to rich environment with high protein content.Desai *et al.* (2016) reported genotype, IC- 269295 with general adaptability while, genotype GJG-3 specifically poor environment for protein content in chickpea.

AMMI biplot located the genotypes HG 2-20, HG 6, HVG 2-30, FS 277, PNB, GG-1, RGC 1038, RGC 1002, RGC 1003 and M-83 near the origin of and represented them generally adapted genotypes with high protein content. The environment,HK 19 was found suitable for the cultivation of all the genotypes. Benakanahalli *et al.* (2021) also reportedIC 415106, IC 420320 and IC 402301as stable genotypes for protein content using AMMI model. C1J, C2Q and BRS Pujante genotypes of cowpea were adjudged as stable genotypes for protein content by Ddamulira *et al.*(2015) in cowpea.

Total soluble sugar (TSS) content

The environment, HS 19was found most favourable environment for high TSS contentas indicated by environmental index, whereas BK 20resulted in low TSS content.

Considering less TSS content as desirable phenotype, one genotype, RGC 1038 with low mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for rich environment. One genotype, HG 563 with low mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

Using Eberhart and Russell’s model in sorghum for TSS content, Kavya *et al.* (2022) suggested hybrids, H 3 and H 4 with general adaptability, hybridH 2 and H 15 specifically adapted to poor and rich environments respectively, with high TSS content. Similarly, Ulaganathan *et al.* (2015) reported hybrid QPM-6 x S.C.B. 7853-1 with specific adaptability for drought environments in maize for TSS content.

AMMI analysis of G x E interaction revealed that performance of HG 2-20, HG 884, HVG 2-30, RGS 3, FS 277, RGC 936 and PNB were little influenced by environmental fluctuations. Therefore, these genotypes were adjudged as stable genotypes with low TSS content. Similarly, HK 19 and BK 19 were found suitable for all the genotypes.

Reducing sugar content

The environment, HK 20 was found most favourable environment for high reducing sugar contentas indicated by environmental index, whereas HS 20 resulted in low reducing sugar content.

Considering less reducing sugar content as desirable, none of the genotype recorded lower mean value than overall mean, significant regression coefficient equal to unity and non-significant deviation from regression were found suitable for all tested environment. Only one genotype, HG 2-20 recorded lower mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for better environment. But, no genotype with lower mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

According to AMMI analysis of G x E interaction the genotypes,HG 3-52, RGC 1017 and RGC 1066 were adjudged as stable genotypes with low reducing sugar content. Similarly, BS19, BK19 and BK20 were found suitable for all the genotypes.

Non-Reducing sugar content

The environment, HS 19was found most favourable environment for high non-reducing sugar contentas indicated by environmental index, whereas BK 19 resulted in low non- reducing sugar content.

Considering less non-reducing sugar content as desirable, No genotypes recorded low mean value than overall mean, significant regression coefficient more than unity and less than withnon-significant deviation from regression. Therefore, none of genotype was found suitable for better environment and for poor environment.

AMMI biplot analysis identified HG 2-20, HG 884, HG 100 and GG-2 as stable genotypes with low non-reducing sugar content across the environments. So these genotypes performed constantly over the wide range of environments. Among the environments, HK 19 was found as stable and suitable.

ADF content

The environment, BS 19was found most favourable environment for high non-reducing sugar contentas indicated by environmental index, whereas HK 19 resulted in low non- reducing sugar content.

Among the genotypes tested, none of the genotype exhibited non-significant deviations from regression as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well.

According to AMMI biplot analysis, the genotypes HG 870, X 10, RGC 1017 and RGC 1003 were found stable and with high ADF content. Among the environments, BS 19 and BK 19were found as stable and suitable.

Lignin content

The environment, HK 19was found most favourable environment for high non-reducing sugar contentas indicated by environmental index, whereas BK 19 resulted in low non- reducing sugar content.

Three genotypes, HG 2-20, RGC 1017 and RGC 1066 recorded high mean value, significant regression coefficient equal to unity and non-significant deviation from regression were found suitable for all tested environment. Four genotypes, HG 884, HG 365, HVG 2-30 and M-83 recorded high mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for better environment. Two genotypes, X-10 and RGS 3 with high mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

Genotypes HG 870, HG 2-20 and RGC 1033 were found with high lignin content and found near the origin in AMMI biplot this indicates the less interaction of these genotypes with environments. Similarly, the environments, HS 19, BS 19, BS 20 and HK 20 were found suitable for the cultivation of all the genotypes included in the study.

Cellulose content

The environment, BS 19was found most favourable environment for high non-reducing sugar contentas indicated by environmental index, whereas HK 19 resulted in low non- reducing sugar content.

Among the genotypes tested, none of genotypeexhibited non-significant deviations from regression as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well.

AMMI analysis showed that genotypes HVG 2-30, FS 277, RGC 936 and HG 75 were stable, with high cellulose content across the environments and had general adaptation. The environmentsBS 19 and BK 19 was found favourable environments for all the genotypes in terms of cellulose content.

Silica content

The environment, BS 20was found most favourable environment for high non-reducing sugar contentas indicated by environmental index, whereas BS 19 resulted in low non- reducing sugar content.

Among the genotypes tested, none of the genotype exhibited non-significant deviations from regression as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well.

Genotypes RGC 1066, RGS 3 and RGC 1033 were found with high overall mean for silica content and found near the origin in AMMI biplot this indicates the less interaction of these genotypes with environments. The environments HS 20 and HK 20 was found favourable environments for all the genotypes.

NDF content

The environment, BS 19was found most favourable environment for high non-reducing sugar contentas indicated by environmental index, whereas HK 19 resulted in low non- reducing sugar content.

Among the genotypes tested, none of the genotypeexhibited non-significant deviations from regression as the genotypes are within the range of minimum deviation from regression, their performance cannot be predicted very well.

AMMI biplot located the genotypes HG 870, HG 100, X-10 and RGC 1003 near the origin of and represented them generally adapted genotypes with high NDF content. The environments,BK 19 and BS 19were found suitable for the cultivation of all the genotypes.

