

**GENETIC DIVERSITY IN RELATION TO SEASONAL
ADAPTABILITY IN GROUNDNUT
(*Arachis hypogaea* L.)**

THESIS

**Submitted to the
Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola
in partial fulfilment of the requirements
for the Degree of**

**DOCTOR OF PHILOSOPHY
IN
AGRICULTURE
(AGRICULTURAL BOTANY)
(Genetics & Plant Breeding)**

**BY
DESHMUKH SUBHASH NARAYANRAO**

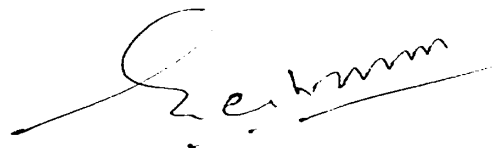
**UNIVERSITY DEPARTMENT OF AGRICULTURAL BOTANY,
POST GRADUATE INSTITUTE,
Dr. PANJABRAO DESHMUKH KRISHI VIDYAPEETH,
AKOLA (M.S.) INDIA**

DECLARATION OF STUDENT

I, hereby, declare that the experimental work and its interpretation of the thesis entitled “**Genetic diversity in relation to seasonal adaptability in groundnut (*Arachis hypogaea* L.)**” or part thereof has not been submitted for any other degree or diploma of any University, nor the data have been derived from any thesis/publication of any University or Scientific Organization. The sources of material used and all assistance received during the course of investigation have been duly acknowledged.

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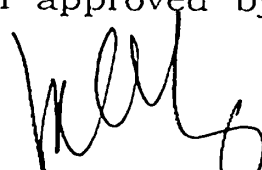


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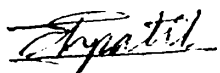
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This is to certify that the dissertation entitled, "**Genetic diversity in relation to seasonal adaptability in groundnut (*Arachis hypogaea* L.)**" submitted in partial fulfilment of the requirements for the degree of "**DOCTOR OF PHILOSOPHY**" in Agriculture (Agriculture Botany/Genetics and Plant Breeding) of Dr.Panjabrao Deshmukh Krishi Vidyapeeth, Akola is a record of bonafide research work carried out by **Shri Subhash Narayanrao Deshmukh** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee.

Place: Akola
Date : 7/6/2004


(Dr.V.K.Mohod)
Chairman
Advisory Committee

COUNTERSIGNED



Associate Dean,
Post Graduate Institute
Dr.Panjabrao Deshmukh Krishi Vidyapeeth, Akola

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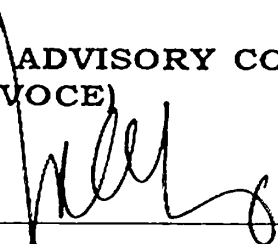
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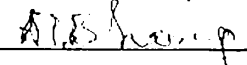
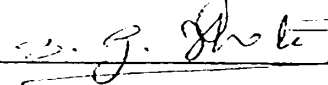
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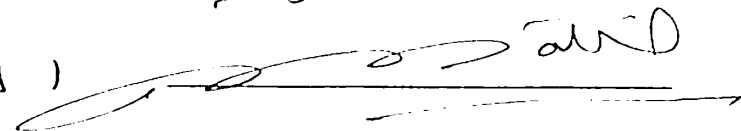
Member (Prof.A.T.Bhongle)

Member (Prof.S.G.Thote)

External member (Dr. J. V. Patil)





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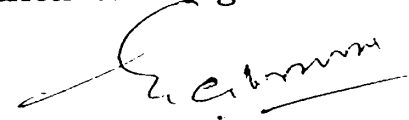
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(S.N.Deshmukh)

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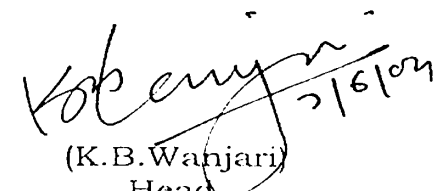
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LIST OF ABBREVIATIONS AND ACRONYMS USED

DM	:	Days to maturity
F	:	Days to 50 per cent flowering
H	:	Height of main axis
HKW	:	Hundred kernel weight
HPS	:	Hand picked selected
HPW	:	Hundred pod weight
KY	:	Kernel yield per plant
O	:	Oil content
P	:	Primary branches per plant
PO	:	Number of pods per plant
PY	:	Pod yield per plant
S	:	Secondary branches per plant
SH	:	Shelling per cent
SMK	:	Sound mature kernel per cent

THESIS ABSTRACT

- a) Title of the thesis : **Genetic diversity in relation to seasonal adaptability in groundnut (*Arachis hypogaea* L.)**
- b) Full name of the student : Subhash Narayanrao Deshmukh
- c) Name and address of major advisor : Dr.Vandan Mohod,
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- i) Signature of the student : 
- j) Signature, Name and address of forwarding authority : 
(K.B. Wanjari)
Head,
Univ. Dept. of Agril. Botany,
Dr.Panjabrao Deshmukh Krishi
Vidyapeeth, Akola

ABSTRACT

The experimental material comprised of 50 genotypes of Spanish bunch habit group of groundnut (24 varieties and 26 germplasm lines) was grown over 2 successive seasons i.e. *Kharif* 2002 and summer 2003 and 2 dates of sowings i.e. recommended date and 10-20 days early in each season with an objectives to estimate genetic divergence for grouping, to estimate $g \times e$ interaction and stability parameters of some of the

components of yield for adaptability and to identify the superior genotypes on the basis of genetic diversity and phenotypic stability for their use in future groundnut breeding programme. The data were recorded for 13 agronomic characters.

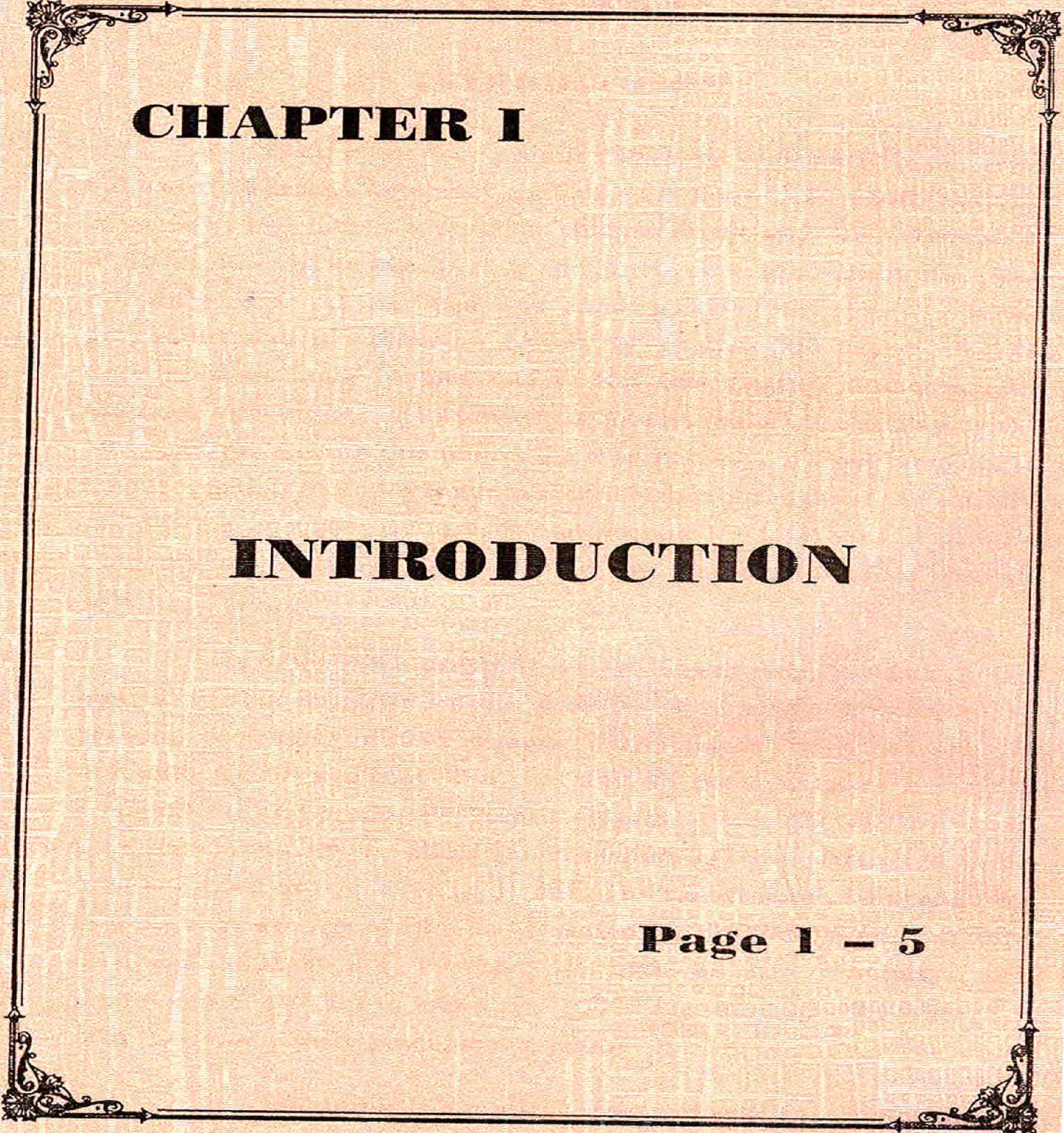
Differences between genotypes and environments were highly significant for all characters. Analysis of dispersion showed highly significant differences for aggregate effect of all characters under separate as well as pooled environments. D^2 analysis was carried out separately for each date, pooled over dates of each season and pooled over seasons. Fifty genotypes were grouped into 7-10 clusters in individual as well as pooled over environments D^2 analysis. Hundred pod weight, shelling percentage and sound mature kernel per cent contributed maximum toward genetic divergence. The canonical analysis showed good agreement with the D^2 analysis. Grouping on the basis of pooled over environments appeared to be more useful. Five varieties, viz., J 11, Jyoti, MH 1, SB XI and TMV 2 and five germplasm lines viz., NC Ac 7790, PI 268782, PI 268829, Pearl and U 1-1-1 consistently occupied the same cluster in separate ~~Kharif, summer~~ and pooled over environments, i.e. E_1 , E_2 , E_3 , E_4 , E_1+E_2 , E_3+E_4 and $E_1+E_2+E_3+E_4$ indicating seasonal adaptability.

Genotype x environment interactions were significant for seven component characters of yield viz., days to 50 per cent flowering, height of main axis, primary and secondary branches per plant, mature pods per plant, shelling per cent and days to maturity. The linear components of $g \times e$ were significant for these seven characters only suggesting genotypes differed from each other in respect of their linear response for these characters. The pooled deviation (non-linear) were non significant for all characters indicating the large part of $g \times e$ interactions were accounted by linear components and thus, predictable.

Stability analysis made it possible to identify the genotypes having average stability, above average stability and below average stability. However, general adaptability or average stability is more important. In present investigation five germplasm lines viz., Ah 1, NC Ac 7785, NC Ac

7790, Span cross and U 2-4-5 (earliness) were having average stability for days to 50 per cent flowering. Six released varieties viz., GG 2, Girnar 1, J 11, TKG 19A, TG 17 (dwarfness) and ALR 3 (tallness) and four germplasm lines viz., NC Ac 7782, NC Ac 7790, PI 268642 and pearl (dwarfness) showed average stability for height of main axis. Released varieties viz., Pol. 2 and Girnar 1 were found to be generally adaptable for primary and secondary branches per plant respectively. Three germplasm lines viz., Teja Amra Local, U 2-4-5 and U 2-12-1 showed average stability for mature pods per plant. Five varieties, viz., GG 2, Jyoti, MH 1, SB XI and TMV 2 and eight germplasm lines viz., Ah 4515, Ah 6649, NC Ac 7782, PI 268782, PI 268829, PI 268642, Starr and U 2-12-1 were found to be generally adaptable for shelling per cent. Four varieties viz., J 11, Jyoti, MH 1 and SB XI (earliness) were having average stability for days to maturity.

On the basis of inter cluster distance and phenotypic stability, 13 cross combinations for *Kharif* and four for summer have been suggested. In addition remaining eight cross combinations from pooled analysis over seasons should also be attempted for wider adaptability i.e. Span cross x Ah 1, TKG 19 A x Span cross, Starr x Ah 1, NC Ac 7782 x U 2-12-1, TKG 19 A x U 2-12-1, NC Ac 7782 x Span cross, TKG 19 A x Ah 1 and TKG 19 A x Starr. Four cross combinations viz., U 2-4-5, GG 2, Girnar 1 and U 2-12-1 x Ah 1 have been particularly selected to isolate useful transgrates for *Kharif* and summer adaptations.



CHAPTER I

INTRODUCTION

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CHAPTER I

INTRODUCTION

Groundnut or peanut (*Arachis hypogaea* Linn.) was cultivated in South American continent for more than 1500 years by indigenous Red Indian population. Subsequently, with the colonization of South America by the Spanish and Portuguese, groundnut plant was introduced into Africa, Asia and some parts of Europe. In India, groundnut has a cultivation history of around 200 years. It was introduced in India in first half of the 16th Century and gradually assumed agricultural importance and became major oilseed crop by the 19th century. During this period the crop has spread from the place of its introduction in South India to newer niches throughout the country and by the late 20th century, it had occupied a total area of around eight million hectares, largely comprising the semi-arid belt (Prasad, 1993).

Now, in the gamut of annual oilseed crops grown in India, groundnut has occupied a prime position. It is grown in *kharif* (rainy season), *rabi*/summer and summer seasons (post rainy season). It accounts for 35 per cent (7 m ha) and 45 per cent (8 m t) of total cropped area and production respectively under oilseeds with average of 11 q ha⁻¹ productivity. Maharashtra's share is 6 per cent (0.43 m ha area and 0.49 m t production) in both groundnut area and production in India with average of 12 q ha⁻¹ productivity. In Vidarbha, groundnut occupies 18800 ha area in *kharif* and 9800 ha area in summer with production of 13700 t in *kharif* and 10500 t in summer with average of 10 q ha⁻¹ productivity (Anonymous, 2003).

Groundnut is a primary source of vegetable oil which is of high quality preferred by the consumers in many parts of the country and contributes nearly 40 per cent of the vegetable oils in India. Thus, edible oil economy in India would be related to quantum of groundnut production. Although the genetic potential of 35-40 q/ha has been

demonstrated, the unit area production on national basis has remained stagnated at 9-10 q/ha for several years as against 25 q/ha average production of China.

Now a days groundnut is considered to be the high energy food crop globally. Thus, it is used as dual purpose crop for extraction of both edible oil as well as kernels which are directly used for consumption. As a result, demand for groundnut kernel for table purpose has increased in domestic as well as in foreign market. Export is touching new heights, particularly of HPS kernels. India is exporting merely 1.5 lakh t of groundnut kernels as against 10 lakh t of international demand as per WTO.

The botanical name of groundnut is derived from two Greek words *Arachis* and *hypogaea*. *Arachis* means a legume and *hypogaea* means below ground referring to the geocarpic nature of pod formation. The genus *Arachis* belongs to the sub-tribe Stylosanthineae in the tribe Hedysareae of the family Fabaceae and sub-family Papilionaceae. The species *hypogaea* is placed in section Axonomorphae and series Amphiploides. It consists of two sub-species, viz., *hypogaea* and *fastigiata* with two botanical varieties each viz., *hypogaea* (type 'Virginia') and *hirsuta* (type 'Peruano') and *fastigiata* (type 'Valencia') and *vulgaris* (type 'Spanish'). Type 'Virginia' consists of two sub-types Virginia runner and Virginia bunch. In India, groundnut varieties under cultivation fall in three botanical groups viz., Spanish, Valencia and Virginia. These can be divided as per growth habit in three groups viz., Bunch (Spanish/Valencia), Semi-spreading (Virginia bunch) and Spreading (Virginia runner) (Gibbons *et al.*, 1972).

In Vidarbha predominantly Spanish bunch (ssp. *fastigiata*, var. *vulgaris*) or erect genotypes are preferred. Therefore, for present investigation, this group has been chosen. Special features of this botanical type are early maturity; erect; light green foliage; pod bearing in a cluster at the base of the plant; round, plumpy and non-

dormant seeds with light rose testa; main axis is reproductive and sequential branching pattern.

The cultivated groundnut species, *Arachis hypogaea* is an annual and a tetraploid with $2n = 4x = 40$ chromosomes (Kawakami, 1930). It must be amphidiploid of *A.batizocoi* and *A.cardenasii* (Smart *et al.*, 1978) and they reported that the cultivated groundnut *A.hypogaea* has two genomes, A and B. The A genome was assumed to have been derived from *A.cardenasii*, a diploid member of section *Arachis* and B genome from *A.batizocoi*, another diploid member from the same section. The distinction between the two genomes lies in the presence of a small chromosome in the A genome which is absent in the B genome. This chromosome is designated as 'A' chromosome by Hosted (1936).

According to Singh *et al.* (1992), South America is the native and centre of origin for the genus *Arachis*. The wild *Arachis* species are found in Argentina, Brazil, Bolivia, Paraguay and Uruguay.

Genetic diversity between genotypes or species might arise due to geographical separation or genetic barriers in crossability. In groundnut breeding it plays an important role because crosses between the lines of diverse origin, generally display a greater heterosis. D^2 technique helps in the selection of genetically diverse parents for their exploitation in hybridization programmes to isolate potential transgrates.

The most remarkable feature of this legume, groundnut is its adaptability. Within a short period, it has spread to several parts of the world. Stability over seasons or across environments requires a low genotype x environment interaction. Yield stability is genetically controlled and hence selection for yield can be effective. Phenotype is the function of genotype, environment and its interaction. Stability analysis is an important tool to the breeders in understanding the adaptability of crop variety and predicting response of various

genotypes over a wide range of changing micro and macro environments. Use of adaptable genotypes helps in achieving stabilization in crop production over locations or seasons. Use of stable genotypes in hybridization programme will lead to development of phenotypically stable high potential cultivars.

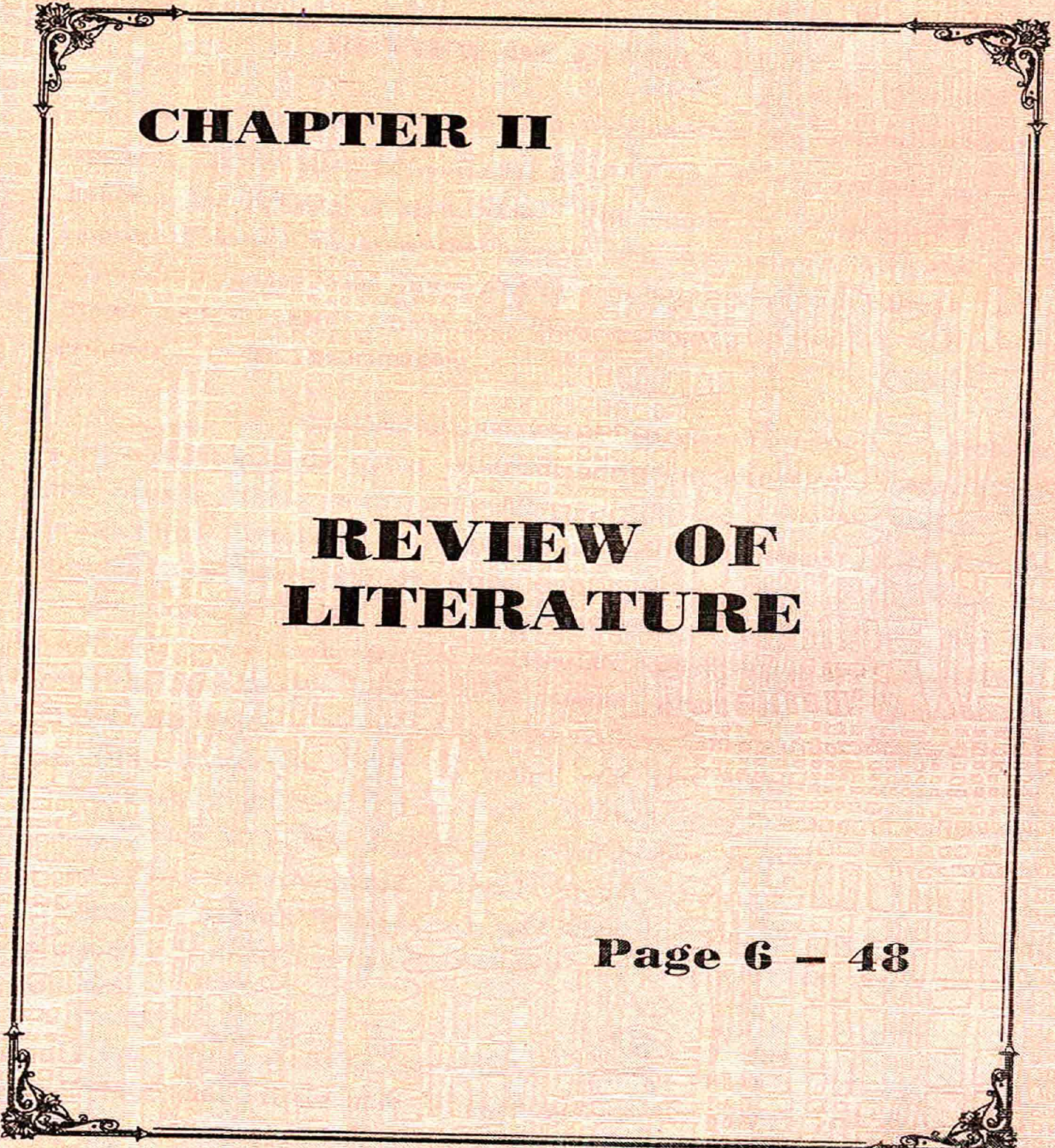
In India, large number of varieties suitable for different cropping systems have been developed and released at national level. However, national productivity remains at low level probably due to lack of wider adaptability. Varietal component being the major contributor for high yields seems to be not performing consistently. Similarly, it is assumed that there is least genetic diversity within habit groups in the Indian groundnut varieties (ISOR, 1993). For instance, apparently it is observed that most of the varieties in India are similar in their characters. AK 12-24 and SB XI of Maharashtra J 11 of Gujarat and TMV 2 of Tamil Nadu are found to be very difficult to differentiate and distinguish. ICGS 11 and ICGS 44 developed and released by ICRISAT are identical. It is, therefore, necessary to test Indian groundnut varieties of Spanish bunch habit group by subjecting them to multi-environments (*kharif* and *summer*) and measure the degree of divergence between varieties as well as describe their performance in a specific environment.

It is known that varieties/genotypes differ in their response to varying environments. And it is likely that the measures of genetic divergence of the genotypes under different environmental conditions are influenced by the stability of the characters. Therefore, Verma *et al.* (1973) were of the opinion that multivariate analysis based on multi-environment test would be more informative and meaningful than one based on a single environment. Jain and Pandya (1984) stated that for the improvement of any crop species the genetic diversity for characters of economic importance is almost a pre-requisite for a plant breeder to start with. Similarly, the stability of productivity of the varieties developed by him is equally important. Therefore, the role of

genetic diversity in breeding for wide adaptation is of paramount importance for an effective breeding programme.

The present investigation was conducted on 24 Indian groundnut varieties belonging to the Spanish bunch habit group, released for cultivation over years in different groundnut growing states/zones and 26 germplasm lines belonging to Spanish bunch habit group representing the variation in crop with the following objectives.

- 1) To estimate the degree of genetic divergence among some Indian groundnut varieties/germplasm lines under *kharif* and summer seasons,
- 2) To estimate stability parameters and extent of genotype x environment interaction with reference to some of the components of yield for identifying most stable and fairly dynamic variety with specific adaptability and
- 3) To identify the superior genotypes on the basis of genetic diversity and phenotypic stability for their use in future groundnut breeding programme.



CHAPTER II

REVIEW OF LITERATURE

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CHAPTER II

REVIEW OF LITERATURE

Groundnut, an annual legume rich in oil and protein, is presently cultivated in 80 countries from 40°N to 40°S in tropical and warm temperature regions of the world. The edible oil of groundnut is an important source of fat in the human diet, especially in Asia and Africa. Groundnut is also used directly as food in primary form in Europe, United States and Canada. There has been a major increase in food use of groundnut in the United States.

The classification of cultivated species of groundnut is based on growth habit, namely, bunch, semi-spreading and spreading. Gibbons (1966) has classified them on the basis of type of branching into two groups. The crosses between these two categories i.e. bunch and spreading have revealed restriction of recombination (John *et al.*, 1954). There is, therefore, an obvious need for a classification of the varieties on genetic criteria (Shew *et al.*, 1972). The application of multivariate and stability analysis helps in selecting genetically diverse and stable genotypes for hybridization programme. To be more meaningful, the multivariate analysis must be based on multi-environment test to cancel out the bias due to genotype-environment interaction (Verma *et al.*, 1973). It was observed that heterotic F_1 s generate a higher frequency of productive derivatives in advance generations when compared to non-heterotic F_1 s (Arunachalam, 1993). In groundnut, several reports are available on genetic divergence and phenotypic stability but no information on correlation of these two aspects is available.

The available literature on genetic diversity and stability in groundnut and relationship between genetic divergence and phenotypic stability in other crops has been reviewed as under.

2.1. Genetic Divergence in Groundnut

The concept of "genetic distance" has been of vital utility in many contexts and several measures of distance have been proposed but Mahalanobis' generalized distance (Mahalanobis, 1930, 1936 and Rao, 1952) occupied a unique place in plant breeding. D^2 statistic and canonical analysis are now most frequently used for classificatory purpose. While the former gives a quantitative measurement of divergence among genotypes, the latter serves the same purpose in term of spatial distance. Besides, both ventures define the relative contribution of different characters to differentiation among genotypes.

Sangha (1971) studied 27 spreading varieties of groundnut for divergence with regards to 6 characters. Multivariate analysis revealed that 100 grain weight and number of pods contributed most to the diversity. Genetic divergence was not apparently related to the geographic diversity.

Multivariate analysis for the nature of divergence among 24 varieties of groundnut for 17 characters were carried out and grouped in to three clusters with 7, 13 and 4 varieties, respectively (Shew *et al.*, 1972). According to him the characters important for grouping were plant height, days to first flowering, days to peak period of flowering, growth habit, leaf colour and resistance to *Cercospora*. It was found that the clustering pattern of the varieties did not follow their geographic origin. The grouping done by Mahalanobis' D^2 statistics was confirmed by canonical analysis.

Genetic diversity in another set of 27 spreading groundnut varieties from diverse sources was studied by Sangha (1973) in respect of secondary branches, lateral spread, fruiting nodes per primary branch, number of pods, pod yield and 100-kernel weight. High significant differences were observed among the varieties. On rank basis, fruiting nodes per primary branch contributed maximum to diversity (20.5%), followed by lateral spread (19.5%). However 100-kernel weight contributed least (13.4%).

The varieties were arranged into 6 clusters. Spatial pattern of clusters was not corresponding to geographical diversity. Varieties occurring in distinct clusters showed maximum diversity.

Twenty seven bunch groundnut varieties were examined by Sandhu and Sangha (1974) for genetic divergence by using multivariate analysis. The varieties differed among themselves with respect to 6 characters, viz., pod yield, length of primary branches, the number of fruiting nodes per primary branch, number of vegetative nodes per primary branch, number of vegetative nodes per secondary branch and number of pods. The analysis of inter-cluster and intra-cluster average D^2 values showed that the varieties could be classified into 7 groups. The divergence between the populations could not be related to their geographical distribution. The force of differentiation appeared different at inter-cluster and intra-cluster levels. Number of pods was the only character which was found a potential force of divergence at both the levels of differentiation.

Representative samples of 160 varieties equally divided among Spanish Bunch (SB), Valencia Bunch (VL), Virginia Bunch (VB) and Virginia Runner (VR) subgroups and between Indian and exotic cultivars in each subgroup were studied by Durgaprasad (1981). The genotypes were assessed for the degree of genetic diversity among them by Mahalanobis' distance statistic. Substantial diversity was found within and between the 4 subgroups. Overlapping of SB and VL within clusters was common. But they did not group with VB or VR in any of the three experiments. Indian and exotic cultivars were found together in any clusters showing that their identity was arbitrary. No relationship was found between geographic diversity and genetic diversity of the varieties. High degree of stability was found in the pattern of clustering of the varieties.

One hundred and forty four genotypes of groundnut of diverse origin were studied to estimate the diversity using Mahalanobis' D^2 statistic and classified them into 16 clusters. Intra-cluster distance (D) were ranging

from 10.30 to 45.82. The characters days to maturity and days to flowering were important in differentiating the genotypes (Sigamani, 1981).

Thirty one Virginia-type varieties were subjected to Mahalanobis' D^2 test and grouped them under 10 clusters. Plant height, number of matured pods, number of secondary branches and 100-kernel weight were found to be the potent factors for identifying genetically diverse genotypes in groundnut (Reddy *et al.*, 1984).

Nadaf *et al.* (1986) determined genetic diversity by using multivariate analysis (D^2 statistic) among the 83 bunch groundnut genotypes which were selected at random having wide geographic distribution. Clustering pattern resulted in grouping of 83 genotypes into 9 distinct clusters irrespective of their geographic isolation. Pod yield was found to be potential source of divergence at inter cluster level. The sources of differentiation were different at inter and intra-cluster levels. Crossing programme is suggested between various genotypes for different characters by identifying potential parents based on cluster means and genetic diversity.

Divergence analysis among 24 Spanish bunch genotypes of groundnut was carried out using Mahalanobis' D^2 statistic by Golakiya and Makne (1991). The results revealed that the genotypes were grouped into six clusters. Grouping of genotypes in different clusters was not related to their geographical origin indicating that the geographical isolation may not be the only factor for genetic diversity. The intra and inter-cluster average D^2 values indicated maximum divergence between cluster IV and VI followed by II and IV. Genotypes for important characters like pod yield, kernel yield, 100-kernel weight, oil and recovery percentage recording maximum mean performance were grouped into clusters II, III and VI. The genotypes like Chico, Barberton, JL 24, TG 18 A, KU No.203 and PBNG 17 were found potential parents based on cluster means and genetic diversity. The pod yield, kernel yield, days to 50 per cent flowering, primary branches, developed pods, recovery percentage and 100-kernel weight contributed considerably accounting for 90 per cent of total divergence.

Katule *et al.* (1991) studied the genetic divergence among 18 geographically diverse genotypes of groundnut (Semi spreading) and also studied the relationship between genetic and geographic divergence. The D^2 values ranged from 26.88 to 493.23 indicating wide range of diversity among the genotypes for the characters studied. After computing the individual D^2 values, 18 genotypes were grouped into eight clusters. Cluster III consisted of maximum five genotypes and cluster I included four genotypes each having different geographic origin indicating that the geographic diversity is not related to genetic diversity in this crop. The intra cluster values were ranged from 5.18 (Cluster II) to 8.45 (Cluster III). The inter-cluster distance were ranged from 9.50 (Cluster V and VII) to 22.20 (Cluster III and VIII). Based on ranks, 100-kernel weight (18.95%), green weight of pods (17.64%), lateral spread (10.45%) and shelling per cent (10.45%) were the most important yield components contributing towards divergence. The genotypes belonging to the cluster III and VIII may be utilized in hybridization programme for further improvement in the progenies for yield components like 100-kernel weight and green weight of pods as they have shown maximum diversity.

Yadav *et al.* (1991) assessed the nature and magnitude of genetic divergence in 39 genotypes of groundnut using D^2 statistic. The material exhibited wide genetic diversity. With the help of multivariate analysis the population was grouped into 10 clusters. Cluster I was found to be the most compact group and comprised of high yielding genotypes. Inter-cluster D^2 value between cluster IV and IX was maximum. The assessment of genetic diversity is likely to be more fruitful in elite material. From this point of view TG 9, MH 11, ICGV 86008, ICGS 11, ICGS 1 and JL 24 were found to be the most promising genotypes and should be used in further crossing programme in groundnut.

Bansal and Satija (1992) with Discriminant Function Index evaluated genetic diversity of 90 groundnut genotypes belonging to different growth habits. The study indicated that genetic diversity existed among the

genotypes having diverse plant types and this can be very efficiently used to exploit heterosis in groundnut.

Golakia and Makne (1992) carried out analysis of genetic diversity using Mahalanobis' D^2 statistic in 35 genotypes of Virginia runner groundnut. These genotypes were grouped into seven clusters. Cluster I had the maximum number of genotypes. The analysis further indicated that the genotypes of common geographic origin or same location were grouped into different clusters which suggested a lack of relationship between genetic and geographic diversity. The intra and inter-cluster average D^2 values indicated maximum statistical distance between cluster II and VII followed by cluster VI and VII. Cluster VII recorded highest mean kernel yield per plant, pod yield per plant, biomass yield per plant and recovery percentage.

Katule *et al.* (1992) assessed genetic diversity among 18 eco-geographically diverse genotypes of groundnut. Out of these, fourteen genotypes belonged to var. *vulgaris* and four to var. *fastigiata* of the ssp. *fastigiata*, Waldron. According to D^2 analysis, these genotypes were grouped into eight clusters which indicated the large amount of diversity in these genotypes. Maximum genotypes were grouped in cluster I, which involved eleven genotypes. Some genotypes from different eco-geographical regions were accommodated in the same cluster. On the other hand, the genotypes from the same eco-geographical region were distributed in different clusters. These results indicated that the geographical diversity was not revealed to the genetic diversity. Intra and inter-cluster distances were worked out. The intra-cluster values ranged from 0.00 (Cluster II and VIII) to 10.17 (Cluster I). Maximum inter-cluster distance was observed between cluster VII and VIII (26.83), followed by cluster III and VIII (25.50). These values suggested presence of wide diversity between these groups. Maximum mean value for 100-kernel weight was observed in cluster VII. The genotypes belonging to the cluster II showed maximum mean values for pod yield. The genotype MLM of the cluster V recorded minimum value for pod yield, number of mature pods and fresh weight of haulm, whereas the genotype Ah 7149 of the cluster II had highest mean values for these characters. The per cent

contribution of each character in grouping the genotype was worked out. A height of main stem was the most important character (19.61), followed by shelling percentage (16.99), number of mature pods (14.38) and 100-kernel weight (13.72). The genotypes having diverse characters like the number of mature pods, 100-kernel weight, shelling percentage and fresh weight of haulm which contributed maximum to the diversity should be selected for hybridization and subsequently for further improvement in pod yield of bunch groundnut.

Reddy and Reddy (1993) studied the nature and magnitude of genetic divergence in 48 genotypes of groundnut using Mahalanobis' D^2 values and reported considerable diversity in the material studied. The population was grouped into 11 clusters. Clusters I, VI and III were larger and included more than half of the total population. The geographical diversity was not related to genetic diversity. 100-pod weight, number of secondaries per plant and harvest index contributed considerably and accounted to 80 per cent of total divergence. The results obtained by D^2 analysis were confirmed by canonical analysis.

Varman and Raveendran (1996) made an attempt to study the nature and magnitude of genetic divergence in three way cross hybrid populations of groundnut. A set of 60 three way cross F_1 hybrid populations derived from 6 bunch groundnut varieties viz., ICGS 44, Girnar 1, ALR 2, JL 24, GG 2 and CO 2 were raised. By clustering technique, all the combinations were grouped into 5 clusters. Among them cluster III was found to have 16 combinations and II had 13 combinations. Of the remaining clusters, cluster I and IV were represented by 11 each and V had only nine combinations. It was observed that crosses originating from the same grand parental combinations were found scattered in different clusters. Considering the intra and inter-cluster distances the maximum inter-cluster distance was recorded between cluster I and IV. It was noted that cluster I was highly divergent from cluster V and IV. Lowest intra-cluster value was recorded by the cluster IV indicated that the combinations included in this group showed closeness between them as compared to the crosses included

in cluster I which showed maximum divergence within the group. Cluster V recorded the highest values of pod weight, kernel weight, pod yield and oil content. Similarly, cluster IV registered high values of maturity index and recovery percentage. The highest values of shelling outturn, number of mature pods and number of branches were recorded by the cluster III, II and I respectively.

John and Mysamy (1998) studied the nature and magnitude of genetic divergence for yield, rust resistance and other important component characters in 26 groundnut genotypes of diverse origin and to make selection of best parents for rust (*Puccinia arachidis* Speg.) resistance breeding. Twenty two diverse resistant genotypes of groundnut obtained from the ICRISAT, Hyderabad and four varieties viz., JL 24, VRI 2, TMV 2 and Robout 33-1 formed the material for this study. Observations were recorded on eight metric traits. Multivariate analysis of genetic divergence using Mahalanobis' D^2 statistic was carried out. The common dispersion matrix was used for a simultaneous test of significance of differences in the mean values of eight characters studied, using Wilk's Criterion and the original means were transformed to uncorrelated variables. On the basis of D^2 values, the genotypes were grouped into clusters. The analysis of variance revealed highly significant differences among 26 genotypes for the eight characters. The analysis of dispersion using Wilk's Criterion revealed highly significant differences among the genotypes for the aggregate of eight characters. D^2 analysis established the presence of moderate genetic diversity among these types by formation of 3 clusters, congregating all the rust resistant genotypes with diverse origin in cluster I and rust susceptible high yielding adopted varieties in cluster II and III. The clustering pattern showed the absence of parallelism between geographical and genetic diversities. The least intra-cluster distance was observed in cluster I and high in cluster II. The minimum intra-cluster distance existed in cluster I between ICG 10030A and ICG 10978 might be due to the common origin. Similarly, high intra-cluster distance within cluster II indicated the possibility of inter breeding among these varieties for

improvement of yield. It was earlier reported that varieties included in a particular cluster with high order of divergence between them will be the best breeding material for achieving maximum genetic advance with regard to yield *per se*. Selection within this cluster must be exercised based on the highest mean values for the desirable traits which had profound influence on yield. The inter-cluster distance was found to be the highest between the clusters I and III and the least between II and III. The dissimilarity between geographic and genetic diversities might be seen from the clustering pattern of the genotypes studied. The cluster I had the highest pod yield per plant and low values for per cent disease index for rust. The cluster III had the highest number of mature pods per plant. The genotypes from cluster I and III may be utilized in crossing to create a wide spectrum of variability and to select for segregants with high pod yield and rust resistance.

It was concluded that the geographic diversity is not related to genetic diversity in groundnut. Multivariate analysis revealed that 100-kernel weight, matured pods per plant, plant height, pod yield, days to maturity, days to flowering, secondary branches, kernel yield, 50 per cent flowering, primary branches and shelling per cent contributed most to the diversity. The results obtained by D^2 analysis were confirmed by canonical analysis. The common dispersion matrix was used for a simultaneous test of significance of differences in the mean values of characters studied using Wilk's criterion. It was observed that crosses originating from the same grandparental combination were found scattered in different clusters.

2.2. Stability Analysis in Groundnut

To reduce genotype x environment interactions, the breeder has to select stable genotypes that interact less with the environment, in which they have to be grown and may be more flexible. Stability in productivity through low $g \times e$ interaction for yield contributing characters is of interest to the plant breeder. It is known that some varieties or genotypes or germplasm lines of crop plants are widely adapted and others are not. A dynamic approach to the interpretation of varietal adaptation to varying environments

was developed by Finley and Wilkinson (1963). From the analysis, the varieties specifically adapted to good or poor environments and those showing general adaptability could be identified. Improvement in this model was made by Eberhart and Russell (1966). They introduced one more parameters (S^2_{di}), in addition to two parameters proposed by Finley and Wilkinson ($\bar{X}_i$ and b_i).

The overall conclusion would be average stability ($b_i \approx 1.0$), below average stability ($b_i > 1.0$), above average stability ($b_i < 1.0$). When average stability is associated with high mean, varieties have general adaptability. When associated with low mean, varieties are poorly adapted to all environments. Below average stability means specific adaptability to favourable environments. Above average stability means specific adaptability to unfavourable environment. Mean performance should be high or low considering the character as desire and S^2_{di} should be non-significant in all cases. The term stable variety has been used for a variety that performs above average in all environments. Hence, the stable variety has high or low mean as desire ($\bar{X}_i$), unit regression ($b_i \approx 1.0$) and the deviations from regression as small as possible ($S^2_{di} \approx 0$).

The reaction of Spanish, Valencia, Virginia bunch and runner varieties and strains were studied in wet and dry growing seasons in Brazil by Wessling (1966). He found that the Spanish/Valencia types grew best during the wet season, but they were unable to maintain their superiority over the other types during dry season. The Virginia bunch types were least affected by climatic conditions unless at extremes. He concluded that the summer types were divisible into 2 groups, one reacting similarly to the Spanish/Valencia types and the other to the Virginia bunch types.

Genotype x environment interaction was measured in Taiwan using 13 groundnut cultivars grown at 10 locations for 2 years. Both cultivar x year and cultivar x location interactions were small for yield but

the cultivar x year x location interaction was highly significant (Chen and Wan, 1968).

Ojomo and Adelana (1970) in a study of cultivar x environment interaction with 16 cultivars grown at 3 locations for 3 years in Western Nigeria found significant both cultivar x location and cultivar x year x location interactions.

Three varieties of groundnut representing spreading, bunch and semi-spreading forms were planted and the number of flowers opened were recorded per plant from the commencement of flowering to maturity. On maturity, the plants were uprooted and the number of pegs and pods were recorded per plant, to work out different ratios and percentages of fertilization. Seasonal variation was very marked in the bunch and spreading forms, whereas in the semi-spreading varieties it was more or less stable (Joshi and Rajipara, 1971).

Five bunch genotypes of groundnut were tested with the local variety in 19 environments at 7 locations in different agro climatic areas of Saurashtra region of Gujarat, where the bunch varieties are grown. SB 11 or J 11 proved a stable yielder under varied conditions showing a wide adaptability and potentiality to utilize all optimum conditions (Joshi *et al.*, 1972).

In USA, 6 groundnut lines representing 3 botanical groups were studied under 2 long-day and 2 short-day photoperiodic treatments and found that the characters related to flowering and fruiting were greatly different under short-day treatment than under long-day treatments (Wynne *et al.*, 1973).

Singh *et al.* (1975) in their investigation, an attempt was made to evaluate eight promising spreading varieties of groundnut for their level of performance and stability for pod yield over four locations in Punjab. The differences in stability were mainly due to the linear regression.

The variety M 13 had average stability and high level of performance for pod yield and hence it was an ideal variety in the material under study.

Twelve groundnut varieties for 2 years at 4 locations were studied by Sangha and Jaswal (1975). The performance of varieties in different years was quite uniform but was inconsistent at different locations. There was a little phenotypic stability in 'C 148', others exhibited no stability or adaptability at all. The small and non-significant variety x year interaction indicated that the performance of different varieties in different years was quite similar and suggested that little would be gained by testing the varieties for more than 2 years.

A significant genotype x environment interaction was found for pod yield, 100-seed weight and length of primary and secondary branches but not for the number of mature pods and number of primary branches when the parental, F₁, F₂, F₃, BC₁ and BC₂ generations of C 501 x AK 12-24 and C 501 x Ah 6595 at 2 sites were evaluated in groundnut (Sandu and Khehra, 1977).

Four trials with five varieties of groundnut representing upright bunch, spreading bunch and runner were conducted. Early sowing resulted in high pod yield but reduced shelling percentage. All the characters studied showed significant variety x sowing date interactions. MH 383 was the highest yielding variety at each sowing date (Nur and Gasim, 1978).

In Georgia, USA, large and significant cultivar x location x year interaction and small, year x cultivar and location x cultivar interactions were observed for groundnut grown in 2 years field trial, in respect of pod yield, percentage of sound matured kernels, extra large kernels, fancy size pods and 100-kernel weight (Tai and Hammons, 1978).

Wynne and Isleib (1978) estimated genotype x environment interaction in nine Virginia cultivars (five commercial releases and four late generation breeding lines) in two separate studies for five years in North Carolina (Virginia production area of USA). A substantial cultivar x location

x year second order interaction was observed for yield in both studies. Both cultivar x location and cultivar x year interactions were small when compared to the variation among cultivars. They concluded that no advantage could be gained by sub dividing the production area into sub areas for breeding or testing purposes.

Data from 26 trials with 3-4 groundnut varieties indicated that varieties reacted differently to environments. Some being superior under cool-cloudy conditions and the others under warm-sunny condition. The cultivars were sensitive to changes in the environment before the fruit filling than during the actual fruit filling phase (Williams *et al.*, 1978).

Eleven varieties of groundnut grown in three environments were assessed for phenotypic stability for pod yield, shelling percentage, 100-kernel weight and oil content. The magnitude of the linear component of the genotype x environment interaction was high for pod yield, 100-kernel weight and oil content. Of the varieties studied, '28-206' gave the highest yield and was stable for yield but not for other characters (Yadava and Kumar, 1978a).

Yadava and Kumar (1978b) also studied 17 genotypes in 4 environments to estimate genotype x environment interactions and stability parameters for 100-kernel weight, oil content and shelling percentage. The linear and non-linear portions of the genotype x environment interactions were significant for all the 3 traits. In all the environments 'Faizpur 1-5' had consistently high 100-kernel weight and oil content and 'Ah 6279' had high shelling percentage. Genotype x environment interactions were significant for these characters. The stability parameters for the different traits were apparently governed by independent genetic systems.

Genotype x environment interaction for pod yield kg/ha and maturity days was studied by growing thirteen genotypes of groundnut in four different years. Pooled analysis of variance indicated that linear portion of genotype x environment interaction was significant for both the characters. However, non-linear portion of genotype x environment interaction was significant only for maturity days. The genotype 'Georgia

119-20' was found to be high yielding, stable with unit response ($b_i \approx 1.00$) indicating its suitability to all kinds of tested environments. Further, the genotype NC 4 x was found to be early maturing and stable with average response. Utilization of these genotypes in future breeding programme is also advocated. No association existed between the mean values and both parameters of stability (b_i and S^2d_i) which indicated that both the parameters of stability are governed by different gene systems (Yadava and Kumar, 1979).

In a groundnut 17 cultivars were grown at 4 locations for 3 years at North Ghana. Average seed yields for the 4 sites were 1.45, 1.16, 0.90 and 1.10 t/ha respectively. While the cultivar x year interaction was not significant for most yield components, the cultivar x location interaction was significant for seed yield and 100-seed weight and the interaction between cultivar x location x year was large and highly significant. It was concluded that in this area cultivar should be evaluated for >1 year at 8 locations using 4 replication trials (Mercer-Quarshie, 1980).

Wynne and Coffelt (1980) determined yield and percentage of sound matured kernels and of extra large kernels in a 2 years study for 9 crosses with 8 lines per cross in F_4 and F_5 generations at 2 locations in North Carolina and Virginia groundnut belt in USA. Cross populations and lines within crosses were significantly different for all traits. Cross populations interacted with the year-location environments for all traits and lines within crosses interacted with the environment for all traits except yield.

The experimental material consisted of eighteen genotypes of groundnut which were grown during three years. These three environments would be referred to as E I, E II and E III respectively. The data were recorded for 100-kernel weight, shelling percentage and oil content. The data were subjected to pooled regression analysis to test the significance of genotype x environment interaction. Further, the stability parameters ($\bar{Y}_i$, b_i and S^2d_i) with regard to individual genotype were estimated. Results indicated that genotype 7-1 recorded moderate 100-kernel weight (40.67 g),

below average response and non-significant S^2di which indicated suitability for poor environments. For shelling percentage, C 421 was sorted out with above average shelling percentage (74.03), average response ($bi \approx 1.05$) and was also stable. This indicated the suitability of this genotype over all the testing environments. Regarding oil content, it was noticed that none of the genotypes possessed the average response ($bi \approx 1$) and non-significant value for S^2di (deviation from regression) for this character which are the requisites of an ideal variety (Yadava *et al.*, 1980).

In a review on genotype x environment interaction in groundnut Wynne and Gregory (1981) opined that although genotype x environment interactions varied with the material tested and the site chosen for testing, genotype x environment interaction in groundnut appeared to be similar to those in several other autogamous species. The yield of a groundnut cultivar in each individual experiment is unique and the environmental conditions differentiating the tests cannot be grouped according to year or location. This is not surprising, considering the indeterminate nature of the groundnut plant.

Data from Oklahoma peanut performance tests were used to estimate genotype x environment interaction variance components for 4 traits. The objectives of this study were to determine, if it would be advantageous to select cultivars for specific regions and to determine the most efficient combination of years, locations and replications to use when evaluating peanut lines. Evidence was obtained that genotypes performed consistently between irrigated and non-irrigated locations for the traits studied. The variance of the difference between two cultivars or lines was calculated using various combinations of years, locations and replications. Results indicated that the time presently allotted for testing could be reduced without sacrificing accuracy. Also it is important to include at least one irrigated and one dryland location in the testing programme (Dashiell *et al.*, 1982).

Patel *et al.* (1983) tested 6 genotypes against M 13 and GAUG 10 at 9 different locations for 2 years for stability. The analysis of variance revealed significant differences in pod yield among the varieties in both the years. Variety x environment interactions were highly significant. Significant deviation from regression indicated that the performance could not be predicted.

Twelve Virginia type peanut cultivars were evaluated for kernel yield in a total of 29 test environments in southern and northern Queensland. The cultivar x environment (c x e) interaction was significant. Pattern analysis revealed that cultivars of dissimilar genetic origin had different productivity responses across environments (Shorter and Norman, 1983).

Schilling *et al.* (1983) conducted a study to examine the relationship among sibling components of two peanut multilines and to determine if the multilines perform in a more stable manner across environments than any single component. Partitioning of genotype x environment interaction sum of squares, regression analyses and stability variances were used to assess stability over environments (2 years and 4 locations) for two multilines and their four components. For one multiline, three of four component lines were not significantly different from the multiline for yield nor did deviations from regression and stability variances differed among components. Conversely, components of the second multiline displayed significant variability for yield, regression coefficients and deviations from regression. However, the multiline performed in a stable manner with relatively high yields and low deviations from regression. Mean yield regression coefficients and deviations from regression were seen to be useful parameters in the formation of a multiline. This study, however, suggests that pure lines of peanuts can be identified that are as stable across environments as multilines.

Reddy *et al.* (1984) stated that seasonal differences in groundnut yields are more pronounced than varietal differences. The magnitude of the variety x season interaction was high. Virginia forms of

groundnut were found less interactive than Spanish types. Individual varieties which were stable across seasons would be identifiable. Study indicated the possibility of shift to Virginia forms during *rabi*. Hybridization among the three sub species did not result in spectacular yield improvements. Further scope for selection was indicated and modified breeding procedures for greater selection gains were suggested.

Patil *et al.* (1984) evaluated six promising varieties of groundnut for level and stability of yield over four environments in Western Maharashtra. The differences in stability were mainly due to linear regression. The variety M 13 had good stability ($b_i = 0.99$) and was second best in yielding ability (1503 kg/ha) and had lowest S^2_{di} (0.25) while TMV 10 had given the highest yield (1664 kg/ha) with moderate stability ($b_i = 1.12$ and $S^2_{di} = 1.2835$). Hence, M 13 and TMV 10 were observed to be ideal genotypes.

Stability analysis with respect to pod yield, maturity days, 100-kernel weight, shelling percentage and oil content was conducted in bunch group of groundnut (12 genotypes over 3 different environments). Pooled analysis of variance indicated the significance of genotype x environment interaction mean squares for all the traits. The regression M.S. (Linear component) and remainder M.S. (non-linear component) were found to be significant for all the characters except for pod yield. The magnitude of linear component was higher for pod yield and maturity, whereas, for remaining characters, the reverse was true. Evaluation of individual genotypes suggested that a genotype GC 90 had high pod yield and oil content and medium kernel weight, average response and low deviation around regression slope for both the characters. The use of genotype GC 90 in the breeding programme is advocated because it possessed high pod yield and oil content and was also stable (Kumar *et al.*, 1984).

In 3 habit groups of groundnut, variety x season interactions were studied and found that Virginia bunch was less interactive than Spanish bunch types. In general, seasonal yield differences were greater

than varietal differences and variety x season interaction was high (Reddy *et al.*, 1984).

Swarnlata *et al.* (1984) examined the stability of performance of six Virginia varieties, two Spanish varieties and their 33 advance generation mutants and eight cross derivatives in *Kharif* (rainy) and *rabi* (post rainy) seasons under two fertility levels. Stability of pod and kernel yields per plant as well as per m² plant spread basis were examined. Average yield was highest in *rabi* under high fertility. The mutants of MK 374, M 13 and R 33-1 Virginia type varieties were significantly superior than the parental varieties and the varieties derived from hybridization. The mutants m 97, m 68 and m76 of MK 374, m 130 of R 33-1 and m 92 of M 13 were high yielding and stable in performance. These can be grown in both the seasons. The stability of some of the compact mutants can be improved by manipulating higher plant density.

Habib *et al.* (1986) studied eight promising bunch genotypes over four locations in Karnataka State representing varying environmental conditions and data were evaluated for their stability of pod yield performance. Stability differences were assessed on the basis of linear regression of genotypes on environmental index and deviation from linear function along with their mean performances. The variety Dh 8, had good stability and high level of performance for pod yield and hence it was concluded that Dh 8 was the suitable variety available in the materials evaluated for their stability performance.

The stability of four peanut multiline populations plus their component lines were determined over a 4 years period at 2 locations in Florida. The study was undertaken to provide information concerning the stability of both yield and market quality factors. G x E interactions were highly significant for pod yield and 5 quality characters including fancy pods percentage, shelling percentage, 100-kernel weight, extra large kernel percentage, SMK yield. Large differences in yield and market quality traits were not found between sib-lines. However, differences were found in stability estimated from regression coefficients and deviation from regression

of multilines compared to their component lines, possibly due to the buffering action resulting from greater genetic variability. Multilines did not have greater stability in all cases, but the differences between the multiline and its least stable component line was generally greater than the difference between the multiline and its most stable component line. This research indicated that the chance of improving the yield stability and market acceptability of peanut cultivars is increased when the multiline approach is used (Norden *et al.*, 1986).

Bhole *et al.* (1987) studied eight promising variety of groundnut viz., R 33-1, G 201, UF 70-103, EC 21130, J 1, TG 17, J 2 and SB XI at seven locations during summer to test the phenotypic stability in respect of pod yield as per Eberhart and Russell model. Pooled analysis of variance for pod yield showed that there were significant differences amongst environments and genotypes and G x E interaction was also significant which revealed that the genotypes interacted with environmental conditions. As per stability parameters, i.e., phenotypic index (Pi) ($P_i = \text{Genotype mean} - \text{Grand mean}$), linear regression (bi) and deviations from regression function (S^2_{di}), the cultivars UF 70103 and J 2 can be considered as the most desirable varieties for summer cultivation under favourable and medium environmental conditions, respectively.

Study was undertaken to estimate the stability of performance of some cross derivatives of groundnut by Patra and Mohanty (1987). Of the 7 cross derivatives, OG 35-1, OG 9-2, OG 66-2, OG 49-1, OG 13-1, OG 71-3 and Kisan and 3 checks TG 3, AK 12-24 and J 11 tested in 7 different seasons at Chiplima, OG 35-1, Kisan and J 11 were found to be general adapters for yield. OG 9-2 had an average stability but low yield and showed adoption to high yielding environments as it gave high yield in the winters. OG 13-1 showed a below average stability ($b > 1.0$) and performed better during the seasons when the environmental indices were higher. Rest of the entries were suitable during the seasons when the environmental indices were negative. The yield stability showed association with stability of shelling percentage, sound mature kernel percentage and 100-kernel weight,

but more flexible association with mature, immature and tender pods per plant and pod per unit weight.

Dwivedi *et al.* (1988) studied stability of seed mass in confectionery groundnut. Significant G x E interaction was observed for both pod yield and seed mass. Among the varieties included in the trial the cultivar, Rabot 33-1 had the smallest b value (0.72) and therefore appeared most stable for seed mass. However, it is not suitable for confectionery use because of its lighter seed mass (51g). A general increase in the 'b' value with the increase in seed mass indicated the sensitivity of this characteristic to environmental changes in this line. Two lines, ICGV 86573 and ICGV 86725 recorded mean 100 seed mass greater than 70g. However, ICGV 86725 was more stable compared to ICGV 86573.

Ravindranath *et al.* (1988) studied seven Virginia bunch genotypes of groundnut, derived out of three cross combinations and blended to give 3 mixed populations (genotypic blends) and the performance of these mixed populations was evaluated together with the constituent pure lines and local control varieties under irrigated and rainfed conditions (2 environments). Data were recorded on 6 quantitative characters including pod yield per plant. G x E interaction was significant for most characters. For all characters, except number of primaries, mixture 003 + 003-1-26 and 502 + 500-2A were most stable. All genotypes in both pure stands and mixed stands gave better performances under irrigated than rainfed conditions. The genotypic blends performed better than their constituent pure stands in respect of several characters in both environments.

Anderson *et al.* (1989) assessed means of yield and qualitative traits in multilocation tests in the final stages of breeding line evaluation. Due to large environmental variation and genotype x environment interactions, it is often desirable to compare stability of lines over a range of environments. The objective of this study was to use various stability parameters, to try and determine the stability of experimental breeding lines. Using data from regional advanced peanut breeding line yield trials conducted over 3 years and four locations in Virginia and North Carolina, the

stability of peanut cultivars and breeding lines was compared. Stability variance was found to be highly correlated (0.91-1.00) with covariate adjusted stability variance. In many instances, the stability variance parameters produced similar results to pairwise regressions and dissimilarity measures when compared with standard cultivars. However, the distance parameters and regressions provided more precise information on relative responses in varying environments of two advanced breeding lines being considered for release. This allowed for direct comparison to cultivars targeted for replacement. NC 18411 had equal mean yields and qualitative traits but better stability than breeding line NC 18423. Regression analysis indicated that NC 18423 performed best in good environments but worse than most other cultivars in poor environments. Means and stability of value per kilogram and value per hectare were highly correlated with percentage of sound mature kernels and yield (0.92 – 0.99), respectively. A comparison of means and stability parameters was effective in discerning superiority of peanut breeding lines for potential release and use by growers.

Kandaswami *et al.* (1989) examined the stability of performance of twelve Spanish bunch groundnut genotypes in eight environments covering different locations, seasons under irrigated and rainfed conditions. VG 19 and Ah 8407 were significantly superior in yield potential over the grand mean but were unstable. These can be grown in well distributed rainfall and irrigated conditions. None of the genotypes showed stability for pod yield and twelve other traits. Five genotypes VG 19, Ah 165/S, Ah 8407, Ah 8457 and CO 1 which showed stability for many of the yield component traits, were identified as ideal genotypes for hybridization and selection of a stable genotype with high yield for further exploitation. The ratio of non-linear and linear components revealed the preponderance of linear component for number of mature pods, number of primary branches, 100-kernel weight, pod yield per plot, shelling per cent, pod to peg ratio and 100-pod weight.

Varman and Raveendran (1989) studied groundnut cultures comprising five each in Virginia bunch and runner to obtain information on

the stability parameters for pod yield, shelling outturn and kernel weight and also to identify the best genotype. The data showed that the mean sum of squares due to G x E interaction were significant only for pod yield and kernel size. Hence, further analysis was not done in respect of shelling percentage. Among the two characters, pod yield and hundred kernel weight, the linear component of G x E interaction was significant only for pod yield. This indicated that there was no linear response for hundred kernel weight. Hence, it appeared meaningful to carry out the stability analysis only for pod yield. Among the genotypes JSP 6 (1649 kg/ha) and ICG 2271 (1582 kg/ha) have recorded significantly higher yield than the check TMV 10 (1273 kg/ha). Out of the two, JSP 6 recorded a regression coefficient of 2.57 which was significantly higher than unity. This suggests that this genotype is adapted only to favourable environment. The next best variety ICG 2271 had a regression coefficient of 1.19 which was equal to unity. This also possesses a non significant S²d. Hence, this variety satisfied all the three requirements of a stable genotype.

Varman *et al.* (1989) worked out phenotypic stability estimates both under stress and stress free environments, for three consecutive years involving seven groundnut genotypes. The phenotypic responsiveness and stability were estimated for productivity and kernel quality characters (dry pod yield, shelling per cent, 100-kernel weight and SMK per cent). The genotype RSHY 1 exhibited high mean performance for yield and quality characters indicating the average unit responsiveness across the environments. However, the stability was poor. JL 24 produced bold kernels even under stress conditions. All other genotypes exhibited similar pattern of stability and responsiveness.

Padma and Reddy (1990) made effort to obtain information on the stability of various physiological characters such as vegetative dry matter, total dry matter, leaf area index, peg number, filled pod number, 100-kernel weight and pod yield over a range of environments. Two seasons i.e. *kharif* and *rabi* with four varieties viz., Gangapuri, JL 24, K 3 and M 13, two irrigation treatments and three dates of sowing in each

season. None of the varieties could be classified as stable for peg number, 100-kernel weight and pod yield based on regression values. M 13 performed better under favourable environment and JL 24 under unfavourable environments for these parameters. These studies clearly showed that first date of sowing in both the seasons and *rabi* among two seasons were found to be the best.

Singh *et al.* (1990) studied 5 released Spanish bunch groundnut varieties (JL 24, J 11, Kisan, Jawan and AK 12-24) under five different conditions (created by sowing dates) in rainy season and residual moisture condition in winter season. The data on pod yield were analysed for variance in each date of sowing and pooled analysis was carried out. Stability parameters were computed. JL 24 having the highest mean performance level can be grouped under below average stability ($b > 1.0$ and S^2d significantly high), it can not adjust to change in environment as revealed from the stability parameters. Kisan and Jawan can be grouped under average stability ($b = 1.0$ and S^2d in negative). But the performance of AK 12-24 and J 11 could be predicted and they were grouped under above average stability ($b < 1.0$ and S^2d is moderate). These varieties may not be suitable for favourable environments.

Veerabadran *et al.* (1990) stated that the larger the interaction, the lesser are the chances of progress under selection in a breeding programme. In the present investigation, five varieties of groundnut were studied in five environments (*Kharif* and summer). The analysis of variance for pod yield revealed non significant differences among the genotypes and environments revealing that the genotypes showed similar reaction in different seasons. The phenotypic stability was measured by three parameters. The entry G 201 registered high mean yield with unit regression coefficient of 1.002 and comparatively less deviation from regression showing stability. The variety Co 1 was considered to possess stability under favourable environments registering the unit regression coefficient value of 1.085 and more deviation from regression coefficient. The genotype Dh 3-20

was specially suited for unfavourable environment as reflected by low b value and low deviation value.

Padma *et al.* (1991) conducted 2 field experiments during *kharif* and *rabi* with 4 cultivars (Gangapuri, JL 24, Kadiri 3, M 13) and 3 dates of sowing to assess the effect of irrigations on the yield of groundnut. The late sown crop yielded less than the early sown crop in both the seasons. Pod filling was most affected, while pod number was least affected under moisture stress conditions. There was a significant cultivar x sowing date interaction. Pod yield decreased significantly in delayed sowings. In *kharif* season the performance of cultivars K 3 followed by M 13 was more stable in irrigated as well as in rainfed conditions either with normal or delayed sowing. But the duration of M 13 (Virginia runner) was 27 days more than JL 24 and Gangapuri. However, for fitting into a multiple cropping system, a short duration cultivar like JL 24 can be chosen. In *rabi* season, under normal sowing conditions M 13 followed by Gangapuri exhibited better yield performance. Kadiri 3 or Gangapuri can be preferred to M 13 for delayed sowings.

Bansal *et al.* (1992) evaluated groundnut genotypes belonging to three diverse growth habits viz., bunch (Spanish bunch), spreading (Virginia runner) and semi-spreading (Virginia bunch) in four environments indicated sufficient inter as well as intra group variability for all traits. Yield and quality traits were affected by environmental fluctuation suggesting the need to identify genotype with least environmental influence. Genotypes yielded better in sandy soil in comparison to loamy soil. Spreading and semi-spreading groups of genotypes had almost equal yield potential, whereas yield was low in bunch group of genotypes. Analysis of variance revealed significant differences among genotypes, environments and genotype x environment interaction for all morphological traits indicating that sufficient variability were available among genotypes and the genetic expressions were highly influenced by environment. This suggests the need to identify genotypes with stable performances.

Nagabhushanam and Prasad (1992) conducted an experiment during 4 seasons viz., post-rainy seasons, rainy seasons and late rainy seasons with 14 different genotypes of groundnut to evaluate them for a wide range of characters. The genotypes were grouped under categories 1, 2, 3 and 4 for canopy development at 60 days, based on canopy diameter, canopy circumference and total dry matter. Genotypes belonging to category 1 represented the most compact canopy type, whereas those of category 4 represented the most spreading type. Categories 2 and 3 represented medium compact and medium spreading types respectively. Since the extreme types, i.e., categories 1 and 4 showed instability for kernel yield, higher level of stability for this trait seem to be associated with intermediate levels of canopy development, represented by canopy categories 2 and 3. For overall stability in pod and kernel yields, the most stable genotypes were PGN 1, MH 2, BC 28, compact mutant of M 13, 32-2-5 and TMV 2 NLM pertaining to canopy categories 2 and 3.

Patra *et al.* (1992) studied heterogenous population of AK 12-24, Spanish groundnut, with that of its 9 component lines, viz., BGS 1, 2, 3, 4, 5, 6, 7, 8 and 9 isolated from the farmer's bulk population of AK 12-24 by pureline selection method. Besides, another heterogenous population was synthesized by mixing all the 9 purelines in equal proportion and included in the study. A study was conducted during summer, rainy and winter seasons at 2 locations. The mix population showed up to 17 per cent increase in pod yield compared with the mean yield of some of its component lines. The population x environment interaction was highly significant for pod yield, indicating the differential response of the populations at different environments. The difference in stability of the mix population and their component lines was recorded. However, no consistent predictable pattern was apparent for the mean and stability values. Some of the component pure lines, were more stable than either of their base or mix populations. However, improvement in yield by multiline or heterogenous population approach can not be ruled out in groundnut. The proportion of different component lines in the mix population is to be worked out for getting advantage in yield.

Dwivedi *et al.* (1993) stated that the quality of edible oil is now receiving increasing consideration from consumers and processors. They conducted the study to investigate the effects of environments on oil content and fatty acid composition in peanut. The correlation between oil content and oil quality parameters was also studied. Thirteen peanut genotypes were grown in 12 environments for the study. Significant genotype, environment and G x E interaction effects were observed for oil content, individual fatty acid content and derived oil quality parameters. Oil content ranges from 45-50 per cent in multilocation evaluation. Out of thirteen genotypes tested, ICG 5856, ICG 5369 and ICGV 87124 could be used in breeding for improved oil quality.

Singh and Sinha (1993) studied 51 groundnut genotypes. Out of that, 37 were Spanish type and 14 were Virginia bunch type, to find out the G x E interaction for yield and quality components at 4 locations. Highly significant differences were observed among the genotypes for all the six characters studied (initial plant population, number of pegs per plant, number and weight of pods per plant, shelling percentage and oil content). The differences among the environments were also highly significant for all characters. Genotype x environment interactions were highly significant for initial plant population and pegs per plant. For the expression of these characters, the linear component was more important than the non linear one, although both the components were significant. All the genotypes could be classified as suitable for high, medium and low yielding environments. For pod per plant, genotypes ICGS 30 and G 201 were most stable G 201 appeared most stable genotype over the different environments for pod weight, while CGS 4018 and ICGS 5 were most desirable genotypes for shelling percentage. Likewise, BAU 6 was the most stable genotype for oil content. It may thus be concluded that the genotype G 201 was stable for number of pegs, number and weight of pods per plant, the three important primary yield contributing characters.

Raut *et al.* (1993) conducted an experiment during winter (*rabi*), summer and rainy season to study stability of kernel yield and its related

characters with 5 genotypes of groundnut (JL 24, SB 11, TKG 19A, NCAC 589 and PI 270792) and concluded that TKG 19 A was widely adaptable genotype and may be used for cultivation during any season and secondly NCAC 589 may be efficiently exploited under conditions of high input management. Environment + (genotype x environment) component was significant for pod yield, oil content, duration for flowering, height and spread of the plant. The 100-kernel weight, harvest index, shelling (%) and maturity period showed the presence of environment (linear) component. TKG 19A showed the highest kernel weight (14.35 g) and absence of genotype x environment interaction for kernel yield. NCAC 589 proved promising for intensive cultivation owing to its predictable high performance for kernel yield ($b_i = 2.85$) and the related characters and for non fluctuating maturity period.

Varman and Manoharan (1993) concluded that groundnut genotype VG 77 was the best performer for all the characters. For shelling percentage, hundred pod and kernel weight JL 24, VG 55 and J 1 were found to be stable. Ten groundnut genotypes (6 cultures and 4 released varieties) were studied in four locations during *kharif* for stability parameters. Genotype x environment interaction was not significant for pod yield and significant for all other characters (Shelling percentage, 100-pod weight, 100-kernel weight). Genotype x environment (linear) component was significant except for pod yield. This indicated that the stability parameter, regression coefficient (b) estimated by linear component of the response to a change in environment was different for various genotypes under study. Another component of variation for stability, variance due to pooled deviation was also highly significant except for pod yield which indicated that differences in stability for the characters among the genotypes was due to both the linear and deviations from the linear function.

Reddy and Gupta (1994) studied 46 genotypes of groundnut belonging to Spanish and Virginia bunch botanical forms over three micro environments and estimated stability parameters for pod yield and four associated traits with a view to identify genotype with reasonable degree of

stability for yield. Spanish types were more stable compared to Virginia types. Among the characters studied, 100 seed weight exhibited better stability across the environments. None of the genotypes, however, was found to be superior over all the three environments. The genotypes 559, 563 and 551 were found to perform better under irrigated conditions, while the genotypes 564, 565 and 571 were found suitable to moisture stress conditions and 4081-4 and 4069-1B had shown no response to change in environments and therefore, suitable to both irrigated and moisture stress conditions. The crop sown under irrigated conditions showed better performance over rainfed with and without supplemental irrigation.

Sojitra and Pethani (1994) stated that phenotypically stable lines are of great significance for a crop like groundnut which is considered to be an unpredictable oilseed legume. Therefore, twenty nine diverse bunch type groundnut genotypes including 27 Spanish and two Valencia were evaluated (out of that 6 were released cultivars) for adaptability under summer condition across four environments for pod yield and to identify high yielding stable genotypes. Both linear and non linear portions of $G \times E$ interactions accounted for the expression for pod yield. However, the predictable portion was significantly higher than the non predictable portion. Most of the genotypes were responsive to the fluctuation in agro-climatic conditions. The genotype J (E) 1 showed wider adaptability across the environments as indicated by higher pod yield (13.0 g/plant) coupled with average responsiveness ($b \approx 1$) and stable nature ($S^2d \approx 0$). Mean pod yield of the genotypes JB 210, J (E) 3, J 17 and GG 2 was significantly high and coupled with high response, but they were unstable to environmental changes as indicated by significant S^2d values. The genotypes ICGS 11, ICGS 44, NRGS (E) 6, Starr and JB 224 exhibited medium adoption across the environments. From these findings it was concluded that high pod yield coupled with high response, resulted in instability, while medium yield in combination with medium response leads to greater stability. The genotype J (E) 1, a released variety for Gujarat state in the name of GG 4 showed wider

adaptability across the environments as indicated by their higher mean performance, response coupled with stability.

Kandaswami *et al.* (1995) studied 15 groundnut genotypes under eight environments and came to the conclusion that the genotypes showing stability were not high yielders and the high yielders were found to be sensitive to environment and unstable. Different set of genes were found to operate in different locations and in different seasons. In this study the magnitude of genotype environment interaction was low under rainfed conditions compared to irrigated conditions. Significant positive genotypic correlation obtained in the location-wise and season-wise analysis indicated that the genes acting under rainfed conditions are similar in the particular location or season. Negative correlation coefficients indicated that the set of genes that acted under one location in irrigated conditions were not similar to that acted under irrigated conditions at another location. To realise optimum yield potential in groundnut, there is a need to identify ideal genotypes to different locations as well as to different seasons.

Singh and Sohu (1995) determined the stability of two groundnut multilines alongwith their four respective component lines with two checks over 12 unilocation environments. Each multiline was constructed from a different cross (multiline 1 from M 145 x NCAc 1107 and multiline 2 from M 37 x NCAc 1107) in F_8 by compositing equal proportions of seed from four phenotypically similar sib lines. The $G \times E$ interaction was highly significant for pod yield. The multilines were stable across environments but some component lines (pure lines) were superior in pod yield and were also as stable as the multilines themselves.

Astanto Kasno *et al.* (1996) carried out stability analysis for pod yield of 10 groundnut genotypes, resistant/tolerant to late leaf spot and drought at 15 locations. The combined analysis of variance for pod yield revealed highly significant differences among genotypes, environments, and $G \times E$ interaction. Groundnut varieties that show small or if possible, no $G \times E$ interaction are desirable because of their stable performance across a wide range of environments.

Adomon *et al.* (1997) conducted a cultivar trials comparing nine early maturing and 14 medium maturing peanut lines over 3 years at 5 sites in Northern Benin and suggested that both phenotypic and physiological yield models should be used in the identification of lines with desirable adaptive attributes. ;

Mathur *et al.* (1997) investigated seven promising groundnut varieties each from Virginia (M 145, Chitra, M 13, No.334, Chandra, GAUG 10 and G 17) and Spanish botanical groups (Dh 8, GG 2, MH 2, Trisul Mahali, JL 24, TMV 2 and J 11) received from SAARC (South Asia Association for Regional Co-operation). Two separate trials during four rainfed *kharif* seasons were conducted. Observations were recorded on 100-pod weight (HPW), 100-kernel weight (HKW), shelling percentage (SP) and sound mature kernel percentage (SMK %). The components of G x E interactions were estimated separately for Virginia and Spanish types. In Virginia trial, for HKW, all the varieties had shown stability in performance over the years (Since S^2d values were non-significant). Chitra was highly unstable variety for SP. All varieties were found to be phenotypically stable for SMK % as shown by non significant S^2d estimates. M 145 had b value significantly lower than unity, thus, reflecting its ability to perform better in inferior/poor environment (above average stability), while Chitra has a potential to perform better in normal environment (since b value was at par with unity) thus showing average stability over the years. In Spanish trial, all the seven varieties showed non significant S^2d values for all the four traits, except Dh 8 for HKW, TMV 2 for SP and Trisul Mahali for SMK per cent, indicating no change in performance over years. However, if we consider significant high mean b and S^2d together, the varieties JL 24 and GG 2 for HPW, GG 2 for HKW, J 11 and GG 2 for SP and J 11, MH 2, JL 24 and GG 2 for SMK per cent were found to be stable over years. It may be concluded that the variety M 13 among Virginia and GG 2 among Spanish types were stable for most of the yield traits over years in Saurashtra region.

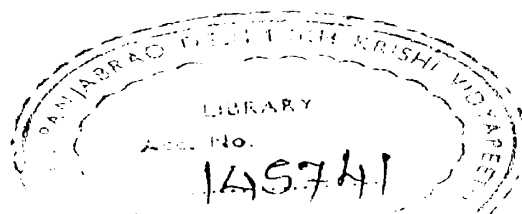
Lal *et al.* (1998) worked out G x E interaction of Spanish bunch groundnut genotypes during *rabi*/summer. The experimental material consisted of ten genotypes including three released varieties and experiments were conducted at ten locations. Highly significant differences were observed for both pod and kernel yields. Likewise, environments also differed significantly for both the characters. Significant mean squares due to genotype x environment (G x E) interaction indicated that the genotypes interacted significantly with the environments. The magnitude of linear component was, however, higher than non linear component suggesting the possibility of prediction across the environments. TG 31, R 9248 and ICGV 86590 possessed higher mean performances than the population mean (29.4 q/ha) coupled with non significant unit regression and the least deviation from regression for pod yield. Similarly, TG 31, R 9248, ICGS 11 and ICGV 86590 exhibited mean kernel yield more than population mean (19.4 q/ha) with non significant unit regression and the least deviation from regression. Among the average yielder, TG 32 exhibited non significant unit regression and deviation from regression for both the characters. These genotypes may be considered as stable and potential genotypes for peninsular region of India or may be used in hybridization programme for ensuring increased and stable yield.

Singh and Singh (1998) studied stability of two groundnut multilines alongwith their component lines (4 each) and five advanced/approved lines over twelve environments. Analysis of variances indicated that mean squares due to environments (linear) and pooled deviation (non-linear) were highly significant for all the characters, demonstrated that differences in stability among genotypes were due to both regression and deviations from regression. However, those due to genotype x environment (linear) were significant when tested against pooled error except for shelling percentage indicated that variation in performance of genotypes when grown over environments were predictable for all the characters except shelling percentage. Multiline M 1 and its component lines were unstable for pod yield. Multiline M 2 was statistically at par with its components for pod yield and was stable, whereas its components were unstable. The

investigation indicated the chance of improving pod yield stability and some other characters through multiline approach.

Patil *et al.* (1998) studied six groundnut genotypes viz., AK 107, 135, 159, 208, TAG 24 and TG 26 for phenotypic stability of seed yield over four years and came to the conclusion that the genotype AK 107, AK 135 and TG 26 had regression value nearing to unity and had high mean yield. Among these three genotypes AK 107, TG 26 had low and non significant S^2d and hence, these two were stable under fluctuating environmental conditions and hence can be used for cultivation in fluctuating environments also for improving the productivity of the crop.

Sojitra and Pethani (1998) stated that higher pod yield leads to the higher seed weight on the basis of their study with twenty nine bunch groundnut genotypes, evaluated under four environments and estimation of the stability parameters for 100 seed weight. Both predictable and non predictable components of genotypes x environment ($G \times E$) interaction were found important for expression of these traits. However, linear portion was significantly higher than non linear portion. Seventeen genotypes showed linear and 11 genotypes non linear sensitivity. Therefore prediction of performance was perfect in the case of 17 genotypes. Prediction of performance was not possible in the case of genotype JB 224 which showed significant b and S^2d values. The bold seeded genotype EC 100827 and small seeded genotype JB 215 showed wider adaptation as manifested by higher seed weight, unit b value coupled with non significant S^2d . The bold seeded genotype JB 210 and small seeded genotype J 18 were highly responsive and suitable for favourable environment as evident from the non significant S^2d value coupled with high responsiveness ($b > 1$). Bold seeded genotypes J 17, GG 2, J (E) 1, JB 223 and CGC 3 as well as small seeded genotypes ICGS 11, J 11, NRCG 4, JB 187, J (E) 336 and GAUG 1 were suitable for adverse environments as evident from the non significant deviation from regression slope ($S^2d \approx 0$) and less responsiveness ($b < 1$). The use of these genotypes as



a parent in breeding programmes or for general cultivation after testing over a wide range of environments can be advocated.

Senapati and Roy (1999) stated that adaptability is an important criterion for developing improved varieties and tested 60 groundnut genotypes, collected from diverse sources under five environments for stability analysis. Considering three parameters, three genotypes viz., Improved Spanish Bunch, NG 5-9 and MCAC 2664 possessed high degree of stability ($S^2_{di} = 0$), nearly unit response and positive phenotypic index, thus they had wider adaptability to be suited equally to all the environments. Though ICG 9331 attained high degree of stability but it was poorly adapted to all seasons due to its negative phenotypic index. Non-significant value of S^2_{di} associated with $b_i > 1$ and positive phenotypic index of seven genotypes viz., JL 53, MC 434, ICGPRS 225, Guyabita Bunch, ICES 44-1, EC 259704 and MCAC 765 indicated their adaptability specifically for better/favourable/rich environments. Non significant S^2_{di} associated with $b_i < 1$ and positive phenotypic index of eight genotypes viz., JL 24, NCAc 17546, JL 58, Manfredi 118, MCAC 2327, EC 24392, ICGS 11 and MH 383 revealed their adaptability specifically to poor/unfavourable environments. These adaptable genotypes may be utilized in the future breeding work of groundnut for the development of high yielding lines.

Azad *et al.* (2000) studied genotype x environment interaction thereby stability in performance for pod yield in five groundnut mutants/varieties across eight environments at seven locations over three consecutive seasons. Genotype x environment interaction was significant. Mutant 3 produced the highest pod yield, followed by Zhigabadam and D₁/62-30. Dhaka 1 and the mutant D₁/86-54 showed negative phenotypic indices and was considered unstable. The mutant D₁/62-30 appeared most stable exhibiting positive phenotypic index, nearer unit regression with deviation from linearity non-significant different from zero. In contrast, mutant 3 and Zingabadam appeared unstable.

Minimol *et al.* (2000) studied 10 genotypes of groundnut (AK 107, 135, 143, 159, 205, 237, 240, 247, TAG 24 and TG 26) in six environments in two seasons, i.e. *kharif* and summer, for six quantitative traits viz., seed weight per plant, shelling per cent, HPW, HKW, Pod yield per plot, oil content and worked out stability. G x E interactions were observed to be significant for all traits. Non-linear components of G x E interactions were important for shelling percentage, pod yield per plot and oil content. For seed weight per plant and 100-pod weight, however, linear as well as non-linear components were observed to be important. Genotypes AK 205, AK 135, AK 237, AK 240 and AK 159 were considered to be stable genotypes for pod yield and majority of yield contributing traits and were identified as ideal genotypes for future breeding programme as one of the parents or components of base population.

Senapati and Sarkar (2002) stated that the stability of yield in different groundnut genotypes was ultimately imparted through the stability of their different component characters in additive fashion. They estimated the phenotypic stability for yield and seven yield related traits of 34 groundnut genotypes grown over four environments. The mean squares due to genotypes, environments and G x E were found highly significant for all the characters. The linear and non-linear component of genotype x environment interactions were also significant against all the characters. The magnitude of linear variance was significantly high against non linear variance for number of primary branches, number of secondary branches and pod number could be accounted mainly by the linear regression. TCF 1717 had very high pod yield and was stable for yield, number of primary branches, shelling percentage and seeds per pod. G 64-206 had high pod yield and was stable for pod yield, primaries number, pod number, shelling percentage and seeds per pod. ICGPRS 221 also had high pod yield and was stable for yield, maturity days, 100 seed weight and seeds per pod.

It was concluded that varieties interacted differently to different environment. Seasonal differences were more pronounced than varietal differences. Multiline performed in a stable manner with relatively high yield

and low deviation from regression. However, it is possible to identify pure lines of peanut that are as stable as multiline across environments. Similarly, genotypic blends performed better than their constituent pure stands in respect of several characters. Market acceptability of peanut cultivars is increased when the multiline approach is used. First date of sowing in both the seasons was found to be the best. Late sown crop yielded less in both seasons. Early sowing resulted in high pod yield but reduced shelling percentage. Significant genotype x environment interactions were found for pod yield, 100-kernel weight, number of mature pods, number of primary branches, oil content, shelling per cent, SMK per cent and seed mass etc. Linear component of the genotype x environment interactions were high for pod yield, 100-kernel weight, oil content, maturity days etc. Non-linear portion of the genotype x environment interactions were significant for 100-kernel weight, oil content, shelling percentage, maturity days etc.

2.3. Genetic Diversity Under Multiple Environments

In the expression of genetic diversity, there is impact of environment on the genetic distance exhibited by genotypes. Sensitivity to environmental variation casts doubt on the reliability of D^2 analysis in a single environment and points to the need of making such studies under multiple environmental condition. Such studies will also help the breeder in identifying the most suitable environments under which D^2 analysis should be conducted to have a more realistic picture of genetic divergence (Prasad and Singh, 1990). Raut *et al.* (1985) revealed that change in environments alters clustering pattern due to genotype - environment interactions. Literature on this aspect in groundnut is not available. Therefore, information available in other crops has been reviewed as under.

Murty *et al.* (1973) studied nature of differentiation between 20 varieties of linseed of diverse origin over two seasons utilizing multivariate analysis. The differences among the varieties were significant for all the characters in both the years. The differences among the varieties for the aggregate of characters tested by Wilk's Λ criterion revealed highly significant

differences among the populations for both the years. The material could be grouped into seven clusters. The number and composition of the clusters remained the same in both the years in spite of considerable seasonal differences. The three exotic types formed three distinct and widely divergent clusters situated in approximately the same positions from each other in both the years. Cluster VI and VII were close to each other and they were the most divergent from the rest of the clusters. The disposition of the first five clusters revealed that cluster V containing an exotic type was distinct from the cluster I, II, III and IV. The stability of the grouping was confirmed by the canonical analysis also indicating the utility of multivariate analysis in analysing intra-specific differentiation. It was found that the amount of genetic divergence between any two clusters was not related to the distance between the geographical areas from which they came. Considerable diversity among the peninsular types was observed which could be related to the diverse ecological conditions within this region. The seven derived types which are rust resistant revealed an irregular pattern of distribution among the clusters but could be related to the region of their adaptation.

Prasad and Singh (1990) tested sixty four genotypes of maize (*Zea mays* L.) belonging to different geographical regions of the world under six different environments with a view to assess the impact of environments on the expression of genetic diversity. There was better expression of genetic diversity under winter environment than in rainy season, which indicated the need to conduct such analysis under more favourable environmental conditions to have a better picture of genetic differentiation between genotypes. The results also reflected that pairs of genotypes showing consistent D^2 value across the environments should be utilized in the breeding programme to evolve high yielding stable varieties. Higher significant differences were existed among the genotypes for all the characters in all the six environments. The mean values based on all the 64 genotypes for the different traits varied from environment to environment, which indicates differential impact of environment on the gene expression which ultimately affected the phenotypic expression. The expression of genetic diversity was better in the winter season environments as compared

to rainy season. The maximum intra and inter cluster distance (D^2 values) in E_2 were found to be 65.2 and 982.1 respectively, while the same in E_4 were only 34.7 and 199.8 respectively. The large intra and inter cluster distances under winter season environments reflected that there was better expression of genetic differentiation under winter season environments. In spite of large variations in mean performance and D^2 values, a few genotypes occupied the same cluster in all the six environments, indicating that they were relatively stable and can be utilized in the breeding programme to evolve high yielding stable varieties.

Singh *et al.* (1990) evaluated forty-four desi and sixteen Kabuli diverse genotypes of chickpea (*Cicer arietinum* L.) in three environments. Environments were created by sowing the material at an interval of fortnight. The results revealed that sixty genotypes were grouped into six clusters in E_1 and E_2 whereas in seven clusters in E_3 . Clustering pattern was influenced by environments to a quite large extent. Eleven genotypes of cluster II in environment 3 were present in cluster I of environment I. The magnitude of inter and intra cluster distance between the groups was similar in environments I and II, whereas it was lowest in environment 3.

Bargale and Billore (1992) utilized multivariate analysis to find out genetic divergence among 28 faba bean (*Vicia faba*) populations comprising 7 diverse strains and their 21 hybrids under better management (E_1) and poor management conditions (E_2). Genotypes were grouped into 5, 4 and 2 cluster in E_1 , E_2 and pooled respectively. A maximum inter cluster divergence was observed between genotypes of cluster I and V (262.86) and minimum was found in I and II (105.71) under E_1 . In E_2 , the maximum inter cluster divergence was noticed in cluster III and IV (103.15) and minimum in I and III (71.36), whereas in pooled analysis there were only two clusters showing inter cluster distance of 41.23. The intra cluster divergence varied from 0.00 to 100.81, 40.63 to 76.87 and 22.88 to 37.78 under E_1 , E_2 and pooled respectively. The inter and intra cluster D^2 values of distribution of hybrids vis-à-vis their respective parents across the clusters suggested that there was appreciable genetic divergence among the parents as well as

hybrids. Data also indicated that certain genotypes changed their relative grouping under different environments which suggested the differential expression of gene under different environments. Genotypes JV 3 and JV 21, JV 34 and JV 68, JV 34 and JV 70, JV 68 and JV 70 were present together in the same cluster in all the three analysis indicating lack of substantial divergence between them. The study indicated no relationship between parental diversity and heterosis, though, heterosis is considered to be the function of diversity. Geographical distribution had no relation with genetic divergence.