Hemicellulose content

The environment, HS 20was found most favourable environment for high non-reducing sugar contentas indicated by environmental index, whereas BK 19 resulted in low non- reducing sugar content.

Two genotypes, HG 870, HG 100 and GG-1 recorded high mean value, significant regression coefficient equal to unity and non-significant deviation from regression was found suitable for all tested environment. RGC 1038 was found stable but poorly adapted as it showed low mean than the overall mean. Only one genotype, RGC 1017 recorded high mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for better environment. Likewise, only one genotype, HG 6 with high mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

AMMI biplot analysis identified HG 884, HG 870, FS 277, RGC 1017, RGC 1066 and HG 75 as stable genotypes with high hemicellulose content across the environments. So these genotypes performed constantly over the wide range of environments. Among the environments, BS 20 was found as stable and suitable for hemicellulose content.

Bacterial leaf blight intensity

The environment, BK 19was found most favourable environment for high bacterial leaf blight intensity incited by as (indicated by *Xanthomonas axonopodis pv cyamopsidis*) environmental index, whereas HS 19 resulted in low bacterial leaf blight intensity.

Out of 25 genotypes, 17 genotypes, HG 2-20, HG 884, HG 870, HG 563, , HG 3-52, HG 100, X-10, GG-2, RGC 1017, RGC 1038, RGC 1055, RGC 1002, RGC 1003, RGC 1066, RGS 3, RGC 1033 and HG 75 recorded low mean value than overall mean, significant regression coefficient equal to unity and non-significant deviation from regression were found suitable for all tested environments with less susceptibility against bacterial leaf blight while, HVG 2-30, FS 277 and PNB were found stable but, highly susceptible in all the environments. Only one genotype, RGC 936 recorded low mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression were found suitable for better environment. Likewise, only two genotypes, HG 6 and GG-1with low mean value than overall mean, significant regression coefficient less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment.

Using Eberhart and Russell's model, Kumar *et al.* (2017) suggested chickpea genotype, GCP 105 with general adaptability while, genotypes BG 372, Pant G 186, GCP 105 and DCP 92-3 specifically adapted to rich with least dry root rot and stunt disease in chickpea. Similarly, Mukherjee *et al.* (2013) reported 24 genotypes of rice showing stable resistance against rice blast disease and found suitable for poor environments. Rubiales *et al.* (2014) studied resistance of faba bean accessions against *O. crenata* and *O. foetida* and reported cultivar *Baraca* and accessions V-1268, V-1302, V-1301, V-268, V-231, V-319 and V-1272 with stable resistance across the environments.

AMMI analysis of G x E interaction revealed that bacterial leaf blight intensity in HG 870, HG 563, X-10, RGC 1055, RGC 1002 and RGS 3 were little influenced by environmental fluctuations. These were the less susceptible genotypes across the environments. Similarly, in environment BS 19 all the genotypes were found least susceptible against bacterial leaf blight.Persaud *et al.* (2018) using the AMMI model, reported consistent expression of high level of resistance by rice genotype FL 127, FG12–08 and FG12–273 against rice blast while, Onverwagt Back, autumn 2016 and Black Bush Polder, spring 2015 were observed to be the most representative environment in Guyana. Similarly, Mukherjee*et al.* (2013) reported a group of 28 genotypes showing consistent resistance against rice blast. Stable resistance was reported by Pariyo *et al.* (2015) in six cassava genotypes namely, against cassava brown streak disease using AMMI model. Tekalign *et al.* (2017) identified six genotypes with most stable resistance against Chocolate spot disease and Kulumsa site of Ethiopia for providing best discriminating ability for the genotypes in faba bean.

5.8 Molecular diversity analysis using SSR markers

Polymorphic Information Content (PIC) refers to the value of a marker for detecting polymorphism. PIC depends on the total allele numbers and their distribution frequency (Bostein *et al.*, 1980; Anderson *et al.*, 1993). The PIC value is very useful as it indicates the quality (discriminatory power) of the marker based on allelic frequency of alleles detected (Pandey *et al.*, 2012). The PIC value is often used to measure the informativeness of a genetic marker for linkage studies (Guo and Elston, 1999; Shete *et al.*, 2000) .Markers with PIC more than 0.5 are efficient in discriminating genotypes and extremely useful in detecting the polymorphism rate at a particular locus (DeWoody *et al.*, 1995). In the present study, 23 polymorphic SSR markers amplified a total of 49 bands. The number of alleles per locus ranged between 2 to 4, the average being alleles per locusand the majority of primers *i.e.*, 15 out of 23 amplified two bands. The maximum number of alleles was amplified by primer

CTN 08, CTN 09, CTN 37 and CTN 239 (4-alleles). Out of 23, polymorphic markers *viz*., GDR 2, GDR 4, GDR 9, GDR 10, CTN 08, CTN 09, CTN 37 and CTN 230 were the most informative whereas CTN 01 (PIC=0.074) and CTN 224 (PIC=0.211) were the least informative among the primers. In the present investigation, the number of alleles amplified per marker has no relationship with the PIC values.

Utility of microsatellite markers for assessment of genetic diversity among cultivars has been done in cluster bean. In the present investigation, dendrogram was constructed using ‘SIMQUAL’ sub-programme of NTSYS-pc (version 2.02) software (Numerical Taxonomy and Multivariate Analysis System Programme, Rohlf, 1997). The reliability of the dendrogram was assessed using online procedure, which was carried out with DendroUPGMA computer program. The dendrogram indicated the division of the 25 cluster bean genotypes into two major clusters at the similarity coefficient of 0.45. Similar variability was observed using RAPD markers in guar (Punia *et al.*, 2009; Pathak *et al.*, 2010; Sharma *et al.*, 2013 and Kumar *et al.*, 2015b). Number of genotypes in a study decides the extent of genetic variation available to plant breeders for crop improvement. Till now, in many studies have been carried out regarding genetic diversity in cluster bean includes only a few genotypes, such as, 18 (Punia *et al.*, 2009), 15 (Sharma *et al.*, 2013) In the present investigation, genotypes developed in different geographical regions are grouped together, indicating independence of genetic diversity from geographical diversity. Similarly, earlier reported that the clustering pattern of cluster bean genotypes was not related to geographical origins**.**Kumar *et al.* (2015a) also reported that PNB and HG-3-52 were found in same cluster, similar to present study. It is apparent from the grouping pattern that most of genotypes have been bred from same genetic material most probably through selection as most of them cluster in same group. Re-circulation of same genotype also is a reason of narrow genetic base of the released cultivars. The range of genetic distance based on SSR was on average lower than phenotypic data, which may reflect the influence of the environment on plant performance or limited diversity in studied genotypes. The result is in agreement with Pabal *et al.* (2013) who reported narrow genetic in cluster bean.

CHAPTER-V

SUMMARY AND CONCLUSION

The present investigation entitled- “Molecular diversity and stability analysis for seed yield and its components in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]” was carried out during the summer and *kharif* seasons in the year 2019 and 2020 at two locations Dry land research area, CCSHAU, Hisar and Regional research station, Bawal (Rewari). The experimental material consisted of 25 cluster bean genotypes grown under Randomized block design in three replications. Observations were recorded for ten qualitative and 26 quantitative characters. The data were subjected (1) to study the genotype x environment interaction patterns. (2) To study association of yield with its component traits in various environments. (3) To study molecular diversity in clusterbean genotypes using SSR markers.

In present study the morphological characterization of 25 genotypes was carried out for ten characters. Out of which two characters namely, position of first trifoliate leaf and first cluster was found in consistent within the replication in each environment. Most of the genotypes were found dwarf with dark green, pubescent leaf with serrated leaf margin. The flower in most of the genotypes was found pink while, pods were found pubescent in most of the cases. The square seed shape was found common in most of the genotypes. Great variability was observed for seed colour which consisted of five classes with light grey as most common seed colour. In general, genotypes responded differently for various traits under different seasons.

HG 6 was found shortest genotypes with early flowering and maturity in all the seasons. Pods on main stem and seeds per pod were found maximum in RGC 1066 while, pods per plant were found maximum in HG 2-20. Lowest pods per cluster were found in RGC 936 while, GG 2 was found with shortest pods. RGC 1038 was found highly branched while, HG 3-52 was found with boldest seed and highest gum content. Highest number of clusters per plant, biomass per plot and seed yield per plot found with HG 2-20. RGC 1055 was found with highest harvest index and protein content. Least TSS, reducing sugar and non-reducing sugar were found with HG 563. Maximum hemicellulose content was found in RGS 3. HG 75 showed highest ADF, lignin, cellulose, silica and NDF content and also recorded least BLB intensity across the environment. High coefficient of phenotypic and genotypic variation and high heritability along with high GAM were observed in plant height, pods on main stem, pods per plant, pods per cluster, seeds on pod and branches per plant indicating these characters could be improved through direct selection for high-yielding cluster bean breeding. Similarly, Moderate coefficient of phenotypic and genotypic variation and high heritability along with high GAM were observed in gum content, and BLB disease intensity. The selection for gum content while, selection against BLB intensity would result into high-yielding cluster bean varieties. Seed yield per plant was positively and significantly associated with pods on main stem, pods per plant, seed per pod, branches per plant, 100 seed weight, biomass per plot, harvest index, cluster per plant, indicating simultaneous selection based on these characters would be effective for seed yield. BLB intensity was positively and significantly correlated with protein content, total soluble sugar content, reducing sugar content, non-reducing sugar content whereas, negative and significant correlation was observed between BLB intensity and gum, ADF, lignin, cellulose, silica and NDF content. Clusters per plant, pods on main stem, pod length, branches per plant, biomass per plot, plant height, 100 seed weight and days to maturity towards seed yield while, ADF content, silica content and protein content towards BLB disease intensity would be selected as important ones for cluster bean improvement programme.

Stable genotypes identified on the basis of Eberhart and Russell's model (1966):

Genotypes *viz.* HG 884, HG 3-52, HG 100, X 10, GG 2, RGC 1017, RGC 1038, RGC 1055, RGC 1002 and RGS 3 were found suitable for all environments for plant height. HG 2-20, HG 870, HG 563, HG 3-52, X 10, GG 2, RGC 1017, RGC 1038, RGC 1003, RGC 1066 and RGC 1033 for all environments for days to 50% flowering. Genotypes, HG 100, RGC 1017 and RGC 1003 found suitable for poor environments for days to maturity. For pods per cluster, genotypes, HG 2-20, HG 884 and X-10 were found suitable for unfavourable environment. HG 870 and RGC 1055 were found suitable for rich environment while, genotypes, GG-2, RGC 1003 and RGC 1033 were found suitable for poor environment for pod length. For seeds per pod genotypes, HG 2-20, HG 884, HG 870, X-10, RGC 1033 and RGC 1038 were found suitable for all environments. Similarly, for 100 seed weight, genotype HG 563 while, for harvest index genotype, HG 884, HG 870, HG 3-52, HG 6, RGC 1017, RGC 1038 and, RGC 1066 were found suitable for all environments. For cluster per plant, HG 2-20, HG 884 and HG 563 was found suitable for all environments. Genotype, RGC 1066 was found suitable for all environments for seed yield per plot. For gum content, HG 2-20, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X-10, GG-1, RGC 1066, RGC 1033 were found suitable for all environments. RGC 1066 was found suitable for poor environment protein content. The genotypes RGC 1038 and HG 563 were found suitable genotypes for rich and poor environments, respectively for TSS content. HG 2-20 found suitable for better environment for reducing sugar content. For lignin content, HG 884, HG 365, HVG 2-30 and M-83 were found suitable for rich while, X-10 and RGS 3 were found suitable for poor environment. The genotype RGC 1017 was found suitable for rich while, HG 6 was found suitable for poor environment for hemicellulose content. For low BLB intensity genotypes HG 6 and GG-1 were found suitable for poor environment.

Among the environments, the environment, HS 19 was found to be most favourable production environment for most of the characters *viz.*, days to 50% flowering, pods on main stem, pods per plant, pods per cluster, seeds per pod, pod length, biomass per plant, clusters per plant, seed yield per plot, gum content, TSS content and non-reducing sugar content. Whereas, BK 19 was found to be the most unfavourable for days to maturity, pods on main stem, pods per plant, pods per cluster, seeds per pod, pod length, branches per plant, biomass per plant, clusters per plant, seed yield per plot, gum content, non-reducing sugar content and BLB intensity.