Ray *et al.* (1995) studied the nature and magnitude of the genetic divergence in 20 rice genotypes (*Oryza sativa* L.) from diverse pedigree by multivariable D² analysis under two locations. The genotypes were grouped under 5 and 4 clusters of varying constellations. The clustering pattern of the genotypes showed that genetic diversity is appreciably related to geographic diversity. On the basis of the present study, suggestion has been made for selecting parents so as to initiate a crossing programme for increased yield and wider adaptation.

Rao and Gomathinayagam (1997) assessed genetic divergence among 40 drought tolerant rice genotypes planted simultaneously under semi-dry condition at two different locations. Genetic divergence has not been found to be related with geographic diversity. Differential response of the genotypes to the environments has altered the clustering pattern between environments. Favourable environment yielded in lesser number of clusters by exploiting high genetic potential of different traits expressed by genotypes. Genotype with stable genotypic environment interaction in the expression of different traits were tend to group together in one cluster in both the environments. Such stable genotypes with higher order of genetic divergence will provide best breeding material for the exploitation of heterosis and high degree of variability in segregating generations.

It can be concluded that the clustering pattern was influenced by environments to a quite large extent. To have a better picture of genetic

diversity, conduct experiment under more favourable environment. In spite of large variation in mean performance and D^2 values, a few genotypes occupied the same cluster in all environments. Pairs of genotypes showing consistent D^2 value across the environments or genotypes occupied same cluster in all environments should be utilized in the breeding programme.

2.3. Relationship between Genetic Divergence and Phenotypic Stability

As it is known that varieties differ in their response to varying environments and therefore, it is likely that the measures of genetic divergence of the populations under different environmental conditions are influenced by the stability of the characters. Hence, it is felt desirable to relate the estimates of stability parameters with genetic diversity between the populations over different seasons (Rana and Murty, 1971). The literature on relationship between genetic divergence and phenotypic stability is not available in groundnut. Therefore, the information available in other crops has been reviewed as under.

Rana and Murty (1971) studied twenty improved varieties representing the variation in Eu-sorghum. Varieties were grown over four successive years and six important characters related to productivity were recorded. Genetic divergence was estimated for each year and also on the basis of pooled analysis by using D^2 statistic. Material could be grouped into six clusters. The composition of clusters varied in different years and different from that based on the pooled analysis. The varieties of first cluster of pooled analysis entered in different clusters in different years. Fourteen varieties were found relatively stable in their grouping over years. They were either very early or very late and were relatively photoinsensitive. The interactors were highly photosensitive with varying degree of maturity. It was observed that the magnitude of intra-cluster D^2 was the least in pooled analysis. The inter-cluster divergence over years did not show any regular pattern. Regression analysis showed that none of the varieties was found to be uniformly stable for all the characters. The spectrum of the variation in

the varieties stable in grouping indicated that genotypes with different constellations of characters were relatively stable in their grouping. Therefore, selection of parents for stability of performance does not in any way influence the variability for characters responsible for productivity. Stability of grouping could be related more to the past history of selection rather than stability for any single trait.

Verma *et al.* (1973) studied 78 varieties of soybean belonging to different geographical and latitudinal zones of the world at three locations under two fertility levels, thus constituting six environments. The varieties differed significantly from each other for each of the traits. The test by Wilk's criterion revealed that these varieties differed for all the 13 characters. The varieties could be grouped into eleven clusters. The largest cluster comprised of 33 varieties from five geographical regions. Four clusters were represented only by one variety each. The dispersion matrix used for D^2 analysis was also used for canonical analysis. The first canonical root λ_1 accounted for 73 per cent of the variation and λ_2 for 10 per cent of total variation. The coefficients in the first two canonical vectors Z_1 and Z_2 indicated that days to flowering followed by 100-grain weight, days to maturity and plant height constituted the major axis of differentiation. Days to maturity, 100-grain weight, pod length and per cent oil in that order formed the secondary axis of differentiation accounting for nearly 10 per cent variation. The cluster means and regression coefficients are two important stability parameters. Varieties belonging to diverse D^2 clusters not only differed in their mean yield but also in their response for yield in varying environments. Since response to environment is a genetic character, grouping on the basis of regression analysis for yield to choose genetically diverse and stable yielding parents was found to be as reliable as the elaborate multivariate analysis. The bringing together of diverse gene constellations for several attributes will provide stability of performance over wider areas.

Jag Shoran (1982) evaluated material comprised of 100 genotypes of pigeonpea [*Cajanus cajan* (Linn.) Millsp.] from India and other seven countries at three locations during two seasons. The Mahalanobis' generalized distance (D^2) was employed to determine the degree of divergence between $n(n-1)/2$ pairs of genotypes and thereafter clusters were formed by using Tocher's method. Stability parameters for grain yield were estimated following Eberhart and Russell model. The material could be grouped into 26-30 diverse clusters under different environments. The clusters formed by D^2 analysis in each environment differed in their mean yield as well as regression coefficients. The diversity of genotypes in different clusters was reflected in diversity of linear responses for grain yield in different environments. Therefore, the grouping of genotypes based on regression analysis for grain yield was observed parallel to the grouping done on the basis of multivariate analysis. It is expected that the crosses between genotypes from diverse clusters and having different means and regression coefficients can bring together diverse gene groups and therefore may provide a mechanism for the stability in grain yield.

Jain and Pandya (1984) investigated 32 chickpea (*Cicer arietinum* L.) genotypes of diverse origin in six environments for yield per plant. Genetic divergence (D^2) was calculated as described by Rao (1952) and stability parameters were estimated following Eberhart and Russell model (1966). In this investigation, by and large, genotypes included in the same cluster had identical means but the linear responses were not the same. However, genotypes included in the same cluster had almost identical non-linear responses. From this relationship it can be concluded that either of the analysis may be effectively used to select diverse parents for any crossing programme. Therefore, grouping of material into different clusters based on regression analysis was found to be reliable as that of Mahalanobis' D^2 statistic.

Mahto (1995) studied nineteen genotypes of linseed (*Linum usitatissimum* L.) in three environments and stability parameters were

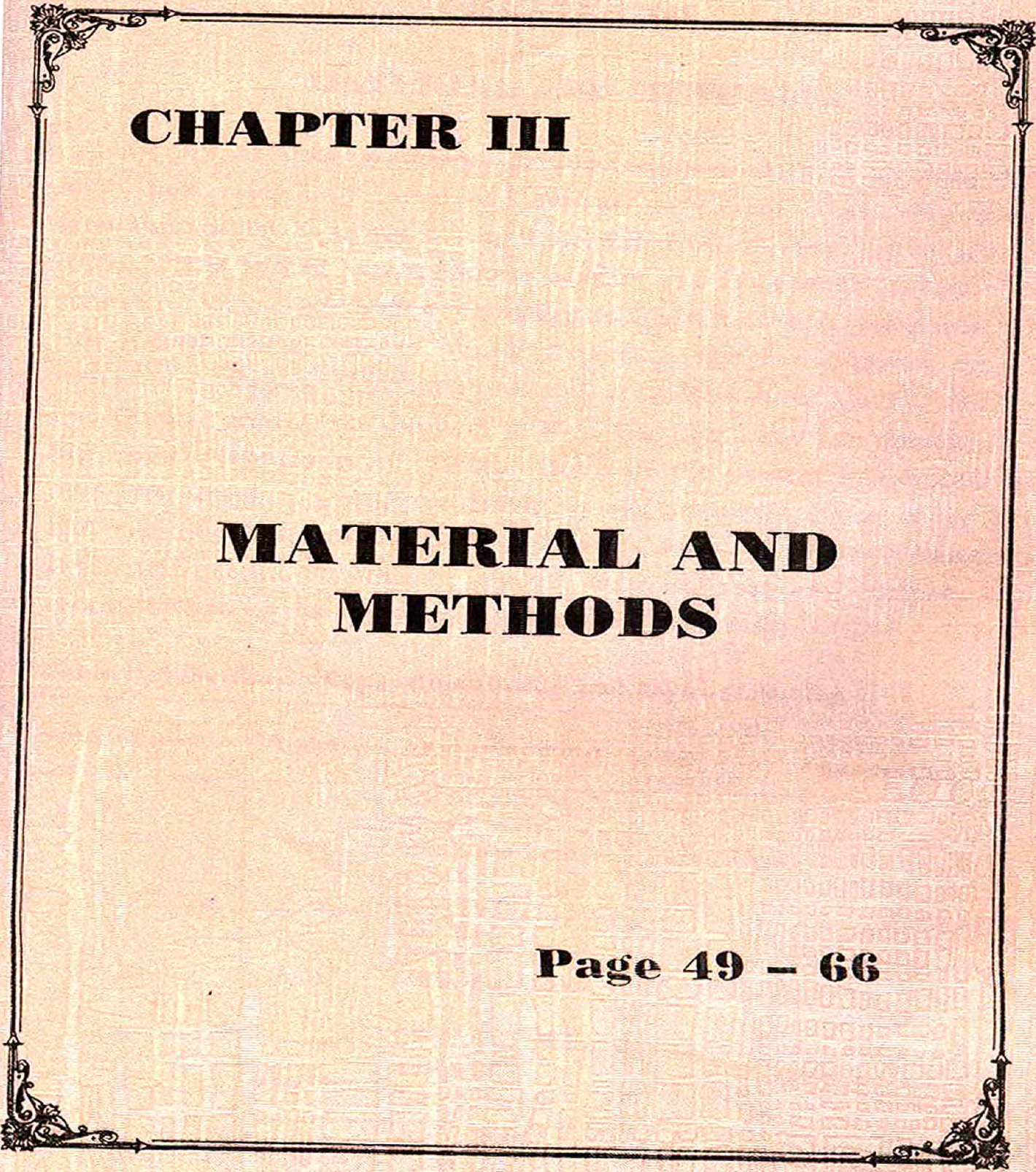
estimated for yield and yield attributes. G x E (Linear) interaction was significant for number of branches per plant and highly significant for plant height, number of seeds per capsule and number of capsules per plant. The environment III gave the highest yield and was favourable for most of the characters. Based on D^2 values, 19 genotypes were grouped into seven clusters. Twelve genotypes were sorted out on the basis of stability and genetic divergence for yield and yield attributes. Six belonged to cluster I, two to cluster II, and one each to cluster III, V, VI and VII. Therefore, considering the D^2 analysis and stability of yield and yield attributes making crosses among the selected genotypes of cluster IV (BAUL 9 and BAUL 159-4) with the genotype of cluster VI (BAUL 135) was recommended as maximum inter-cluster distance (49.769) was noticed between cluster IV and VI which indicated wider genetic diversity between themselves and was expected to provide enough genetic variability to select for high yielding and stable segregates in the segregating generations.

Mahto and Singh (1996) studied twenty strains of linseed (*Linum usitatissimum* L.) over four environments. Pooled data of nine characters over environments were analysed for D^2 estimates. Mean sum of squares for the most characters revealed highly significant differences due to strains, environments and strain x environment interaction for all characters. Stability of individual strains was worked out on the basis of two stability parameters, regression coefficient (bi) and deviation from regression (S^2di). Further 7 strains were selected with high seed yield per plant (higher than grand mean over environments) and stable for seed yield and for other yield contributing characters.

Patil (1997) studied a set of 35 safflower (*Carthamus tinctorius* L.) germplasm lines to identify genetically diverse and stable genotypes under rainfed and irrigated conditions over 2 years and 2 locations. Five characters were considered for investigation. The linear component of G x E was significant for seed yield, days to 50 per cent flowering, number of capitula per plant and oil content, suggested that genotypes differed from each other

in respect to their linear response for these characters. The pooled deviation (non-linear) were significant for all traits except for days to 50 per cent flowering in rainfed situation, suggesting unpredictable response. From stability parameters stable genotypes were identified for further use in breeding programme. Considerable genetic diversity was present among 35 genotypes as per D^2 estimates. Nine clusters were formed in combined over irrigated and rainfed conditions. There was no relationship between genetic diversity and geographic diversity in this material. Plant height and days to 50 per cent flowering contributed maximum towards the genetic divergence. On the basis of inter-cluster distance, five crosses in rainfed, six crosses in irrigated and three crosses in combined over rainfed and irrigated conditions were suggested. In addition, different sets of double crosses were suggested for breeding safflower varieties for wide adaptation and specific adaptation.

It was concluded that genotypes included in the same cluster had identical means, but cluster means and regression coefficients were differed in each environment. Regression analysis showed that none of the varieties was found to be uniformly stable for all the characters. Bringing together of diverse gene constellations for several attributes will provide stability of performance over wider areas. Magnitude of intra-cluster divergence was least in pooled analysis whereas, inter-cluster divergence over years did not show any regular pattern.



CHAPTER III

MATERIAL AND METHODS

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CHAPTER III

MATERIAL AND METHODS

In India, groundnut is grown in three seasons, i.e. rainy (85% area), post rainy (10% area) and summer (5% area). The rainy season groundnut which is grown during the South West monsoon period (June – November) is spread over the entire country and is generally rainfed. The post rainy season groundnut is confined to South India and raised mostly in rice (*Oryza sativa*) fallows during October – March. Summer crop is restricted to Central India in the States of Maharashtra, Madhya Pradesh and Gujarat grown from January to May. The post rainy and summer crop are irrigated (Reddy *et al.*, 1992). Therefore the present investigation on performance test of groundnut genotypes was conducted during *kharif* 2002 and summer 2003 on the field of Oilseeds Research Unit, Dr.Panjabrao Deshmukh Krishi Vidyapeeth, Akola. Four different environments were created by sowing the crop on different dates (Table 3.1).

Table 3.1: Seasons of experimentation and dates of sowing

Environments	Seasons	Date of sowing	Effective date of sowing	Date of harvesting
E ₁	<i>Kharif</i>	10/6/2002 (Sown in dry condition before onset of monsoon)	19/6/2002	As per maturity in the month of October
E ₂	<i>Kharif</i>	28/6/2002 (Sown after sufficient rains as recommended)	28/6/2002	As per maturity in the month of October
E ₃	<i>Summer</i>	4/1/2003 (Sown early)	4/1/2003	As per maturity in the month of May
E ₄	<i>Summer</i>	24/1/2003 (Sown as recommended)	24/1/2003	As per maturity in the month of May

Genetic material consisted of Spanish bunch type, 24 released varieties and 26 promising germplasm lines were chosen to represent a diversity of genetic background and geographical origin. Pure seeds of these 50 genotypes were collected from the Senior Research Scientist, Crop Research Unit (Oilseeds), Dr.Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Table 3.2).

Table 3.2: Set of test material

Sr. No.	Genotypes	State for which released/origin
Varieties (Spanish Bunch)		
1.	AK 12-24	Maharashtra
2.	AK 159	Vidarbha region of Maharashtra
3.	ALR 3	Tamil Nadu
4.	CO 1	Tamil Nadu
5.	CO 2	Tamil Nadu
6.	GAUG 1	Gujarat
7.	GG 2	Gujarat
8.	Girnar 1	Entire country
9.	ICG (FDRS) 10	Maharashtra
10.	J 11	Gujarat
11.	JL 24 (Phule Pragati)	Maharashtra
12.	JL 220 (Vyas)	Maharashtra
13.	Jyoti	Madhya Pradesh
14.	KRG 1	Karnataka
15.	MH 1	Haryana
16.	POL 2	Karnataka
17.	S 206	Karnataka
18.	SB XI	Maharashtra
19.	Spanish Improved	Maharashtra and Karnataka
20.	TAG 24	Vidarbha region of Maharashtra
21.	TKG 19 A	Konkan and Vidarbha region of M.S.
22.	TG, 17	Maharashtra
23.	TG 26	Maharashtra, Gujarat and Andhra Pradesh
24.	TMV 2	Tamil Nadu
Germplasm Lines (Spanish Bunch)		
25.	Ah 1	India
26.	Ah 4104-2	India
27.	Ah 4515	India
28.	Ah 6649	Tanzania
29.	Comet	United States
30.	NC Ac 7776	United States
31.	NC Ac 7777	United States

Sr. No.	Genotypes	State for which released/origin
32.	NC Ac 7778	United States
33.	NC Ac 7780	United States
34.	NC Ac 7782	United States
35.	NC Ac 7783	United States
36.	NC Ac 7785	United States
37.	NC Ac 7787	United States
38.	NC Ac 7790	United States
39.	PI 268782	Zimbabwe
40.	PI 268829	Zimbabwe
41.	PI 268642	Zimbabwe
42.	Pearl	United States
43.	Starr	United States
44.	Span cross	United States
45.	Span white	United States
46.	Taiwan selection	Taiwan
47.	Teja Amra local	India
48.	U 1-1-1	Sudan
49.	U 2-4-5	Sudan
50.	U 2-12-1	Sudan

AK=Akola; ALR=Aliyarnagar; CO=Coimbatore

GAUG=Gujarat Agril. Univ. Groundnut; GG=Gujarat Groundnut;

ICG (FDRS)=ICRISAT Groundnut (Foliar Diseases Resistant Strain);

J=Junagadh; JL=Jalgaon; KRG=Karnataka Groundnut;

MH=Moongphali Haryana; POL=Pollachi; S=Selection; SB=Spanish Bunch;

TAG=Trombay Akola Groundnut; TKG=Trombay Konkan Groundnut;

TG=Trombay Groundnut; TMV=Tindivanam; Ah=*Arachis hypogaea*;

NC Ac= North Carolina Accession; PI= Plant Introduction; U=Uganda

3.1. Soil Fertility Status

Soils of the experimental farm of Oilseeds Research Unit, Dr.PDKV, Akola are moderately deep to deep. Soils had pH 7.8 (slightly alkaline in reaction) electrical conductivity was 0.144 dSm⁻¹. Organic carbon content was medium in range (0.585%), whereas the available N and Phosphorous was low i.e. 188.2 and 27.2 kg/ha respectively and available K content was high (242.1 kg/ha).

3.2. Details of Layout

All the trials were conducted with following details

- | | | | |
|-----|----------------------|---|--|
| 1) | Design of experiment | : | Randomized Complete Block Design |
| 2) | Replications | : | Four |
| 3) | Genotypes | : | 50 |
| 4) | Plot size | : | 2.00 m x 0.90 m (3 rows of 2 meter long) |
| 5) | Spacing | : | 30 cm x 10 cm |
| 6) | Method of sowing | : | Dibbling (one seed/hill) |
| 7) | Fertilizer dose | : | 25:50:0 NPK kg/ha as recommended |
| 8) | Plant protection | : | As per recommendations |
| 9) | Date of sowing | : | As given in Table 1 |
| 10) | Date of harvesting | : | As per maturity |

Other recommended packages of practices were followed during crop growth period.

3.3. Observations Recorded

Data on following 13 quantitative characters were recorded on five randomly selected competitive plants from each plot, except days to 50 per cent flowering and days to maturity.

1) Days to 50 per cent flowering:

Days to 50 per cent flowering were recorded on commencement of flowering in 50 per cent of the total plants in a plot.

2) Height of main axis (cm):

Height of main axis (n) was recorded in cm from the base (first pair of primaries) of the plant to the growing tip of main axis (n) at the time of maturity.

3) Primary branches per plant:

Primary branches (n + 1) are the lateral branches located on main axis (n), which were counted.

4) Secondary branches per plant:

Secondary branches (n + 2) are located on primary branches (n+1) which were counted.

5) Number of mature pods per plant:

Number of mature pods means fully developed pods which were counted at the time of maturity.

6) Hundred pod weight (g):

Hundred pod weight was recorded in grams by weighing fully developed 100 dry pods.

7) Hundred kernel weight (g):

Hundred kernel weight was recorded in grams by weighing random sample of 100 seeds, obtained from fully developed dry pods.

8) Shelling per cent:

Shelling per cent was calculated by following formula.

$$\text{Shelling \%} = \frac{\text{Weight of seeds}}{\text{Weight of pods}} \times 100$$

9) Sound mature kernel per cent:

Sound mature kernel per cent was calculated by following formula.

$$\text{SMK \%} = \frac{\text{Weight of well developed seeds}}{\text{Weight of seeds}} \times 100$$

It is the weight of sound mature seeds recovered from the kernel yield and expressed as per cent.

10) Oil content(%):

Oil content in seed was estimated by NMR (Nuclear Magnetic Resonance) technique on instrument (OXFORD NMR Analyser - NEWPORT 4000) available in Instrumentation Cell, Dr.PDKV, Akola as described by Sagare and Naphade (1983).

11) Days to maturity:

Days to maturity was recorded by summation of days from sowing (effective date of sowing) to maturity.

12) Pod yield per plant (g):

Pod yield was recorded in grams after weighing total clean and matured dry pods obtained from five plants under observations and mean was calculated.

13) Kernel yield per plant (g):

Kernel yield was recorded in grams after shelling of pod obtained from five observation plants and mean was calculated.

3.4. Climate and Weather Conditions

Akola is geographically located at $20^{\circ}8'$ N latitude and 77° E longitude at the altitude of 278 metres above mean sea level in the sub-tropical zone. Rainfall received mostly from South-West monsoon amounted to 717.6 mm annually.

Monthly weather for the crop season 2002 (*khari*f) and 2003 (Summer) recorded by Meteorological Observatory, Dr.PDKV, Akola were as under.

Kharif 2002:

Sr. No.	Month	Rainfall (mm)	No. of rainy days	Temperature (°C)		Relative humidity (%)		Sunshine hours per day
				Max.	Min.	Morning	Evening	
1	June	240.6	11	36.3	25.4	58	40	5.2
2	July	53.4	3	32.9	23.8	76	51	5.6
3	August	194.7	15	28.8	22.2	89	75	2.4
4	September	110.7	5	31.2	21.5	85	58	5.2
5	October	35.2	2	34.6	18.7	72	35	10.4
6	November	2.3	1	31.9	14.1	72	43	9.1
	Total	636.9	37					

Summer 2003:

Sr. No.	Month	Rainfall (mm)	No. of rainy days	Temperature (°C)		Relative humidity (%)		Sunshine hours per day
				Max.	Min.	Morning	Evening	
1	January	0.0	0	29.9	12.4	65	32	7.6
2	February	2.2	0	33.1	16.0	66	26	8.4
3	March	0.0	0	37.0	18.1	44	22	8.1
4	April	0.0	0	40.7	25.9	36	16	8.6
5	May	0.0	0	42.3	28.1	41	18	9.0
6	June	75.6	7	36.6	26.5	67	41	6.3
	Total	77.8	7					

3.5. Statistical and Biometrical Analyses:

The data were subjected to the following statistical and biometrical analyses:

3.5.1. Multivariate analysis of genetic divergence:

D^2 values were obtained by the model developed by Mahalanobis (1928, 1930 and 1936) to determine divergence among genotypes in terms of "generalized group distance". The grouping of genotypes was done by Tocher's method described by Rao (1952). Canonical roots were calculated by method suggested by Rao (1952) to represent the varieties in the graphical form.

3.5.1.1. ' Analysis of variance and covariance:

The analysis of variance was performed to measure the variation among genotypes for all the characters. The analysis of covariance was performed to measure the variation occurring simultaneously in two characters. The statistical model used was as follows:

$$Y_{ijk} = \mu + g_{ij} + b_k + c_{ijk}$$

Where,

Y_{ijk} = Phenotypic performance of ij^{th} genotype in k^{th} block

μ = general mean

g_{ij} = effect of the ij^{th} genotype

b_k = effect of the k^{th} block

c_{ijk} = environmental effect

Analysis of variance and covariance based on this model has the following form:

Source of variation	d.f.	Variance X_i	Covariance X_{ij}	Variance X_j
Replications	(r-1)	$\sigma_{ii} + g. \sigma_{rii}$	$\sigma_{ij} + g. \sigma_{rii}$	$\sigma_{jj} + g. \sigma_{rjj}$
Genotypes	(g-1)	$\sigma_{ii} + r. \sigma_{g.ii}$	$\sigma_{ij} + r. \sigma_{gij}$	$\sigma_{jj} + r. \sigma_{g.jj}$
Error	(r-1) (g-1)	σ_{ii}	σ_{ij}	σ_{jj}

Where,

g = Number of genotypes

r = Number of replications

σ_{ii} = Error variance for trait i

σ_{jj} = Error variance for trait j

$\sigma_{r.ii}$ = Variance associated with replications for trait i

$\sigma_{r.jj}$ = Variance associated with replications for trait j.

- $\sigma_{r.ii}$ = Variance associated with replications for trait i
 $\sigma_{r.jj}$ = Variance associated with replications for trait j.
 σ_{gii} = Genotypic variance of trait i
 σ_{gjj} = Genotypic variance of trait j
 σ_{ij} = Error covariance for trait i and j
 σ_{rij} = Replication covariances for trait i and j
 σ_{gij} = Genotypic covariances for trait i and j

3.5.1.2. Wilk's criterion:

Test of significance of differences can be accomplished in two ways, i.e. by simple ANOVA (Univariate analysis of variance) and by Wilk's statistic for aggregate traits (Multivariate analysis of dispersion, Rao, 1952). An analysis of variance was carried out for all the characters X_1 to X_{13} . Significance of differences among genotypes for all or majority of characters would justify further calculation of D^2 . However, pooled differences can be determined by Wilk's criterion which follow V-statistic representing χ^2 distribution (at pq d.f., p being the number of traits and q the d.f. for varieties) was computed as,

$$\Lambda = \frac{|E|}{|E + G|} = \left[\frac{\text{Determinant of error matrix}}{\text{Determinant of error + variety matrix}} \right]$$

The $|E|$ and $|E + G|$ are found out from the inverted/reduced matrices of variance and covariance of error and error + genotype, respectively by pivotal condensation method.

Further V-statistics was calculated.

As 'V' (Stat.) = $m \log_e$

Where,

$$m = \frac{n - (p + q + 1)}{2}$$

n = d.f. for error + d.f. for genotypes

p = number of significant characters

q = d.f. for genotypes (g-1)

e = 2.7183

Calculated 'V' (statistics) was tested at pq d.f. at 5 per cent level of significance.

3.5.1.3. Transformation of correlated variables (X_s) into uncorrelated (Y_s) variables:

The computation is very much simplified when the characters under study are independent. Therefore, it was preferred to transform the correlated variables to uncorrelated ones and then worked out D^2 values. Transformation was done by using pivotal condensation method (Rao, 1952). The inverse matrix of the original genotypic variance covariance matrix was computed to derive the relationship by which the original character mean (X_1 - X_{13}) were transformed to an uncorrelated set of variables (Y_1 - Y_{13}).

3.5.1.4. Computation of D^2 values:

In terms of variance and covariance the D^2 values were obtained as suggested by Mahalanobis (1936).

$$pD^2 = \sum_{i=1}^p \sum_{j=1}^p W_{ij} (X^1_i - X^2_i) (X^1_j - X^2_j)$$

Where,

X^1_i and X^2_i = The mean of i^{th} character in the first and second genotype respectively.

W_{ij} = Inverse of variance and covariance matrix

For each combination the mean deviation, i.e., $Y^1_i - Y^2_i$ with $i = 1, 2, \dots, p$, was computed and D^2 was calculated as sum of these deviations, i.e., $\sum (Y^1_i - Y^2_i)^2$.

3.5.1.5. Significance of D^2 values:

The significance of D^2 values were tested against the table value of X^2 for p degrees of freedom, where p was the total number of characters included in this study. If the calculated value of D^2 was higher than table value of X^2 it was considered significant and vice versa.

3.5.1.6. Contribution of individual characters towards divergence:

In all the combinations (i.e. 650 in this case) each character was ranked on the basis of $d_i = Y^j_i - Y^k_i$ values. Rank 1 was given to the highest mean difference and rank 13 to the lowest mean difference. Finally, number of times each character appearing first in ranking was calculated and per cent contribution was worked out taking $650 = 100$.

3.5.1.7. Group constellation (Cluster formation):

The grouping of genotypes was done by Tocher's method described by Rao (1952). The criterion used in clustering was that any two varieties belonging to same cluster should show a smaller D^2 value than those belonging to different clusters. In this method, the two genotypes having smallest distance from each other were considered first to which a third genotype having smallest average D^2 value from the first two genotypes was added. Then comes the nearest fourth genotype and so it goes on. At certain stage when it was felt that after adding a particular genotype, there was abrupt increase in the average D^2 , this genotype was not added in that cluster. Similarly, a second cluster was formed. Thus the process was continued till all the genotypes were included into one or other cluster.

3.5.1.8. Canonical analysis:

It is complementary to D^2 -statistic. In canonical analysis uncorrelated variables (Y_s) are handled differently.

a) Development of A-matrix:

Find out simple sum of squares (SS) and sum of products (SP) of uncorrelated Y-variables (Y_1 - Y_{13}) and it was arranged in matrix form (diagonals were SS and off-diagonals were SP). Thus, matrix of variances and covariances (matrix A) was obtained.

i) Derivation of canonical vector 1 (Z_1):

Determination of the canonical variates was done by iteration starting with trial (unit) Vector (1, -1) each row of the matrix was multiplied and a derived vector, which was better approximation, was obtained. This procedure was repeated until stable values of the vector were obtained. The vector was standardized by dividing each element by square root of the sum of squares of all the elements.

ii) Deriving canonical root 1 (λ_1):

The highest element of the last iteration which was used as divider to get the best approximated vector served as λ_1 (Lambda 1), the first canonical root.

b) Development of B-matrix:

From the $(i, j)^{th}$ element squares of the matrix A, the product λ_1 x i^{th} element x j^{th} element of the first vector was subtracted to obtain the reduced matrix (matrix B).

i) Derivation of canonical vector 2 (Z_2) and canonical root 2 (λ_2):

The procedure followed in the case of matrix-A was repeated to obtain the second and third canonical roots.

c) Development of other matrices:

Reduced matrices C, D etc were also developed just like B-matrix from A-matrix. However, this may not require if $\lambda_1 + \lambda_2$ account for >80% variation.

d) Mean of canonical variates:

The two means (Z_1 and Z_2) were obtained for each of the 50 groundnut genotypes.

e) $\lambda_1 - \lambda_2$ chart:

If $(\lambda_1 + \lambda_2) > 80\%$, a two dimensional pictorial representation (Scatter diagram) of all the varieties was possible.

3.5.1.9. Computation of intra-cluster divergence:

The average intra-cluster distance was obtained by using following formula.

$$D^2 = \frac{\sum D^2 i}{N}$$

Where,

$\sum D^2 i$ = Sum of distance between all possible combinations of genotypes involved in a cluster

n = Possible combinations

3.5.1.10. Computation of inter-cluster divergence:

The average inter-cluster distance was calculated using all possible D^2 values between genotypes included in any two clusters.

3.5.1.11. Cluster means:

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included in that cluster.

3.5.2. Analysis of G x E interaction and estimation of stability parameters:

The phenotypic value (P) measured on a suitable scale is not equal to genotypic value (G) when the genotype is grown under more than one environment (E), i.e., $P \neq G + E$. But $P = G + E + (G \times E)$. Presence of G x E interaction underlies the stability of genotypes and influences the adaptability of improved strains.

The stability parameters were estimated utilizing the regression technique or model as suggested by Eberhart and Russell (1966). This model, $Y_{ij} = \mu_i + \beta_i I_j + \sigma_{ij}$, defines stability parameters that may be used to describe the performance of a genotype over a series of environments.

Where,

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

μ_i = Mean of the i^{th} genotype over all environments.

β_i = Regression coefficient that measures the response of the i^{th} genotype to varying environments.

σ_{ij} = Deviation from regression of the i^{th} genotype at j^{th} environment.

I_j = Environmental index obtained as the mean of all genotypes at the environment minus the grand mean.

$$I_j = \left(\sum_i Y_{ij} / g \right) - \left(\sum_i \sum_j Y_{ij} / gn \right), \sum_j I_j = 0$$

Where,

$\sum_i Y_{ij}$ = Total of all the genotypes at j^{th} environment.

$\sum_i \sum_j Y_{ij}$ = Grand total

g = Genotype 1 to 50

n = Environment 1 to 4

3.5.2.1. Bartlett's test for homogeneity of error variance:

For *kharif* (2 environments) and summer (2 environments) conditions, respective error mean squares were used to test the homogeneity of variance with Bartlett's test (Snedecor and Cochran, 1967).

$$\bar{S}^2 = \frac{E}{\sum_{i=1}^E} \frac{1}{K_i} \left[\sum_{i=1}^E K_i S_i^2 \right]$$

Where,

$\bar{S}^2$ = Pooled error mean squares,

K_i = Error degrees of freedom associated with i^{th} experiment

E = Number of experiments

S_i^2 = Error mean squares of i^{th} experiment

$$\chi^2 = \frac{\left[\sum_{i=1}^E K_i \log_e \bar{S}^2 - \sum_{i=1}^E K_i \log_e S_i^2 \right]}{C}$$

Where,

$$C = 1 + \frac{1}{3(E-1)} \left[\sum_{i=1}^E \frac{1}{K_i} - \frac{1}{\sum_{i=1}^E K_i} \right]$$

Calculated χ^2 was compared with table χ^2 value for (E-1) d.f. at 5 and 1 per cent level of significance.

The error means squares were heterogenous after transformation as described by Hinz and Eagles (1976). Thus, error mean

squares were assumed to be homogenous in this situation and data were analysed over all environments on the original scale.

3.5.2.2. Estimation of regression coefficient (bi):

It is the regression of the performance of each variety under different environments on the environmental means over all the genotypes. The b_i was estimated by using following formula.

$$b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

Where,

$\sum_j Y_{ij} I_j$ = Sum of products

$\sum_j I_j^2$ = Sum of squares

Analysis of variance for stability

Sr. No.	Source	d.f.	S.S.	M.S.	F
1	Total	ng-1	$\sum_i \sum_j Y_{ij}^2 - C.F.$		
2	Genotypes (G)	g-1	$\frac{1}{n} \sum_i Y_{i.}^2 - C.F.$	MS ₁	MS ₁ /MS ₃
3	Environment (E.) + V x E.	g (n-1)	$\sum_i \sum_j Y_{ij}^2 - \sum_i Y_{i.}^2 / n$		
4	Env. (linear)	1	$\frac{1}{g} \sum_j (\sum_i Y_{ij} I_j)^2 / \sum_j I_j^2$		
5	G x Env. (linear)	g-1	$\sum_j [(\sum_i Y_{ij} I_j)^2 / \sum_j I_j^2] - \text{Env. (linear) S.S.}$	MS ₂	MS ₂ /MS ₃
6	Pooled deviation	g(n-2)	$\sum_i \sum_j \sigma_{ij}^2$	MS ₃	MS ₃ /MS ₄
	Genotype 1 . . .	n-2 . . .	$\left[\sum_j Y_{ij}^2 - \frac{(Y_{i.})^2}{n} \right] - \frac{(\sum_j Y_{ij} I_j)^2}{\sum_j I_j^2}$		

	Genotype (G)	n-2	$\left[\sum_j Y_{gj}^2 - \frac{Y_{g.}^2}{n} \right] - \frac{(\sum_j Y_{gj} I_j)^2}{\sum_j I_j^2}$ $= \sum_j \sigma^2_{gj}$		
7	Pooled error	n(r-1) (g-1)	Pooled replications x genotypes SS over environment M'e	MS ₄ = M'e	

n = Number of environments, g = Number of genotypes,

r = Number of replications, I = Environmental Index,

Y_{ij} = basic observation, i.e., mean of the i^{th} genotype over replications in j^{th} environment

M'e = Pooled σ^2_e/r

3.5.2.3. Deviation from regression (S^2_{di}):

The deviation from regression of each genotype was estimated using following formula.

$$S^2_{di} = \left[\sum_j \hat{\sigma}^2_{ij} / (n-2) \right] - S^2_e / r$$

Where,

$$\sum_j \hat{\sigma}^2_{ij} = \left[\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{n} \right] - \frac{(\sum_j Y_{ij} I_j)^2}{\sum_j I_j^2}$$

S^2_e / r = Estimate of the pooled error (or the variance of a genotype means at the j^{th} location)

Standard error of b was calculated by using following formula to test the significance of b_i that does not differ from zero by using approximate 't' test at 5 and 1 per cent level of significant.

$$SE(b) = \sqrt{\frac{MS \text{ due to pooled deviation}}{\sum_j I_j^2}}$$

The hypothesis that any regression coefficient does not differ from unity was also tested by the appropriate 't' test.

An approximate test of the deviations from regression for each variety was obtained as below.

$$F \approx (\sum_j \hat{\sigma}_{ij}^2 / n - 2) / \text{Pooled error}$$

3.5.3. Relationship between genetic divergence and phenotypic stability:

The relationship between genetic diversity and phenotypic stability was studied by many workers (Rana and Murty, 1971 in sorghum; Verma *et al.* 1973 in soybean; Shoran, 1982 in pigeonpea; Jain and Pandya, 1984 in chickpea; Mahto, 1995 and Mahto and Singh, 1996 in Linseed). Therefore, in the present investigation, the efforts have been made to understand the relationship between genetic divergence and phenotypic stability for yield and yield contributing traits in groundnut.

3.5.4. Selection of parents for hybridization programme:

- a) Selection of parents for hybridization from different clusters was done on the basis of mean statistical distance ($\bar{D}$) suggested by Bhatt (1970). According to him the crosses between parents belonging to different clusters having same or higher inter-cluster distance than the mean statistical distance ($\bar{D}$) may be attempted.
- b) Selection of parents for hybridization on the basis of stability and higher mean performance belonging to different clusters was done. It is assumed that crosses among selected genotypes based on genetic divergence and stability analysis may provide enough genetic diversity to select for high yield and stable segregates in the segregating generations.

CHAPTER IV

EXPERIMENT FINDINGS

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CHAPTER IV

EXPERIMENTAL FINDINGS

The results of the present study on “Genetic diversity in relation to seasonal adaptability in groundnut” carried out over two seasons (*khariif* and *Summer*) and two dates in each season at Central Research Station, Dr.PDKV, Akola with 50 genotypes (24 varieties and 26 germplasm lines) are presented below in this chapter.

4.1. Analysis of Variance

The data collected on 13 traits of agronomic importance were subjected to analysis of variance for different characters under each environment and pooled environments. Test for homogeneity using Bartlett's test was performed for error variance of each environment and was found to be homogenous in respect of all traits. The variation among genotypes was highly significant for all the characters in all environments indicating the presence of considerable genetic variability for the characters under study (Table 4.1). Pooled analysis of variance (Table 4.2) revealed that the mean squares due to seasons and dates were highly significant for all the characters except sound mature kernel per cent and oil per cent. The mean squares due to season x dates were highly significant for all the characters except primary branches per plant. It was also revealed from the Table 4.2 that the genotypic differences were significant for all the characters under study. Genotype x season interactions were highly significant in all the characters. The mean squares due to genotype x date were significant for all the characters, except primary branches per plant and oil content (%). The interaction due to genotypes x seasons x dates were significant for all the characters, except primary branches per plant, shelling per cent and oil content (Table 4.2). Pooled ANOVA (Table 4.3) revealed that the mean squares due to environments and genotypes were highly significant for all the characters.

Table 4.1: Analysis of variance for different characters under each environment

Sr. No.	Characters	Source of variation	d.f.	Mean squares			
				E ₁	E ₂	E ₃	E ₄
1	2	3	4	5	6	7	8
1.	Days to 50% flowering	Replications	3	2.9533	2.9650	0.3125	1.6133
		Genotypes	49	4.9086**	5.1838**	30.4796**	17.4935**
		Error	147	0.8275	0.8494	1.7436	1.0589
2.	Height of main axis (cm)	Replications	3	7.7189	3.1486	2.5523	20.4388
		Genotypes	49	140.4072**	136.5674**	65.7406**	42.8637**
		Error	147	1.3744	3.1502	1.2105	1.2585
3.	Primary branches per plant	Replications	3	0.3251	0.3782	0.2407	0.3889
		Genotypes	49	0.8171**	0.6648**	1.6450**	1.8373**
		Error	147	0.1029	0.1014	0.1059	0.1472
4.	Secondary branches per plant	Replications	3	0.1789	0.3864	0.2561	1.5222
		Genotypes	49	2.6519**	3.9584**	21.6037**	17.0410**
		Error	147	0.1629	0.1229	0.2968	0.3542
5.	Mature pods/plant	Replications	3	3.8163	1.6738	2.2706	0.9597
		Genotypes	49	50.1878**	45.6084**	23.6394**	36.2208**
		Error	147	1.0925	1.8103	0.9612	1.1590
6.	100-pod weight (g)	Replications	3	5.2331	0.4346	1.0081	1.6758
		Genotypes	49	360.9881**	347.6274**	339.9879**	364.9452**
		Error	147	2.0076	3.0476	2.0123	2.1035
7.	100-kernel weight (g)	Replications	3	4.7699	0.2130	1.3107	2.8153
		Genotypes	49	63.6187**	60.8690**	83.3649**	80.2156**
		Error	147	0.9184	1.3977	1.0749	1.0744
8.	Shelling (%)	Replications	3	9.1249	3.3121	0.1900	4.1938
		Genotypes	49	123.0618**	152.0119**	84.5456**	96.9201**
		Error	147	1.7524	1.8405	1.6018	1.3782
9.	Sound mature kernel (%)	Replications	3	4.7003	6.8055	12.0011	0.7900
		Genotypes	49	145.7902**	178.3737**	119.4118**	108.7560**
		Error	147	1.8016	2.1116	1.9897	1.5809
10.	Oil content (%)	Replications	3	2.7500	2.7863	0.9575	1.9028
		Genotypes	49	30.7090**	35.1263**	21.7952**	26.5613**
		Error	147	0.7098	0.8658	1.2293	1.1024
11.	Days to maturity	Replications	3	14.2067	1.6983	2.9650	2.0600
		Genotypes	49	58.6122**	48.1960**	79.2985**	64.3078**
		Error	147	1.1488	2.5283	1.9276	2.0838
12.	Pod yield/plant	Replications	3	1.5946	0.5747	0.8247	0.3094
		Genotypes	49	16.5434**	17.3801**	9.9982**	14.4153**
		Error	147	0.6741	0.4237	0.5339	0.6400
13.	Kernel yield/plant	Replications	3	1.0313	0.2481	0.3537	0.2149
		Genotypes	49	9.1346**	8.6811**	5.4479**	7.5751**
		Error	147	0.3277	0.1938	0.2487	0.2937

** P ≤ 0.01

Table 4.2: Analysis of variance for different characters over two seasons and two dates

Sr. No.	Source of variation	d.f.	Mean squares												
			Days to 50% flowering	Height of main axis (cm)	Primary branches per plant	Secondary branches per plant	Mature pods per plant	100-pod weight (g)	100-kernel weight (g)	Shelling %	Sound mature kernel %	Oil content (%)	Days to maturity	Pod yield/ plant	Kernel yield/ plant
1	Replications	3	3.640	21.952	0.924	0.581	1.796	0.740	3.597	3.988	15.666	0.178	3.308	0.764	0.468
2	Seasons	1	57088.205**	35125.751**	118.888**	1899.745**	542.522**	535.790**	110.633**	536.281**	0.002	2.509	85367.120**	61.550**	16.331**
3	Dates	1	4851.125**	1654.275**	17.111**	25.992**	170.940**	24.325**	72.180**	521.968**	6.195	1.155	3042.000**	46.803**	36.338**
4	Seasons x dates	1	5660.480**	94.394**	0.002	6.882**	168.361**	676.936**	202.709**	35.955**	610.053**	338.260**	400.445**	41.360**	21.223**
5	Genotypes	49	43.153**	261.015**	3.511**	29.205**	92.914**	1346.688**	267.755**	430.097**	521.049**	104.500**	149.367**	32.663**	18.375**
6	Genotypes x season	49	9.970**	115.607**	1.256**	15.318**	57.488**	41.060**	11.440**	22.455**	21.678**	8.292**	92.367**	22.072**	10.794**
7	Genotypes x dates	49	2.406**	3.984**	0.074	0.369*	1.915*	10.724**	4.639**	2.660**	5.016**	0.729	4.916**	1.589**	0.720**
8	Genotypes x seasons x dates	49	2.536**	4.973**	0.123	0.363*	3.339**	15.076**	4.235**	1.328	4.588**	0.671	3.764**	2.014**	0.950**
9	Error (c)	597	1.124	1.782	0.115	0.240	1.272	2.295	1.127	1.683	1.886	1.003	1.982	0.572	0.259
10	Total	799	89.020	71.211	0.564	5.375	11.606	89.955	19.005	30.640	36.112	8.181	126.001	4.135	2.165

* $P \leq 0.05$, ** $P \leq 0.01$

Table 4.3 : Analysis of variance for different characters under pooled environments

Sr. No.	Source of variation	d.f.	Mean squares												
			Days to 50% flowering	Height of main axis (cm)	Primary branches per plant	Secondary branches per plant	Mature pods/plant	100 pod weight (g)	100 kernel weight (g)	Shelling %	Sound mature kernel %	Oil content (%)	Days to maturity	Pod yield/plant	Kernel yield/plant
1	Replications	3	3 640	21.952	0.924**	0.581	1.796	0.740	3.597	3.988	15.666**	0.178	3.308	0.764	0.468
2	Environments	3	22533.271**	12291.474**	45.334**	644.206**	293.941**	412.350**	128.507**	364.734**	205.417**	113.975**	29603.188**	49.904**	24.630**
3	Interaction	9	1.405	3.969	0.136	0.588	2.308	2.537	1.837	4.278	2.877	2.739*	5.875	0.847	0.460
4	Total	15	4508.225**	2465.066**	9.333**	129.310**	60.532**	84.140**	27.523**	76.311**	45.943**	24.474**	5924.824**	10.641**	5.296**
5	Genotypes	49	43.153**	261.015**	3.511**	29.205**	92.914**	1346.688**	267.755**	430.097**	521.049**	104.500**	149.367**	32.663**	18.375**
6	Error	735	1.890	9.703	0.188	1.257	5.187	6.292	2.247	3.077	3.582	1.428	8.274	2.166	1.044

* $P \leq 0.05$, ** $P \leq 0.01$

4.2. Mean Performance of Genotypes in Different Environments

The mean values based on all the 50 genotypes for the different traits varied from environment to environment which indicates differential impact of environment on the gene expression which ultimately affected the phenotypic expression (Table 4.4). Days required for 50 per cent flowering was maximum in E_3 (50.2850), whereas it was lowest in E_1 (28.07). Height of main axis was maximum in E_1 (35.7305 cm) and it was minimum in E_4 (19.602 cm). Primary and secondary branches were more in summer season environments (E_3 and E_4) than for the rainy season environments (E_1 and E_2). The mean values for 100-pod weight and 100-kernel weight were higher in E_4 (68.851 g and 28.458 g respectively) compared to E_3 (65.3745 g and 26.7075 g respectively). Shelling per cent was low in E_2 (64.379%) and it was high in E_3 (67.632%). The mean values for sound mature kernel per cent and oil per cent indicated that there was less influence of environments. However, sound mature kernel per cent and oil per cent were comparatively more in E_1 (88.2195 %) and E_4 (44.654 %) respectively. Crop matured in less days in E_2 (102.365), whereas it took maximum days in E_3 (126.925). Surprisingly, *kharif* environment E_1 (dry sowing before onset of monsoon) produced highest pod and kernel yield per plant (7.3155 g and 4.8925 g) respectively.

4.3. Analysis of Dispersion Using Wilk's Criterion

Analysis of dispersion has been presented in Table 4.5. The analysis of dispersion for the test of significance of differences in the mean values based on Wilk's Criterion revealed highly significant differences between the genotypes for the aggregate of 13 characters, justifying thereby, the need to calculate D^2 values. Therefore, D^2 values were estimated for all the possible pair wise combinations of the 50 genotypes for four different environments separately (E_1 , E_2 , E_3 and E_4), pooling *kharif* season environments ($E_1 + E_2$), pooling summer season environments ($E_3 + E_4$) and pooling all environments ($E_1 + E_2 + E_3 + E_4$).

Table 4.4: Mean performance for different characters under different environments

Sr. No.	Characters	Character means in different environments			
		E ₁	E ₂	E ₃	E ₄
1.	Days to 50% flowering	28.0700	28.4650	50.2850	40.0400
2.	Height of main axis (cm)	35.7305	33.5415	23.1650	19.6020
3.	Primary branches per plant	4.7555	4.4595	5.5230	5.2340
4.	Secondary branches per plant	0.8450	0.6700	4.1125	3.5665
5.	Mature pods/plant	13.4010	11.5590	10.8365	10.8295
6.	100-pod weight (g)	67.5630	65.3745	67.3600	68.8510
7.	100-kernel weight (g)	28.3150	26.7075	28.0520	28.4580
8.	Shelling (%)	66.4185	64.3790	67.6320	66.4405
9.	Sound mature kernel (%)	88.2195	86.2970	86.4695	88.0400
10.	Oil content (%)	44.6180	43.2415	43.4295	44.6540
11.	Days to maturity	104.8500	102.3650	126.9250	121.6100
12.	Pod yield/plant	7.3155	6.3770	6.3060	6.2770
13.	Kernel yield/ plant	4.8925	4.1405	4.2810	4.1805

Table 4.5: Analysis of dispersion

Sr. No.	Source of variation	d.f.	Mean Squares			
			E ₁	E ₂	E ₃	E ₄
1.	Genotypes	49	9.7476 E12**	1.2873 E13**	1.7528 E13**	2.7211 E13**
2.	Error	146	1.4395 E-07	2.9757 E-06	1.4248 E-06	9.2499 E-07
3.	Total	195	2.4494 E12	3.2348E12	4.4045 E12	6.8377 E12

Table continued:

Sr. No.	Source of variation	d.f.	Mean Squares		d.f.	Mean squares
			E ₁ + E ₂	E ₃ + E ₄		E ₁ + E ₂ + E ₃ + E ₄
1.	Genotypes	49	4.3452 E16**	6.6547 E16**	49	3.5910 E19
2.	Error	342	1.7424 E-06	3.8864 E-05	734	1.0231 E-01
3.	Total	391	5.4454 E15	8.3397 E15	783	2.2472 E18

** P ≤ 0.01

4.4. Contribution of Individual Character Towards Genetic Divergence

The contribution of each character towards genetic divergence has been presented in Table 4.6. In E_1 , the contribution of 100-pod weight to the total divergence was maximum (29.96%), followed by sound mature kernel per cent (17.39 %) and height of main axis (13.88%). Relatively less contribution was made by other characters. In E_2 also, the contribution of 100-pod weight to the total divergence was maximum (28.0%), followed by sound mature kernel per cent (18.94%) and shelling per cent (17.8%). Relatively less contribution was made by other characters. In E_3 also, the contribution of 100-pod weight to the total divergence was maximum (33.06%), followed by secondary branches per plant (14.86%) and sound mature kernel per cent (10.53%). Relatively less contribution was made by other characters. In E_4 also, the contribution of 100-pod weight was maximum (33.71%) to the total divergence, followed by sound mature kernel per cent (17.63%) and shelling per cent (12.82%). Relatively less contribution was made by other characters.

In pooled *kharif* season environments ($E_1 + E_2$), the contribution of 100-pod weight was maximum (30.53%) to the total divergence followed by sound mature kernel per cent (17.06%), shelling per cent (16.98%) and height of main axis (11.10%). Relatively less contribution was made by other characters. In pooled summer season environments ($E_3 + E_4$), the contribution of 100-pod weight to the total divergence was maximum (23.43%), followed by shelling per cent (18.12%), secondary branches per plant (18.04%) and sound mature kernel per cent (13.80%). Relatively less contribution was made by other characters. In pooled estimates of all environments ($E_1 + E_2 + E_3 + E_4$), the contribution of 100-pod weight to the total divergence was maximum (30.69%), followed by sound mature kernel per cent (22.61%) and shelling per cent (21.88%). Relatively less contribution was made by other characters.

Table 4.6: Contribution of each character towards genetic divergence under different environments

Sr. No	Characters	E ₁		E ₂		E ₃		E ₄		E ₁ + E ₂		E ₃ + E ₄		E ₁ + E ₂ + E ₃ + E ₄	
		Times ranked 1 st	% contribution	Times ranked 1 st	% contribution	Times ranked 1 st	% contribution	Times ranked 1 st	% contribution	Times ranked 1 st	% contribution	Times ranked 1 st	% contribution	Times ranked 1 st	% contribution
1.	Days to 50% flowering	1	0.08	2	0.16	10	0.82	7	0.57	1	0.08	7	0.57	17	1.39
2.	Height of main axis(cm)	170	13.88	77	6.29	99	8.08	46	3.76	136	11.10	55	4.49	18	1.47
3.	Primary branches/plant	0	0.00	5	0.41	9	0.73	6	0.49	3	0.24	14	1.14	10	0.82
4.	Secondary branches/plant	10	0.82	77	6.29	182	14.86	105	8.57	29	2.37	221	18.04	12	0.98
5.	Mature pods/plant	64	5.22	45	3.67	32	2.61	38	3.10	80	6.53	44	3.59	16	1.31
6.	100-pod weight (g)	367	29.96	343	28.00	405	33.06	413	33.71	374	30.53	287	23.43	376	30.69
7.	100-kernel weight (g)	67	5.47	64	5.22	110	8.98	98	8.00	76	6.20	76	6.20	107	8.73
8.	Shelling %	110	8.98	218	17.80	107	8.73	157	12.82	208	16.98	222	18.12	268	21.88
9.	Sound mature kernel (%)	213	17.39	232	18.94	129	10.53	216	17.63	209	17.06	169	13.80	277	22.61
10.	Oil content (%)	53	4.33	72	5.88	16	1.31	23	1.88	68	5.55	47	3.84	107	8.73
11.	Days to maturity	87	7.10	11	0.90	114	9.31	70	5.71	18	1.47	80	6.53	15	1.22
12.	Pod yield/plant	78	6.37	74	6.04	11	0.90	46	3.76	22	1.80	3	0.24	2	0.16
13.	Kernel yield/plant	5	0.41	5	0.41	1	0.08	0	0.00	1	0.08	0	0.00	0	0.00

4.5. Grouping of Genotypes into Different Clusters

Grouping of genotypes was done by Tocher's method and is presented in Table 4.7. In E_1 , all the genotypes were grouped into nine clusters. Cluster I was the largest involving 35 genotypes from different geographical origin. Eight genotypes were grouped in cluster IV. The remaining clusters (II, III, V, VI, VII, VIII and IX) contained only one genotype. In E_2 , all the genotypes were grouped into seven clusters. Cluster I was the largest involving 41 genotypes from different geographical origin. Four genotypes were grouped in cluster III. The remaining clusters (II, IV, V, VI and VII) contained only one genotype. In E_3 , all the genotypes were grouped into nine clusters. The cluster I was the largest involving 20 genotypes from different geographical origin. Eleven, eight, four and three genotypes were grouped in cluster IV, V, VII and II respectively. The remaining clusters (III, VI, VIII and IX) contained only one genotype. In E_4 , all the genotypes were grouped into ten clusters. The cluster I was the largest involving 22 genotypes from different geographical origin. Cluster II and III were the next large clusters which involve 11 and 10 genotypes respectively belonging to diverse origin. The remaining clusters (IV, V, VI, VII, VIII, IX and X) contained only one genotype.

In *kharif* condition pooled over 2 environments ($E_1 + E_2$), all the genotypes were grouped into ten clusters. The cluster I was the largest involving 26 genotypes from different geographical origin. Cluster II was second largest cluster involving 11 genotypes and cluster V involved six genotypes of diverse origin. The remaining clusters (III, IV, VI, VII, VIII, IX and X) contained only one genotype. In summer condition pooled over 2 environments ($E_3 + E_4$), all the genotypes were grouped into nine clusters. The cluster I was the largest involving 20 genotypes, whereas cluster III and cluster II involved 13 and 11 genotypes respectively from different geographical origin. The remaining clusters (IV, V, VI, VII, VIII and IX) contained only one genotype. In pooled analysis over all environments ($E_1 + E_2 + E_3 + E_4$), all the genotypes were grouped into eight clusters. The cluster I was the largest, involving 19 genotypes, as well as eleven genotypes were

grouped in cluster III and eight each in cluster II and IV from diverse geographical origin. The remaining clusters (V, VI, VII and VIII) contained only one genotype.

Table 4.7: Clustering pattern of groundnut genotypes in each environment and pooled environments

Environ-ments	Clus-ter No.	Total No.of genot-ypes	Genotypes included in the cluster		
E ₁ (Kharif 2002)	I	35	(39) PI 268782 (40) PI 268829 (14) KRG 1 (49) U 2-4-5 (36) NCAc 7785 (42) Pearl (17) S 206 (30) NCAc 7776 (32) NCAc 7778 (10) J 11 (48) U 1-1-1 (1) AK 12-24	(18) SB XI (38) NCAc 7790 (24) TMV 2 (7) GG-2 (16) POL.2 (6) GAUG 1 (35) NCAc 7783 (8) Gimar 1 (15) MH 1 (41) PI 268642 (29) Comet (13) Jyoti	(9) ICG (FDRS) 10 (28) Ah 6649 (19) Spanish Improved (33) NCAc 7780 (3) ALR 3 (34) NCAc 7782 (26) Ah 4104-2 (27) Ah 4515 (50) U 2-12-1 (47) Teja Amra Local (2) AK 159
	II	1	(11) JL 24		
	III	1	(22) TG 17		
	IV	8	(31) NCAc 7777 (37) NCAc 7787 (45) Span white	(12) JL 220 (5) CO 2 (46) Taiwan Selection	(21) TKG 19A (4) CO 1
	V	1	(43) Starr		
	VI	1	(23) TG 26		
	VII	1	(25) Ah 1		
	VIII	1	(44) Span cross		
	IX	1	(20) TAG 24		
E ₂ (Kharif 2002)	1	41	(39) PI 268782 (40) PI 268829 (27) Ah 4515 (10) J 11 (13) Jyoti (18) SB XI (17) S 206 (41) PI 268642 (32) NCAc 7778 (15) MH 1 (38) NCAc 7790 (30) NCAc 7776 (24) TMV 2 (48) U 1-1-1	(42) Pearl (29) Comet (49) U 2-4-5 (14) KRG 1 (47) Teja Amra Local (1) AK 12-24 (16) Pol. 2 (35) NCAc 7783 (2) AK 159 (11) JL 24 (6) GAUG 1 (28) Ah 6649 (19) Spanish Improved (33) NCAc 7780	(34) NCAc 7782 (9) ICG (FDRS) 10 (3) ALR 3 (26) Ah 4104-2 (22) TG 17 (8) Gimar 1 (36) NCAc 7785 (7) GG 2 (46) Taiwan Selection (12) JL 220 (50) U 2-12-1 (23) TG 26 (20) TAG 24

Table 4.7 Continued -

Environ-ments	Clus-ter No.	Total No.of genot-ypes	Genotypes included in the cluster		
	II	1	(45) Span white		
	III	4	(31) NCAc 7777	(4) CO 1	
			(37) NCAc 7787	(21) TKG 19A	
	IV	1	(43) Starr		
	V	1	(44) Span cross		
	VI	1	(25) Ah 1		
E ₃ (Summer 2003)	VII	1	(5) CO 2		
	I	20	(17) S 206 (47) Teja Amar Local (48) U 1-1-1 (16) Pol.2 (6) GAUG 1 (24) TMV 2 (10) J 11	(38) NCAc 7790 (42) Pearl (13) Jyoti (39) PI 268782 (40) PI 268829 (8) Girnar 1 (15) MH 1	(18) SB XI (9) ICG (FDRS) 10 (27) Ah 4515 (36) NCAc 7785 (1) AK 12-24 (11) JL 24
	II	3	(31) NCAc 7777	(37) NCAc 7787	(49) U 2-4-5
	III	1	(2) AK 159		
	IV	11	(19) Spanish Improved (26) Ah 4104-2 (46) Taiwan Selection (34) NCAc 7782	(41) PI 268642 (22) TG 17 (12) JL 220 (5) Co 2	(45) Span white (4) Co 1 (33) NCAc 7780
	V	8	(14) KRG 1 (50) U 2-12-1 (29) Comet	(43) Starr (23) TG 26 (7) GG 2	(44) Span cross (20) TAG 24
	VI	1	(28) Ah 6649		
	VII	4	(30) NCAc 7776 (32) NCAc 7778	(3) ALR 3 (35) NCAc 7783	
	VIII	1	(25) Ah 1		
	IX	1	(21) TKG 19A		
E ₄ (Summer 2003)	I	22	(10) J 11 (13) Jyoti (39) PI 268782 (40) PI 268829 (38) NCAc 7790 (24) TMV 2 (15) MH 1 (29) Comet	(27) Ah 4515 (43) Starr (14) KRG 1 (48) U, 1-1-1 (47) Teja Amra Local (6) GAUG 1 (18) SB XI (7) GG 2	(42) Pearl (36) NCAc 7785 (41) PI 268642 (32) NCAc 7778 (19) Spanish Improved (17) S 206
	II	11	(11) JL 24 (34) NCAc 7782 (46) Taiwan Selection (26) Ah 4104-2	(22) TG 17 (2) AK 159 (1) AK 12-24 (12) JL 220	(28) Ah 6649 (3) ALR 3 (21) TKG 19A
	III	10	(31) NCAc 7777 (37) NCAc 7787 (45) Span white (9) ICG (FDRS) 10	(16) Pol.2 (49) U 2-4-5 (8) Girnar 1 (30) NCAc 7776	(4) Co 1 (33) NCAc 7780

Table 4.7 Continued -

Environ- ments	Clus- ter No.	Total No. of genot- ypes	Genotypes included in the cluster		
	IV	1	(23) TG 26		
	V	1	(35) NCAc 7783		
	VI	1	(20) TAG 24		
	VII	1	(44) Span cross		
	VIII	1	(50) U 2-12-1		
	IX	1	(25) Ah 1		
	X	1	(5) Co 2		
Pooled E ₁ + E ₂ (Kharif 2002)	I	26	(39) PI 268782 (40) PI 268829 (14) KRG 1 (49) U 2-4-5 (10) J 11 (36) NCAc 7785 (17) S 206 (42) Pearl (32) NCAc 7778	(30) NCAc 7776 (48) U 1-1-1 (38) NCAc 7790 (18) SB XI (41) PI 268642 (1) AK 12-24 (15) MH 1 (24) TMV 2 (13) Jyoti	(29) Comet (16) Pol 2 (35) NCAc 7783 (7) GG 2 (6) GAUG 1 (9) ICG (FDRS) 10 (47) Teja Amra Local (8) Girnar 1
	II	11	(11) JL 24 (34) NCAc 7782 (22) TG 17 (19) Spanish Improved	(26) Ah 4104-2 (28) Ah 6649 (33) NCAc 7780 (46) Taiwan Selection	(3) ALR 3 (12) JL 220 (21) TKG 19A
	III	1	(27) Ah 4515		
	IV	1	(50) U 2-12-1		
	V	6	(31) NCAc 7777 (37) NCAc 7787	(45) Span white (20) TAG 24	(5) Co 2 (4) Co 1
	VI	1	(23) TG 26		
	VII	1	(2) AK 159		
	VIII	1	(43) Starr		
	IX	1	(44) Span cross		
	X	1	(25) Ah 1		
Pooled E ₃ + E ₄ (Summer 2003)	I	20	(10) J 11 (13) Jyoti (39) PI 268782 (40) PI 268829 (38) NCAc 7790 (27) Ah 4515 (24) TMV 2	(11) JL 24 (19) Spanish Improved (46) Taiwan Selection (34) NCAc 7782 (1) AK 12-24 (26) Ah 4104-2 (15) MH 1	(41) PI 268642 (18) SB XI (48) U 1-1-1 (6) GAUG 1 (42) Pearl (32) NCAc 7778
	II	11	(31) NCAc 7777 (37) NCAc 7788 (45) Span white (12) JL 220	(9) ICG (FDRS) 10 (16) Pol.2 (49) U 2-4-5 (30) NCAc 7776	(4) Co 1 (8) Girnar 1 (5) Co 2
	III	13	(17) S 206 (47) Teja Amra Local (14) KRG 1 (29) Comet (43) Starr	(36) NCAc 7785 (50) U 2-12-1 (23) TG 26 (7) GG 2 (20) TAG 24	(44) Span cross (2) AK 159 (35) NCAc 7783

Table 4.7 Continued -

Environ-ments	Clus-ter No.	Total No.of genot-ypes	Genotypes included in the cluster		
	IV	1	(22) TG 17		
	V	1	(21) TKG 19 A		
	VI	1	(28) Ah 6649		
	VII	1	(25) Ah 1		
	VIII	1	(3) ALR 3		
	IX	1	(33) NCAc 7780		
Pooled E ₁ +E ₂ +E ₃ +E ₄ (Kharif 2002 and Summer 2003)	I	19	(39) PI 268782 (40) PI 268829 (10) J 11 (13) Jyoti (27) Ah 4515 (14) KRG 1 (29) Comet	(17) S 206 (36) NCAc 7785 (47) Teja Amra Local (38) NCAc 7790 (41) PI 268642 (18) SB XI (1) AK 12-24	(24) TMV 2 (15) MH 1 (32) NCAc 7778 (48) U 1-1-1 (42) Pearl
	II	8	(11) JL 24 (19) Spanish Improved (34) NCAc 7782	(26) Ah 4104-2 (22) TG 17 (28) Ah 6649	(46) Taiwan Selection (6) GAUG 1
	III	11	(7) GG 2 (23) TG 26 (35) NCAc 7783 (30) NCAc 7776	(49) U 2-4-5 (8) Gimnar 1 (16) Pol. 2 (9) ICG (FDRS) 10	(2) AK 159 (20) TAG 24 (3) ALR 3
	IV	8	(31) NCAc 7777 (37) NCAc 7780 (45) Span white	(5) CO. 2 (12) JL 220 (4) CO.1	(33) NCAc 7780 (21) TKG 19A
	V	1	(43) Starr		
	VI	1	(44) Span cross		
	VII	1	(50) U 2-12-1		
	VIII	1	(25) Ah 1		

4.6. Canonical Analysis

The values to the canonical vectors and canonical roots have been presented in Tables 4.8 to 4.14. In E₁, the first two canonical roots accounted for 55.24 per cent of the observed variability in the material ($\lambda_1 = 35.04\%$ and $\lambda_2 = 20.20\%$). However, the overall contribution of the first five canonical roots to the total variability among 50 genotypes was 84.79 per cent suggesting the completion of major portion of differentiation in the first five phases. Hundred pod weight, pod yield per plant, days to maturity and 100-kernel weight were important sources of variation in 1st vector. In 2nd vector, sound mature kernel per cent, height of main axis, mature pods per

plant, 100-pod weight and shelling per cent were important sources of variation. In 3rd vector shelling per cent, sound mature kernel per cent, 100-pods weight, pod yield per plant and 100-kernel weight shared major source of variation. In 4th vector, height of main axis, shelling per cent, pod yield per plant, and 100-kernel weight were important sources of variation. In 5th vector, days to maturity, sound mature kernel per cent and 100-kernel weight shared major sources of variation (Table 4.8).

Table 4.8 : Values of canonical vectors (Z) and canonical roots (λ) in E₁ (Kharif 2002)

Sr. No.	Characters	Canonical vectors				
		1 st Vector Z ₁	2 nd Vector Z ₂	3 rd Vector Z ₃	4 th Vector Z ₄	5 th Vector Z ₅
1.	Days to 50% flowering	0.03397	0.03434	0.02281	0.05789	0.06879
2.	Height of main axis(cm)	-0.01100	0.56509	-0.50238	0.32373	-0.46821
3.	Primary branches/plant	-0.03958	0.00411	-0.06990	-0.08121	-0.02551
4.	Secondary branches/plant	-0.00013	0.00600	-0.09624	0.07656	-0.23186
5.	Mature pods/plant	-0.19551	0.27574	-0.00897	-0.44569	-0.10620
6.	100 pod weight (g)	0.73246	0.27238	0.27842	-0.14865	-0.25702
7.	100 kernel weight (g)	0.21972	0.06550	0.17291	0.15974	0.17286
8.	Shelling %	-0.40102	0.14335	0.49307	0.30324	-0.06709
9.	Sound mature kernel (%)	-0.07807	0.68551	0.29169	-0.01914	0.45824
10.	Oil content (%)	-0.01305	-0.00309	0.10435	-0.63477	-0.17942
11.	Days to maturity	0.22643	0.06777	-0.48732	-0.03695	0.60550
12.	Pod yield/plant	0.39264	-0.15793	0.20960	0.29142	-0.02647
13.	Kernel yield/plant	0.04047	0.07004	-0.07035	-0.22716	0.01999

Canonical roots	Account for 100 %	Total
$\lambda_1 = 3497.55$	35.04 %	35.04 %
$\lambda_2 = 2015.76$	20.20 %	55.24 %
$\lambda_3 = 1334.79$	13.37 %	68.61 %
$\lambda_4 = 896.86$	8.99 %	77.60 %
$\lambda_5 = 717.82$	7.19 %	84.79 %

In E₂, the first two canonical roots accounted for 53.01 per cent of the observed variability in the material ($\lambda_1 = 29.51\%$ and $\lambda_2 = 23.50\%$). However, the overall contribution of first five canonical roots to the total variability among 50 genotypes was 80.89 per cent suggesting the completion of major portion of differentiation in the first five phases. Hundred pod

weight, sound mature kernel per cent, pod yield per plant, 100-kernel weight and height of main axis were important sources of variation in 1st vector. In 2nd vector, shelling per cent, sound mature kernel per cent, oil content, pod yield per plant, mature pods per plant and height of main axis were important sources of variation. In 3rd vector, sound mature kernel per cent and shelling per cent shared major source of variation. In 4th vector, sound mature kernel per cent, oil content, height of main axis and days to maturity were important sources of variation. In 5th vector, height of main axis, 100-kernel weight, secondary branches per plant and days to maturity shared major source of variation (Table 4.9).

Table 4.9 : Values of canonical vectors (Z) and canonical roots (λ) in E_2 (Kharif 2002)

Sr. No.	Characters	Canonical vectors				
		1 st Vector	2 nd Vector	3 rd Vector	4 th Vector	5 th Vector
		Z_1	Z_2	Z_3	Z_4	Z_5
1.	Days to 50% flowering	0.04715	0.01556	0.03949	0.03181	0.01635
2.	Height of main axis(cm)	0.20877	0.16963	-0.32782	0.26470	0.47804
3.	Primary branches/plant	-0.01566	0.01246	-0.11667	-0.00575	-0.00590
4.	Secondary branches/plant	-0.02121	-0.05498	-0.49171	0.00541	0.18392
5.	Mature pods/plant	0.01007	0.19390	-0.35935	-0.00785	-0.09555
6.	100 pod weight (g)	0.77530	-0.24764	0.09684	-0.30065	-0.31821
7.	100 kernel weight (g)	0.24863	0.06777	-0.02307	-0.15609	0.33740
8.	Shelling %	-0.16099	0.68862	0.16597	-0.51630	0.00459
9.	Sound mature kernel (%)	0.38389	0.47836	0.39680	0.53998	0.09810
10.	Oil content (%)	0.02935	0.26640	-0.34842	0.35319	-0.66037
11.	Days to maturity	0.03542	-0.18588	-0.07461	0.21763	0.14283
12.	Pod yield/plant	0.32515	0.21773	-0.41495	-0.28935	0.07625
13.	Kernel yield/plant	-0.09676	0.09126	-0.11134	-0.00873	-0.20292

Canonical roots	Account for 100 %	Total
$\lambda_1 = 2084.89$	29.51 %	29.51 %
$\lambda_2 = 1659.81$	23.50 %	53.01 %
$\lambda_3 = 766.42$	10.85 %	63.86 %
$\lambda_4 = 696.38$	9.86 %	73.72 %
$\lambda_5 = 506.50$	7.17 %	80.89 %

In E_3 , the first two canonical roots accounted for 58.15 per cent of the observed variability in the material ($\lambda_1 = 41.88\%$ and $\lambda_2 = 16.27\%$).

However, the overall contribution of first four canonical roots to the total variability among 50 genotypes was 76.31 per cent suggesting the completion of major portion of differentiation in the first four phases. Hundred pod weight, pod yield per plant, 100-kernel weight, days to maturity and sound mature kernel per cent were important sources of variation in 1st vector. In 2nd vector, secondary branches per plant, shelling per cent, sound mature kernel per cent, height of main axis and oil content were important sources of variation. In 3rd vector, height of main axis, 100-pod weight, secondary branches per plant and 100-kernel weight shared major source of variation. In 4th vector, 100-kernel weight, days to maturity, secondary branches per plant and primary branches per plant were important sources of variation (Table 4.10).

Table 4.10: Values of canonical vectors (Z) and canonical roots (λ) in E₃ (Summer 2003)

Sr. No.	Characters	Canonical vectors			
		1 st Vector Z_1	2 nd Vector Z_2	3 rd Vector Z_3	4 th Vector Z_4
1.	Days to 50% flowering	0.04554	0.16401	0.03645	0.03235
2.	Height of main axis(cm)	-0.08788	0.30099	0.38679	-0.43368
3.	Primary branches/plant	-0.06884	0.10482	0.06691	0.17776
4.	Secondary branches/plant	-0.14276	0.56812	0.29585	0.33079
5.	Mature pods/plant	-0.11163	0.12058	0.12248	-0.15564
6.	100 pod weight (g)	0.72579	-0.03016	0.34069	-0.21155
7.	100 kernel weight (g)	0.34952	0.19712	0.22623	0.47854
8.	Shelling %	-0.05243	0.51525	-0.00791	-0.22373
9.	Sound mature kernel (%)	0.15602	0.34201	-0.57648	-0.33330
10.	Oil content (%)	0.01554	0.29919	0.27592	0.00509
11.	Days to maturity	0.30132	0.16031	-0.40577	0.40498
12.	Pod yield/plant	0.43057	-0.01223	-0.04037	-0.21596
13.	Kernel yield/plant	-0.01313	0.01385	0.00279	-0.00734

Canonical roots	Account for 100 %	Total
$\lambda_1 = 3757.23$	41.88 %	41.88 %
$\lambda_2 = 1459.61$	16.27 %	58.15 %
$\lambda_3 = 1006.01$	11.21 %	69.36 %
$\lambda_4 = 623.55$	6.95 %	76.31 %

In E₄, the first two canonical roots accounts for 57.93 per cent of the observed variability in the material ($\lambda_1 = 32.92$ % and $\lambda_2 = 25.01$ %).

However, the overall contribution of the first four canonical roots to the total variability among 50 genotypes was 75.46 per cent suggesting the completion of major portion of differentiation in the first four phases. Hundred pod weight and pod yield per plant were important sources of variation in 1st vector. In 2nd vector, sound mature kernel per cent, shelling per cent, 100-kernel weight, oil content and secondary branches per plant were important sources of variation. In 3rd vector, mature pods per plant, 100-kernel weight, height of main axis, secondary branches per plant and 100-pod weight shared major source of variation. In 4th vector, secondary branches per plant, primary branches per plant and height of main axis were important sources of variation (Table 4.11).

Table 4.11 : Values of canonical vectors (Z) and canonical roots (λ) in E₄ (Summer 2003)

Sr. No.	Characters	Canonical vectors			
		1 st Vector	2 nd Vector	3 rd Vector	4 th Vector
		Z ₁	Z ₂	Z ₃	Z ₄
1.	Days to 50% flowering	0.00815	0.17380	0.03682	0.02083
2.	Height of main axis(cm)	-0.01792	0.18796	0.22838	0.14176
3.	Primary branches/plant	-0.05244	0.03315	-0.07206	0.31101
4.	Secondary branches/plant	-0.15054	0.23165	0.21050	0.70713
5.	Mature pods/plant	-0.11797	0.07727	0.45907	0.07971
6.	100 pod weight (g)	0.82649	0.19803	0.18961	0.06030
7.	100 kernel weight (g)	0.10546	0.33820	0.23712	-0.38918
8.	Shelling %	-0.35153	0.42653	0.14134	-0.42864
9.	Sound mature kernel (%)	-0.02407	0.63615	-0.47052	0.07641
10.	Oil content (%)	0.08594	0.30866	0.07290	0.12725
11.	Days to maturity	0.06175	0.04533	-0.58217	0.06416
12.	Pod yield/plant	0.35520	-0.00815	-0.08499	-0.10668
13.	Kernel yield/plant	0.06753	-0.19008	0.03522	-0.00159

Canonical roots	Account for 100 %	Total
$\lambda_1 = 2893.80$	32.92 %	32.92 %
$\lambda_2 = 2198.41$	25.01 %	57.93 %
$\lambda_3 = 932.96$	10.61 %	68.54 %
$\lambda_4 = 608.08$	6.92 %	75.46 %

In Kharif condition pooled over 2 environments ($E_1 + E_2$), the first two canonical roots accounted for 53.12 per cent of the observed variability in the material ($\lambda_1 = 31.99\%$ and $\lambda_2 = 21.13\%$). However, the overall contribution of the first six canonical roots to the total variability among 50 genotypes was 86.96 per cent indicating that the major portion of differentiation was completed in the first six phases. Hundred pod weight, 100-kernel weight, pod yield per plant and days to maturity were important sources of variation in 1st vector. In 2nd vector, sound mature kernel per cent, shelling per cent, height of main axis, mature pods per plant and 100-pod weight were important sources of variation. In 3rd vector, shelling per cent, 100-pod weight, 100-kernel weight and pod yield per plant shared major source of variation. In 4th vector, 100-kernel weight, height of main axis, days to maturity and sound mature kernel per cent were important sources of variation. In 5th vector, sound mature kernel per cent and days to maturity shared major source of variation. In 6th vector, 100 kernel weight, days to maturity, mature pods per plant and oil content were important sources of variation (Table 4.12).

In summer condition pooled over 2 environments ($E_3 + E_4$), the first two canonical roots accounted for 51.12 per cent of the observed variability in the material ($\lambda_1 = 29.97\%$ and $\lambda_2 = 21.15\%$). However, the overall contribution of first six canonical roots to the total variability among 50 genotypes was 84.56 per cent suggesting the completion of major portion of differentiation in the first six phases. Shelling per cent, secondary branches per plant, mature pods per plant and sound mature kernel per cent were important sources of variation in 1st vector. In 2nd vector, hundred pod weight, sound mature kernel per cent, days to maturity, oil content, secondary branches per plant and shelling per cent were important sources of variation. In 3rd vector, sound mature kernel per plant, shelling per cent and days to maturity shared major source of variation. In 4th vector, 100-pod weight, shelling per cent, height of main axis and 100-kernel weight were important sources of variation. In 5th vector, 100-kernel weight and days to maturity shared major source of variation. In 6th vector, height of main axis,

sound mature kernel per cent and primary branches per plant were important sources of variation (Table 4.13).

Table 4.12 : Values of canonical vectors (Z) and canonical roots (λ) in pooled E_1+E_2 (Kharif 2002)

Sr. No.	Characters	Canonical vectors					
		1 st Vector	2 nd Vector	3 rd Vector	4 th Vector	5 th Vector	6 th Vector
		Z_1	Z_2	Z_3	Z_4	Z_5	Z_6
1.	Days to 50% flowering	0.03715	0.05131	0.02923	0.06315	0.01836	0.10881
2.	Height of main axis(cm)	0.09448	0.37607	-0.67052	0.24616	-0.38992	-0.35315
3.	Primary branches/plant	-0.3441	-0.01550	-0.08969	-0.08081	-0.06908	0.03427
4.	Secondary branches/plant	0.01798	-0.02867	-0.12170	0.01500	-0.35254	0.15011
5.	Mature pods/plant	-0.12728	0.21746	-0.19809	-0.36536	-0.21067	0.28901
6.	100 pod weight (g)	0.80140	0.20568	0.30489	-0.21050	-0.13221	-0.17776
7.	100 kernel weight (g)	0.19720	0.17447	0.15410	0.31654	-0.30691	0.726777
8.	Shelling %	-0.48510	0.45711	0.45087	0.08236	-0.29737	-0.09385
9.	Sound mature kernel (%)	0.04347	0.68821	-0.04458	0.13419	0.62934	0.06502
10.	Oil content (%)	-0.04250	0.16517	-0.19085	-0.74870	0.04318	0.20751
11.	Days to maturity	0.14590	-0.13404	-0.32919	0.19854	0.21558	0.34021
12.	Pod yield/plant	0.15985	0.07506	0.14328	-0.04102	-0.16116	-0.15666
13.	Kernel yield/plant	-0.07074	0.03700	0.01273	-0.15562	-0.06089	0.00578

Canonical roots	Account for 100 %	Total
$\lambda_1 = 2150.24$	31.99 %	31.99 %
$\lambda_2 = 1420.21$	21.13 %	53.12 %
$\lambda_3 = 765.96$	11.40 %	64.52 %
$\lambda_4 = 602.14$	8.96 %	73.48 %
$\lambda_5 = 552.89$	8.23 %	81.71 %
$\lambda_6 = 352.71$	5.25 %	86.96 %

Table 4.13 : Values of canonical vectors (Z) and canonical roots (λ) in pooled $E_3 + E_4$ (Summer 2003)

Sr. No.	Characters	Canonical vectors					
		1 st Vector	2 nd Vector	3 rd Vector	4 th Vector	5 th Vector	6 th Vector
		Z ₁	Z ₂	Z ₃	Z ₄	Z ₅	Z ₆
1.	Days to 50% flowering	0.05804	0.17250	0.00518	0.12333	0.15115	0.05292
2.	Height of main axis (cm)	0.13627	0.08855	-0.11799	0.28829	0.11045	0.77528
3.	Primary branches/plant	0.07869	0.02938	-0.23904	-0.28844	0.19312	0.18147
4.	Secondary branches/plant	0.40000	0.23481	-0.77695	-0.21592	-0.15599	-0.12598
5.	Mature pods/plant	0.20319	-0.08219	-0.03774	0.14726	-0.27994	-0.02368
6.	100 pod weight (g)	-0.55414	0.56549	-0.22999	0.43875	-0.21227	-0.08010
7.	100 kernel weight (g)	0.09138	0.15686	-0.08283	0.27966	0.76338	-0.09774
8.	Shelling %	0.58762	0.21552	0.28810	0.40805	-0.07843	-0.32289
9.	Sound mature kernel (%)	0.18548	0.53396	0.40212	-0.34266	-0.14853	0.35621
10.	Oil content (%)	0.12104	0.32793	0.08434	-0.08094	-0.09870	-0.13531
11.	Days to maturity	-0.19011	0.33458	0.10758	-0.43463	0.31339	-0.24181
12.	Pod yield/plant	-0.15684	0.03100	0.00155	-0.00801	-0.23912	0.06595
13.	Kernel yield/plant	-0.00858	-0.05709	0.02640	0.00461	-0.06179	-0.13617

Canonical roots	Account for 100 %	Total
$\lambda_1 = 1598.59$	29.97 %	29.97 %
$\lambda_2 = 1128.14$	21.15 %	51.12 %
$\lambda_3 = 599.22$	11.23 %	62.35 %
$\lambda_4 = 453.57$	8.50 %	70.85 %
$\lambda_5 = 422.11$	7.91 %	78.76 %
$\lambda_6 = 309.65$	5.80 %	84.56 %

In pooled environments over 2 seasons ($E_1 + E_2 + E_3 + E_4$) the first two canonical roots were found to account for 59.61 per cent of the observed variability in the material ($\lambda_1 = 33.92\%$ and $\lambda_2 = 25.69\%$). However, the over all contribution of first five canonical roots to the total variability among 50 genotypes was 86.38 per cent suggesting that the major portion of differentiation was completed in the first five phases. Hundred pod weight and pod yield per plant were important sources of variation in 1st vector. In

2nd vector, sound mature kernel per cent, shelling per cent, 100-pod weight, 100-kernel weight and days to maturity were important sources of variation. In 3rd vector, 100-kernel weight, shelling per cent, 100-pod weight and secondary branches per plant contributed to source of variation. In 4th vector, sound mature kernel per cent, 100-kernel weight and days to 50 per cent flowering were important sources of variation. In 5th vector, 100-kernel weight, oil content, primary branches per plant and days to maturity shared major source of variation (Table 4.14).

Table 4.14: Values of canonical vectors (Z) and canonical roots (λ) in pooled $E_1+E_2+E_3+E_4$ (Kharif 2002 and Summer 2003)

Sr. No.	Characters	Canonical vectors				
		1 st Vector	2 nd Vector	3 rd Vector	4 th Vector	5 th Vector
		Z_1	Z_2	Z_3	Z_4	Z_5
1.	Days to 50% flowering	0.02128	0.15203	0.10237	0.12259	0.09195
2.	Height of main axis(cm)	0.01073	0.10097	0.03474	0.06989	0.03399
3.	Primary branches/plant	-0.04234	-0.03443	-0.03001	0.06210	0.20387
4.	Secondary branches/plant	-0.05109	0.03704	0.18984	-0.06187	0.03042
5.	Mature pods/plant	-0.09816	0.02235	-0.01754	-0.18465	0.14031
6.	100 pod weight (g)	0.77782	0.31885	0.25130	-0.37593	-0.25792
7.	100 kernel weight (g)	0.09414	0.22914	0.57693	0.29558	0.65433
8.	Shelling %	-0.59013	0.39894	0.44783	-0.31424	-0.32002
9.	Sound mature kernel (%)	-0.02893	0.75370	-0.42533	0.36181	-0.10743
10.	Oil content (%)	-0.07808	0.16883	-0.34212	-0.68033	0.53566
11.	Days to maturity	0.05942	0.19756	-0.23014	0.05303	0.16776
12.	Pod yield/plant	0.11321	-0.11190	-0.05893	0.09912	0.00395
13.	Kernel yield/plant	-0.00145	-0.04685	0.01121	-0.06697	-0.06718

Canonical roots	Account for 100 %	Total
$\lambda_1 = 899.55$	33.92 %	33.92 %
$\lambda_2 = 681.16$	25.69 %	59.61 %
$\lambda_3 = 320.34$	12.08 %	71.69 %
$\lambda_4 = 211.27$	7.97 %	79.66 %
$\lambda_5 = 178.13$	6.72 %	86.38 %

4.7. Intra and Inter-Cluster Distance

Average intra and inter-cluster statistical distance among thirteen quantitative characters calculated by Tocher's method are presented in Tables 4.15 to 4.21. In E_1 , the intra cluster distance ranged from 0 to 19.54. Cluster IV possessed the highest intra-cluster distance ($D=19.54$), followed by cluster I ($D=16.10$). The cluster in which only one genotype was grouped, the intra-cluster distance was zero. The average inter-cluster distance was maximum between clusters VI and VII ($D=38.84$), followed by VII and VIII ($D=38.31$), IV and VIII ($D=35.0$), V and VII ($D=34.09$), III and VIII ($D=33.24$), VII and IX ($D=32.03$) and II and VIII ($D=30.7$) (Table 4.15). In E_2 , the intra-cluster variation ranged from 0 to 18.11. Cluster III possessed the highest intra cluster distance ($D=18.11$), followed by cluster I ($D=14.3$). The clusters comprised of only one genotype had zero intra cluster distance. The average inter-cluster distance was maximum between cluster V and VI ($D=34.74$) followed by cluster IV and VI ($D=33.03$), cluster III and VI ($D=31.44$) and Cluster V and VII ($D=31.21$) (Table 4.16). In E_3 , the intra-cluster distance ranged from 0 to 18.01. Cluster VII possessed the highest intra-cluster distance ($D=18.01$), followed by cluster V ($D=17.06$) and cluster IV ($D=15.5$). The clusters comprised of only one genotype had zero intra-cluster distance. The average inter-cluster distance was maximum between cluster V and cluster IX ($D=35.41$), followed by cluster V and VIII ($D=34.19$), cluster II and VIII ($D=33.98$), Cluster II and IX ($D=33.07$) and cluster I and IX ($D=30.08$) (Table 4.17). In E_4 , the intra-cluster distance ranged from 0 to 17.22. Cluster III possessed the highest intra-cluster distance ($D=17.22$), followed by cluster II ($D=14.7$) and cluster I ($D=13.14$). The cluster in which only one genotype was grouped, the intra-cluster distance was zero. The average inter-cluster distance was maximum between clusters VIII and IX ($D=37.5$), followed by cluster IV and IX ($D=35.62$), Cluster VII and IX ($D=34.87$), Cluster V and IX ($D=34.62$), Cluster VII and X ($D=29.49$), Cluster V and X ($D=28.22$) and Cluster II and VIII ($D=28.03$) (Table 4.18).