Stable genotypes identified on the basis of AMMI model (1997):

General adaptation:

Genotypes, HG 3-52, HG 884, RGC 1033, RGS 3, RGC 1017, RGC 1055, RGC 1002, GG-2, GG-1, RGC 1038, HG 870, HG 6, HG 563, RGC 936, HG 365 and HG 2-20 for plant height; HG 884, HG 870, HG 365, RGC 1033, RGC 1003, RGC 1066, GG-2, GG-1, HG 2-20, HG 563, RGC 1017, X-10, HG 100, RGS 3, RGC 1038, HG 3-52 and RGC 1055 for days to 50% flowering; RGC 1003, RGC 936, GG-2, RGC 1017, RGC 1002, HG 365, X-10, RGC 1066, RGC 1055, HG 100, RGC 1038, HG 3-52, HG 563, RGC 1033, HG 2-20, GG-1, HG 884, HG 870, RGS 3 and HG 6 for days to maturity; HG 2-20, HG 884, HG 870, HG 563, HG 365 and X-10 for pods on main stem; HG 100, HG 3-52 and RGS 3 for pods per plant; HG 2-20, HG 100, GG-1 and RGC 1002 for pod length; HG 2-20, HG 884, HG 870, HG 563, X 10 and RGC 1033 for seeds per pod; HG 870, HG 365, RGC 1002, RGC 1003 and RGC 1033 for branches per plant; HG 563 for 100 seed weight; HG 100, X-10, RGC 1038, RGC 1066, RGS 3 and RGC 1033 for biomass per plot, HG 2-20, HG 884, HG 870, HG 563, X-10, RGC 1017, RGC 1038, RGC 1066, RGS 3 and RGC 1033 for harvest index; HG 870, HG 3-52, HG 100, RGC 1038, RGS 3 and RGC 1033 for clusters per plant; HG 100, GG-2, RGC 936, RGC 1038, RGC 1066 and HG 870 for seed yield per plot; HG 870, HG 365, HG 100, X-10, GG-1, RGC 1066 and RGC 1033 for gum content; HG 2-20, HG 6, HVG 2-30, FS 277, PNB, GG-1, RGC 1038, RGC 1002, RGC 1003 and M-83 for protein content; HG 2-20, HG 884, HVG 2-30, RGS 3, FS 277, RGC 936 and PNB for TSS content; HG 3-52, RGC 1017 and RGC 1066 for reducing sugar content; HG 2-20, HG 884, HG 100 and GG-2 for non-reducing sugar content; HG 870, X 10, RGC 1017 and RGC 1003 for ADF content; HG 870, HG 2-20 and RGC 1033 for lignin content; HVG 2-30, FS 277, RGC 936 and HG 75 for cellulose content; RGC 1066, RGS 3 and RGC 1033 for silica content; HG 870, HG 100, X-10 and RGC 1003 for NDF content; HG 884, HG 870, FS 277, RGC 1017, RGC 1066 and HG 75 for hemicellulose content and HG 870, HG 563, X-10, RGC 1055, RGC 1002 and RGS 3 for BLB intensity, were found suitable for all the tested environments.

Specific adaptation:

For plant height, genotype RGC 1033 found suitable for BS 20; for days to 50% flowering, the best adapted genotypes for BS 20 was HG 6, for BK 20 was RGC 936, for BS 19 was RGS 3, for HK 19 and HK 20 was HG 75 and for BK 19 and HS 20 was M 83; in case of days to maturity, the best adapted genotypes for HS 19 was HG 6, for BS 19 was PNB, for HK 19 and HK 20 were HVG 2-30 and FS 277.For pods on main stem, for BK 20 was M 83, BS 19 and HK 19 was FS 277, for BK 19 and BK 20 were HG 75 and for HS 19 was RGC 1066; in case of pods per plant, the best adapted genotypes for HK 20 was GG 2, for BS 19 and BS 20 was HVG 2-30, for BK 19 and BK 20 were HG 884, M 83 and FS 277, for HS 19 was RGC 1017, for HK 19 were RGC 1038 and RGC 1066 and for HS 20 was X 10; the best adapted genotypes for BK 20 was HG 75, for HK 20 were HG 884 and GG 2, for BS 19 was RGC 1066, for HS 19 was FS 277 and for HS 20 were GG1 and M 83 for pod per cluster; the best adapted genotypes for HK 19 was RGC 1055, for HS 19 was RGC 1017, for HS 20was RGC 1066, for HK 20 was PNB and for BK 19 and BS 19 was M 83 pod length; in case of branches per plant, the best adapted genotypes for BS 20 was HG 563, for BK 20 was M 83, for HS 20 was RGC 1003, for HK 19 was HG 365 and for HK 20 was GG 1; for 100 seed weight, for BS 19 was HG 3-52 and RGC 1038, for BS 20 and HK 19 was RGS 3, for BK 19 were GG 2, RGC 1002, RGC 1003, and M 83, for HK 20 were HG 75, for HS 19 was HG 2-20; and for BK 20 was HG 870; in case of biological yield per plot, the best adapted genotypes for BK 20 was HVG 2-30 and for BS 20 were HG 100 and RGC 1033; the best adapted genotypes for harvest index for BS 19 was RGC 1003, for BK 19 and BK 20 were RGS 3 and RGC 1033 and for BS 20 and HS 20 was GG 2; for cluster per plant the best adapted genotypes for BK 20 were HVG 2-30 and M 83, for BS 19 was HG 6, for BK 19 and HK 20 was HG 75, for HK 19 were HG 2-20 and HG 563, for HS 19was RGC 1017 and for BS 19 was HG 870; for seed yield per plot, the best adapted genotypes for HK 19 and BS 19 was GG 2, for HK 20 were RGS 3 and RGC 1033and for BS 20 and BK 20 was HG 100; in case of gum content, the best adapted genotypes for HS 20 were HG 75 and GG 1, for BS 20was RGC 1017and for HG 20 was HG 3-52; for protein content, the best adapted genotypes for BK 19 and BK 19 were HG 6, RGC 1055 and RGC 1066 and for BS 20 were HG 563 and HG 3-52; the best adapted genotypes for BS 20 was HG 75, for BK 19 was RGC 1017, for BS 19 was HVG 2-30, for BK 20 was RGC 1003, for HK 20 were RGC 1038 and RGC 1055 and for HK 19 was PNB for TSS content; for reducing sugar content, the best adapted genotype for HS 19 was RGC 1066, for BK 20 was HG 3-52, for BS 19 were HG 884 and RGC 1017 and for BS 20 were HG 100 and HG 75; for non-reducing sugar content, the best adapted genotypes for BS 19 was HG 884, for BK 19 were HVG 2-30 and RGC 1017, for BS 20 were HG 870, RGC 1002 and HG 75 for HK 19 were PNB and RGC 936and for BK 20 was RGC 1003; the best adapted genotypes for HK 20 was GG 2, for BK 19 were HG 2-20 and HG

870, for BS 20 was HG 100, for HK 19 was HG 365, for HS 19 were HVG 2-30 and PNBand for BK 20were RGS 3 and M 83 for ADF content; in case of lignin content, the best adapted genotypes for HS 20 was RGC 936, for BS 19 was RGC 1055, for BK 19 was HG 3-52, for BK 20 was HG 884 and for BS 20was PNB; in case of cellulose content, the best adapted genotypes for HK 20 was RGC 936, for BK 19 was HG 365, for BS 19 was RGC 1003 and for HK 19 were HG 6 and PNB; the best adapted genotypes for BK 20 was FS 277, for HS 19 was HG 870, for HK 20 was RGC 936, for HS 20 was RGC 1002, for BS 19 was RGS 3, for HK 19 was GG 1 and for BS 20 was HG 100 for silica content; the best genotypes for BK 20 was HG 100, for HS 19was HG 3-52, for HK 19 was HG 884, for HK 20was FS 277, for BK 19 was RGC 1003, for BS 20 was HG 2-20 and for BS 19 was RGC 1038 for NDF content; the best adapted genotypes for BK 19 was RGC 1002, for BS 20, BK 20, HS 19 and HS 20 were HG 884 and GG 1 and for BS 19 was X 10 for hemicellulose content and the best adapted genotypes for BS 20 was RGC 936, for HK 19 was HVG 2-30, for BK 20 was RGC 1017, for BS 19 was X 10, for HS 20 were HG 365 and GG 1 and for HS 19 was HG 6 for BLB intensity.

Markers used in the present investigation were moderately informative as the mean PIC value was less than 0.5 (0.41/marker). The highest genetic similarity value was found between genotypes RGC1038 & RGC 1002 (0.8529) followed by HG 6 and HG 870 (0.7526) and HG6 and HVG 2-30 (0.7500). This finding can be confirmed from the fact that HVG 2-30 served as a parent in the pedigree of HG 6. The lowest genetic similarity was found between genotype HG 884 and HG 2-20 (0.2895) followed by HG 884 and FS 277 (0.3077) and GG 2 and FS 277 (0.3256). Therefore, hybridization among these genotypes can manifest heterosis and superior transgressive segregants. Most of the important cultivated varieties such as HG870, RGC1038, X10, HG100, HG563, RGS3, RGC1055, RGC1066 and RGC 1033 grouped together in Cluster II. These results indicated that important cultivars in cluster bean have a high level of genetic similarity and have a narrow genetic base. In the present investigation, genotypes developed in different geographical regions are grouped together, indicating independence of genetic diversity from geographical diversity.

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Annexure I

Weekly weather data at CCS HAU Hisar centre (2019)

Standard Week	Dates	Temperature		Relative Humidity		Average Wind Speed	Bright Sunshine	Rainfall
		Maximum	Minimum	(%)	(%)			
		°C	°C	M	E	Km/Hour	Hour	(mm)
1	January 1-7	18.90	5.70	95	66	3.40	3.30	7.30
2	January 8-14	19.30	5.60	93	60	2.40	4.40	0.00
3	January 15-21	20.40	4.90	90	55	2.30	5.00	0.00
4	January 22-28	18.20	4.80	99	63	3.10	4.60	6.50
5	Jan 29-Feb 4	17.10	5.30	96	65	3.60	3.90	0.00
6	February 5-12	21.00	6.90	92	56	3.90	5.70	0.00
7	February 13-18	20.00	9.70	94	67	4.00	3.10	0.00
8	February 19-25	22.20	9.00	89	50	5.10	5.60	0.00
9	Feb 26-Mar 4	18.30	7.00	81	47	4.40	5.10	14.80
10	March 5-11	24.20	8.50	88	38	3.80	8.20	0.00
11	March 12-18	24.90	9.10	91	48	3.70	6.10	0.00
12	March 19-25	28.90	11.80	80	42	4.20	7.20	0.00
13	Mar 26-Apr 01	32.60	13.50	81	28	3.20	7.30	0.00
14	April 2-8	36.00	16.00	74	28	3.80	8.00	7.30
15	April 9-15	36.90	20.00	69	27	5.60	7.00	0.00
16	April 16-22	32.90	17.20	81	37	5.20	7.20	8.20
17	April 23-29	40.70	20.60	56	19	5.30	8.50	0.00
18	April 30-May 6	40.10	20.80	48	23	6.00	9.30	0.00
19	May 7-13	40.50	21.70	48	20	5.50	7.90	0.00
20	May 14-20	35.70	20.50	82	37	6.00	8.30	59.80
21	May 21-27	38.00	22.70	61	26	4.70	8.90	0.00
22	May 28-Jun 03	43.80	25.20	53	18	4.60	9.90	0.00
23	June 4-10	43.50	25.80	55	17	5.60	8.80	0.00
24	June11-17	41.80	26.00	67	36	7.40	8.30	55.10
25	June 18-24	35.70	24.60	78	43	6.70	8.20	20.30
26	June 25-July 01	39.10	25.50	77	44	5.50	7.60	29.70
27	July 02-08	38.60	26.20	74	56	6.50	6.50	1.80
28	July 09-15	37.20	27.30	73	57	9.90	0.70	13.40
29	July 16-22	32.50	23.70	93	70	6.20	4.50	81.50
30	July 23-29	33.20	25.30	88	73	6.40	3.80	23.70
31	July 30-Aug 5	33.80	25.10	87	67	5.60	5.30	17.70
32	August 06-12	34.60	27.00	87	68	7.20	6.30	63.00
33	August 13-19	33.30	25.50	89	70	5.70	4.50	15.40
34	August 20-26	35.60	25.80	86	56	4.70	8.20	0.00
35	August 27-02	36.20	27.40	84	55	5.20	6.90	0.00
36	September 03-09	35.70	27.00	89	59	4.10	6.20	27.70
37	September 10-16	37.00	27.10	88	51	5.10	6.60	0.00
38	September 17-23	35.10	25.20	84	49	6.80	6.70	0.00
39	September 24-30	33.40	24.30	84	58	6.90	7.20	2.20
40	October 01-07	31.80	21.00	92	50	4.10	5.50	2.60
41	October 08-14	32.70	17.60	90	39	2.90	7.50	0.00
42	October 15-21	34.10	18.40	79	34	4.50	7.30	0.00
43	October 22-28	31.90	14.90	79	31	2.10	6.50	0.00
44	Oct 29-Nov 04	30.70	16.20	90	40	1.30	1.80	0.00
45	November 05-11	28.40	12.70	85	36	4.10	6.60	0.30
46	November12-18	26.80	12.70	86	41	3.10	2.50	0.00
47	November 19-25	26.70	10.90	88	42	2.50	4.70	0.00
48	Nov 26-02 Dec	22.60	12.10	92	62	3.50	2.80	12.00
49	December 03-09	23.10	6.00	88	47	1.50	6.20	0.00
50	December 10-16	19.20	8.30	95	74	3.80	2.20	4.50
51	December 17-23	13.70	6.10	99	81	3.20	1.10	0.00
52	December 24-31	12.30	2.40	98	79	2.40	2.00	0.00