Table 4.15 : Average intra and inter cluster distance $D = \sqrt{D^2}$ in E_1 (*Kharif 2002*)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	16.10	20.33	20.48	23.52	20.61	21.61	27.14	22.23	24.34
II		0.00	10.34	21.92	25.47	26.18	16.20	30.70	21.22
III			0.00	19.96	25.51	26.48	20.01	33.24	23.80
IV				19.54	25.91	28.96	27.76	35.00	24.96
V					0.00	19.06	34.09	27.21	27.46
VI						0.00	38.84	20.34	18.22
VII							0.00	38.31	32.03
VIII								0.00	26.90
IX									0.00

$$\bar{D} = 25.18$$

Table 4.16: Average intra and inter cluster distance $D = \sqrt{D^2}$ in E_2 (*Kharif 2002*)

Cluster	I	II	III	IV	V	VI	VII
I	14.30	19.11	20.39	19.82	19.53	26.13	22.47
II		0.00	15.62	20.11	27.99	27.90	19.86
III			18.11	22.91	29.28	31.44	20.78
IV				0.00	25.52	33.03	28.32
V					0.00	34.74	31.21
VI						0.00	27.69
VII							0.00

$$\bar{D} = 24.95$$

Table 4.17: Average intra and inter cluster distance $D = \sqrt{D^2}$ in E_3 (*Summer 2003*)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	12.65	18.51	14.92	18.60	16.29	17.16	18.47	27.79	30.08
II		11.64	19.17	22.94	19.95	25.86	19.94	33.98	33.07
III			00.00	16.04	19.81	20.68	14.63	23.64	26.80
IV				15.50	24.06	18.91	21.19	18.52	21.38
V					17.06	23.33	22.85	34.19	35.41
VI						00.00	21.92	22.40	27.36
VII							18.01	28.78	29.98
VIII								00.00	14.07
IX									00.00

$$\bar{D} = 22.85$$

Table 4.18 :Average intra and inter cluster distance $\bar{D} = \sqrt{D^2}$ in E_4 (Summer 2003)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	13.14	17.88	20.81	16.08	18.93	18.30	16.11	20.44	27.30	20.84
II		14.70	21.22	24.48	23.69	20.25	23.66	28.03	18.55	18.64
III			17.22	23.29	19.75	19.70	27.53	21.94	27.15	20.75
IV				0.00	17.28	19.84	17.38	17.51	35.62	27.64
V					0.00	22.74	20.25	18.39	34.36	28.22
VI						0.00	24.20	21.31	24.18	17.68
VII							0.00	21.68	34.87	29.49
VIII								0.00	37.50	26.32
IX									0.00	19.20
X										0.00

$$\bar{D} = 22.91$$

In pooled over environments of *kharif* ($E_1 + E_2$), the intra-cluster variation ranged from 0 to 17.05. Cluster V possessed the highest intra-cluster distance ($D=17.05$), followed by cluster II ($D=13.39$) and cluster I ($D=11.33$). The clusters comprised of only one genotype had zero intra cluster distance. The average inter-cluster distance was maximum between cluster VI and Cluster X ($D=33.94$), followed by cluster IX and X ($D=33.73$), Cluster IV and X ($D=31.62$), cluster VIII and X ($D=30.91$), cluster V and IX ($D=27.17$), Cluster V and X ($D=26.82$), cluster II and X ($D=25.72$) and cluster VII and VIII ($D=25.26$) (Table 4.19). In pooled over environments of summer (E_3+E_4), the intra cluster distance ranged from 0 to 13.16. Cluster III possessed the highest intra cluster distance ($D=13.16$), followed by cluster II ($D=12.72$) and cluster I ($D=10.49$). The clusters comprised of only one genotype had zero intra-cluster distance. The average inter-cluster distance was maximum between cluster III and cluster V ($D=22.69$), followed by cluster III and VII ($D=21.65$), cluster V and VI ($D=20.86$), Cluster III and IX ($D=20.80$) and cluster III and cluster VIII ($D=19.97$) (Table 4.20). In pooled over environments of both seasons ($E_1+E_2+E_3+E_4$), the intra cluster distance ranged from 0 to 10.84. Cluster IV possessed the highest intra cluster distance ($D=10.84$), followed by cluster III ($D=9.02$), cluster II ($D=6.66$) and cluster I ($D=6.45$). The cluster in which only one genotype was grouped, the intra-cluster distance was zero. The average inter-cluster distance was maximum between cluster VI and cluster VIII ($D=20.74$), followed by cluster

VII and VIII ($D=20.53$), cluster IV and VI ($D=18.44$) and cluster V and VIII ($D=17.48$) (Table 4.21).

Table 4.19: Average intra and inter cluster distance $D = \sqrt{D^2}$ in pooled E_1+E_2 (Kharif 2002)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	11.33	16.07	13.96	14.84	19.23	16.64	14.34	18.21	17.54	24.94
II		13.39	19.27	22.36	19.51	22.26	17.94	21.04	25.72	18.20
III			0.00	14.52	21.67	20.45	12.58	21.09	14.91	24.48
IV				0.00	19.68	16.42	18.51	15.18	16.25	31.62
V					17.05	22.66	20.53	22.87	27.17	26.82
VI						0.00	18.77	16.22	17.51	33.94
VII							0.00	25.26	15.65	23.71
VIII								0.00	24.35	30.91
IX									0.00	33.73
X										0.00

$$\bar{D} = 20.66$$

Table 4.20: Average intra and inter cluster distance $D = \sqrt{D^2}$ in pooled $E_3 + E_4$ (Summer 2003)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	10.49	15.21	13.79	13.76	18.24	12.85	15.89	16.21	18.10
II		12.72	16.49	14.98	17.57	18.02	17.35	16.24	15.15
III			13.16	17.60	22.69	17.81	21.65	19.97	20.80
IV				0.00	11.27	17.64	10.81	12.20	11.81
V					0.00	20.86	13.35	14.00	18.03
VI						0.00	16.81	18.36	18.74
VII							0.00	15.30	13.59
VIII								0.00	16.76
IX									0.00

$$\bar{D} = 16.39$$

Compiled intra and inter-cluster distance are presented in Table 4.22. It was observed that the magnitudes of intra and inter cluster distance were least in pooled analysis. It was also observed that environment played a significant role in the expression of genetic diversity between genotypes. The expression of genetic diversity was better in the *kharif* season environments compared to summer season environments indicating that there was better expression of genetic differentiation under *kharif* season environments as compared to summer season environments.

Table 4.21: Average intra and inter cluster distance $D = \sqrt{D^2}$ in pooled $E_1+E_2+E_3+E_4$ (Kharif 2002 and Summer 2003)

Cluster	I	II	III	IV	V	VI	VII	VIII
I	6.45	8.97	8.52	12.83	10.14	9.40	10.91	14.93
II		6.66	10.65	11.97	11.77	14.36	15.33	9.93
III			9.02	12.24	11.92	11.84	11.36	15.68
IV				10.84	13.55	18.44	14.37	13.61
V					0.00	13.84	9.37	17.48
VI						0.00	11.67	20.74
VII							0.00	20.53
VIII								0.00

$\bar{D} = 13.08$

Table 4.22 : Average intra and inter cluster distance $D = \sqrt{D^2}$ in different environments and pooled over environments

Clus- ters	Environ- ment	Clusters									
		I	II	III	IV	V	VI	VII	VII	IX	X
I	E_1	16.10	20.33	20.48	23.52	20.61	21.61	27.14	22.23	24.34	-
	E_2	14.30	19.11	20.39	19.82	19.53	26.13	22.47	-	-	-
	E_3	12.65	18.51	14.92	18.60	16.29	17.16	18.47	27.79	30.08	-
	E_4	13.14	17.88	20.81	16.08	18.93	18.30	16.11	20.44	27.30	20.84
	E_1+E_2	11.33	16.07	13.96	14.84	19.23	16.64	14.34	18.21	17.54	24.94
	E_3+E_4	10.49	15.21	13.79	13.76	18.24	12.85	15.89	16.21	18.10	-
	$E_1+E_2+E_3+E_4$	6.45	8.97	8.52	12.83	10.14	9.40	10.91	14.93	-	-
II	E_1		0.00	10.34	21.92	25.47	26.18	16.20	30.70	21.22	-
	E_2		0.00	15.62	20.11	27.99	27.90	19.86	-	-	-
	E_3		11.64	19.17	22.94	19.95	25.86	19.94	33.98	33.07	-
	E_4		14.70	21.22	24.48	23.69	20.25	23.66	28.03	18.55	18.64
	E_1+E_2		13.39	19.27	22.36	19.51	22.26	17.94	21.04	25.72	18.20
	E_3+E_4		12.72	16.49	14.98	17.57	18.02	17.35	16.24	15.15	-
	$E_1+E_2+E_3+E_4$		6.66	10.65	11.97	11.77	14.36	15.33	9.93	-	-
III	E_1			0.00	19.96	25.51	26.48	20.01	33.24	23.80	-
	E_2			18.11	22.91	29.28	31.44	20.78	-	-	-
	E_3			0.00	16.04	19.81	20.68	14.63	23.64	26.80	-
	E_4			17.22	23.29	19.75	19.70	27.53	21.94	27.15	20.75
	E_1+E_2			0.00	14.52	21.67	20.45	12.58	21.09	14.91	24.48
	E_3+E_4			13.16	17.60	22.69	17.81	21.65	19.97	20.80	-
	$E_1+E_2+E_3+E_4$			9.02	12.24	11.92	11.84	11.36	15.68	-	-
IV	E_1				19.54	25.91	28.96	27.76	35.00	24.96	-
	E_2				0.00	25.52	33.03	28.32	-	-	-
	E_3				15.50	24.06	18.91	21.19	18.52	21.38	-
	E_4				0.00	17.28	19.84	17.38	17.51	35.62	27.64
	E_1+E_2				0.00	19.68	16.42	18.51	15.18	16.25	31.62
	E_3+E_4				0.00	11.27	17.64	10.81	12.20	11.81	-
	$E_1+E_2+E_3+E_4$				10.84	13.55	18.44	14.37	13.61	-	-

Table 4.22 Continued -

Clusters	Environment	Clusters									
		I	II	III	IV	V	VI	VII	VII	IX	X
V	E ₁					0.00	19.06	34.09	27.21	27.46	-
	E ₂					0.00	34.74	31.21	-	-	-
	E ₃					17.06	23.33	22.85	34.19	35.41	-
	E ₄					0.00	22.74	20.22	18.39	34.36	28.22
	E ₁ +E ₂					17.05	22.66	20.53	22.87	27.17	26.82
	E ₃ +E ₄					0.00	20.86	13.35	14.00	18.03	-
	E ₁ +E ₂ +E ₃ +E ₄					0.00	13.84	9.37	17.48	-	-
VI	E ₁						0.00	38.84	20.34	18.22	-
	E ₂						0.00	27.69	-	-	-
	E ₃						0.00	21.92	22.40	27.36	-
	E ₄						0.00	24.20	21.31	24.18	17.68
	E ₁ +E ₂						0.00	18.77	16.22	17.51	33.94
	E ₃ +E ₄						0.00	16.81	18.36	18.74	-
	E ₁ +E ₂ +E ₃ +E ₄						0.00	11.67	20.74	-	-
VII	E ₁							0.00	38.31	32.03	-
	E ₂							0.00	-	-	-
	E ₃							18.01	28.78	29.98	-
	E ₄							0.00	21.68	34.87	29.49
	E ₁ +E ₂							0.00	25.26	15.65	23.71
	E ₃ +E ₄							0.00	15.30	13.59	-
	E ₁ +E ₂ +E ₃ +E ₄							0.00	20.53	-	-
VIII	E ₁								0.00	26.90	-
	E ₂								0.00	-	-
	E ₃								0.00	14.07	-
	E ₄								0.00	37.50	26.32
	E ₁ +E ₂								0.00	24.35	30.91
	E ₃ +E ₄								0.00	16.76	-
	E ₁ +E ₂ +E ₃ +E ₄								0.00	-	-
IX	E ₁									0.00	-
	E ₂									-	-
	E ₃									0.00	-
	E ₄									0.00	19.20
	E ₁ +E ₂									0.00	33.73
	E ₃ +E ₄									0.00	-
	E ₁ +E ₂ +E ₃ +E ₄										-
X	E ₁										-
	E ₂										-
	E ₃										-
	E ₄										0.00
	E ₁ +E ₂										0.00
	E ₃ +E ₄										-
	E ₁ +E ₂ +E ₃ +E ₄										-

4.8. Cluster Means

The cluster means of all the characters are presented in Table 4.23 to 4.29. In E₁, for days to 50 per cent flowering the cluster mean was lowest in cluster VII (26.25) while it was highest in cluster III (28.25), followed by cluster I and IV which had similar cluster means (28.16). For height of main axis, the highest cluster mean was recorded by cluster VII (48.00), followed by cluster I (37.25). The lowest cluster mean for this trait was recorded by cluster IX (18.05), followed by cluster VI (18.25). For primary branches per plant, the cluster mean was high in cluster VIII (4.85), followed by cluster I (4.82) and cluster IV (4.73). For secondary branches per plant, the cluster mean was high in cluster IV (1.23) followed by cluster VII (1.15) and cluster VI (1.0). For mature pods per plant, the cluster mean was highest in cluster VIII (20.35), followed by cluster VII (17.15) and cluster IX (17.02). For 100-pod weight and 100-kernel weight, the cluster means were highest in cluster VII (95.35 and 36.47 respectively), followed by cluster II (86.13 and 33.83 respectively). The lowest cluster means for these characters were recorded by cluster VIII (54.80 and 25.17 respectively), followed by cluster VI (55.17 and 26.48 respectively). For shelling per cent the highest cluster mean was recorded by cluster VIII (78.97), followed by cluster VI (72.05). For sound mature kernel per cent, the highest cluster mean was noticed in cluster III (94.55), followed by cluster II (92.53) and cluster VII (92.53). For oil content, the highest cluster mean was recorded by cluster VIII (48.17), followed by cluster IX (47.8) and cluster VII (47.65). For days to maturity, the lowest cluster mean was found in cluster VIII (98.75), followed by cluster IX (99.25). The highest cluster mean for this trait was recorded by cluster III (110.50), followed by cluster IV (108.06). For pod yield per plant, cluster mean was highest in cluster VII (11.15), followed by cluster VIII (10.27). For kernel yield per plant, the highest cluster mean was possessed by cluster VIII (8.13) followed by cluster VII (7.15) (Table 4.23).

Overall study of cluster means from Table 4.23 for all the characters (1 to 13) has provided information as under.

Characters	F	H	P	S	PO	HPW	HKW	SH	SMK	O	DM	PY	KY
	1	2	3	4	5	6	7	8	9	10	11	12	13
Highest in cluster	III	VII	VIII	IV	VIII	VII	VII	VIII	III	VIII	III	VII	VIII
Lowest in cluster	VII	IX	-	-	-	VIII	VIII	-	-	-	VIII	-	-

Cluster III: Possessed the highest cluster means for days to 50 per cent flowering, sound mature kernel per cent and days to maturity (3).

Cluster IV: Showed the highest cluster mean for secondary branches per plant (1)

Cluster VII: Possessed the highest cluster means for height of main axis, 100-pod and kernel weight and pod yield per plant and the lowest cluster mean for days to 50 per cent flowering (5).

Cluster VIII: Had the highest cluster means for primary branches per plant, mature pods per plant, shelling per cent, oil content and kernel yield per plant and lowest cluster mean for 100-pod weight, 100-kernel weight and days to maturity (8).

Cluster IX: Possessed the lowest cluster mean for height of main axis (1).

In E₂, for days to 50 per cent flowering, the lowest cluster mean was recorded by cluster II and VI (27.25) and it was highest in cluster III (29.06), followed by cluster VII (29.00). For height of main axis, the highest cluster mean was possessed by cluster VI (45.22), followed by cluster I (33.92). The lowest cluster mean for this trait was noticed in cluster II (24.83). For primary branches per plant, the cluster means were high in cluster VI and VII which were similar (4.75). For secondary branches per plant, the highest cluster mean was recorded by cluster VII (5.30), followed by cluster VI (0.70). For mature pods per plant, the highest cluster mean was found in cluster V (18.25) followed by cluster VI (16.65) and cluster I (11.82). For 100-pod weight, the highest cluster mean was recorded by

cluster VI (94.22) and it was lowest in cluster V (52.65). For 100-kernel weight, the highest cluster mean was observed in cluster VI (35.63) and it was lowest in cluster III (24.09). For shelling per cent, highest cluster mean was recorded by cluster V (78.60), followed by cluster IV (69.93). For sound mature kernel per cent, the highest cluster mean was registered by the cluster VI (91.30), followed by cluster I (87.64) and cluster V (87.03). For oil content, the highest cluster mean was recorded by cluster V (47.55), followed by cluster VI (47.10). For days to maturity, the lowest cluster mean was shown by the cluster V (96.00), followed by cluster VI (98.25). The highest cluster mean for this trait was recorded by cluster VII (106.5), followed by cluster III (105.06). For pod and kernel yield per plant, the highest cluster means were found in cluster VI (12.43 and 7.72 respectively), followed by the cluster V (8.93 and 7.00 respectively) (Table 4.24).

Overall study of cluster mean from Table 4.24 for all the characters (1 to 13) has provided information as under

Characters	F	H	P	S	PO	HPW	HKW	SH	SMK	O	DM	PY	KY
	1	2	3	4	5	6	7	8	9	10	11	12	13
Highest in cluster	III	VI	VI,VII	VII	V	VI	VI	V	VI	V	VII	VI	VI
Lowest in cluster	II, VI	II	-	-	-	V	III	-	-	-	V	-	-

Cluster II: Recorded the lowest cluster means for days to 50 per cent flowering and height of main axis (2).

Cluster III: Possessed the highest cluster means for days to 50 per cent flowering and lowest cluster mean for 100-kernel weight (2).

Cluster V: Showed the highest cluster means for mature pods per plant, shelling per cent and oil content and lowest cluster means for 100-pod weight and days to maturity (5).

Cluster VI: Recorded the highest cluster means for height of main axis, primary branches per plant, 100-pod and 100-kernel weight, sound mature kernel per cent, pod and kernel yield per plant and lowest value for days to 50% flowering (8).

Cluster VII: Had the highest cluster means for primary branches per plant, secondary branches per plant and days to maturity (3).

Table 4.23 : Cluster means for 13 characters in E₁ (Kharif 2002)

Sr. No.	Characters	I	II	III	IV	V	VI	VII	VIII	IX
1.	Days to 50% flowering	28.16	28.00	28.25	28.16	28.00	28.00	26.25	27.00	27.00
2.	Height of main axis(cm)	37.25	33.90	32.80	33.19	33.08	18.25	48.00	33.20	18.05
3.	Primary branches/plant	4.82	4.50	4.20	4.73	4.20	4.40	4.60	4.85	4.40
4.	Secondary branches/plant	0.78	0.5	0.15	1.23	0.90	1.00	1.15	0.75	0.70
5.	Mature pods/plant	14.00	11.90	13.18	9.59	10.50	13.20	17.15	20.35	17.02
6.	100 pod weight (g)	65.49	86.13	79.40	72.77	60.85	55.17	95.35	54.80	72.15
7.	100 kernel weight (g)	27.61	33.83	32.92	29.50	28.02	26.48	36.47	25.17	30.42
8.	Shelling %	67.68	71.15	64.78	57.59	71.38	72.05	64.30	78.97	68.72
9.	Sound mature kernel (%)	89.65	92.95	94.55	81.25	82.68	90.38	92.53	89.15	80.90
10.	Oil content (%)	44.98	45.58	43.88	43.69	32.70	41.38	47.65	48.17	47.80
11.	Days to maturity	104.68	103.75	110.50	108.06	100.50	100.25	101.25	98.75	99.25
12.	Pod yield/plant	7.52	6.93	8.82	5.43	5.60	6.38	11.15	10.27	9.95
13.	Kernel yield/plant	5.09	4.93	5.70	3.13	4.00	4.57	7.15	8.13	6.82

In E₃, for days to 50 per cent flowering, the lowest cluster mean was recorded by cluster VIII (48.00), followed by cluster VII (48.38). The highest cluster mean for this trait was registered by cluster IX (54.50), followed by cluster III (51.25). For height of main axis, the cluster mean was high in cluster VIII (24.55) while it was low in cluster II (19.35). For primary branches per plant, the highest cluster mean was recorded by cluster II (5.92), followed by cluster VI (5.70) and cluster I (5.68). For secondary branches per plant, the highest cluster mean was found in the cluster VI (9.88), followed by cluster I (5.15). For mature pods per plant, the highest

cluster mean was recorded by the cluster V (13.79), followed by cluster VI (12.10) and cluster I (11.12). For 100-pod weight, the highest cluster mean was observed in the cluster VIII (92.82), followed by cluster IX (85.55). The lowest cluster mean for this character was recorded by the cluster V (59.08), followed by cluster II (60.75). For 100-kernel weight, the highest cluster mean was possessed by the cluster IX (45.50), followed by cluster VIII (36.75). The lowest cluster mean for this character was recorded by cluster II (24.02), followed by cluster VII (25.08). For shelling per cent, the highest cluster mean was exhibited by cluster V (72.32), followed by cluster I (68.76). For sound mature kernel per cent, the highest cluster mean was recorded by the cluster VI (92.40), followed by cluster VII (91.11). For oil content, the highest cluster mean was noticed in the cluster III (49.35), followed by cluster VIII (47.05). For days to maturity, the lowest cluster mean was recorded by the cluster V (124.38), followed by cluster I (125.40). The highest cluster mean for this trait was registered by cluster IX (136.0), followed by cluster VII (133.06). For pod yield per plant, the highest cluster mean was recorded by cluster VIII (8.05), followed by cluster VI (7.97) and cluster IX (7.40). For kernel yield per plant, the highest cluster mean was found in cluster VI (5.43), followed by cluster V (5.30) and cluster VIII (5.25) (Table 4.25).

Table 4.24 : Cluster means for 13 characters in E₂ (*Kharif* 2002)

Sr. No	Characters	I	II	III	IV	V	VI	VII
1.	Days to 50% flowering	28.47	27.25	29.06	28.25	28.00	27.25	29.00
2.	Height of main axis(cm)	33.92	24.83	30.09	31.50	31.80	45.22	32.75
3.	Primary branches/plant	4.46	4.30	4.36	4.20	4.70	4.75	4.75
4.	Secondary branches/plant	0.60	0.30	0.51	0.15	0.25	0.70	5.30
5.	Mature pods/plant	11.82	7.80	8.09	9.45	18.25	16.65	8.85
6.	100 pod weight (g)	64.49	77.10	67.06	59.00	52.65	94.22	73.28
7.	100 kernel weight (g)	26.65	25.80	24.09	26.98	24.42	35.63	33.67
8.	Shelling %	65.60	59.13	51.57	69.93	78.60	62.15	53.40
9.	Sound mature kernel (%)	87.64	71.32	79.46	79.43	87.03	91.30	74.65
10.	Oil content (%)	43.48	43.17	41.48	30.50	47.55	47.10	45.33
11.	Days to maturity	102.30	102.50	105.06	100.25	96.00	98.25	106.50
12.	Pod yield/plant	6.48	4.57	4.13	5.10	8.93	12.43	5.47
13.	Kernel yield/plant	4.26	2.70	2.11	3.58	7.00	7.72	2.92

Table 4.25: Cluster means for 13 characters in E₃ (Summer 2003)

Sr. No	Characters	I	II	III	IV	V	VI	VII	VIII	IX
1.	Days to 50% flowering	50.56	48.58	51.25	50.98	49.91	50.00	48.38	48.00	54.50
2.	Height of main axis (cm)	24.28	19.35	21.73	22.66	24.21	22.25	20.43	24.55	21.33
3.	Primary branches/plant	5.68	5.92	5.10	5.27	5.49	5.70	5.43	4.90	5.50
4.	Secondary branches/plant	5.15	2.69	0.30	3.09	4.91	9.88	1.56	3.30	1.55
5.	Mature pods/plant	11.12	9.18	10.45	9.72	13.79	12.10	8.43	9.70	8.57
6.	100 pod weight (g)	64.50	60.75	68.35	77.81	59.08	71.90	62.13	92.82	85.55
7.	100 kernel weight (g)	27.17	24.02	25.35	30.51	27.02	27.35	25.08	36.75	45.50
8.	Shelling %	68.76	58.61	68.63	66.23	72.32	68.05	65.15	65.40	60.75
9.	Sound mature kernel (%)	87.95	78.02	86.35	86.08	83.30	92.40	91.11	88.50	85.60
10.	Oil content (%)	43.93	40.75	49.35	43.11	42.45	43.47	44.13	47.05	40.50
11.	Days to maturity	125.40	128.00	127.00	127.34	124.38	132.75	133.06	130.50	136.00
12.	Pod yield/plant	6.14	4.63	6.28	6.58	7.32	7.97	4.49	8.05	7.40
13.	Kernel yield/plant	4.23	2.71	4.32	4.34	5.30	5.43	2.93	5.25	4.50

Overall study of cluster means from Table 4.25 for all the characters (1 to 13) has provided information as under.

Characters	F	H	P	S	PO	HPW	HKW	SH	SMK	O	DM	PY	KY
	1	2	3	4	5	6	7	8	9	10	11	12	13
Highest in cluster	IX	VIII	II	VI	V	VIII	IX	V	VI	III	IX	VIII	VI
Lowest in cluster	VIII	II	-	-	-	V	II	-	-	-	V	-	-

Cluster II: Exhibited the highest cluster mean for primary branches per plant and lowest cluster means for height of main axis and 100-kernel weight (3).

Cluster III: Possessed the highest cluster mean for oil content (1).

Cluster V: Exhibited the highest cluster means for mature pods per plant and shelling per cent and cluster mean was lowest for 100-pod weight and days to maturity (4).

Cluster VI: Registered the highest cluster means for secondary branches per plant, sound mature kernel per cent and kernel yield per plant (3).

Cluster VIII: Exhibited the highest cluster mean for height of main axis, 100-pod weight and pod yield per plant and the lowest cluster mean for days to 50 per cent flowering (4).

Cluster IX: Had the highest cluster means for days to 50 per cent flowering, 100-kernel weight and days to maturity (3).

In E₄, for days to 50 per cent flowering, the lowest cluster means were recorded by cluster V and VIII (35.75), whereas it was highest in cluster IV (42.25), followed by cluster X (41.00). For height of main axis, the highest cluster mean was shown by cluster VIII (24.05), followed by cluster IX (23.13). The lowest cluster mean for this trait was recorded by cluster V (14.30), followed by cluster VI (15.48) and cluster IV (15.85). For primary branches per plant, the highest cluster mean was found in cluster VII (5.55), followed by cluster II (5.38) and cluster I (5.34). For secondary branches per plant, the highest cluster mean was recorded by cluster X (6.60), followed by cluster I (4.33). For mature pods per plant, the highest cluster mean was possessed by the cluster VI (19.80), followed by cluster IV (16.05). For 100-pod weight, the highest cluster mean was recorded by the cluster IX (96.78), followed by cluster X (79.38). The lowest cluster mean for this character was exhibited by cluster V (52.05), followed by cluster VIII (53.35). For 100-kernel weight, the highest cluster mean was recorded by cluster IX (36.90), followed by cluster X (35.65). The lowest cluster mean for this trait was observed in cluster VIII (22.23), followed by cluster V (23.15). For shelling per cent, the highest cluster mean was registered by cluster VII (77.72), followed by cluster IV (70.97). For sound mature kernel per cent, the highest cluster mean was recorded by the cluster V (91.53), followed by cluster VII (91.20). For oil content, the highest cluster mean was recorded by the cluster

VI (48.28), followed by cluster IX (48.20) and cluster VII (48.05). For days to maturity, the lowest cluster mean was noticed in cluster VI (115.25), followed by cluster X (118.0). The highest cluster mean for this trait was present in cluster II (125.82), followed by cluster VII (124.25). For pod yield per plant, the highest cluster mean was recorded by cluster VI (12.98), followed by cluster X (8.55). For kernel yield per plant, the highest cluster mean was observed in the cluster VI (9.07), followed by cluster IX (5.30) (Table 4.26).

Overall study of cluster mean from Table 4.26 for all the characters (1 to 13) has provided information as under.

Characters	F	H	P	S	PO	HPW	HKW	SH	SMK	O	DM	PY	KY
	1	2	3	4	5	6	7	8	9	10	11	12	13
Highest in cluster	IV	VIII	VII	X	VI	IX	IX	VII	V	VI	II	VI	VI
Lowest in cluster	V & VIII	V	-	-	-	V	VIII	-	-	-	VI	-	-

Cluster II: Possessed highest cluster mean for days to maturity (1).

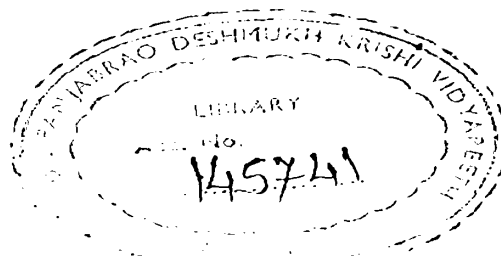
Cluster IV: Exhibited highest cluster mean for days to 50 per cent flowering (1).

Cluster V: Recorded highest cluster means for sound mature kernel per cent and lowest cluster mean for days to 50 per cent flowering, height of main axis and 100-pod weight (4).

Cluster VI: Registered highest cluster means for mature pods per plant, oil content, pod yield per plant and kernel yield per plant and lowest cluster mean for days to maturity (5).

Cluster VII: Possessed highest cluster mean for primary branches per plant and shelling per cent (2).

Cluster VIII: Had highest cluster means for height of main axis and lowest cluster mean for days to 50 per cent flowering and hundred kernel weight (3).



Cluster IX: Possessed highest cluster means for 100-pod and 100-kernel weight (2).

Cluster X: Recorded highest cluster mean for secondary branches per plant (1).

Table 4.26 : Cluster means for 13 characters in E₄ (Summer 2003)

Sr. No.	Characters	I	II	III	IV	V	VI	VII	VIII	IX	X
1.	Days to 50% flowering	40.80	40.89	38.38	42.25	35.75	39.00	39.00	35.75	38.25	41.00
2.	Height of main axis (cm)	20.54	20.03	17.41	15.85	14.30	15.48	20.27	24.05	23.13	20.75
3.	Primary branches/plant	5.34	5.38	5.14	4.40	4.00	4.90	5.55	5.25	4.35	5.30
4.	Secondary branches/plant	4.33	3.18	2.47	2.65	0.00	3.70	4.60	2.90	2.83	6.60
5.	Mature pods/plant	11.11	9.63	10.38	16.05	6.70	19.80	9.40	12.30	10.35	12.60
6.	100 pod weight (g)	64.94	77.66	69.47	57.08	52.05	71.38	54.90	53.35	96.78	79.38
7.	100 kernel weight (g)	28.40	32.57	24.06	26.48	23.15	29.33	25.60	22.23	36.90	35.65
8.	Shelling %	68.73	66.03	60.76	70.97	63.42	69.93	77.72	69.57	65.05	59.40
9.	Sound mature kernel (%)	89.63	90.27	83.77	89.13	91.53	83.97	91.20	75.47	89.65	78.68
10.	Oil content (%)	44.57	45.00	44.23	41.17	41.85	48.28	48.05	42.10	48.20	45.33
11.	Days to maturity	120.09	125.82	121.22	121.25	120.00	115.25	124.25	120.00	123.50	118.00
12.	Pod yield/plant	6.13	6.21	5.88	7.10	3.47	12.98	5.05	6.55	8.15	8.55
13.	Kernel yield/plant	4.22	4.12	3.59	5.03	2.20	9.07	3.92	4.55	5.30	5.07

In pooled environments of *kharif* (E₁+E₂), for days to 50 per cent flowering, the lowest cluster mean was recorded by cluster X (26.75), followed by cluster IV (26.88). The highest cluster mean for this trait was recorded by cluster III (30.00), followed by cluster II (29.02). For height of main axis, the highest cluster mean was possessed by the cluster X (46.61), followed by cluster III (41.75). The lowest cluster mean for this trait was

recorded by cluster VI (17.45), followed by cluster V (27.96). For primary branches per plant, the highest cluster mean was noticed in cluster III (5.53), followed by cluster IV (5.32). For secondary branches per plant, the cluster mean was high in cluster III (2.40), followed by cluster VI (1.25). For mature pods per plant, the highest cluster mean was recorded by the cluster VII (22.00), followed by the cluster III (21.17). For 100-pod weight, the highest cluster mean was exhibited by cluster X (94.79) and it was lowest in cluster IX (53.72). For 100-kernel weight, the highest cluster mean was

Table 4.27: Cluster means for 13 characters in pooled $E_1 + E_2$ (Kharif 2002)

Sr. No.	Characters	I	II	III	IV	V	VI	VII	VIII	IX	X
1.	Days to 50% flowering	28.13	29.02	30.00	26.88	27.96	28.13	27.75	28.13	27.50	26.75
2.	Height of main axis(cm)	36.01	35.58	41.75	34.70	27.96	17.45	31.05	32.29	32.50	46.61
3.	Primary branches/plant	4.59	4.54	5.53	5.32	4.57	4.35	4.85	4.20	4.78	4.68
4.	Secondary branches/plant	0.73	0.49	2.40	0.28	1.26	1.25	0.05	0.52	0.50	0.93
5.	Mature pods/plant	12.43	11.55	21.17	13.85	9.71	12.27	22.00	9.98	19.30	16.90
6.	100 pod weight (g)	61.98	77.00	63.25	54.53	69.66	54.58	66.36	59.92	53.72	94.79
7.	100 kernel weight (g)	26.29	30.94	29.39	22.11	26.00	26.11	29.83	27.50	24.80	36.05
8.	Shelling %	66.59	64.14	69.22	69.35	57.32	71.36	66.60	70.65	78.79	63.22
9.	Sound mature kernel (%)	88.68	90.77	83.90	74.95	76.61	89.26	89.95	81.05	88.09	91.91
10.	Oil content (%)	44.27	43.24	45.54	41.34	44.15	40.13	51.08	31.60	47.86	47.38
11.	Days to maturity	103.81	105.13	100.00	100.00	104.19	99.75	102.63	100.38	97.38	99.75
12.	Pod yield/plant	6.61	7.11	10.60	6.69	5.22	5.65	11.20	5.35	9.60	11.79
13.	Kernel yield/plant	4.41	4.57	7.35	4.65	3.08	4.03	7.49	3.79	7.56	7.44

recorded by cluster X (36.05) and it was lowest in cluster IV (22.11). For shelling per cent, the highest cluster mean was found in cluster IX (78.79), followed by cluster VI (71.36). For sound mature kernel per cent, the highest cluster mean was recorded by cluster X (91.91), followed by cluster II (90.77). For oil content, the highest cluster mean was registered by cluster VII (51.08), followed by cluster IX (47.86). For days to maturity, the lowest cluster mean was recorded by cluster IX (97.38), followed by clusters VI and X with similar means (99.75). The highest cluster mean for this trait was present in cluster II (105.13), followed by cluster V (104.19) and cluster I (103.81). For pod yield per plant, the highest cluster mean was recorded by cluster X (11.79), followed by cluster VII (11.20) and cluster III (10.60). For kernel yield per plant, the highest cluster mean was noticed in cluster IX (7.56), followed by cluster VII (7.49) and cluster X (7.44) (Table 4.27).

Overall study of cluster means from Table 4.27 for all the characters (1 to 13) has provided information as under.

Characters	F	H	P	S	PO	HPW	HKW	SH	SMK	O	DM	PY	KY
	1	2	3	4	5	6	7	8	9	10	11	12	13
Highest in cluster	III	X	III	III	VII	X	X	IX	X	VII	II	X	IX
Lowest in cluster	X	VI	-	-	-	IX	IV	-	-	-	IX	-	-

Cluster II: Recorded highest cluster mean for days to maturity (1).

Cluster III: Exhibited highest cluster mean for days to 50 per cent flowering, and primary branches per plant and secondary branches per plant (3).

Cluster IV: Recorded lowest cluster mean for 100-kernel weight (1).

Cluster VI: Possessed lowest cluster mean for height of main axis (1).

Cluster VII: Recorded highest cluster means for mature pods per plant and oil content (2).

Cluster IX: Registered highest cluster means for shelling per cent and kernel yield per plant and lowest cluster means for 100-pod weight and days to maturity (4).

Cluster X: Recorded highest cluster means for height of main axis, 100-pod weight, 100-kernel weight, sound mature kernel per cent and pod yield per plant and lowest cluster mean for days to 50 per cent flowering (6).

In pooled environments of summer (E_3+E_4), for days to 50 per cent flowering, the lowest cluster mean was recorded by cluster IX (41.63) and it was highest in cluster V (48.13). For height of main axis, the highest cluster mean was noticed in cluster VIII (25.89), followed by cluster VII (23.84). The lowest cluster mean for this trait was recorded by cluster IX (15.73). For primary branches per plant, the highest cluster mean was possessed by cluster VIII (6.25). For secondary branches per plant, the highest cluster mean was recorded by cluster VI (8.98), followed by cluster I (4.68). For mature pods per plant, the highest cluster mean was registered by cluster III (12.64), followed by cluster VI (12.34). For 100-pod weight, the highest cluster mean was recorded by cluster VII (94.80), followed by cluster V (84.60) and cluster IX (84.41). The lowest cluster mean for this trait was observed in cluster III (59.99). For 100-kernel weight, the highest cluster mean was recorded by cluster V (43.09) and it was lowest in cluster IX (24.54). For shelling per cent, the highest cluster mean was exhibited by cluster III (70.52). For sound mature kernel per cent, the highest cluster mean was recorded by cluster VI (92.99), followed by cluster IV (92.95). For oil content, the highest cluster mean was shown by cluster VII (47.63), followed by cluster I (44.88). For days to maturity, the lowest cluster mean was recorded by cluster III (121.79), followed by cluster II (123.69). The highest cluster mean for this trait was found in cluster VIII (137.50), followed by cluster V (133.38). For pod yield per plant, the highest cluster mean was recorded by cluster VII (8.10), followed by cluster VI (7.51) and cluster IV (7.39). ~~For kernel yield per plant, the cluster mean was highest in cluster VII~~ (5.28), followed by cluster VI (5.09) (Table 4.28).

Table 4.28 : Cluster means for 13 characters in pooled E₃ + E₄ (Summer 2003)

Sr. No.	Characters	I	II	III	IV	V	VI	VII	VIII	IX
1	Days to 50% flowering	46.19	43.89	44.74	46.13	48.13	45.38	43.13	45.63	41.63
2	Height of main axis (cm)	22.02	19.43	22.29	19.02	20.39	20.27	23.84	25.89	15.73
3	Primary branches/plant	5.54	5.43	5.24	4.25	5.25	5.71	4.63	6.25	4.28
4	Secondary branches/plant	4.68	2.97	3.86	0.28	1.50	8.98	3.06	0.00	1.75
5	Mature pods/plant	10.10	10.46	12.64	10.48	8.90	12.34	10.02	9.70	8.73
6	100 pod weight (g)	68.99	68.67	59.99	80.80	84.60	73.16	94.80	72.39	84.41
7	100 kernel weight (g)	29.66	25.88	26.16	34.72	43.09	27.59	36.83	28.14	24.54
8	Shelling %	68.98	61.03	70.52	66.11	59.17	67.60	65.22	61.31	64.82
9	Sound mature kernel (%)	89.92	82.44	86.03	92.95	86.44	92.99	89.07	91.04	86.63
10	Oil content (%)	44.88	44.05	43.04	41.95	40.95	44.29	47.63	44.70	40.81
11	Days to maturity	124.37	123.69	121.79	127.25	133.38	130.13	127.00	137.50	126.88
12	Pod yield/plant	5.88	6.05	6.82	7.39	6.39	7.51	8.10	5.94	6.51
13	Kernel yield/plant	4.06	3.70	4.82	4.89	3.78	5.09	5.28	3.70	4.25

Overall study of cluster means from Table 4.28 for all the characters (1 to 13) has provided information as under.

Characters	F	H	P	S	PO	HPW	HKW	SH	SMK	O	DM	PY	KY
	1	2	3	4	5	6	7	8	9	10	11	12	13
Highest in cluster	V	VIII	VIII	VI	III	VII	V	III	VI	VII	VIII	VII	VII
Lowest in cluster	IX	IX	-	-	-	III	IX	-	-	-	III	-	-

Cluster III: Exhibited the highest cluster means for mature pods per plant and shelling per cent and the lowest cluster means for 100-pod weight and days to maturity (4).

Cluster V: Possessed the highest cluster means for days to 50 per cent flowering and 100-kernel weight (2).

Cluster VI: Exhibited the highest cluster means for secondary branches per plant and sound mature kernel per plant (2).

Cluster VII: Registered the highest cluster means for 100-pod weight, oil content, pod yield per plant and kernel yield per plant (4).

Cluster VIII: Exhibited the highest cluster means for height of main axis, primary branches per plant and days to maturity (3).

Cluster IX: Had the lowest cluster means for days to 50 per cent flowering, height of main axis and 100-kernel weight (3).

In pooled environment of both seasons ($E_1+E_2+E_3+E_4$), for days to 50 per cent flowering, the lowest cluster mean was recorded by cluster VII (33.63), followed by cluster VIII (34.94). The highest cluster mean for this character was exhibited by cluster II (37.53). For height of main axis, the highest cluster mean was recorded by cluster VIII (35.22), followed by cluster VII (30.99). The lowest cluster mean for this trait was observed in cluster III (24.85). For primary branches per plant, the highest cluster mean was possessed by cluster VII (5.45), followed by cluster VI (5.28) and cluster I (5.13). For secondary branches per plant, the highest cluster mean was recorded by cluster V (3.20), followed by cluster I (2.83). For mature pods per plant, the highest cluster mean was recorded by the cluster VI (14.65), followed by cluster VIII (13.46) and cluster VII (13.32). For 100-pod weight and 100-kernel weight the highest cluster means were noticed in the cluster VIII (94.79 and 36.44 units respectively) and it was lowest in cluster VII (54.44 and 22.52 units respectively). For shelling per cent, the highest cluster mean was recorded by cluster VI (78.53), followed by cluster V

(71.21). For sound mature kernel per cent, the highest cluster mean was found in cluster II (91.70), followed by cluster VIII (90.49). For oil content, the highest cluster mean was recorded by cluster VI (47.72), followed by cluster VIII (47.50). For days to maturity, the lowest cluster mean was shown by cluster V (110.00) and it was highest in cluster II (115.32), followed by cluster IV (115.21). For pod yield and kernel yield per plant, the highest cluster mean was recorded by cluster VIII (9.94 and 6.36 unit, respectively), followed by cluster VI (7.34 and 5.78 unit, respectively) and cluster II (6.91 and 4.62 units respectively) (Table 4.29).

Table 4.29: Cluster means for 13 characters in pooled $E_1 + E_2 + E_3 + E_4$ (Kharif 2002 and Summer 2003)

Sr. No.	Characters	I	II	III	IV	V	VI	VII	VIII
1.	Days to 50% flowering	37.23	37.53	35.95	36.36	37.25	36.00	33.63	34.94
2.	Height of main axis (cm)	29.82	29.71	24.85	25.03	28.86	27.64	30.99	35.22
3.	Primary branches/ plant	5.13	4.96	4.91	4.85	4.44	5.28	5.45	4.65
4.	Secondary branches/plant	2.83	2.55	1.63	1.63	3.20	2.69	1.77	1.99
5.	Mature pods/plant	11.97	11.06	13.03	8.88	11.02	14.65	13.32	13.46
6.	100 pod weight (g)	63.43	76.87	62.72	73.37	63.47	54.69	54.44	94.79
7.	100 kernel weight (g)	27.59	31.61	25.30	28.28	28.16	25.43	22.52	36.44
8.	Shelling %	68.92	67.12	64.88	58.38	71.21	78.53	69.82	64.22
9.	Sound mature kernel (%)	88.76	91.70	87.32	80.77	81.51	89.08	75.01	90.49
10.	Oil content (%)	44.48	43.52	44.57	42.90	35.78	47.72	41.51	47.50
11.	Days to maturity	113.28	115.32	113.95	115.21	110.00	112.06	111.50	113.38
12.	Pod yield/plant	6.54	6.91	6.87	5.40	6.21	7.34	6.56	9.94
13.	Kernel yield/plant	4.52	4.62	4.48	3.17	4.43	5.78	4.57	6.36

Overall study of cluster means from Table 4.29 for all the characters (1 to 13) has provided the information as under.

Characters	F	H	P	S	PO	HPW	HKW	SH	SMK	O	DM	PY	KY
	1	2	3	4	5	6	7	8	9	10	11	12	13
Highest in cluster	II	VIII	VII	V	VI	VIII	VIII	VI	II	VI	II	VIII	VIII
Lowest in cluster	VII	III	-	-	-	VII	VII	-	-	-	V	-	-

Cluster II: Possessed highest cluster means for days to 50 per cent flowering, sound mature kernel per cent and days to maturity (3).

Cluster III: Exhibited lowest cluster mean for height of main axis (1).

Cluster V: Possessed highest cluster means for shelling per cent and lowest cluster mean for days to maturity (2).

Cluster VI: Showed highest cluster means for mature pods per plant, shelling per cent and oil content (3).

Cluster VII: Possessed highest cluster mean for primary branches per plant and lowest cluster means for days to 50 per cent flowering, 100-pod weight and 100-kernel weight (4).

Cluster VIII: Registered highest cluster means for height of main axis, 100-pod weight, 100-kernel weight, pod yield per plant and kernel yield per plant (5).

4.9. Analysis of Variance for Stability

The ANOVA for stability as per Eberhart and Russell (1966) for 13 characters have been presented in Table 4.30. The mean squares due to genotypes and environments were significant for all characters. Genotype x environment interaction was observed to be highly significant for seven characters, viz., days to 50 per cent flowering, height of main axis, primary

Table 4.30: Analysis of variance for stability of different characters over four environments (two *Kharif* and two *Summer*, 2002-2003)

Sr No	Source of variation	df	Mean squares												
			Days to 50% flowering	Height of main axis (cm)	Primary branches per plant	Secondary branches per plant	Mature pods per plant	100-pod weight (g)	100-kernel weight (g)	Shelling %	Sound mature kernel %	Oil content (%)	Days to maturity	Pod yield/ plant	Kernel yield/ plant
1.	Replication within Env.	12	0.491	2.116	0.083	0.146	0.545	0.531	0.569	1.057	1.528	0.529	1.308	0.206	0.116
2.	Genotypes	49	10.788**	65.254**	0.878**	7.301*	23.228**	336.672**	66.939**	107.524**	130.262**	26.125**	37.342*	8.163**	4.594**
3.	Env. x (Geno x Env.)	150	113.884**	71.630**	0.345	4.532	6.594	7.522**	2.301**	3.983	3.582**	1.361**	156.268**	2.346	1.141**
4.	Environments	3	5633.316**	3072.870**	11.334**	161.052**	73.485**	103.026**	32.128**	91.143**	51.230**	28.463**	7400.798**	12.476**	6.157**
5.	Genotypes x Environment	147	1.243**	10.360**	0.121**	1.337**	5.229**	5.573	1.693	2.204**	2.609	0.808	8.421**	2.140	1.039
6.	Environments (Lin.)	1	16899.953**	9218.610**	34.001**	483.155**	220.455**	309.079**	96.383**	273.428**	153.689**	85.368**	22202.393**	37.428**	18.472**
7.	Genotypes x Env. (Lin.)	49	2.813**	27.390**	0.292**	3.866**	8.911**	3.323	0.837	4.067**	1.054	0.193	22.656**	2.157	0.633
8.	Pooled deviation	100	0.449	1.838	0.035	0.071	3.320	6.564	2.078	1.247	3.320	1.094	1.277	2.038	1.217
9.	Pooled error	588	0.280	0.437	0.029	0.059	0.314	0.573	0.279	0.411	0.468	0.244	0.481	0.142	0.056
10.	Total	199	88.499	70.060	0.476	5.214	10.690	88.569	18.217	29.478	34.775	7.459	126.955	3.779	1.991

* $P \leq 0.05$, ** $P \leq 0.01$

branches per plant, secondary branches per plant, mature pods per plant, shelling per cent and days to maturity and it was non-significant for six characters viz., 100-pod weight, 100-kernel weight, sound mature kernel per cent, oil content, pod yield per plant and kernel yield per plant. Hence, stability analysis was not necessary to be done in respect of these six characters. Environment + (Genotype x Environment) component was highly significant for eight characters, viz., days to 50 per cent flowering, height of main axis, 100-pod weight, 100-kernel weight, sound mature kernel per cent, oil content, day to maturity and kernel yield per plant. Environment (Linear) component was highly significant for all characters genotype x Environment (Linear) component was highly significant for seven characters viz., days to 50 per cent flowering, height of main axis, primary branches per plant, secondary branches per plant, mature pods per plant, shelling per cent and days to maturity. This indicated that there was no linear response for rest of the six characters. Hence, it appeared meaningful to carry out the stability analysis only for seven characters listed above. Pooled deviation (Non-linear) component was non significant for all the characters indicating no change in performance over environments.

4.10. Estimates of Stability Parameters

Mean performance of different genotypes for seven characters under each of the four environments and estimates of stability parameters have been presented in Table 4.31 to 4.37. The genotypes plotted on graphs, mean versus bi values, are presented in Fig. 4.1 to 4.7 for the same characters.

4.10.1. Days to 50 per cent flowering

On an average, less days to 50 per cent flowering was taken by germplasm line (50) U 2-12-1 (33.63 days) whereas, maximum days was taken by another germplasm line (27) Ah 4515 (40.13 days). Regression coefficient was recorded to be significant for 13 genotypes. Eleven genotypes viz., (12) JL 220, (13) Jyoti, (17) S 206, (25) Ah 1, (32) NC Ac 7778, (36) NC

Ac 7785, (38) NC Ac 7790, (39) PI 268782, (44) Span cross, (47) Teja Amra Local and (49) U 2-4-5 recorded 'b' values around unity with non significant S^2di . Two varieties viz., (6) GAUG 1 and (7) GG 2 showed unit regression and significant S^2di . If selection has to be made for genotypes which took less days for 50 per cent flowering with general adaptability the genotypes viz., (25) Ah 1, (36) NC Ac 7785, (38) NC Ac 7790, (44) Span cross and (49) U 2-4-5 have to be selected. If selection has to be made for genotypes which took less days for 50 per cent flowering with specific adaptability to unfavourable environment, the four varieties viz., (9) ICG (FDRS) 10, (10) J 11, (14) KRG 1, (20) TAG 24 and nine germplasm lines viz., (30) NC Ac 7776, (31) NC Ac 7777, (33) NC Ac 7780, (37) NC Ac 7787, (40) PI 268829, (45) Span white, (46) Taiwan selection, (48) U 1-1-1 and (50) U 2-12-1 have to be selected (Table 4.31 and Fig 4.1).

Table 4.31: Mean performance and stability parameters for days to 50 per cent flowering

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
1.	AK 12-24	28.25	28.50	49.00	41.50	36.81	0.957	1.30*
2.	AK 159	27.25	28.25	51.25	40.25	36.75	1.067	-0.20
3.	ALR 3	30.25	29.25	50.25	41.00	37.69	0.933	0.21
4.	CO 1	28.00	30.00	49.75	41.50	37.31	0.957	1.08*
5.	CO 2	28.25	29.00	53.00	41.00	37.81	1.101*	-0.10
6.	GAUG 1	26.00	27.00	47.75	40.25	35.25	0.989	1.85*
7.	GG 2	28.00	29.00	50.75	42.00	37.44	1.027	0.73*
8.	Girnar 1	27.25	27.00	50.75	41.25	36.56	1.087	0.63*
9.	ICG (FDRS) 10	27.50	28.00	48.75	37.75	35.50	0.942	0.26
10.	J 11	27.00	27.00	47.75	37.75	34.88	0.939	-0.21
11.	JL 24 (Phule Pragati)	28.00	28.00	54.00	40.75	37.69	1.169	0.25
12.	JL 220 (Vyas)	28.00	28.75	49.75	40.00	36.63	0.973	-0.24
13.	Jyoti	27.75	29.25	50.00	39.50	36.63	0.972	0.12
14.	KRG 1	28.00	28.25	48.00	39.50	35.94	0.910	-0.08
15.	MH 1	30.25	29.75	54.50	44.25	39.69	1.124	0.41
16.	POL 2	27.00	27.00	47.00	36.00	34.25	0.891	0.78*
17.	S 206	28.75	28.25	50.00	40.25	36.81	0.978	-0.06
18.	SB 11	28.00	29.00	52.00	43.00	38.00	1.087	1.14*

Table 4.31: Continued –

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
19.	Spanish Improved	30.00	30.00	54.00	42.75	39.19	1.089*	-0.24
20.	TAG 24	27.00	27.25	47.00	39.00	35.06	0.915	0.28
21.	TKG 19A	29.75	30.50	54.50	41.75	39.13	1.093	0.45
22.	TG 17	28.25	28.75	51.75	40.50	37.31	1.052	-0.22
23.	TG 26	28.00	28.25	52.75	42.25	37.81	1.128	0.06
24.	TMV 2	29.50	29.00	55.25	42.25	39.00	1.171*	0.24
25.	Ah 1	26.25	27.25	48.00	38.25	34.94	0.967	-0.18
26.	Ah 4104-2	29.75	30.00	54.25	42.25	39.06	1.100*	-0.12
27.	Ah 4515	29.25	30.75	56.50	44.00	40.13	1.203*	-0.01
28.	Ah 6649	29.00	29.25	50.00	40.75	37.25	0.953	-0.20
29.	Comet	29.00	29.75	54.00	42.00	38.69	1.113*	-0.16
30.	NCAc 7776	26.00	27.00	46.25	36.75	34.00	0.894*	-0.15
31.	NCAc 7777	28.25	27.75	48.00	37.50	35.38	0.896	0.41
32.	NCAc 7778	28.00	29.00	50.00	39.00	36.50	0.967	0.17
33.	NCAc 7780	27.25	27.00	46.00	37.25	34.38	0.857*	-0.20
34.	NCAc 7782	30.50	30.00	51.25	42.00	38.44	0.958	0.01
35.	NCAc 7783	26.75	27.00	47.00	35.75	34.13	0.895	0.99*
36.	NCAc 7785	27.50	27.75	50.00	38.75	36.00	1.008	-0.03
37.	NCAc 7787	27.50	28.00	47.00	39.00	35.38	0.884	0.05
38.	NCAc 7790	27.25	26.75	49.25	38.50	35.44	1.006	-0.03
39.	PI 268782	27.75	29.00	50.00	39.25	36.50	0.976	0.07
40.	PI 268829	28.00	28.00	47.75	39.00	35.69	0.901*	-0.18
41.	PI 268642	30.00	31.25	55.00	42.75	39.75	1.099	0.18
42.	Pearl	29.00	30.00	53.00	42.75	38.69	1.074	-0.03
43.	Starr	28.00	28.25	51.75	41.00	37.25	1.075*	-0.26
44.	Span cross	27.00	28.00	50.00	39.00	36.00	1.017	-0.09
45.	Span white	27.25	27.25	47.00	38.00	34.88	0.899*	-0.24
46.	Taiwan Selection	28.25	28.00	49.00	39.00	36.06	0.945	-0.16
47.	Teja Amra Local	28.00	28.00	50.00	40.25	36.56	1.004	-0.16
48.	U 1-1-1	27.50	28.25	48.00	38.75	35.63	0.915*	-0.24
49.	U 2-4-5	27.75	28.00	50.75	38.75	36.31	1.026	0.38
50.	U 2-12-1	26.75	27.00	45.00	35.75	33.63	0.815*	-0.05
	Mean	28.07	28.47	50.29	40.04	36.72	1.000	
	SE (m) ±	0.45	0.46	0.66	0.51	0.34	SE (bi) 0.036	
	CD at 5%	1.27	1.29	1.85	1.44	0.95		
	CD at 1%	1.68	1.70	2.44	1.90	1.26		

* P ≤ 0.05, ** P ≤ 0.01

4.10.2. Height of main axis (cm)

Average height of main axis was minimum in variety (20) TAG 24 (16.58 cm) and it was maximum in germplasm line (25) Ah 1 (35.23 cm). Regression coefficient was recorded to be significant for 16 genotypes. Twelve genotypes viz., (3) ALR 3, (7) GG 2, (8) Girnar 1, (10) J 11, (21) TKG

Days to 50 per cent flowering

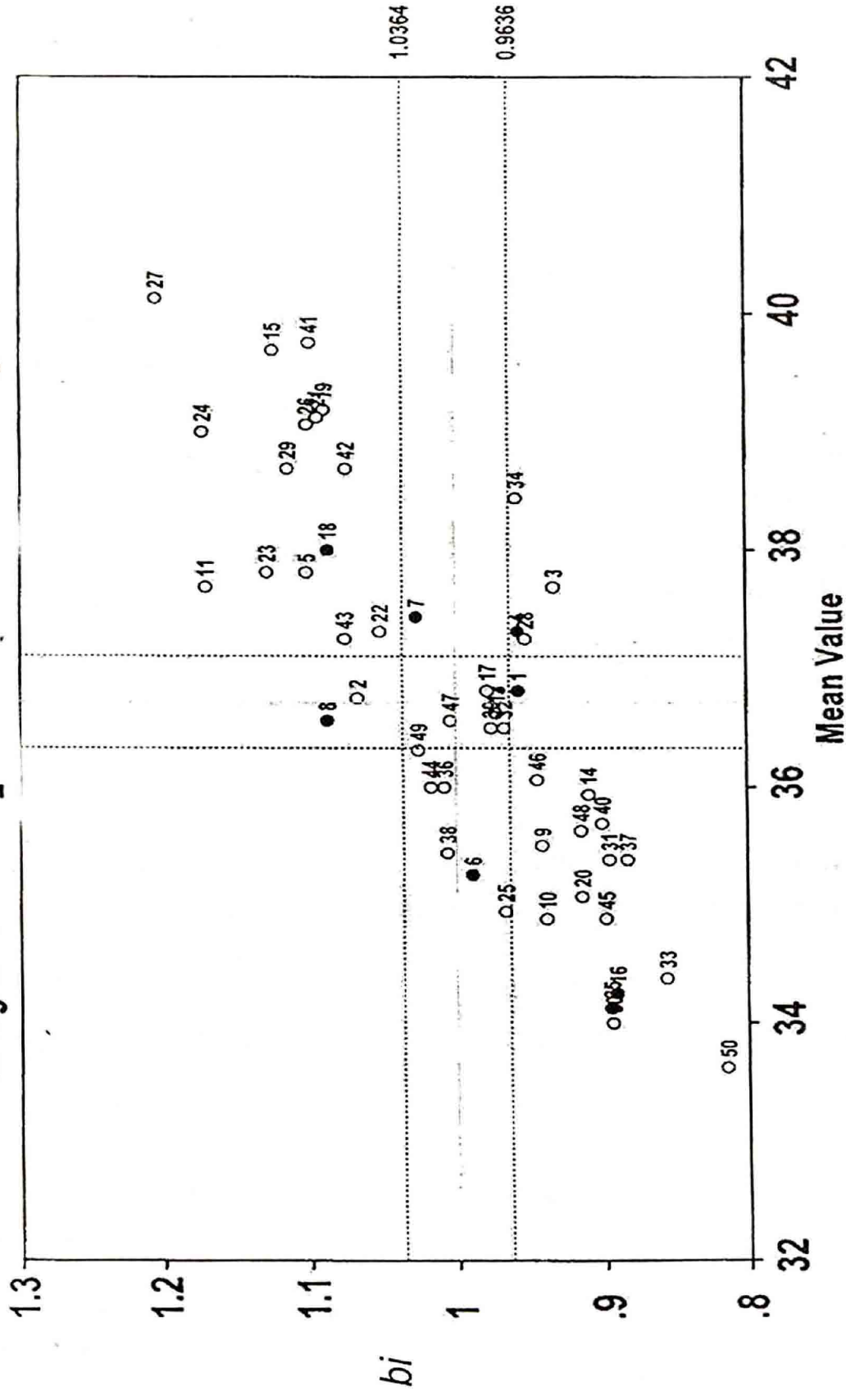


Fig.4.1: Stability parameters in respect of days to 50 per cent flowering
(Mean performance, bi and S^2di)

- Solid symbols indicate significant S^2di

19A, (22) TG 17, (34) NC Ac 7782, (36) NC Ac 7785, (38) NC Ac 7790, (41) PI 268642, (42) Pearl and (49) U 2-4-5 possessed 'b' values around unity. Out of these two genotypes viz., (36) NC Ac 7785 and (49) U 2-4-5 showed significant deviation from regression. Non significant deviation from regression was shown by 32 genotypes. If selection has to be made for dwarfness with general adaptability, the genotypes viz., (7) GG 2, (8) Girnar 1, (21) TKG 19A, (34) NC Ac 7782, (38) NC Ac 7790, (41) PI 268642 and (42) Pearl have to be selected. If selection has to be made for tallness with general adaptability, the genotype viz., (3) ALR 3 has to be selected. If selection has to be made for dwarfness with specific adaptability to favourable environment, the varieties viz., (9) ICG (FDRS) 10 and four germplasm lines viz., (32) NC Ac 7778, (33) NC Ac 7780, (35) NC Ac 7783 and (37) NC Ac 7787 have to be selected. If selection has to be made for tallness with specific adaptability to favourable environment, three varieties viz., (6) GAUG 1, (14) KRG 1 and (24) TMV 2 and three germplasm lines viz., (26) Ah 4104-2, (28) Ah 6649 and (47) Teja Amra Local can be selected. If selection has to be made for dwarfness with specific adaptability for unfavourable environment, the released varieties viz., (2) AK 159, (12) JL 220, (15) MH 1, (20) TAG 24 and (23) TG 26 have to be selected. If selection has to be made for tallness with specific adaptability for unfavourable environment, the released varieties viz., (1) AK 12-24, (4) CO 1, (16) Pol. 2 and (18) SB XI have to be selected (Table 4.32 and Fig. 4.2).

Table 4.32 : Mean performance and stability parameters for height of main axis (cm)

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
1.	AK 12-24	36.00	34.40	25.30	22.38	29.52	0.854*	-0.45
2.	AK 159	32.35	29.75	21.73	20.15	25.99	0.758*	0.07
3.	ALR 3	39.60	37.90	28.20	23.58	32.32	0.979	-0.09
4.	CO 1	35.20	34.30	25.65	22.55	29.43	0.801*	-0.27
5.	CO 2	34.65	32.75	23.40	20.75	27.89	0.872*	-0.42
6.	GAUG 1	42.95	40.80	24.33	18.83	31.73	1.525*	-0.11
7.	GG 2	30.35	28.50	18.35	13.50	22.68	1.028	-0.07
8.	Girnar 1	30.80	29.10	18.23	13.65	22.94	1.062	-0.22
9.	ICG (FDRS) 10	37.00	32.70	20.30	16.70	26.68	1.236	0.33
10.	J 11	35.70	33.95	23.93	20.23	28.45	0.963	-0.42
11.	JL 24 (Phule Pragati)	33.90	31.85	26.05	20.45	28.06	0.758	1.76*

Table 4.32 : Continued -

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
12.	JL 220 (Vyas)	31.50	28.05	18.88	17.00	23.86	0.889	0.51
13.	Jyoti	41.55	35.50	23.45	20.45	30.24	1.256	2.80*
14.	KRG 1	41.95	38.60	27.30	22.28	32.28	1.140	-0.23
15.	MH 1	33.90	30.60	21.68	19.80	26.49	0.865	0.39
16.	POL 2	36.43	33.95	25.70	22.00	29.52	0.865	-0.28
17.	S 206	37.58	33.63	30.25	28.65	32.53	0.481*	1.66*
18.	SB 11	34.50	34.15	26.78	24.45	29.97	0.651*	-0.18
19.	Spanish Improved	37.88	34.65	30.15	21.60	31.07	0.848	8.00*
20.	TAG 24	18.05	16.00	16.80	15.48	16.58	0.089*	0.69
21.	TKG 19A	34.05	32.15	21.33	19.45	26.74	0.943	0.11
22.	TG 17	32.80	31.50	20.83	17.23	25.59	0.986	-0.28
23.	TG 26	18.25	16.65	16.85	15.85	16.90	0.098*	0.13
24.	TMV 2	43.25	41.25	25.55	22.60	33.16	1.347*	0.66
25.	Ah 1	48.00	45.23	24.55	23.13	35.23	1.667	5.05*
26.	Ah 4104-2	42.30	38.80	27.05	22.60	32.69	1.194*	-0.26
27.	Ah 4515	43.50	40.00	24.75	22.43	32.67	1.349	1.18*
28.	Ah 6649	41.05	38.30	22.25	18.30	29.98	1.449*	-0.04
29.	Comet	31.90	30.35	30.10	24.25	29.15	0.350	5.22*
30.	NCAc 7776	40.28	37.65	17.35	15.50	27.69	1.653	4.06*
31.	NCAc 7777	25.98	21.50	19.25	16.85	20.89	0.459	2.76*
32.	NCAc 7778	36.75	33.85	19.48	16.65	26.68	1.284*	0.32
33.	NCAc 7780	33.95	30.85	16.95	14.50	24.06	1.241	0.56
34.	NCAc 7782	32.95	31.10	20.00	18.90	25.74	0.925	0.79
35.	NCAc 7783	33.65	31.55	16.70	14.30	24.05	1.265	0.81
36.	NCAc 7785	36.35	34.00	27.53	19.10	29.24	0.948	6.16*
37.	NCAc 7787	33.85	32.40	17.30	13.90	24.36	1.301	0.44
38.	NCAc 7790	33.95	32.70	21.25	17.40	26.33	1.051	-0.19
39.	PI 268782	42.55	40.80	22.50	19.50	31.34	1.525*	1.75*
40.	PI 268829	42.50	39.90	19.25	17.40	29.76	1.678	4.28*
41.	PI 268642	34.15	32.75	20.45	17.48	26.21	1.078	-0.03
42.	Pearl	34.15	33.80	22.10	18.35	27.10	1.027	0.44
43.	Starr	33.08	31.50	28.50	22.38	28.86	0.561	3.99*
44.	Span cross	33.20	31.80	25.30	20.28	27.64	0.755	0.95*
45.	Span white	26.05	24.83	22.60	18.45	22.98	0.400*	1.49*
46.	Taiwan Selection	44.23	43.45	23.33	20.30	32.83	1.617	3.49*
47.	Teja Amra Local	45.20	44.00	27.23	22.25	34.67	1.483*	0.62
48.	U 1-1-1	36.55	34.80	29.53	22.25	30.78	0.784	4.73*
49.	U 2-4-5	35.70	34.65	21.50	20.05	27.98	1.055	1.35*
50.	U 2-12-1	35.55	33.85	30.50	24.05	30.99	0.606	4.35*
	Mean	35.73	33.54	23.17	19.60	28.01	1.000	
	SE (m) $\pm$	0.59	0.89	0.55	0.56	0.78	SE (bi) 0.100	
	CD at 5%	1.64	2.48	1.54	1.57	2.16		
	CD at 1%	2.16	3.28	2.03	2.07	2.84		

* $P \leq 0.05$, ** $P \leq 0.01$

Height of main axis (cm)

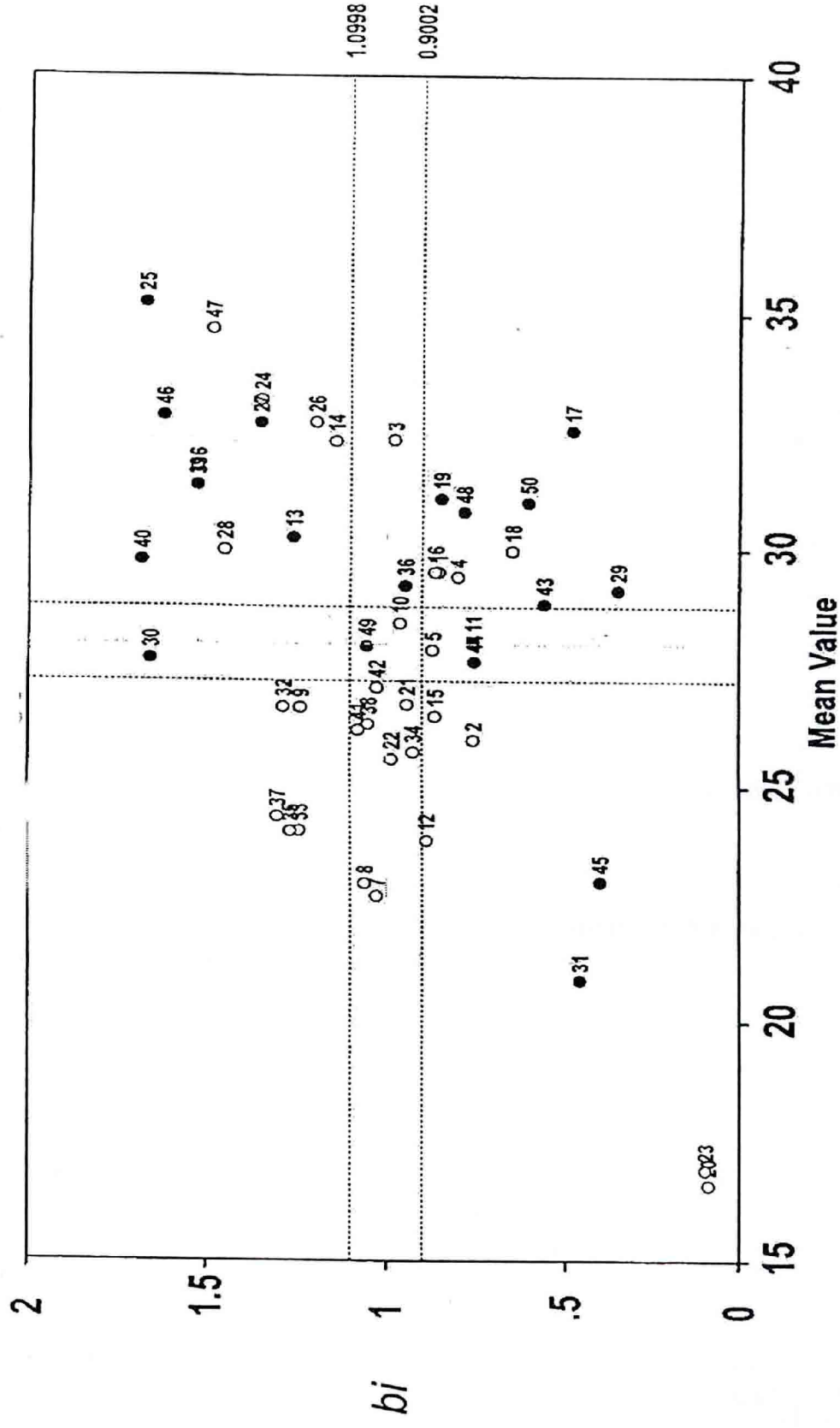


Fig.4.2: Stability parameters in respect of height of main axis
(Mean performance, bi and S^2_{di})

- Solid symbols indicate significant S^2_{di}

4.10.3. Primary branches per plant

Average primary branches was maximum in germplasm line (42) Pearl (6.19) and it was minimum in germplasm line (35) NC Ac 7783 (3.95). Regression coefficient or sensitivity was found to be significant for 13 genotypes. Ten genotypes, viz., (7) GG 2, (9) ICG (FDRS) 10, (11) JL 24, (16) POL.2, (17) S 206, (19) Spanish Improved, (20) TAG 24, (24) TMV 2, (38) NC Ac 7790 and (40) PI 268829 recorded '*bi*' value around unity. Except five genotypes, all other showed non significant deviation from regression ($S^2di \approx 0$). If selection has to be made for general adaptability only one variety (16) Pol.2 has to be selected. If selection has to be made for specific adaptability to favourable environment ($bi > 1.0$), four varieties, viz., (3) ALR 3, (10) J 11, (12) JL 220 and (13) Jyoti and seven germplasm lines viz., (29) Comet, (36) NC Ac 7785, (42) PI 268642, (44) Span cross, (46) Taiwan selection, (46) Teja Amra Local and (48) U 1-1-1 have to be selected. If selection has to be made for specific adaptability to unfavourable environment ($bi < 1.0$) one variety viz., (5) Co 2 and four germplasm lines viz., (28) Ah 6649, (30) NC Ac 7776, (37) NC Ac 7787 and (49) U 2-4-5 have to be selected (Table 4.33 and Fig. 4.3).

Table 4.33: Mean performance and stability parameters for primary branches per plant

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
1.	AK 12-24	4.45	4.25	6.28	6.25	5.31	2.217	0.14*
2.	AK 159	5.00	4.70	5.10	4.58	4.84	0.163	0.05
3.	ALR 3	5.00	4.50	6.40	6.10	5.50	1.873*	-0.01
4.	CO 1	4.60	4.45	4.98	4.65	4.67	0.428*	-0.02
5.	CO 2	5.10	4.75	5.50	5.30	5.16	0.657	-0.02
6.	GAUG 1	5.00	4.60	5.10	4.53	4.81	0.223	0.08*
7.	GG 2	4.75	4.15	5.20	4.90	4.75	0.875	0.00
8.	Girnar 1	4.85	4.10	5.50	5.25	4.93	1.237	0.01
9.	ICG (FDRS) 10	4.15	3.95	5.20	4.85	4.54	1.223	-0.02
10.	J 11	4.50	4.30	6.10	5.80	5.18	1.865	0.02
11.	JL 24 (Phule Pragati)	4.50	4.30	5.20	5.10	4.78	0.915	-0.02
12.	JL 220 (Vyas)	4.50	4.10	6.10	5.75	5.11	2.004*	0.00
13.	Jyoti	4.50	4.20	6.25	6.00	5.24	2.131	0.04
14.	KRG 1	4.63	4.28	5.80	5.00	4.93	1.323	0.02

Table 4.33: Continued-

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
15.	MH 1	4.25	4.15	4.70	4.40	4.38	0.482*	-0.02
16.	POL 2	5.00	4.70	5.85	5.35	5.23	1.022	-0.02
17.	S 206	4.95	4.65	5.60	5.10	5.08	0.795	-0.01
18.	SB 11	4.50	4.30	5.10	4.70	4.65	0.695	-0.02
19.	Spanish Improved	4.90	4.40	5.70	5.30	5.08	1.158	-0.02
20.	TAG 24	4.40	4.05	5.10	4.90	4.61	0.995	-0.03
21.	TKG 19A	4.45	4.15	5.50	5.00	4.78	1.249	-0.02
22.	TG 17	4.20	4.30	4.30	4.20	4.25	-0.001*	-0.03
23.	TG 26	4.40	4.30	4.90	4.40	4.50	0.468	0.01
24.	TMV 2	4.20	4.05	5.10	4.45	4.45	0.908	0.01
25.	Ah 1	4.60	4.75	4.90	4.35	4.65	0.028	0.05
26.	Ah 4104-2	4.40	4.20	4.90	4.70	4.55	0.653*	-0.03
27.	Ah 4515	5.75	5.30	5.45	6.00	5.63	0.208	0.10*
28.	Ah 6649	5.90	5.35	5.70	5.73	5.67	0.214	0.03
29.	Comet	4.95	4.35	6.10	5.80	5.30	1.668*	-0.02
30.	NCAc 7776	5.00	4.90	5.35	5.30	5.14	0.458*	-0.03
31.	NCAc 7777	4.50	3.75	5.65	5.55	4.86	1.857	0.03
32.	NCAc 7778	4.90	4.30	5.95	6.10	5.31	1.714	0.08*
33.	NCAc 7780	4.15	4.15	4.45	4.10	4.21	0.216*	-0.01
34.	NCAc 7782	4.65	4.40	5.90	6.00	5.24	1.649	0.08*
35.	NCAc 7783	4.00	3.80	4.00	4.00	3.95	0.157	-0.02
36.	NCAc 7785	4.75	4.35	6.08	5.85	5.26	1.736	-0.01
37.	NCAc 7787	5.45	5.10	5.70	5.33	5.39	0.425	0.00
38.	NCAc 7790	4.55	4.15	5.25	4.90	4.71	0.983	-0.03
39.	PI 268782	4.70	4.25	5.10	4.90	4.74	0.736	-0.02
40.	PI 268829	4.70	4.40	5.55	5.20	4.96	1.075	-0.03
41.	PI 268642	4.95	4.90	5.10	4.90	4.96	0.138*	-0.02
42.	Pearl	5.45	4.95	7.35	7.00	6.19	2.422*	0.02
43.	Starr	4.20	4.20	4.90	4.45	4.44	0.634	0.00
44.	Span cross	4.85	4.70	6.03	5.55	5.28	1.282	-0.01
45.	Span white	4.40	4.30	4.90	4.80	4.60	0.610*	-0.03
46.	Taiwan Selection	4.85	4.45	6.10	5.75	5.29	1.607*	-0.02
47.	Teja Amra Local	4.50	4.35	6.10	5.55	5.13	1.737	-0.01
48.	U 1-1-1	4.70	5.00	6.80	6.60	6.03	1.726	0.00
49.	U 2-4-5	5.85	5.60	6.40	6.20	6.01	0.749*	-0.03
50.	U 2-12-1	5.30	5.35	5.90	5.25	5.45	0.411	0.05
	Mean	4.76	4.46	5.52	5.23	4.99	1.000	
	SE (m) ±	0.16	0.16	0.16	0.19	0.11	SE (bi) 0.227	
	CD at 5%	0.45	0.45	0.46	0.536	0.30		
	CD at 1%	0.59	0.59	0.60	0.708	0.40		

* P ≤ 0.05, ** P ≤ 0.01

Primary branches per plant

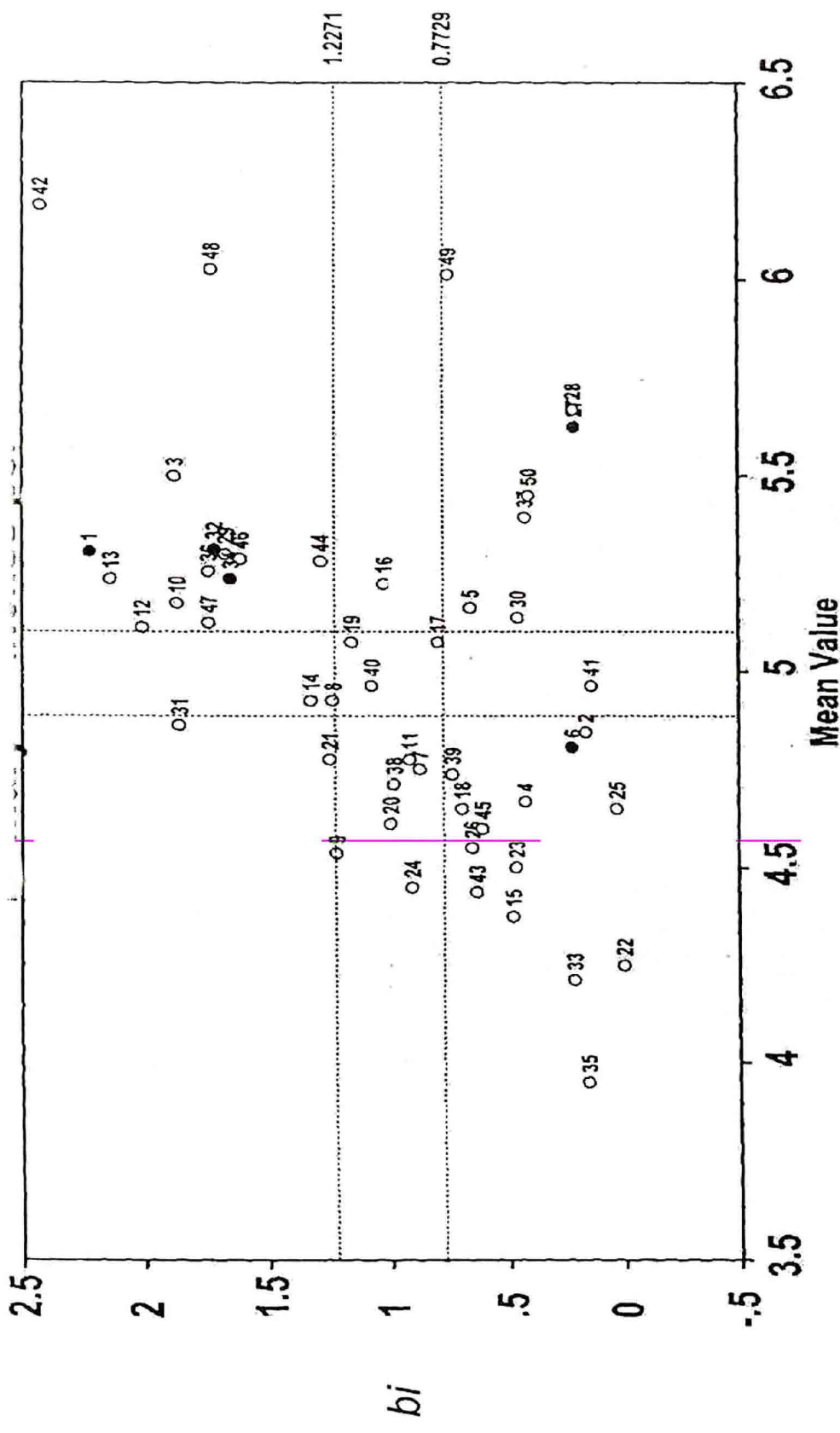


Fig.4.3: Stability parameters in respect of primary branches per plant (Mean performance, bi and S^2di)

- Solid symbols indicate significant S^2di

4.10.4. Secondary branches per plant

Average secondary branches ranged between 0.00 [germplasm line (35) NC Ac 7783] to 5.71 [release variety (5) CO 2]. Regression coefficient or sensitivity was found to be significant for 34 genotypes. Six genotypes, viz., (8) Girnar 1, (9) ICG (FDRS) 10, (16) POL. 2 (20) TAG 24, (24) TMV 2 and (50) U 2-12-1 recorded '*bi*' values around unity (1.00). Except seven genotypes all other showed non significant deviation ($S^2di \approx 0$) from regression. If selection has to be made for general adaptability, only one variety viz., (8) Girnar 1 has to be selected. If selection has to be made for specific adaptability to favourable environment ($bi > 1.0$), four released varieties, viz., (1) AK 12-24, (7) GG 2, (11) JL 24, (13) Jyoti and nine germplasm lines viz., (27) Ah 4515, (28) Ah 6649, (29) Comet, (40) PI 268829, (42) Pearl, (43) Starr, (44) Span cross, (48) U 1-1-1 and (49) U 2-4-5 deserve to be selected. If selection has to be made for specific adaptability to unfavourable environment ($bi < 1.0$) one variety viz., (18) SB XI and one germplasm line viz., (46) Taiwan selection has to be selected (Table 4.34 and Fig. 4.4).