Weekly weather data at RRS Bawal centre (2019)

Standard Week	Dates	Temperature		Relative Humidity		Average Wind Speed	Bright Sunshine	Rainfall
		Maximum	Minimum	(%)	(%)			
		°C	°C	M	E	Km/Hour	Hour	(mm)
1	January 1-7	19.60	5.00	91	52	2.80	4.00	1.50
2	January 8-14	19.70	5.20	92	38	3.30	5.30	-
3	January 15-21	21.20	4.80	90	41	2.10	5.00	-
4	January 22-28	16.60	7.50	93	59	3.80	5.10	11.00
5	Jan 29-Feb 4	18.40	5.60	89	52	3.00	4.40	-
6	February 5-12	20.40	7.20	94	52	3.20	5.30	10.60
7	February 13-18	20.80	9.50	94	58	3.70	4.30	1.70
8	February 19-25	23.10	10.50	88	49	3.50	5.40	0.70
9	Feb 26-Mar 4	20.20	8.80	88	55	3.10	4.20	1.00
10	March 5-11	25.70	9.00	83	29	3.40	7.60	0.40
11	March 12-18	25.20	9.90	87	33	3.10	5.50	-
12	March 19-25	31.40	12.80	78	21	4.00	7.60	-
13	Mar 26-Apr 01	34.90	15.60	74	19	3.60	8.00	-
14	April 2-8	37.80	17.00	65	15	3.00	6.90	6.40
15	April 9-15	37.50	20.50	62	19	4.10	6.80	-
16	April 16-22	32.60	14.40	70	29	3.70	6.80	6.00
17	April 23-29	41.60	16.00	43	9	4.70	8.90	10.70
18	April 30-May 6	40.10	17.70	40	10	5.00	8.70	10.30
19	May 7-13	40.60	19.50	31	13	7.10	7.00	.
20	May 14-20	36.70	21.70	59	25	5.40	8.30	18.00
21	May 21-27	40.00	25.40	58	20	4.70	8.00	4.60
22	May 28-Jun 03	45.00	29.90	38	12	6.40	9.00	-
23	June 4-10	44.70	29.70	49	21	5.00	8.50	-
24	June11-17	39.00	29.40	57	37	8.80	6.70	27.30
25	June 18-24	37.40	26.10	71	37	4.90	7.40	-
26	June 25-July 01	36.60	29.20	61	32	6.60	6.10	39.90
27	July 02-08	37.10	28.90	72	48	5.50	4.70	1.80
28	July 09-15	37.10	28.50	63	43	8.10	3.10	1.70
29	July 16-22	33.00	25.20	88	64	3.00	4.80	88.80
30	July 23-29	33.80	26.80	90	60	4.40	4.10	56.60
31	July 30-Aug 5	33.30	27.20	92	66	2.60	4.10	7.30
32	August 06-12	33.70	26.00	91	66	5.50	4.80	10.20
33	August 13-19	31.80	25.20	92	75	5.50	4.90	92.60
34	August 20-26	34.60	25.10	84	53	4.00	6.50	6.00
35	August 27-02	35.60	26.10	89	57	2.40	6.10	0.70
36	September 03-09	34.80	26.10	95	63	1.10	4.70	141.90
37	September 10-16	36.20	25.30	91	52	1.80	6.20	1.70
38	September 17-23	33.60	23.40	78	57	3.50	4.90	12.40
39	September 24-30	27.20	23.00	94	58	2.70	4.60	-
40	October 01-07	32.60	20.50	92	47	2.90	6.00	7.80
41	October 08-14	33.60	18.80	81	34	1.60	7.40	-
42	October 15-21	34.10	18.70	84	32	1.80	7.40	1.40
43	October 22-28	32.20	16.40	81	32	1.80	7.00	-
44	Oct 29-Nov 04	30.80	18.00	83	40	2.20	2.50	-
45	November 05-11	28.10	14.80	87	41	2.50	5.20	5.00
46	November12-18	28.00	13.10	89	36	3.30	4.00	-
47	November 19-25	26.80	12.50	89	40	1.40	4.40	-
48	Nov 26-02 Dec	24.00	12.00	84	50	3.00	3.10	-
49	December 03-09	23.20	7.50	90	42	1.60	5.00	-
50	December 10-16	18.50	8.20	93	68	3.70	2.00	13.90
51	December 17-23	14.60	5.70	94	73	2.40	2.70	-
52	December 24-31	12.80	3.20	100	87	2.40	2.70	-

Weekly weather data at CCS HAU Hisar centre (2020)

Standard Week	Dates	Temperature		Relative Humidity		Average Wind Speed	Bright Sunshine	Rainfall
		Maximum	Minimum	(%)	(%)			
		°C	°C	M	E	Km/Hour	Hour	(mm)
1	January 1-7	17.30	5.70	96	60	3.10	3.50	0.00
2	January 8-14	17.70	5.70	96	64	3.30	3.30	3.20
3	January 15-21	13.40	4.70	100	82	2.80	2.10	0.00
4	January 22-28	19.20	5.00	97	56	3.90	5.90	7.20
5	Jan 29-Feb 4	18.80	3.90	98	61	3.40	6.30	0.00
6	February 5-12	20.10	2.80	93	46	2.60	7.20	0.00
7	February 13-18	24.70	4.80	93	37	3.60	8.70	0.00
8	February 19-25	23.80	10.50	89	61	6.40	6.40	10.90
9	Feb 26-Mar 4	26.00	12.10	95	55	5.90	6.70	0.20
10	March 5-11	23.10	11.70	90	66	6.10	5.70	61.80
11	March 12-18	23.80	9.80	94	53	4.00	6.50	11.60
12	March 19-25	29.20	14.40	90	52	4.10	6.30	1.50
13	Mar 26-Apr 01	27.60	15.00	92	55	4.40	5.20	20.60
14	April 2-8	31.00	13.40	80	37	3.80	7.90	0.00
15	April 9-15	35.10	17.70	73	24	3.20	7.40	0.00
16	April 16-22	36.10	18.80	71	25	5.30	8.10	0.80
17	April 23-29	34.50	20.20	72	41	5.70	7.60	4.00
18	April 30-May 6	37.50	22.30	70	32	7.00	9.10	18.20
19	May 7-13	37.70	23.10	65	28	7.00	8.40	1.10
20	May 14-20	38.60	20.80	58	20	4.20	9.20	6.60
21	May 21-27	43.20	23.20	47	16	5.10	10.00	0.00
22	May 28-Jun 03	37.00	22.90	74	47	9.60	7.70	13.70
23	June 4-10	36.60	24.60	72	41	5.90	7.60	2.20
24	June11-17	41.50	27.30	66	32	5.50	9.00	0.00
25	June 18-24	39.70	27.00	73	40	7.60	7.90	29.20
26	June 25-July 01	37.40	28.30	74	54	8.10	6.50	14.00
27	July 02-08	38.70	27.90	80	55	8.40	8.70	8.70
28	July 09-15	36.00	26.50	89	64	6.70	8.00	38.40
29	July 16-22	34.60	25.90	92	75	8.70	5.70	111.10
30	July 23-29	34.50	26.80	87	60	4.80	7.30	14.70
31	July 30-Aug 5	36.40	27.00	84	66	5.90	6.60	0.00
32	August 06-12	35.30	27.50	88	62	6.90	6.60	32.80
33	August 13-19	35.30	26.90	90	77	6.50	6.70	17.50
34	August 20-26	32.60	25.40	91	76	7.70	6.40	11.70
35	August 27-02	33.90	25.60	90	64	7.50	6.80	0.00
36	September 03-09	34.20	25.10	94	67	3.40	5.10	32.50
37	September 10-16	36.30	24.90	88	49	3.00	8.30	0.00
38	September 17-23	37.60	24.70	87	48	3.90	7.60	7.00
39	September 24-30	36.90	22.30	85	39	4.10	7.40	0.00
40	October 01-07	36.60	18.20	79	29	3.40	8.20	0.00
41	October 08-14	35.60	16.30	86	28	2.90	7.90	0.00
42	October 15-21	34.20	13.70	76	22	2.60	7.10	0.00
43	October 22-28	33.00	12.80	80	26	2.80	6.50	0.00
44	Oct 29-Nov 04	30.40	9.80	85	24	2.20	5.60	0.00
45	November 05-11	29.70	10.50	91	33	1.10	3.20	0.00
46	November12-18	25.60	12.60	89	50	3.60	2.70	18.20
47	November 19-25	23.10	7.70	88	43	1.90	6.50	0.00
48	Nov 26-02 Dec	23.30	8.40	92	42	2.90	6.60	1.70
49	December 03-09	25.50	9.10	90	53	2.70	5.90	0.00
50	December 10-16	20.80	5.00	96	63	3.40	5.30	0.00
51	December 17-23	19.70	3.00	92	42	2.20	6.20	0.00
52	December 24-31	19.50	2.60	96	51	2.60	5.80	0.00

Weekly weather data at RRS Bawal centre (2020)