Table 4.34: Mean performance and stability parameters for secondary branches per plant

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
1.	AK 12-24	0.50	0.80	6.70	5.98	3.49	1.832*	0.06
2.	AK 159	0.10	0.00	0.30	0.20	0.15	0.068*	-0.06
3.	ALR 3	0.15	0.25	0.00	0.00	0.10	-0.065*	-0.06
4.	CO 1	0.05	0.00	2.03	1.48	0.89	0.566*	-0.05
5.	CO 2	4.25	5.30	6.70	6.60	5.71	0.591	0.29*
6.	GAUG 1	0.20	0.15	5.00	3.90	2.31	1.395*	-0.02
7.	GG 2	0.30	0.00	6.10	5.35	2.94	1.802*	-0.05
8.	Girnar 1	1.85	1.45	5.00	4.45	3.19	1.000	-0.05
9.	ICG (FDRS) 10	0.00	0.00	3.45	2.98	1.61	1.038	-0.05
10.	J 11	1.75	2.60	7.00	5.85	4.30	1.380	0.28*
11.	JL 24 (Phule Pragati)	0.50	0.45	5.93	4.90	2.94	1.604*	-0.04
12.	JL 220 (Vyas)	0.50	0.20	1.45	0.90	0.76	0.281*	0.00
13.	Jyoti	1.00	0.85	6.90	6.10	3.71	1.802*	-0.05

Table 4.34 Continued -

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
14.	KRG 1	0.40	1.00	6.00	4.70	3.03	1.514	0.18*
15.	MH 1	0.85	0.75	1.65	1.30	1.14	0.226*	-0.05
16.	POL 2	0.75	0.55	3.85	3.45	2.15	0.970	-0.06
17.	S 206	0.40	0.20	2.30	2.10	1.25	0.613*	-0.05
18.	SB 11	1.45	1.40	4.05	3.60	2.63	0.779*	-0.06
19.	Spanish Improved	1.25	1.10	3.55	3.05	2.24	0.693*	-0.06
20.	TAG 24	0.70	0.20	3.70	3.70	2.08	1.041	0.05
21.	TKG 19A	0.65	0.40	1.55	1.45	1.01	0.316*	-0.05
22.	TG 17	0.15	0.00	0.30	0.25	0.18	0.067*	-0.06
23.	TG 26	1.00	1.50	3.35	2.65	2.13	0.573	0.07
24.	TMV 2	0.15	0.00	3.60	2.75	1.63	1.014	-0.04
25.	Ah 1	1.15	0.70	3.30	2.83	1.99	0.699*	-0.03
26.	Ah 4104-2	0.15	0.00	4.30	4.10	2.14	1.323	0.01
27.	Ah 4515	2.65	2.15	8.35	7.15	5.08	1.745*	-0.04
28.	Ah 6649	0.50	0.00	9.88	8.08	4.61	2.838*	-0.04
29.	Comet	0.85	0.20	5.30	4.30	2.66	1.398*	-0.01
30.	NCAc 7776	0.60	0.35	1.85	1.10	0.98	0.342*	0.03
31.	NCAc 7777	0.05	0.00	0.60	0.65	0.33	0.190*	-0.05
32.	NCAc 7778	0.15	0.00	4.40	3.95	2.13	1.322*	-0.04
33.	NCAc 7780	0.15	0.00	1.85	1.65	0.91	0.541*	-0.06
34.	NCAc 7782	0.35	0.60	5.60	5.40	2.99	1.606*	0.13*
35.	NCAc 7783	0.00	0.00	0.00	0.00	0.00	0.000*	-0.06
36.	NCAc 7785	2.70	3.35	8.53	7.70	5.57	1.640	0.16*
37.	NCAc 7787	2.05	1.65	2.48	2.83	2.25	0.249*	0.03
38.	NCAc 7790	1.40	0.05	5.80	4.90	3.04	1.513	0.24*
39.	PI 268782	1.30	0.20	5.60	4.95	3.01	1.472	0.12*
40.	PI 268829	1.00	0.55	4.70	3.70	2.49	1.125	-0.01
41.	PI 268642	0.85	0.30	1.10	0.93	0.79	0.149*	0.01
42.	Pearl	0.70	0.20	5.90	5.75	3.14	1.723*	0.11
43.	Starr	0.90	0.15	6.00	5.75	3.20	1.720*	0.11
44.	Span cross	0.75	0.25	5.15	4.60	2.69	1.415*	-0.03
45.	Span white	0.55	0.30	2.30	1.60	1.19	0.508*	-0.01
46.	Taiwan Selection	1.75	1.70	4.85	3.78	3.02	0.856	0.04
47.	Teja Amra Local	1.30	1.25	3.10	3.00	2.16	0.569*	-0.05
48.	U 1-1-1	0.35	0.00	5.60	4.53	2.62	1.592*	-0.05
49.	U 2-4-5	0.75	0.25	5.00	4.55	2.64	1.381*	-0.02
50.	U 2-12-1	0.40	0.15	3.65	2.90	1.78	0.980	-0.05
	Mean	0.85	0.67	4.11	3.57	2.30	1.000	
	SE (m) $\pm$	0.20	0.18	0.27	0.30	0.28	SE (bi) 0.086	
	CD at 5%	0.56	0.49	0.76	0.83	0.78		
	CD at 1%	0.75	0.65	1.01	1.10	1.02		

* $P \leq 0.05$, ** $P \leq 0.01$

Secondary branches per plant

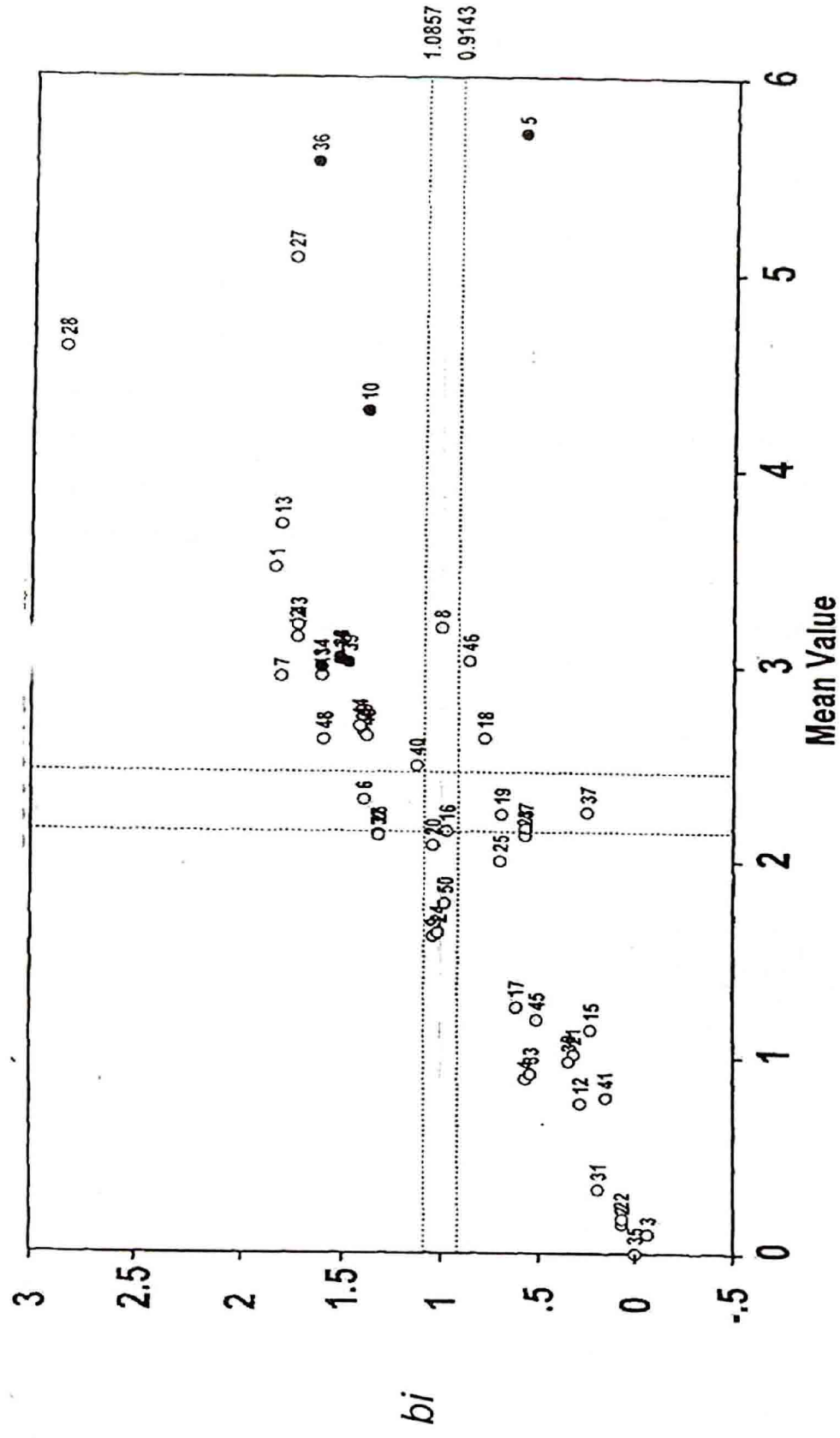


Fig.4.4: Stability parameters in respect of secondary branches per plant
(Mean performance, bi and S²di)

- Solid symbols indicate significant S²di

4.10.5. Mature pods per plant

Maximum number of mature pods was produced by variety (20) TAG 24 (17.22) and minimum by germplasm line (37) NC Ac 7787. Regression coefficient was found to be significant for only one genotype. Thirteen genotypes viz., (6) GAUG 1, (10) J 11, (21) TKG 19A, (22) TG 17, (26) Ah 4104-2, (31) NC Ac 7777, (36) NC Ac 7785, (38) NC Ac 7790, (41) PI 268642, (46) Taiwan selection, (47) Teja Amra Local (49) U 2-4-5 and (50) U 2-12-1 recorded '*bi*' value around unity ($bi \approx 1.00$) with non significant $S^2 di$. Non significant deviation from regression was shown by 15 genotypes. If selection has to be made for general adaptability, three germplasm lines viz., (47) Teja Amra Local, (49) U 2-4-5 and (50) U 2-12-1 may be attempted (Table 4.35 and Fig. 4.5).

Table 4.35: Mean performance and stability parameters for mature pods per plant

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E_1	E_2	E_3	E_4	General Mean	<i>bi</i>	$S^2 di$
1.	AK 12-24	10.80	7.95	11.40	13.75	10.98	-0.602	7.41*
2.	AK 159	23.85	20.15	10.45	11.40	16.46	4.909	11.53*
3.	ALR 3	17.15	15.00	10.70	8.70	12.89	2.832	4.48*
4.	CO 1	11.10	9.30	10.05	12.25	10.68	0.019	2.15*
5.	CO 2	10.70	8.85	11.10	12.60	10.81	-0.390	2.92*
6.	GAUG 1	13.95	12.20	10.60	12.40	12.29	0.952	0.50
7.	GG 2	10.50	8.85	13.35	14.48	11.79	-1.239	6.27*
8.	Gimar 1	14.55	12.50	14.38	15.45	14.22	-0.091	1.97*
9.	ICG (FDRS) 10	11.85	8.95	12.35	14.23	11.84	-0.474	6.34*
10.	J 11	14.45	13.05	10.55	11.75	12.45	1.263	0.40
11.	JL 24 (Phule Pragati)	11.90	9.05	6.33	5.15	8.11	2.366	0.94*
12.	JL 220 (Vyas)	7.10	5.25	7.80	9.25	7.35	-0.493	3.29*
13.	Jyoti	11.05	9.70	10.60	11.28	10.66	0.071	0.40
14.	KRG 1	15.03	12.40	13.55	14.55	13.88	0.421	1.32*
15.	MH 1	12.38	10.70	12.40	12.48	11.99	0.014	0.79*
16.	POL.2	11.05	9.10	11.25	12.10	10.88	-0.191	2.01*
17.	S 206	13.68	12.40	14.33	15.00	13.85	-0.341	1.27*

Table 4.35 : Continued –

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
18.	SB 11	15.05	11.55	15.45	16.15	14.55	-0.203	5.90*
19.	Spanish Improved	14.03	11.60	11.25	13.30	12.54	0.706	1.25*
20.	TAG 24	17.03	13.60	18.45	19.80	17.22	-0.710	9.23*
21.	TKG 19A	11.90	10.10	8.58	9.23	9.95	1.160	-0.16
22.	TG 17	13.18	11.60	11.40	9.55	11.43	1.045	0.58
23.	TG 26	13.20	11.35	15.50	16.05	14.03	-0.921	4.87*
24.	TMV 2	13.05	11.60	11.30	9.05	11.25	1.108	1.08*
25.	Ah 1	17.15	16.65	9.70	10.35	13.46	2.672	7.74*
26.	Ah 4104-2	10.75	9.50	8.58	9.45	9.57	0.676	-0.13
27.	Ah 4515	22.25	20.10	9.40	11.65	15.85	4.426	15.64*
28.	Ah 6649	17.25	15.65	12.10	12.58	14.39	1.870	1.13*
29.	Comet	11.25	9.60	13.10	12.75	11.68	-0.589	2.75*
30.	NCAc 7776	15.45	13.75	7.55	8.50	11.31	2.810	4.83*
31.	NCAc 7777	10.40	8.05	7.58	8.25	8.57	0.981	-0.08
32.	NCAc 7778	13.60	11.15	6.65	7.65	9.76	2.463	1.71*
33.	NCAc 7780	10.15	8.45	10.45	7.00	9.01	0.573	2.82*
34.	NCAc 7782	12.50	11.45	9.58	8.25	10.44	1.364	0.98*
35.	NCAc 7783	11.30	9.85	8.83	6.70	9.17	1.355	1.24*
36.	NCAc 7785	12.40	10.20	9.43	8.30	10.08	1.371	0.04
37.	NCAc 7787	6.33	4.90	7.45	5.60	6.07	-0.042	1.46*
38.	NCAc 7790	9.80	7.90	8.23	7.70	8.41	0.729	-0.12
39.	PI 268782	18.33	17.60	10.40	9.28	13.90	3.187	10.74*
40.	PI 268829	16.90	15.75	10.20	9.45	13.08	2.669	5.58*
41.	PI 268642	9.45	8.20	7.65	6.80	8.03	0.859	-0.10
42.	Pearl	12.50	12.10	10.38	8.85	10.96	1.089	1.30*
43.	Starr	10.50	9.45	12.50	11.65	11.03	-0.564	1.64*
44.	Span cross	20.35	18.25	10.60	9.40	14.65	3.914	10.62*
45.	Span white	8.50	7.80	9.50	8.63	8.61	-0.194	0.33
46.	Taiwan Selection	10.70	9.75	9.60	8.68	9.68	0.605	-0.10
47.	Teja Amra Local	16.30	13.60	12.35	10.65	13.23	1.854	0.60
48.	U 1-1-1	16.60	14.60	11.15	9.35	12.93	2.418	2.92*
49.	U 2-4-5	16.75	13.25	12.50	11.80	13.58	1.796*	-0.19
50.	U 2-12-1	14.10	13.60	13.30	12.30	13.33	0.497	0.00
	Mean	13.40	11.56	10.84	10.83	11.66	1.000	
	SE (m) ±	0.52	0.67	0.49	0.54	0.57	SE (bi) 0.868	
	CD at 5%	1.46	1.88	1.37	1.50	1.58		
	CD at 1%	1.93	2.48	1.81	1.99	2.08		

* P ≤ 0.05, ** P ≤ 0.01

Number of mature pods per plant

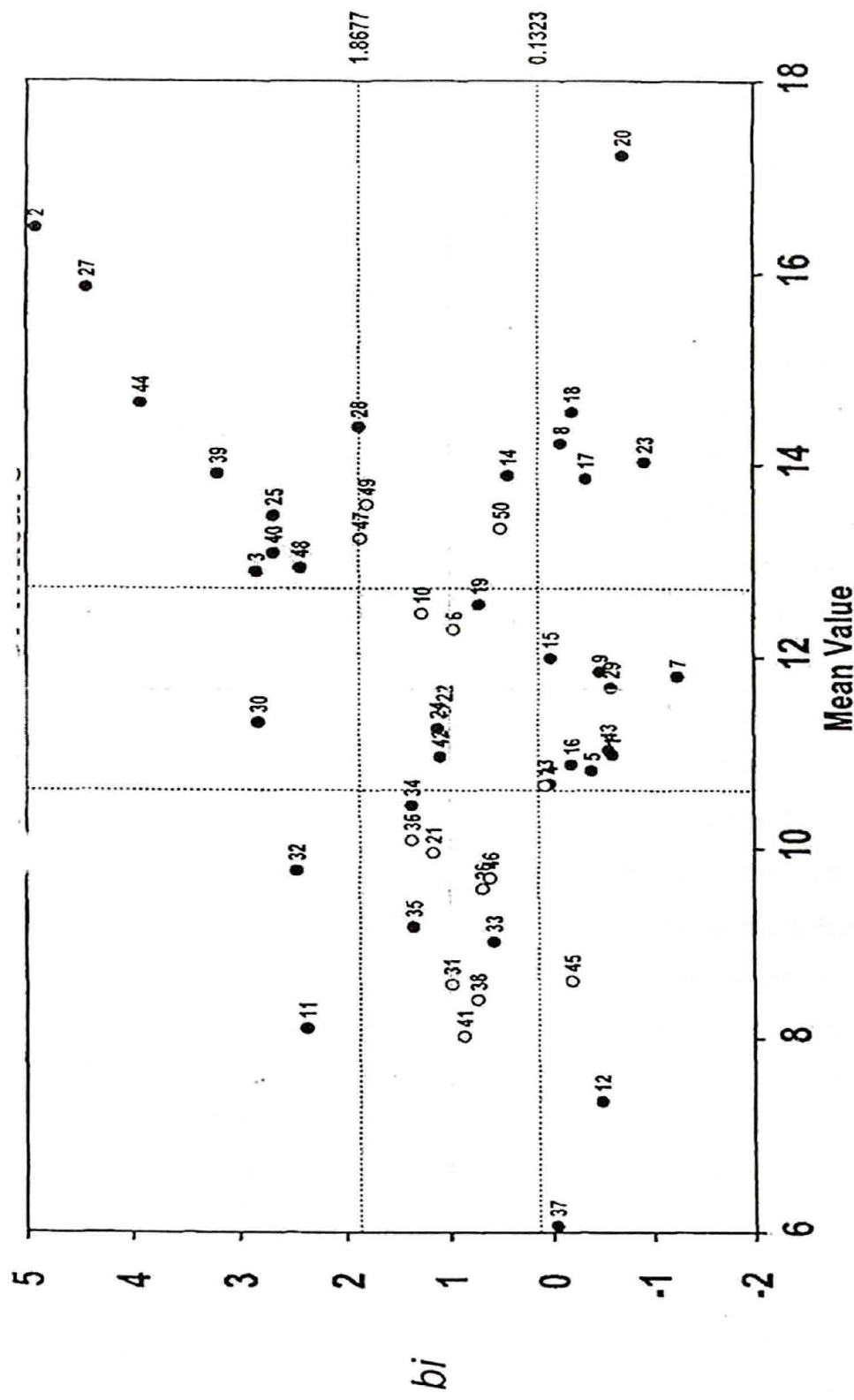


Fig.4.5: Stability parameters in respect of mature pods per plant (Mean performance, bi and S^2di)

- Solid symbols indicate significant S^2di

4.10.6. Shelling percentage

Highest average shelling out-turn was registered by genotype (44) Span cross (78.53%) and it was lowest in variety (4) Co 1 (54.99%). Twenty three genotypes viz., (7) GG 2, (9) TCG (FDRS) 10, (12) JL 220, (13) Jyoti, (15) MH 1, (16) Pol. 2, (18) SB XI, (22) TG 17, (24) TMV 2, (25) Ah 1, (27) Ah 4515, (28) Ah 6649, (30) NC Ac 7776, (34) NC Ac 7782, (35) NC Ac 7783, (39) PI 268782, (40) PI 268829, (41) PI 268642, (42) Pearl, (43) Star, (45) Span white, (48) U 1-1-1 and (50) U 2-12-1 recorded '*bi*' value around unity with non significant S^2di . In all 37 genotypes showed non significant deviation from regression. If selection has to be made for general adaptability, five released varieties, viz., (7) GG 2, (13) Jyoti, (15) MH 1, (18) SB XI and (24) TMV 2 and eight germplasm lines viz., (27) Ah 4515, (28) Ah 6649, (34) NC Ac 7782, (39) PI 268782, (40) PI 268829, (41) PI 268642, (43) Starr, (50) U 2-12-1 may be considered, because they have got high mean performance and unit regression and non significant S^2di . If selection has to be made for specific adaptability to favourable environment, one variety viz., (20) TAG 24 and one germplasm line viz., (36) NC Ac 7785 have to be selected because they registered mean performance greater than over all mean, $bi > 1.0$ and non significant S^2di . If selection has to be made for specific adaptability to unfavourable environment, four varieties viz., (14) KRG 1, (17) S 206, (19) Spanish improved and (23) TG 26 and five germplasm lines viz., (26) Ah 4104-2, (29) Comet, (38) NC Ac 7790, (44) Span cross and (47) Teja Amra Local may to be selected, because of mean performance greater than over all mean, $bi < 1.0$ and non significant S^2di (Table 4.36 and Fig. 4.6).

Table 4.36 Mean performance and stability parameters for shelling percentage

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	Bi	S ² di
1.	AK 12-24	66.80	64.40	72.43	70.90	68.63	2.427	3.86*
2.	AK 159	67.63	65.58	68.63	69.48	67.83	1.022	0.95*
3.	ALR 3	57.20	55.75	62.28	60.35	58.89	1.927	2.57*
4.	CO 1	53.98	49.05	59.68	57.25	54.99	3.262	2.16*
5.	CO 2	56.70	53.40	60.60	59.40	57.53	2.227	1.34*
6.	GAUG 1	61.50	56.48	62.50	60.45	60.23	1.904	0.12
7.	GG 2	70.38	68.90	72.25	70.95	70.62	1.003	-0.29

Table 4.36: Continued -

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	Bi	S ² di
8.	Girnar 1	61.90	58.25	65.53	63.85	62.38	2.243	0.49
9.	ICG (FDRS) 10	62.93	61.60	65.93	65.18	63.91	1.312	0.85
10.	J 11	72.15	70.60	69.05	72.45	71.06	-0.269	3.07*
11.	JL 24 (Phule Pragati)	71.15	67.80	69.58	68.35	69.22	0.604	1.89*
12.	JL 220 (Vyas)	60.20	56.68	61.25	59.80	59.48	1.439	-0.28
13.	Jyoti	70.83	69.45	71.28	71.33	70.72	0.598	-0.25
14.	KRG 1	68.58	67.38	68.25	67.45	67.91	0.273	-0.10
15.	MH 1	70.05	68.13	70.20	69.28	69.41	0.654	-0.24
16.	POL 2	61.65	59.05	63.33	61.65	61.42	1.306*	-0.42
17.	S 206	70.88	70.43	71.48	70.13	70.73	0.275	-0.11
18.	SB 11	73.35	70.90	74.33	72.55	72.78	1.042	-0.25
19.	Spanish Improved	70.38	38.23	69.28	68.33	69.05	0.354	0.74
20.	TAG 24	68.73	65.80	71.58	69.93	69.01	1.768	-0.08
21.	TKG 19A	53.70	50.08	60.75	57.60	55.53	3.199	3.89*
22.	TG 17	64.78	64.30	66.43	65.80	65.33	0.628	-0.11
23.	TG 26	72.05	70.68	72.15	70.98	71.46	0.444	-0.12
24.	TMV 2	70.03	67.28	69.80	68.30	68.85	0.795	0.38
25.	Ah 1	64.30	62.15	65.40	65.05	64.23	1.037	-0.18
26.	Ah 4104-2	70.63	69.43	70.80	69.93	70.19	0.419	-0.30
27.	Ah 4515	70.23	68.23	71.45	70.68	70.14	1.007	-0.36
28.	Ah 6649	67.60	66.18	68.05	67.15	67.24	0.576	-0.37
29.	Comet	71.40	70.48	71.95	71.05	71.22	0.438*	-0.38
30.	NCAc 7776	64.40	62.18	64.50	63.10	63.54	0.720	0.02
31.	NCAc 7777	55.55	51.93	57.83	56.13	55.36	1.829*	-0.33
32.	NCAc 7778	70.38	69.05	68.58	67.43	68.86	-0.141	1.76*
33.	NCAc 7780	66.48	64.98	65.55	64.10	65.28	0.168	0.99*
34.	NCAc 7782	71.88	70.18	72.53	71.25	71.46	0.713	-0.32
35.	NCAc 7783	63.30	62.50	65.25	63.43	63.62	0.778	-0.05
36.	NCAc 7785	66.15	63.95	69.33	68.43	66.96	1.652	0.84
37.	NCAc 7787	56.48	55.23	60.18	58.50	57.59	1.459	0.93*
38.	NCAc 7790	67.88	67.40	69.15	68.15	68.14	0.500	-0.29
39.	PI 268782	66.68	65.53	68.68	67.18	67.01	0.923	-0.20
40.	PI 268829	70.48	68.35	71.05	69.93	69.95	0.840	-0.33
41.	PI 268642	70.70	69.00	71.55	70.25	70.38	0.772	-0.36
42.	Pearl	64.35	61.08	64.38	63.38	63.29	1.067	0.07
43.	Starr	71.38	69.93	72.58	70.95	71.21	0.780	-0.28
44.	Span cross	78.98	78.60	78.83	77.73	78.53	0.036	0.04
45.	Span white	61.88	59.13	63.30	60.90	61.30	1.252	-0.10
46.	Taiwan Selection	62.23	61.35	67.55	65.73	64.21	1.813	3.37*
47.	Teja Amra Local	70.68	69.30	70.50	69.70	70.04	0.377	-0.17
48.	U 1-1-1	63.48	60.85	65.35	63.75	63.36	1.378*	-0.40
49.	U 2-4-5	65.33	63.88	57.83	56.93	60.99	-1.795	17.60*
50.	U 2-12-1	70.70	68.00	71.00	69.58	69.82	0.939	-0.06
	Mean	66.42	64.38	67.63	66.44	66.22	1.000	
	SE (n) ±	0.66	0.68	0.63	0.59	0.44	SE (bi) 0.478	
	CD at 5%	1.85	1.90	1.77	1.64	1.22		
	CD at 1%	2.44	2.50	2.34	2.17	1.60		

* P ≤ 0.05, ** P ≤ 0.01

Shelling per cent

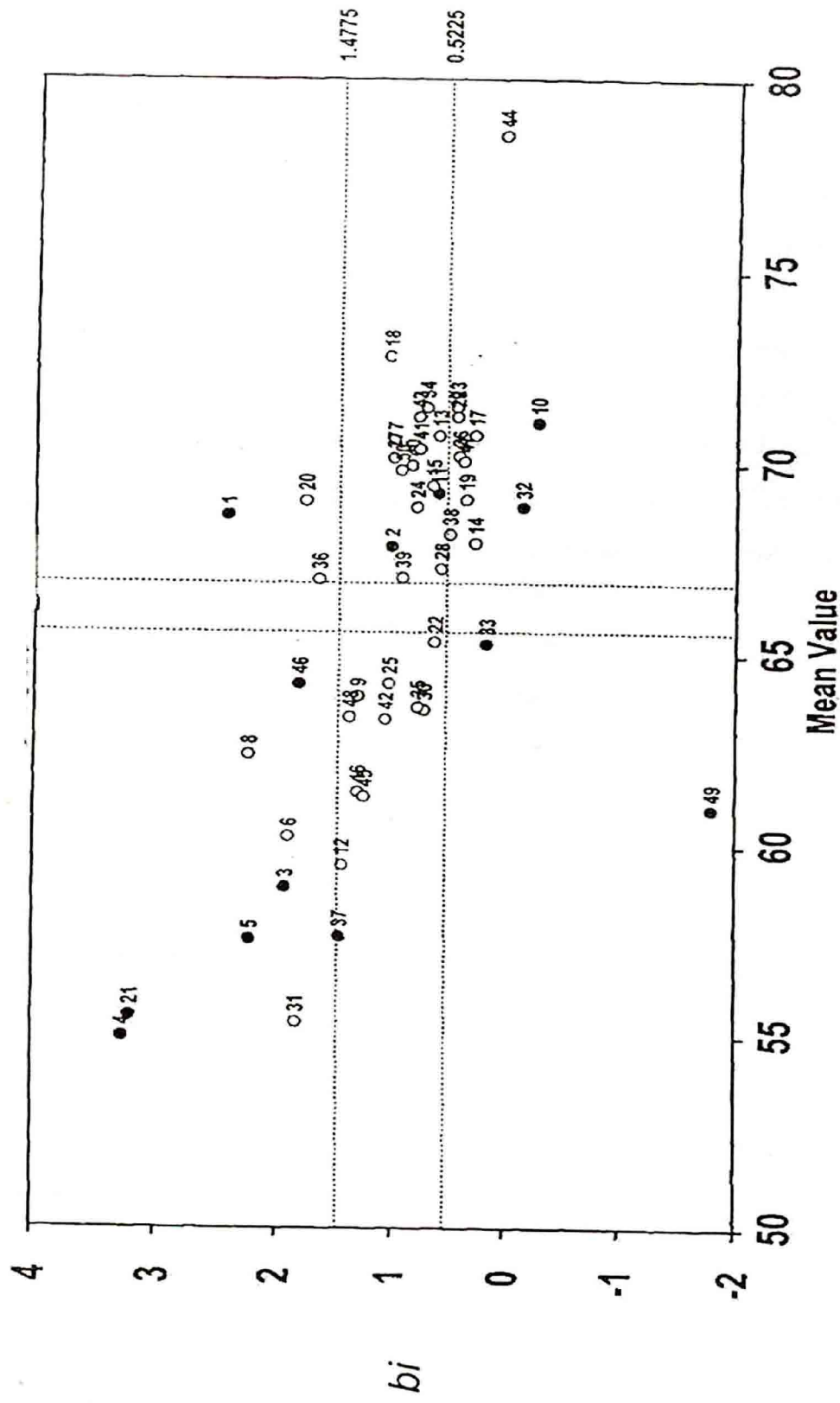


Fig.4.6: Stability parameters in respect of shelling per cent
(Mean performance, bi and S^2di)

• Solid symbols indicate significant S^2di

4.10.6. Days to maturity

Earliest maturing released variety of Spanish bunch group of groundnut was (20) TAG 24 (107.44) while latest maturing was (3) ALR 3 (124.81). Regression coefficient was significant for 21 genotypes. Five genotypes viz., (10) J 11, (13) Jyoti, (15) MH 1, (18) SB 11 and (49) U 2-4-5 recorded '*bi*' values around unity with non significant S^2di . Deviation from regression was non significant for 36 genotypes. If selection has to be made for earliness with general adaptability, four released varieties viz., (10) J 11, (13) Jyoti, (15) MH 1 and (18) SB 11 have to be selected, because they have mean performance smaller than over all mean, $bi \approx 1.0$ and non significant S^2di . If selection has to be made for earliness with specific adaptability to favourable environment, the germplasm lines viz., (26) Ah 4104-2, (29) Comet, (41) PI 268642 and (50) U 2-12-1 have to be selected. If selection has to be made for earliness with specific adaptability to unfavourable environment, the varieties viz., (4) Co 1, (7) GG 2, (8) Girnar 1, (14) KRG 1, (16) Pol.2, (17) S 206 and (20) TAG 24 and germplasm lines viz., (39) PI 368782, (43) Starr and (47) Teja Amra Local may be selected (Table 4.37 and Fig. 4.7).

Table 4.37 : Mean performance and stability parameters for days to maturity

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
1.	AK 12-24	106.25	104.0	125.50	121.50	114.31	0.885*	-0.37
2.	AK 159	103.75	101.50	127.00	122.50	113.69	1.063	-0.12
3.	ALR 3	114.00	110.25	140.00	135.00	124.81	1.221*	0.20
4.	CO 1	104.50	102.75	123.00	118.25	112.13	0.824*	-0.44
5.	CO 2	108.75	106.50	124.25	118.00	114.38	0.672*	1.45*
6.	GAUG 1	110.25	108.50	119.75	115.00	113.38	0.406*	1.40*
7.	GG 2	105.50	102.25	125.00	119.75	113.13	0.901	-0.18
8.	Girnar 1	106.25	104.50	124.00	117.75	113.13	0.763*	0.75
9.	ICG (FDRS) 10	110.25	107.50	131.50	124.75	118.50	0.944	0.33
10.	J 11	104.75	101.00	125.00	120.75	112.88	0.966	0.15
11.	JL 24 (Phule Pragati)	103.75	99.75	129.75	125.00	114.56	1.232*	0.55
12.	JL 220 (Vyas)	108.25	104.75	128.00	123.50	116.13	0.932	-0.10

Table 4.37 : Continued-

Sr. No.	Genotypes	Environmental means				Stability parameters		
		E ₁	E ₂	E ₃	E ₄	General Mean	bi	S ² di
13.	Jyoti	103.75	101.75	126.75	119.50	112.94	0.997	0.54
14.	KRG 1	107.75	105.00	121.25	117.25	112.81	0.631*	-0.03
15.	MH 1	103.00	100.50	125.00	119.25	111.94	0.989	-0.43
16.	POL 2	105.00	102.75	123.00	118.00	112.19	0.810*	-0.36
17.	S 206	104.00	100.75	119.25	115.00	109.75	0.721*	0.09
18.	SB 11	104.50	101.00	127.50	120.00	113.25	1.032	0.79
19.	Spanish Improved	108.75	104.75	129.00	120.75	115.81	0.904	3.39*
20.	TAG 24	99.25	96.75	118.50	115.25	107.44	0.905	0.14
21.	TKG 19A	112.25	108.25	136.00	130.75	121.81	1.119	0.00
22.	TG 17	110.50	105.50	129.50	125.00	117.63	0.937	1.35*
23.	TG 26	100.25	99.25	125.00	121.25	111.44	1.113	1.53*
24.	TMV 2	103.00	98.00	126.00	121.75	112.19	1.127	1.47*
25.	Ah 1	101.25	98.25	130.50	123.50	113.38	1.318*	-0.48
26.	Ah 4104-2	98.00	95.00	125.00	120.25	109.56	1.252*	0.45
27.	Ah 4515	100.75	99.25	129.00	125.50	113.63	1.293	3.22*
28.	Ah 6649	106.25	102.25	132.75	127.50	117.19	1.246*	0.19
29.	Comet	99.75	98.25	128.00	121.00	111.75	1.233*	0.17
30.	NCAc 7776	101.00	100.00	130.25	123.50	113.69	1.270*	0.67
31.	NCAc 7777	109.00	108.00	129.00	124.75	117.69	0.883	-0.08
32.	NCAc 7778	106.00	103.50	137.75	128.75	119.00	1.387*	0.40
33.	NCAc 7780	100.75	98.50	128.00	125.75	113.25	1.288	5.21*
34.	NCAc 7782	101.75	101.00	132.50	128.00	115.81	1.372	3.36*
35.	NCAc 7783	99.50	99.50	124.25	120.00	110.81	1.078	1.91*
36.	NCAc 7785	102.50	101.25	128.00	121.50	113.31	1.107	0.16
37.	NCAc 7787	106.75	101.25	128.00	119.75	113.94	0.989	4.21*
38.	NCAc 7790	108.00	105.25	122.00	118.50	113.44	0.663*	-0.19
39.	PI 268782	105.50	104.00	123.50	119.25	113.06	0.803*	-0.44
40.	PI 268829	104.50	101.25	129.25	121.50	114.13	1.102	0.50
41.	PI 268642	100.75	99.50	125.25	120.50	111.50	1.090	0.33
42.	Pearl	105.00	102.50	130.00	120.75	114.56	1.068	2.80*
43.	Starr	100.50	100.25	122.00	117.25	110.00	0.925	0.57
44.	Span cross	98.75	96.00	129.25	124.25	112.06	1.404*	1.22*
45.	Span white	104.25	102.50	125.25	117.50	112.38	0.889	1.91*
46.	Taiwan Selection	110.75	107.75	131.00	125.00	118.63	0.917	-0.03
47.	Teja Amra Local	107.75	105.25	119.50	118.50	112.75	0.595*	0.95
48.	U 1-1-1	109.25	107.25	123.75	120.00	115.06	0.662*	-0.45
49.	U 2-4-5	105.75	103.50	127.00	122.25	114.63	0.965	-0.45
50.	U 2-12-1	100.25	99.75	126.00	120.00	111.50	1.107	0.78
	Mean	104.85	102.37	126.93	121.61	113.94	1.000	
	SE (m) $\pm$	0.54	0.80	0.69	0.72	0.72	SE (bi) 0.054	
	CD at 5%	1.50	2.22	1.94	2.02	2.00		
	CD at 1%	1.98	2.93	2.56	2.66	2.63		

* $P \leq 0.05$, ** $P \leq 0.01$

Days to maturity

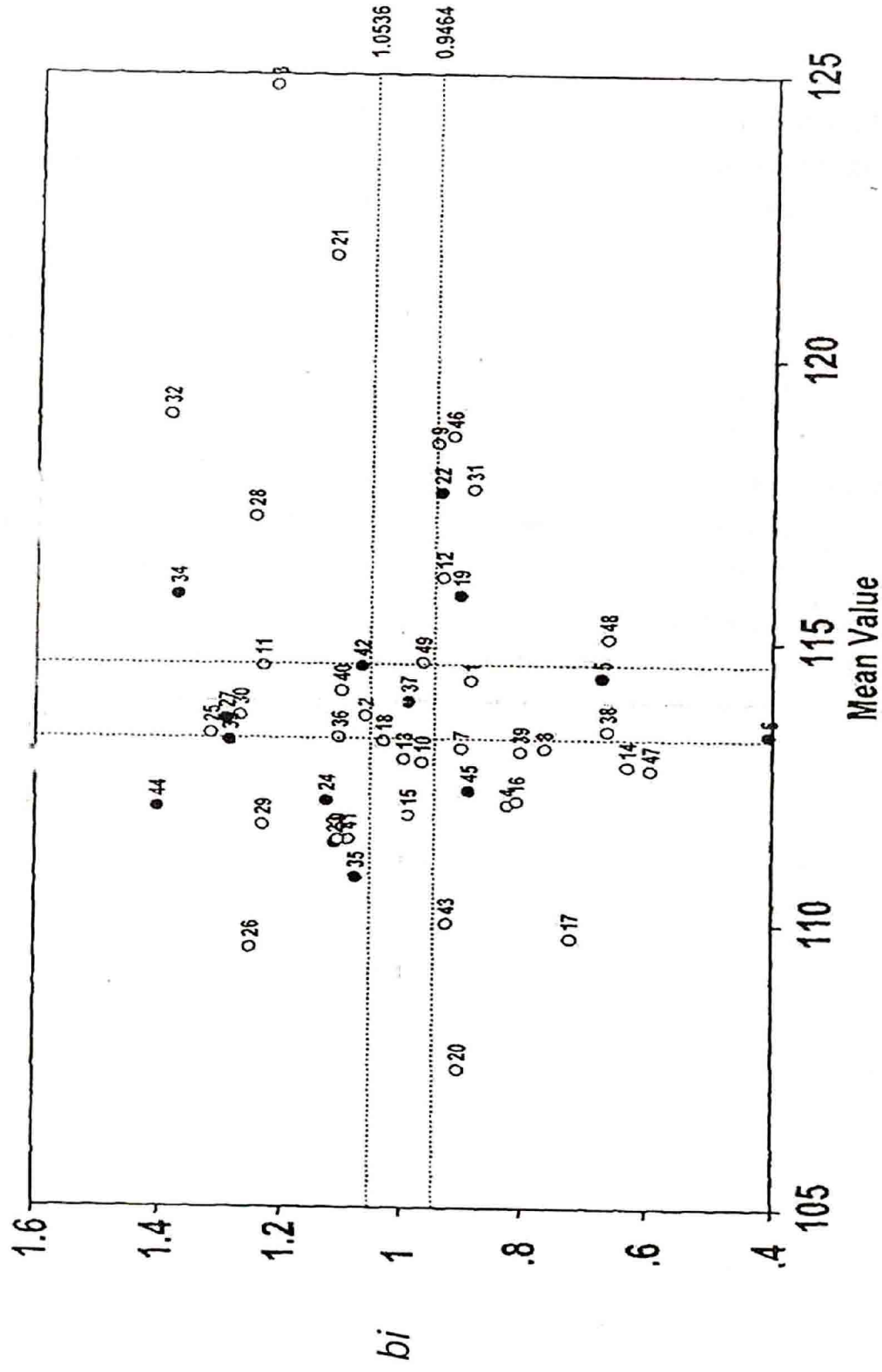


Fig.4.7: Stability parameters in respect of days to maturity
(Mean performance, bi and S^2di)

- Solid symbols indicate significant S^2di

4.11. Genetic Diversity and Adaptability

Adaptability of genotypes for various characters in different clusters has been presented in Table 4.38. The variety (47) Teja Amra Local belonging to cluster I was found adaptable to maximum i.e. five number of characters viz., height of main axis (tallness), primary branches per plant, mature pods per plant, shelling per cent and days to maturity, either generally adaptable, specifically adaptable to favourable environment or specifically adaptable to unfavourable environment. Similarly, other 11 genotypes (five from cluster I, one from cluster II, three from cluster III and one each from cluster VI and VII) belonging to different clusters were found adaptable to four different characters. Twelve genotypes (seven from cluster I, two each from cluster II and cluster III and one from cluster V), 14 genotypes (five from cluster I, one from cluster II, four each from cluster III and cluster IV) and 12 genotypes (one from cluster I, four from cluster II, two from cluster III, four from cluster IV and one from cluster VIII) belonging to different clusters were found adaptable to three, two and one characters respectively.

Table 4.38: Adaptability of genotypes for various characters in different clusters at a glance

Cluster formed (E ₁ +E ₂ +E ₃ +E ₄)	Total No of genotypes	Genotypes included	Origin	Days to 50% flower- ing	Height of main axis (cm)	Prim- ary branc- h-es/ plant	Seco- ndary bran- ches/ plant	Mat- ure pods/ plant	Shell -ing %	Days to matu- rity
				1	2	3	4	5	8	11
I	19	(39) PI 268782	Zimbabwe						+	✓
		(40) PI 268829	Zimbabwe	✓			△		+	
		(10) J11	Gujarat	✓	←(+	△				+
		(13) Jyoti	M.P.			△	△		+	+
		(27) Ah 4515	India				△		+	
		(14) KRG 1	Karnataka	✓	△)→				✓	✓
		(29) Comet	U.S.			△	△		✓	△
		(17) S 206	Karnataka						✓	✓
		(36) NCAc 7785	U.S.	+		△			△	
		(47) Teja Amra Local	India		△)→	△		+	✓	✓
		(38) NCAc 7790	U.S.	+	←(+				✓	
		(41) PI 268642	Zimbabwe		←(+				+	△
		(18) SB XI	M.S.		✓)→		✓		+	+
		(1) AK 12-24	M.S.		✓)→		△			
		(24) TMV 2	T.N.		△)→				+	
		(15) MH 1	Haryana		←(✓				+	+
		(32) NCAc 7778	U.S.		←(△					
		(48) U1-1-1	Sudan	✓		△	△			
		(42) Pearl	U.S.		←(+	△	△			
II	8	(11) JL 24	M.S.				△			
		(19) Spanish improved	M.S. and Karnataka						✓	
		(34) NCAc 7782	U.S.		←(+				+	
		(26) Ah 4104-2	India		△)→				✓	△
		(22) TG 17	M.S.		←(+					
		(28) Ah 6649	Tanzania		△)→	✓	△		+	
		(46) Taiwan selection	Taiwan	✓		△	✓			
		(6) GAUG 1	Gujarat		△)→					

Table 4.38: Continued -

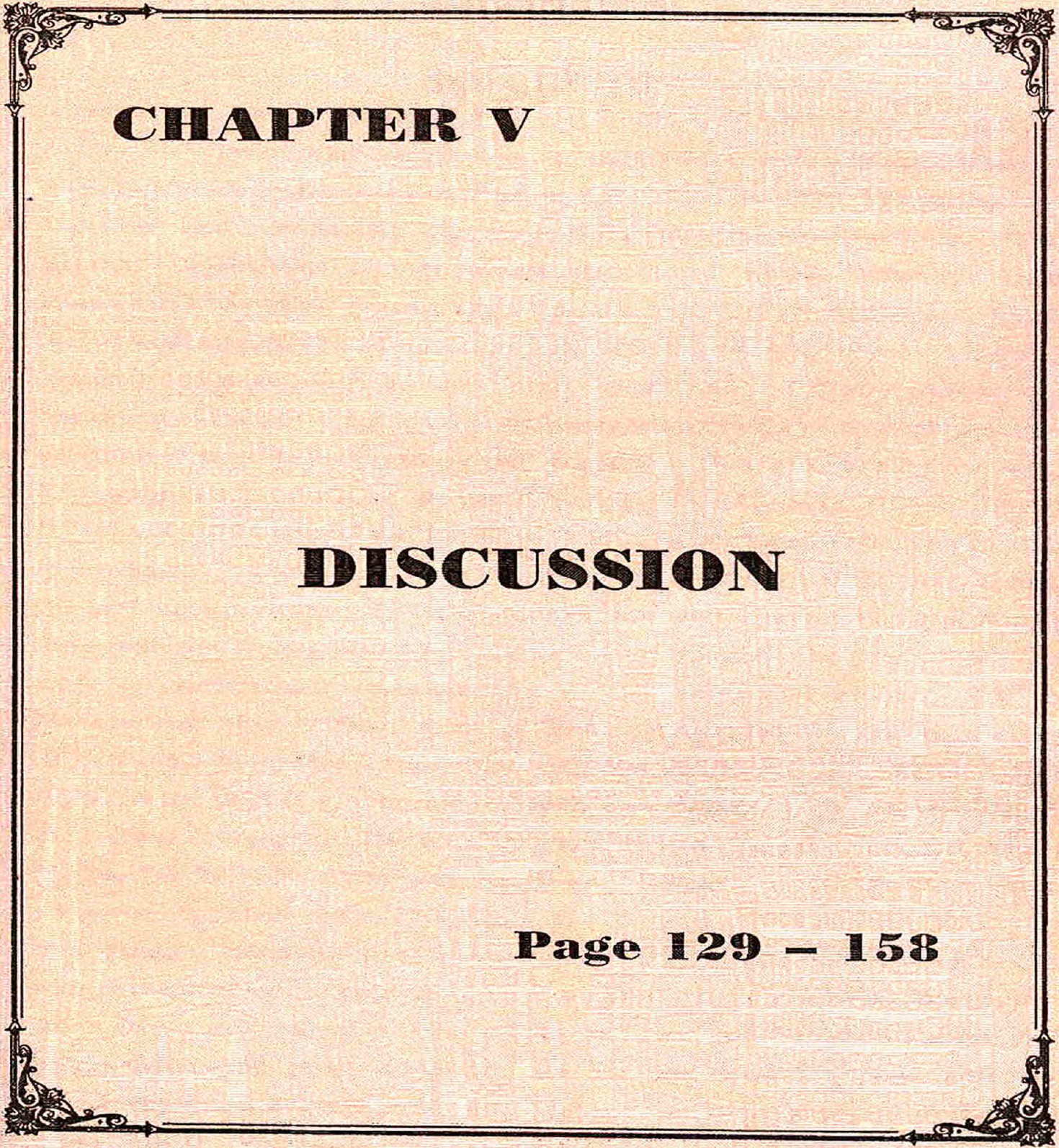
Cluster formed (E ₁ +E ₂ +E ₃ +E ₄)	Total No. of genotypes	Genotypes included	Origin	Days to 50% flowering	Height of main axis (cm)	Prim- ary bran- ches/ plant	Seco- n- dary bran- ches/ plant	Mat- ure pods/ plant	Shell- ing %	Days to matu- rity
				1	2	3	4	5	8	11
III	11	(7) GG 2	Gujarat		←(+		△		+	▽
		(23) TG 26	M.S., Gujarat & A.P.		←(▽				▽	
		(35) NCAc 7783	U.S.		←(△					
		(30) NCAc 7776	U.S.	▽		▽				
		(49) U.2-4-5	Sudan	+		▽	△	+		
		(8) Girnar 1	Entire country		←(+		+			▽
		(16) Pol 2	Karnataka		▽)→	+				▽
		(9) ICG (FDRS) 10	M.S.	▽	←(△					
		(2) AK 159	M.S.		←(▽					
		(20) TAG 24	M.S.	▽	←(▽				△	▽
		(3) ALR 3	T.N.		+)→	△				
IV	8	(31) NCAc 7777	U.S.	▽						
		(37) NCAc 7787	U.S.	▽		▽				
		(45) Span White	U.S.	▽						
		(5) CO 2	T.N.			▽				
		(12) JL 220	M.S.		←(▽	△				
		(4) CO 1	T.N.		▽)→					▽
		(33) NCAc 7780	U.S.	▽	←(△					
		(21) TKG 19 A	M.S.		←(+					
V	1	(43) Starr	U.S.				△		+	▽
VI	1	(44) Span cross	U.S.	+		△	△		▽	
VII	1	(50) U 2-12-1	Sudan	▽				+	+	△
VIII	1	(25) Ah 1	India	+						

+ = Generally adapted genotype/average stability

△ = Specifically adapted genotype to favourable environment/below average stability

▽ = Specifically adapted genotype to unfavourable environment/above average stability

)→ = Tallness and ←(= Dwarfness



CHAPTER V

DISCUSSION

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CHAPTER V

DISCUSSION

Purposeful introduction of improved varieties of groundnut in India was made by Madras Government for 1st time in 1894. The variety was Mauritius and introduction was made from Mozambique (East Africa). The Bombay Department of Agriculture introduced variety Mauritius from Pondicherry, Spanish Peanut and Virginia from United States and Small Japan and Large Japan from Japan in 1901-02 (Reddy, 1988; Reddy and Murthy, 1993). Attempt in crop improvement seems to have paid at the beginning of the 20th Century. The varieties were developed through pureline selection or mass selection from local varieties or from introduced stock, e.g., Kopergaon No.1 (1933), Kopergaon No.3 (1933), AK 8-11 (1940), AK 10 (1940), AK 12-24 (1940) and Karad 4-11 (1957). Systematic attempts in crop improvement in groundnut were started in the state after 1960. As a result, the first cross derivative 'SB XI' developed through recombination breeding at Junagadh and finally tested at Jalgaon was released in the year 1965. ~~The work on varietal improvement was further intensified around 1970 in~~ Maharashtra after establishment of State Agricultural Universities (SAUs). At the same time, close interaction between SAUs, AICORP, ICRISAT and BARC in the field of groundnut research was increased. It had resulted in the release of some varieties in 1980's and 1990's viz., TG 1, TMV 10, M 13, JL 24, TG 17, UF 70103 and ICGS 11. Recently in 2000's three more improved varieties viz., TAG 24, TG 26 and AK 159, developed by hybridization technique have been released for general cultivation giving a wide array of choice to farmers to improve productivity. However, the genetic gains do not truly reflect at farm level to stabilized groundnut production and productivity. The crop is known for its tremendous genetic potential displaying on an average yield of 6.7 tonnes per ha as reported from Israel (Basu, 1993). Therefore, there is need to develop high yielding groundnut variety having greater stability in performance over a number of environments.