Standard Week	Dates	Temperature		Relative Humidity		Average Wind Speed	Bright Sunshine	Rainfall
		Maximum	Minimum	(%)	(%)			
		°C	°C	M	E	Km/Hour	Hour	(mm)
1	January 1-7	19.60	5.70	94	64	1.80	4.00	-
2	January 8-14	18.20	5.10	91	55	3.60	4.80	-
3	January 15-21	16.10	5.90	95	69	3.10	2.60	5.60
4	January 22-28	20.90	6.20	88	41	3.60	6.20	1.40
5	Jan 29-Feb 4	20.00	3.40	94	42	2.20	7.60	10.00
6	February 5-12	20.90	4.30	92	39	2.00	7.50	-
7	February 13-18	25.90	8.10	79	25	4.20	8.70	-
8	February 19-25	24.10	10.20	93	54	3.40	4.80	1.40
9	Feb 26-Mar 4	27.30	12.90	94	52	3.50	5.90	27.80
10	March 5-11	23.50	10.10	92	53	4.70	5.70	28.80
11	March 12-18	25.80	9.40	86	37	3.80	6.90	2.80
12	March 19-25	31.60	14.00	84	32	3.10	5.90	-
13	Mar 26-Apr 01	29.40	14.20	86	38	5.10	6.10	9.40
14	April 2-8	33.30	13.50	76	22	4.30	8.50	4.20
15	April 9-15	36.80	17.20	63	26	4.00	7.70	0.70
16	April 16-22	36.70	20.90	59	36	5.20	7.00	0.70
17	April 23-29	35.80	19.40	66	48	5.50	6.40	14.10
18	April 30-May 6	37.70	22.00	72	42	5.40	8.30	4.90
19	May 7-13	29.00	26.60	65	37	4.60	7.60	1.70
20	May 14-20	40.10	21.20	50	19	5.20	8.40	1.00
21	May 21-27	44.00	24.00	29	8	7.00	9.60	-
22	May 28-Jun 03	37.40	22.20	66	36	8.00	7.70	69.10
23	June 4-10	36.90	22.40	76	43	4.10	6.40	14.80
24	June11-17	40.80	26.30	64	32	4.50	7.40	2.00
25	June 18-24	39.40	25.60	71	39	5.10	7.00	43.10
26	June 25-July 01	38.30	26.40	67	49	6.50	5.10	1.00
27	July 02-08	38.30	22.00	77	45	5.50	7.00	6.40
28	July 09-15	36.20	25.10	81	64	5.20	6.00	12.10
29	July 16-22	35.80	25.50	83	62.1	5.60	3.90	19.50
30	July 23-29	35.10	24.90	86	60	4.70	6.70	14.60
31	July 30-Aug 5	35.70	25.10	86	64	5.00	5.50	37.50
32	August 06-12	35.00	25.90	89	66	5.60	5.20	9.10
33	August 13-19	33.50	25.40	94	80	4.20	4.20	51.20
34	August 20-26	30.80	23.70	94	82	6.30	3.60	44.30
35	August 27-02	32.80	24.20	90	66	5.10	5.00	32.40
36	September 03-09	34.70	23.80	90	65	3.30	4.80	11.30
37	September 10-16	37.10	23.60	87	41	2.60	7.60	-
38	September 17-23	38.10	24.40	69	38	4.10	6.90	-
39	September 24-30	36.80	22.20	69	34	3.90	7.30	9.20
40	October 01-07	37.60	17.60	66	17	4.50	8.20	-
41	October 08-14	36.40	15.8	68	19	2.90	9.10	-
42	October 15-21	35.30	15.8	74	17	2.40	7.50	-
43	October 22-28	34.30	13.00	70	14	2.20	7.20	-
44	Oct 29-Nov 04	31.00	9.50	66	12	2.90	7.50	-
45	November 05-11	30.60	9.00	76	17	2.00	3.20	-
46	November12-18	27.00	10.20	87	43	2.10	4.40	1.40
47	November 19-25	24.60	7.30	86	87	2.60	6.60	-
48	Nov 26-02 Dec	25.10	9.10	82	28	2.90	6.10	-
49	December 03-09	28.20	8.90	87	31	1.70	6.60	-
50	December 10-16	19.30	9.90	90	53	3.00	4.30	-
51	December 17-23	20.30	3.90	73	31	3.70	6.60	-
52	December 24-31	19.40	2.60	92	38	2.60	6.00	-

ABSTRACT

Title of Thesis	**Molecular diversity and stability analysis for seed yield and its components in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]**
Full Name of the Degree Holder	**Ravish Panchta**
Admission Number	2017A31D
Title of the Degree	**Doctor of Philosophy**
Name of Discipline	Genetics and Plant Breeding
Name and Address of Major Advisor	**Dr. S.K. Pahuja** Dean, College of Agriculture, CCSHAU,Hisar-125004
Degree Awarding University	CCS Haryana Agricultural University Hisar-125004 (Haryana),India
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Keywords: AMMI, GxE interaction, stability, molecular diversity, cluster bean

Molecular diversity analysis was carried out to identify adaptable and stable genotypes of cluster bean for non-conventional season. A set of 25 cluster bean genotypes comprising released varieties and elite lines was evaluated under eight environments containing two locations Dry land research area Hisar and RRS Bawal. The experiment was conducted during summer and *kharif* seasons of years 2019 and 2020 in RBD with three replications. The sowing of summer crop was done during first week of March and *kharif* crop was sown between second fortnights of June to first week of July. In general, genotypes responded differently for various traits under different production systems. Morphological characterization of the genotypes was done based on eight qualitative characters. HG 6 was found shortest, early flowering and early maturing genotype. Seed yield per plot, number of cluster per plant and biological yield of HG 2-20 was found highest. Highest gum content was found in HG 3-52 while, HG75 was found least susceptible against bacterial leaf blight intensity. Clusters per plant, pods on main stem, pod length, branches per plant, biomass per plot, plant height, 100 seed weight and days to maturity towards seed yield while, ADF content, silica content and protein content towards BLB disease intensity were found to be important characters for cluster bean improvement.

The G X E interaction was analyzed following two models i) Eberhart and Russell's (1966) and ii) AMMI (1997). The mean sum of squares due to genotype x environment interaction were significant for number of pods per plant, number of pods per cluster, pod length, number of branches per plant, harvest index, total clusters, protein content and seed yield per plot. Genotypes, RGC 1066 for seed yield per plot whereas, for gum content, HG 2-20, HG 870, HG 563, HG 365, HG 3-52, HG 6, HG 100, X-10, GG-1, RGC 1066, RGC 1033 were found suitable for all environments. Similarly, for low BLB intensity 17 genotypes were found suitable for all environments. According to AMMI biplot analysis, HG 100, RGC 1038, RGC 1066 and HG 870 for seed yield per plot; HG 870, HG 365, HG 100, X-10, GG-1, RGC 1066 and RGC 1033 for gum content and HG 870, HG 563, X-10, RGC 1055, RGC 1002 and RGS 3 were found stable with low BLB intensity were found suitable for general adaptation to all the environments. Markers used in the present investigation were moderately informative. Most of the important cultivated varieties were grouped into a cluster indicating important cultivars in cluster bean have a high level of genetic similarity and have a narrow genetic base.

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- Abstracts:3
- Populararticle:3

Signature of student

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