The importance of genetic resources in crop improvement has been repeatedly emphasized. The success of breeders does not depend only on the use of breeding methodology and the selection technique but it is related to successful utilization of variability from broad based and specific gene pools. The evaluation of germplasm is an important prerequisite for its utilization in breeding programme. And on this line the concept of multivariate analysis has been successfully used in crop improvement for choice of divergent parents. As we do in stability analysis, multi environment data should be subjected to work out genetic diversity in available germplasm for identification of diverse, widely adapted and stable genotypes for hybridization. Many approaches are available, but Mahalanobis' D^2 -statistic (1936) and Eberhart and Russell's model (1966) of linear regression analysis have been most commonly used. Therefore, the present investigations were carried out with a view to estimate the degree of genetic divergence among some Indian groundnut varieties/germplasm lines under *kharif* and summer seasons for attaining classification or grouping, to estimate stability parameters and extent of genotype x environment interactions with reference to some of the components of yield for identifying most stable and fairly dynamic varieties with general and specific adaptability and to identify the superior genotypes on the basis of genetic diversity and phenotypic stability for their use in future groundnut breeding programme.

5.1. Genetic Diversity

Analysis of divergence has been in use by plant breeders since long. It has helped them to classify their breeding material into useful groups. This is a measure of the statistical distance between two populations. Involving genetically diverse parents in crossing would be advantageous in the sense that it would provide an opportunity for bringing together gene constellations of divergent origin. Arunachalam (1993) stated that initial step of a breeding programme is as vital as the final improved yield desired by the breeder. An analysis of experimental evidence in the light of underlying genetic concepts suggests a choice of parents on genetic

divergence given by a multivariate measure. Murty *et al.* (1973) revealed that the number and composition of the clusters remained the same in both the years in spite of considerable seasonal differences. However, Singh *et al.* (1990) concluded that the number of clusters and constituent of the clusters varied with the environments. Rana and Murty (1971) found that the varieties of first cluster of pooled analysis entered in different clusters in different years, taking groups based on pooled analysis as the standard.

In the present study a set of 50 genotypes (24 released varieties of different states of India and 26 diverse germplasm lines) were grown in *kharif* and summer seasons on two dates each along with standard check varieties (SB XI, JL 24, TAG 24 and AK 159) and D² analysis was carried out separately for each date, pooling of both dates of each season and pooling of both seasons. The ANOVA of different characters indicated that higher significant differences existed among the genotypes for all the characters in all the four environments (Table 4.1). The pooled ANOVA of different characters indicated that higher significant differences existed among the environments for all the characters (Table 4.3). Also, differences between seasons and dates and interactions between season x dates, genotypes x seasons, genotypes x dates and genotypes x seasons x dates were significant except for few characters (Table 4.2). The analysis of dispersion based on Wilk's criterion also revealed highly significant differences among the genotypes for the aggregate effect of all the characters under each of the four separate environments and three pooled (Table 4.5). Thus both the tests revealed considerable divergence among the genotypes. It indicated that grouping of genotypes can be conducted in the present environments and will be fruitful. Similar results were reported by Murty *et al.* (1973), Prasad and Singh (1990), Singh *et al.* (1990), Bargale and Billore (1992), Reddy and Reddy (1993), Vindhiyavarman and Raveendram (1996) and John Joel and Mysamy (1998). The mean values (Table 4.4) indicate differential impact of environment on gene expression. This sensitivity to environmental variation ~~creates~~ ^{creates} doubt on the reliability of D² analysis in a single environment and points to the need of making such studies under multiple environmental

conditions (Ray *et al.*, 1995). However, Prasad and Singh (1990) concluded that the genotypes should be tested under more favourable environments to have a better picture of genetic divergence between them.

5.1.1. Grouping of genotypes:

Fifty genotypes were grouped into nine clusters in environments 1 and seven clusters in environment 2, whereas ten clusters in pooled analysis of these two *kharif* environments (E_1+E_2). In environments 3 and 4 the genotypes were grouped into nine and ten clusters respectively, whereas nine clusters in pooled analysis of these two summer environments (E_3+E_4). In pooling of these two seasons environments ($E_1+E_2+E_3+E_4$) the genotypes were grouped into eight clusters. In *kharif* environments (E_1 and E_2) 35 and 41 genotypes out of total 50 genotypes were grouped into cluster I. Thus, it indicated that 70 per cent and 82 per cent of the genotypes were genetically similar. Trend was different in summer environments (E_3 and E_4) in which cluster I was largest and included 40 per cent and 44 per cent of genotypes. Jain *et al.* (1981) and Singh *et al.* (1990) also observed that clustering pattern was influenced by environments to a quite large extent. Distribution of genotypes into different clusters were comparatively good in pooled analysis over seasons (38 per cent in cluster I, 16 per cent in cluster II, 22 per cent in cluster III and 16 per cent in cluster IV). Thus, 92 per cent genotypes were grouped in four clusters. Therefore, a combined analysis over years and seasons for assessing divergence would appear to be useful (Rana and Murty, 1971).

Table 5.1 revealed that in spite of variation in mean and D^2 values, a few genotypes (13 varieties and 13 germplasm lines) viz., (1) AK 12-24, (6) GAUG 1, (7) GG 2, (8) Girnar 1, (9) ICG (FDRS) 10, (10) J 11,(13), Jyoti (14) KRG 1, (15) MH 1, (16) Pol. 2, (17) S 206, (18) SB XI, (24) TMV 2 (29) Comet, (30) NC Ac 7776, (32) NC Ac 7778, (35) NC Ac 7783, (36) NC Ac 7785, (38) NC Ac 7790, (39) PI 268782, (40) PI 268829, (41) PI 268642, (42) Pearl, (47) Teja Amra Local, (48) U 1-1-1 and (49) U 2-4-5 showed seasonal adaptability as they occupied the same cluster in two *kharif* (E_1 and E_2) and

pooled *kharif* environments (E_1+E_2) indicating that they are relatively stable and can be utilized in the breeding programme to evolve high yielding stable varieties. Similarly, for summer (E_3 and E_4 and E_3+E_4) the genotypes (6 varieties and 6 germplasm lines) viz., (6) GAUG 1, (10) J 11 (13) Jyoti (15) MH 1, (18) SB XI, (24) TMV 2, (27) Ah 4515, (38) NC Ac 7790 (39) PI 268782, (40) PI 268829, (42) Pearl and (48) U 1-1-1 occupied same cluster and showed seasonal adaptability. Over seasons, in all five released varieties viz., (10) J 11, (13) Jyoti, (15) MH 1, (18) SB XI, (24) TMV 2 and five germplasm lines viz., (38) NC Ac 7790, (39) PI 268782, (40) PI 268829, (42) Pearl and (48) U 1-1-1 consistently occupied the same cluster in pooled and separate analysis, indicating stable performance (Table 5.1). Prasad and Singh (1990) stated that the pairs of genotypes showing stability in their D^2 values across the environments should be used to evolve hybrids with wider adaptability. Same may be true in the varietal improvement programme through hybridization.

Table 5.1: Genotypes occupying same cluster indicating seasonal adaptability

Cluster	Environments	Genotypes occupied same cluster			
I	E_1, E_2, E_3 and E_4	Varieties (7)	(6) GAUG 1	(10) J 11	(13) Jyoti
			(15) MH 1	(17) S 206	(18) SB XI
			(24) TMV 2		
		Germplasm (8)	(27) Ah 4515	(36) NC Ac 7785	(38) NC Ac 7790
			(39) PI 268782	(40) PI 268829	(42) Pearl
			(47) Teja Amra Local		
	E_1, E_2 and E_1+E_2	Varieties (13)	(1) AK 12-24	(6) GAUG 1	(7) GG 2
			(8) Gimar 1	(9) ICG (FDRS) 10	(10) J 11
			(13) Jyoti	(14) KRG 1	(15) MH 1
			(16) Pol. 2	(17) S 206	(18) SB XI
			(24) TMV 2		
		Germplasm (13)	(29) Comet	(30) NC Ac 7776	(32) NC Ac 7778
			(35) NC Ac 7783	(36) NC Ac 7785	(38) NC Ac 7790
			(39) PI 268782	(40) PI 268829	(41) PI 268642
			(42) Pearl	(47) Teja Amra Local	(48) U 1-1-1
	E_3, E_4 and E_3+E_4	Varieties (6)	(6) GAUG 1	(10) J 11	(13) Jyoti
			(15) MH 1	(18) SB XI	(24) TMV 2
		Germplasm (6)	(27) Ah 4515	(38) NC Ac 7790	(39) PI 268782
			(40) PI 268829	(42) Pearl	(48) U 1-1-1

Table 5.1 Continued -

Cluster	Environments	Genotypes occupied same cluster			
I	E ₁ +E ₂ , E ₃ +E ₄ and E ₁ +E ₂ +E ₃ +E ₄	Varieties (6)	(1) AK 12-24	(10) J 11	(13) Jyoti
			(15) MH 1	(18) SB XI	(24) TMV 2
		Germplasm (7)	(32) NC Ac 7778	(38) NC Ac 7790	(39) PI 268782
			(40) PI 268829	(41) PI 268642	(42) Pearl
	E ₁ , E ₂ , E ₁ +E ₂ , E ₃ , E ₄ , E ₃ +E ₄ and E ₁ +E ₂ +E ₃ +E ₄	Varieties (5)	(10) J 11	(13) Jyoti	(15) MH 1
			(18) SB 11	(24) TMV 2	
		Germplasm (5)	(38) NC Ac 7790	(39) PI 268782	(40) PI 268829
			(42) Pearl	(48) U 1-1-1	
II	E ₁ +E ₂ and E ₃ +E ₄	Variety (1)	(12) JL 220		
	E ₁ +E ₂ and E ₁ +E ₂ +E ₃ +E ₄	Verities (3)	(11) JL 24	(19) Spanish Improved	(22) TG 17
		Germplasm (3)	(26) Ah 4104-2	(28) Ah 6649	(34) NC Ac 7782
	E ₃ +E ₄ and E ₁ +E ₂ +E ₃ +E ₄	Nil			
III	E ₃ +E ₄ and E ₁ +E ₂ +E ₃ +E ₄	Varieties (4):	(2) AK 159	(7) GG 2	(20) TAG 24
			(23) TG 26		
		Germplasm (1):	(35) NC Ac 7783		

5.1.2. Relative importance of characters towards genetic divergence:

Relative importance can be known on the basis of the size of coefficients of canonical vectors (Rao, 1952). The results of the canonical analysis in E₁, E₂, pooled E₁ + E₂, E₃, E₄, pooled E₃ + E₄ and pooled over all environments of both the seasons (E₁ + E₂ + E₃ + E₄) revealed that 100-pod weight, pod yield per plant, days to maturity, 100-kernel weight, shelling per cent, sound mature kernel per cent and height of main axis were important sources of variation in vector I. In vector II, sound mature kernel per cent, shelling per cent, secondary branches per plant, 100 pod weight, oil per cent, pod yield per plant, mature pods per plant and height of main axis were important sources of variation. In vector III, shelling per cent, sound mature kernel per cent, height of main axis, mature pods per plant, shelling per cent, 100-kernel weight were important sources of variation.

Shew *et al.* (1972) observed in groundnut that the leaf colour and plant height were important sources of variation in the first vector. In the second vector days to last flowering, hairiness of the leaves and growth habit were important. Verma *et al.* (1973) indicated that days to flowering

followed by 100-grain weight, days to maturity and plant height constituted the major axis of differentiation. Days to maturity, 100-grain weight, pod length and per cent oil in that order formed the secondary axis of differentiation in soybean. The first canonical root λ_1 accounted for 73 per cent of the variation and λ_2 for 10 per cent of total variation. Reddy and Reddy (1993) in groundnut found that 100-pod weight, harvest index and number of secondaries per plant were important sources of variation in the first vector. In the second vector number of secondaries per plant, number of pods per plant, number of mature pods per plant and pod yield were important. The first two vector accounted for 70 per cent and the first three vector for 80.7 per cent of total genetic divergence. Murty *et al.* (1973) observed the important role of height and the minor role of seeds per capsule for primary differentiation and the number of tillers and height at which branching started for secondary differentiation in linseed. Jay Lal Mahto (1995) observed that days to maturity contributed maximum followed by seed yield and plant height in determining genetic divergence in linseed.

In the present study the importance of 100-pod weight, shelling per cent and sound mature kernel per cent towards genetic divergence has been underlined. Canonical analysis also confirmed the importance of these characters. Therefore, if the parents are selected on the basis of 100-pod weight, shelling per cent and sound mature kernel per cent, they are expected to be genetically diverse and can be used in groundnut hybridization programme to expect genetic improvement in desirable direction.

5.1.3. Relationship of genetic diversity with geographic diversity:

From the clustering pattern of 50 groundnut genotypes, it was observed that none of the clusters was solely constituted by the genotypes which had their origin from the same geographical area. In other words the 24 groundnut varieties belonging to Spanish botanical group released for different Indian states and 26 germplasm lines belonging to Spanish botanical group originated from six different countries have been clustered

randomly irrespective of their origins which give an evidence that geographic diversity is not related to genetic diversity in this crop. These results are in conformity with earlier reports of Golakiya and Makne (1992), Katule *et al.* (1992), Reddy and Reddy (1993), John and Mylsamy (1998) on groundnut. Thus, geographic diversity though important, may not be the only factor in determining genetic divergence and the factors other than geographic diversity such as genetic drift, selection pressure and environment may be responsible for differential grouping of genotypes (Sangha, 1971).

5.2. Stability/Adaptability

Evenson *et al.* (1978) defined cultivar stability in terms of yield variability over years at a site and cultivar adaptability in terms of yield variability across sites average over years. A plant breeder must be concerned with both stability and adaptability when selecting among breeding lines (Binswanger and Barah, 1980). Stability and adaptability should be closely related if cultivar x environment interaction are caused by unpredictable environmental variables, such as rainfall, rather than by predictable ones, such as soil type differences that vary across sites but not years (Shorter and Normans, 1983). In present investigation, seasonal influence was very high as well as dates of sowing also influenced characters excepting few. Genotypic differences were found to be pronounced in all characters. Thus, selection for adaptability should result in stability.

5.2.1. Genotype x environment interaction:

The study of g x e interaction will be of immense help as it would lead to the successful evaluation of stable genotype which could either be released for commercial cultivation or be used in future breeding programme (Yadava *et al.* 1980). Varying levels of g x e interaction appear to be common in groundnut resulting in poor stability of performance as earlier reported by Singh *et al.* (1975), Tai and Hammons (1978), Wynne and Isleib (1978), Norden *et al.* (1986), Verma *et al.* (1989), Singh *et al.* (1990), Bansal *et al.* (1992) and Singh and Sohu (1995). Significant mean squares due to g x e interaction show that phenotypic expression of the genotypes

varied in different agro-climatic conditions or genotypes interacted significantly with the environments. Non significant variance due to $g \times e$ interaction indicated that similar reaction of genotypes in different environment for particular trait.

In the present study the mean squares due to $g \times e$ interaction were significant only for seven characters out of 13 characters. Hence further analysis was carried out in respect of seven characters only viz., days to 50 per cent flowering, height of main axis, primary branches per plant, secondary branches per plant, mature pods per plant, shelling per cent and days to maturity. Singh and Chaudhary (1977) stated that in case the variance due to varieties $\times$ locations is found significant the analysis may be further proceeded for estimating the stability parameters. Verman and Raveendran (1989) confirmed this understanding. Norden *et al.* (1986) stated that genotypic stability was analysed with linear regression, because the GE interaction was significant. Singh and Narayanan (1993) stated that, if $g \times e$ interaction is found significant, the stability analysis can be carried out. Raut *et al.* (1993) showed absence of genotype $\times$ environment interaction for kernel yield per plant. Verman and Manoharan (1993) found that the mean sum of squares due to genotypes $\times$ environment interaction were significant for all the characters except pod yield.

A great deal of concern regarding significance of homeostatis in crop species has stimulated plant breeder to develop well buffered cultivars. Phenotypically stable lines are of great significance for a crop like groundnut which is considered to be an unpredictable oilseed legume (Sojitra and Pethani, 1994).

In present study ANOVA for stability revealed that significant mean squares due to genotypes showed degree of genetic variability among the genotypes. Environment + (Genotype $\times$ Environment) mean squares were significant for days to 50 per cent flowering, height of main axis and days to maturity indicated relatively complex kind of interaction and these characters are not stable in expression. Significant mean squares due to environment showed presence of variation over environments. Significant

genotype x environment interaction for days to 50 per cent flowering, height of main axis, primary branches per plant, secondary branches per plant, mature pods per plant, shelling per cent and days to maturity indicated divergent linear response of genotypes to environmental changes. It shows that the best genotype in one environment was not the best in another environment.

The mean squares due to environment (linear) were significant for all the characters under present study indicating that the differences were present between the environments. The linear component of genotype x environment or genotype x environment (linear) mean squares were significant for the seven characters only viz., days to 50 per cent flowering, height of main axis, primary branches per plant, secondary branches per plant, mature pods per plant, shelling per cent and days to maturity. Hence, it appeared meaningful to carry out the stability analysis only for these characters as there was no linear response for remaining characters viz., 100-pod weight, 100-kernel weight, sound mature kernel per cent, oil content, pod yield and kernel yield. The absence of linear response for these characters could be due to the fact that these characters would not change beyond a certain limit of favourable environment as earlier reported by Verman and Raveendran (1989). Significance of G x E (linear) interaction indicated that the differences among the regression coefficient pertaining to various genotypes on the environmental means were real. Similar results were reported by Singh *et al.* (1975) and Patel *et al.* (1983). Dabholkar (1992) stated that the significant mean squares due to G x E (linear) indicate the variation in the performance of genotypes due to the regression of genotypes on environments and hence it can be predicted. The environment (linear) and variety x environment (linear) components of variation were highly significant for seven characters viz., days to 50 per cent flowering, height of main axis, primary branches per plant, secondary branches per plant, mature pods per plant, shelling per cent and days to maturity, confirming the reliability of regression coefficient (b) pertaining to different varieties/germplasm lines on the mean of different environments.

This confirms the findings of Singh *et al.* (1990). As per Verman and Manoharan (1993) and Mathur *et al.* (1997) the significant G x E (linear) interaction indicates that the stability parameters, regression coefficient (b) estimated by linear component of the response to change in environment was different for various genotypes under study. According to Johar Singh and Singh (1998) the mean squares due to genotype x environment (linear) were significant when tested against pooled error for all the characters except shelling percentage. It indicated that variation in performance of genotypes when grown over environments were predictable for all the characters except shelling percentage. As per Patra *et al.* (1992) significant linear component of population x environment indicated the predominance of predictable component.

Variances due to pooled deviation (non-linear) were non significant for all the characters under study, which indicates that the major component for differences in stability for the characters under study in present investigation was due to the linear regression and not due to the deviations from the linear function. This is in agreement with report of Singh *et al.* (1975). Non significant pooled deviation was also reported by Veerabhadran *et al.* (1990).

When both the components of G x E interaction were examined, the magnitude of linear component of G x E interaction was higher for all the seven characters, viz., days to 50 per cent flowering, height of main axis, primary branches per plant, secondary branches per plant, mature pods per plant, shelling per cent and days to maturity indicating the possibility of prediction across the environments and prediction will be more reliable. This observation confirms the findings of Reddy and Gupta (1994), Sojitra and Pethani (1994) and Lal *et al.* (1998).

5.2.2. Phenotypic stability:

Stability of productivity for the characters of economic importance like yield is of interest to the plant breeder. Since yield is a complex character the developing genotypes may show stability for its component characters. The identification of stable genotype is possible only by studying the linear regression slope as a measure of stability as used by Finlay and Wilkinson (1963) and more precisely when both the linear (bi) and the non-linear (S^2di) component of the $g \times e$ interaction are considered for judging the phenotypic stability of an individual genotype (Eberhart and Russell, 1966).

In the present investigation, the phenotypic stability of 50 genotypes, consisted of 24 released varieties and 26 germplasm lines, was measured by three parameters viz., mean performance over environments, the linear regression coefficient and the deviation from regression function. The stability parameters for all 50 genotypes are presented in Fig 4.1 to 4.7 and genotypes selected for general adaptability specific adaptability for favourable environment and specific adaptability for unfavourable environment for seven component characters of yield are presented in Table 5.2, 5.3. and 5.4, respectively.

Table 5.2 revealed that the phenotypic stability of high level for height of main axis was associated with six released varieties, viz., GG 2, Girnar 1, J 11, TKG 19 A, TG 17 (less than mean $-SE m$) and ALR 3 (more than mean $+SE m$). For primary branches per plant Pol. 2 for secondary branches per plant Girnar1 for shelling per cent GG 2, Jyoti, MH 1, SB IX TMV 2 and for days to maturity J 11, Jyoti, MH 1 and SB IX (less than mean $-SE m$) had general adaptability which exhibited $\pm$ mean performance (mean $\pm SE m$), unit regression ($1 \pm SEbi$) and non-significant S^2di . Similarly, 15 germplasm lines had general adaptability for different seven component characters of yield. While selecting parents for further utilization in breeding programme these 11 released varieties and 15 germplasm lines which had average stability may be utilized. Table 5.3 revealed that the specific

adaptability to favourable environment was associated with 12 released varieties and 18 germplasm lines which exhibited $\pm$ mean performance (mean $\pm$ SE m), regression coefficient higher than $1 + SE$ (bi) (below average stability) and non-significant S^2di . Such association between mean performance and stability is not desirable, because one would like to have genotype which are capable of giving high mean performance and high level of phenotypic stability. Table 5.4 revealed that the specific adaptability to unfavourable environment was associated with 17 released varieties and 18 germplasm lines which exhibited $\pm$ mean performance (mean $\pm$ SE m), regression coefficient lower than $1-SE$ (bi) (above average stability) and non-significant S^2di .

Table 5.2: Genotypes selected for general adaptability or average stability for different characters

Sr. No.	Characters	Varieties/Germplasm lines selected for average stability (+)
1.	Days to 50% flowering	Earliness
		(25) Ah 1 (36) NC Ac 7785 (38) NC Ac 7790* (44) Span cross (49) U 2-4-5*
2.	Height of main axis (cm)	Dwarfness
		(7) GG 2* (8) Girnar 1* (10) J 11* (21) TKG 19A (22) TG 17 (34) NC Ac 7782* (38) NC Ac 7790* (41) PI 268642* (42) Pearl
		Tallness
		(3) ALR 3
		(16) Pol. 2
3.	Primary branches/plant	
4.	Secondary branches/plant	(8) Girnar 1*
5.	Mature pods/plant	(47) Teja Amra local (49) U 2-4-5 (50) U 2-12-1*
6.	Shelling per cent	(7) GG 2* (13) Jyoti* (15) MH 1* (18) SB XI* (24) TMV 2 (27) Ah 4515 (28) Ah 6649 (34) NC Ac 7782* (39) PI 268782 (40) PI 268829 (41) P. 268642* (43) Starr (50) U 2-12-1*
7.	Days to maturity	Earliness
		(10) J 11* (13) Jyoti* (15) MH 1* (18) SB XI*

* appeared more than one time

Table 5.3: Genotypes selected for specific adaptation to favourable environment or below average stability for different characters

Sr. No.	Characters	Varieties/Germplasm lines selected for below average stability (A)
		Earliness
1.	Days to 50 per cent flowering	Nil
2.	Height of main axis (cm)	Dwarfness (9) ICG (FDRS)10 (32) NC Ac 7778 (33) NC Ac 7780 (35) NC Ac 7783 (37) NC Ac 7787 Tallness (6) GAUG 1 (14) KRG 1 (24) TMV 2 (26) Ah 4104-2* (28) Ah 6649* (47) Teja Amra Local*
3.	Primary branches/plant	(3) ALR 3 (10) J 11 (12) JL 220 (13) Jyoti* (29) Comet* (36) NC Ac 7785* (42) Pearl* (44) Span cross* (46) Taiwan selection (47) Teja Amra local* (48) U 1-1-1*
4.	Secondary branches/plant	(1) AK 12 24 (7) GG 2 (11) JL 24 (13) Jyoti* (27) Ah 4515 (28) Ah 6649* (29) Comet* (40) PI 268829 (42) Pearl* (43) Starr (44) Span cross* (48) U 1-1-1* (49) U 2-4-5
5.	Mature pods/plant	Nil
6.	Shelling per cent	(20) TAG 24 (36) NC Ac 7785*
7.	Days to maturity	Earliness (26) Ah 4104-2* (29) Comet* (41) PI 268642 (50) U 2-12-1

* appeared more than one time

Table 5.4: Genotypes selected for specific adaptation to unfavourable environment or above average stability for different characters

Sr. No.	Characters	Varieties/Germplasm lines selected for above average stability (∇)
1.	Days to 50 per cent flowering	Earliness
		(9) ICG (FDRS) 10 (10) J 11 (14) KRG 1* (20) TAG 24* (30) NC Ac 7776* (31) NC Ac 7777 (33) NC Ac 7780 (37) NC Ac 7787* (40) PI 268829 (45) Span white (46) Taiwan selection* (48) U 1-1-1 (50) U 2-12-1
2.	Height of main axis (cm)	Dwarfness
		(2) AK 159 (12) JL 220 (15) MH 1 (20) TAG 24* (23) TG 26*
		Tallness
		(1) AK 12-24 (4) CO 1* (16) POL.2* (18) SB XI*
3.	Primary branches/plant	(5) CO 2 (28) Ah 6649 (30) NC Ac 7776* (37) NC Ac 7787* (49) U 2-4-5
4.	Secondary branches/plant	(18) SB XI* (46) Taiwan selection*
5.	Mature pods/plant	Nil
6.	Shelling per cent	(14) KRG 1* (17) S 206* (19) Spanish Improved (23) TG 26* (26) Ah 4104-2 (29) Comet (38) NC Ac 7790 (44) Span cross (47) Teja Amra Local*
7.	Days to maturity	Earliness
		(4) CO 1* (7) GG 2 (8) Gimar 1 (14) KRG 1* (16) POL.2* (17) S 206* (20) TAG 24* (39) PI 268782 (43) Starr (47) Teja Amra Local*

* appeared more than one time

5.3. Relation Between Genetic Diversity and Adaptability

Several studies have been conducted on these two aspects in different crops. However, only a few workers have tried to understand the relationship between these two analytical procedures (Rana and Murty, 1971 in sorghum, Verma *et al.* 1973 in soybean, Jag Shoran, 1982 in pigeonpea, Jain and Pandya, 1984 in chickpea and Mahto, 1995 and Mahto and Singh, 1996 in linseed). Since, such information is scanty in groundnut, an attempt was made to study the inter-relation between genetic divergence and adaptability in Spanish bunch groundnut genotypes.

The mean performance, linear and non-linear responses for different characters of genotypes falling in different clusters in the pooled data over seasons are given in Table 5.5. A close perusal of the table revealed that by and large, genotypes grouped in a single cluster had almost identical mean performances. However, all genotypes having identical means were not necessarily grouped together. It indicated that there were other components of genetic divergence which influence the grouping of genotypes. The regression coefficient of the genotypes of the same cluster did not show common pattern being a heterogeneous combination of poor to highly stable genotypes in each cluster. The highly variable deviation from linearity in the same cluster also were evidence of heterogeneity within each cluster. This results further supported the views of Rana and Murty (1971) and Jain and Panda (1984).

From this relationship, it can be concluded that selection of parents for any crossing programme may be made primarily on the basis of inter cluster distance and intra cluster selection, if more than one genotype is included in cluster, may be made on the basis of general or specific adaptability for maximum number of characters. This is important, since crosses between varieties with similar means but with different regression coefficients can bring together diverse gene constellations and therefore provide mechanism for stability for yield.

Table 5.5: Cluster wise stability parameters for different characters

Cluster formed in pooled over seasons ($E_1+E_2+E_3+E_4$)	Total No. of genotypes	Genotypes included	Origin	(1) Days to 50% flowering				(2) Height of main axis (cm)				(3) Primary branches/ plant				(4) Secondary branches/ plant			
				$\bar{X}_i$	bi	S ² di	$\bar{X}_j$	bi	S ² di	$\bar{X}_i$	bi	S ² di	$\bar{X}_j$	bi	S ² di	$\bar{X}_i$	bi	S ² di	$\bar{X}_j$
I	19	(1) AK 12-24	M.S.	36.8	0.96	1.3*	29.5	0.85*	-0.5	5.3	2.22	0.1*	3.5	1.83*	0.1				
		(10) J 11	Gujarat	34.9	0.94	-0.2	28.5	0.96	-0.4	5.2	1.87	0.0	4.3	1.38	0.3*				
		(13) Jyoti	M.P.	36.6	0.97	0.1	30.2	1.26	2.8*	5.2	2.13	0.0	3.7	1.80*	0.1				
		(14) KRG 1	Karnataka	35.9	0.91	-0.1	32.3	1.14	-0.2	4.9	1.32	0.0	3.0	1.51	0.2*				
		(15) MH 1	Haryana	39.7	1.12	0.4	26.5	0.87	0.4	4.4	0.48*	0.0	1.1	0.23*	-0.1				
		(17) S 206	Karnataka	36.8	0.98	-0.1	32.5	0.48*	1.7*	5.1	0.80	0.0	1.3	0.61*	-0.1				
		(18) SB 11	M.S.	38.0	1.09	1.1*	30.0	0.65	-0.2	4.7	0.70	0.0	2.6	0.78*	-0.1				
		(24) TMV 2	T.N.	39.0	1.17*	0.2	33.2	1.35*	0.7	4.5	0.91	0.0	1.6	1.01	0.0				
		(27) Ah 4515	India	40.1	1.20*	0.0	32.7	1.35	1.2*	5.6	0.21	0.1*	5.1	1.75*	0.0				
		(29) Comet	U.S.	38.7	1.11*	-0.2	29.2	0.35	5.2*	5.3	1.67*	0.0	2.7	1.40*	0.0				
		(32) NC Ac 7778	U.S.	36.5	0.97	0.2	26.7	1.28*	0.3	5.3	1.71	0.1*	2.1	1.32*	0.0				
		(36) NC Ac 7785	U.S.	36.0	1.01	0.0	29.2	0.95	6.2*	5.3	1.74	0.0	5.6	1.64	0.2*				
		(38) NC Ac 7790	U.S.	35.4	1.01	0.0	26.3	1.05	-0.2	4.7	0.98	0.0	3.0	1.51	0.2*				
		(39) PI 268782	Zimbabwe	36.5	0.98	0.1	31.3	1.53*	1.8*	4.7	0.74	0.0	3.0	1.47	0.1*				
		(40) PI 268829	Zimbabwe	35.7	0.90*	-0.2	29.8	1.68	4.3*	5.0	1.08	0.0	2.5	1.13	0.0				
		(41) PI 268642	Zimbabwe	39.8	1.10	0.2	26.2	1.08	0.0	5.0	0.14*	0.0	0.8	0.15*	0.0				
		(42) Pearl	U.S.	38.7	1.07	0.0	27.1	1.03	0.4	6.2	2.42*	0.0	3.1	1.72*	0.1				
		(47) Teja Amra Local	India	36.6	1.00	-0.2	34.7	1.48*	0.6	5.1	1.74	0.0	2.2	0.57*	-0.1				
		(48) U 1-1-1	Sudan	35.6	0.92*	-0.2	30.8	0.78	4.7*	6.0	1.73	0.0	2.6	1.59*	-0.1				
		Mean		37.2	1.02	0.1	29.8	1.06	1.5	5.1	1.29	0.0	2.8	1.23	0.0				
		(6) GAUG 1	Gujarat	35.3	0.99	1.9*	31.7	1.53	-0.1	4.8	0.22	0.1*	2.3	1.40*	0.0				
		(11) JL 24	M.S.	37.7	1.17	0.3	28.1	0.76	1.8*	4.8	0.92	0.0	2.9	1.60*	0.0				
		(19) Spanish Improved	M.S. Karnataka	39.2	1.09*	-0.2	31.1	0.85	8.0*	5.1	1.16	0.0	2.2	0.69*	-0.1				
		(22) TG 17	M.S.	37.3	1.05	-0.2	25.6	0.99	-0.3	4.3	0.00*	0.0	0.2	0.07*	-0.1				
		(26) Ah 4104-2	India	39.1	1.10*	-0.1	32.7	1.19*	-0.3	4.6	0.65*	0.0	2.1	1.32	0.0				
		(28) Ah 6649	Tanzania	37.3	0.95	-0.2	30.0	1.45*	0.0	5.7	0.21	0.0	4.6	2.84*	0.0				
		(34) NC Ac 7782	U.S.	38.4	0.96	0.0	25.7	0.93	0.8	5.2	1.65	0.1*	3.0	1.61*	0.1*				
		(46) Taiwan Selection	Taiwan	36.1	0.95	-0.2	32.8	1.62	3.5*	5.3	1.61*	0.0	3.0	0.86	0.0				
		Mean		37.5	1.03	0.2	29.7	1.17	1.8	4.9	0.80	0.0	2.5	1.30	0.0				
II	8																		

Table 5.5: Continued:

Cluster formed in pooled over seasons (E ₁ •E ₂ •E ₃ •E ₄)	Total No. of genotypes	Genotypes included	Origin	(1) Days to 50% flowering			(2) Height of main axis (cm)			(3) Primary branches/ plant			(4) Secondary branches/ plant		
				$\bar{X}_i$	bi	S ² di	$\bar{X}_i$	bi	S ² di	$\bar{X}_i$	bi	S ² di	$\bar{X}_i$	bi	S ² di
III	11	(2) AK 159	M.S.	36.8	1.07	-0.2	26.0	0.76*	0.1	4.8	0.16	0.1	0.2	0.07*	-0.1
		(3) ALR 3	T.N.	37.7	0.93	0.2	32.3	0.98	-0.1	5.5	1.87*	0.0	0.1	-0.07*	-0.1
		(7) GG 2	Gujarat	37.4	1.03	0.7*	22.7	1.03	-0.1	4.8	0.88	0.0	2.9	1.80*	-0.1
		(8) Gimar 1	Entire country	36.6	1.09	0.6*	22.9	1.06	-0.2	4.9	1.24	0.0	3.2	1.00	-0.1
		(9) ICG (FDRS) 10	M.S.	35.5	0.94	0.3	26.7	1.24	0.3	4.5	1.22	0.0	1.6	1.04	-0.1
		(16) POL 2	Karnataka	34.3	0.89	0.8*	29.5	0.87	-0.3	5.2	1.02	0.0	2.2	0.97	-0.1
		(20) TAG 24	M.S.	35.1	0.92	0.3	16.6	0.09*	0.7	4.6	1.00	0.0	2.1	1.04	0.1
		(23) TG 26	M.S., Guja AP	37.8	1.13	0.1	16.9	0.10*	0.1	4.5	0.47	0.0	2.1	0.57	0.1
		(30) NC Ac 7776	U.S.	34.0	0.89*	-0.2	27.7	1.65	4.1*	5.1	0.46	0.0	1.0	0.34*	0.0
		(35) NC Ac 7783	U.S.	34.1	0.90	1.0*	24.1	1.27	0.8	4.0	0.16	0.0	0.0	0.00*	-0.1
		(49) U 2-4-5	Sudan	36.3	1.03	0.4	28.0	1.06	1.4*	6.0	0.75*	0.0	2.6	1.38*	0.0
IV	8	Mean		35.9	0.98	0.4	24.8	0.92	0.6	4.9	0.84	0.0	1.6	0.74	0.0
		(4) CO 1	T.N.	37.3	0.96	1.1*	29.4	0.80*	-0.3	4.7	0.43*	0.0	0.9	0.57*	-0.1
		(5) CO 2	T.N.	37.8	1.10*	-0.1	27.9	0.87*	-0.4	5.2	0.66	0.0	5.7	0.59	0.3*
		(12) JL 220	M.S.	36.6	0.97	-0.2	23.9	0.89	0.5	5.1	2.00*	0.0	0.8	0.28*	0.0
		(21) TKG 19A	M.S.	39.1	1.09	0.5	26.7	0.94	0.1	4.8	1.25	0.0	1.0	0.32*	-0.1
		(31) NC Ac 7777	U.S.	35.4	0.90	0.4	20.9	0.46	2.8*	4.9	1.86	0.0	0.3	0.19*	-0.1
		(33) NC Ac 7780	U.S.	34.4	0.86*	-0.2	24.1	1.24	0.6	4.2	0.22*	0.0	0.9	0.54*	-0.1
		(37) NC Ac 7787	U.S.	35.4	0.88	0.1	24.4	1.30	0.4	5.4	0.43	0.0	2.3	0.25*	0.0
		(45) Span white	U.S.	34.9	0.90*	-0.2	23.0	0.40*	1.5*	4.6	0.61*	0.0	1.2	0.51*	0.0
		Mean		36.3	0.96	0.2	25.0	0.86	0.7	4.8	0.93	0.0	1.6	0.41	0.0
		(43) Starr	U.S.	37.3	1.08*	-0.3	28.9	0.56	4.0*	4.4	0.63	0.0	3.2	1.72*	0.1
V	1	(44) Span cross	U.S.	36.0	1.02	-0.1	27.6	0.76	1.0*	5.3	1.28	0.0	2.7	1.42*	0.0
VI	1	(50) U 2-12-1	Sudan	33.6	0.82*	-0.1	31.0	0.61	4.4*	5.5	0.41	0.1	1.8	0.98	-0.1
VII	1	(25) Ah 1	India	34.9	0.97	-0.2	35.2	1.67	5.1*	4.7	0.03	0.1	2.0	0.70*	0.0
VIII	1	General mean		36.7	1.00	0.2	28.0	1.00	1.4	5.0	1.0	0.0	2.3	1.0	0.0

Table 5.5: Continued:

Cluster formed in pooled over seasons ($E_1+E_2+E_3+E_4$)	Total No. of genotypes	Genotypes included	Origin	(5) Mature pods per plant				(6) Shelling per cent				(7) Days to maturity			
				$\bar{X}_i$	bi	S ² di	$\bar{X}_i$	bi	S ² di	$\bar{X}_i$	bi	$\bar{X}_i$	bi	S ² di	
I	19	(1) AK 12-24	M.S.	11.0	-0.60	7.4*	68.6	2.43	3.9*	114.3	0.89*	-0.4			
		(10) J 11	Gujarat	12.5	1.26	0.4	71.1	-0.27	3.1*	112.9	0.97	0.2			
		(13) Jyoti	M.P.	10.7	0.10	0.4	70.7	0.60	-0.3	112.9	1.00	0.5			
		(14) KRG 1	Karnataka	13.9	0.42	1.3*	67.9	0.27	-0.1	112.8	0.63*	0.0			
		(15) MH 1	Haryana	12.0	0.01	0.8*	69.4	0.65	-0.2	111.9	0.99	-0.4			
		(17) S 206	Karnataka	13.9	-0.34	1.3*	70.7	0.28	-0.1	109.8	0.72*	0.1			
		(18) SB 11	M.S.	14.6	-0.20	5.9*	72.8	1.04	-0.3	113.3	1.03	0.8			
		(24) TMV 2	T.N.	11.3	1.11	1.1*	68.9	0.80	0.4	112.2	1.13	1.5*			
		(27) Ah 4515	India	15.9	4.43	15.6*	70.1	1.01	-0.4	113.6	1.29	3.2*			
		(29) Comet	U.S.	11.7	-0.59	2.8*	71.2	0.44*	-0.4	111.8	1.23*	0.2			
		(32) NC Ac 7778	U.S.	9.8	2.46	1.7*	68.9	-0.14	1.8*	119.0	1.39*	0.4			
		(36) NC Ac 7785	U.S.	10.1	1.37	0.0	67.0	1.65	0.8	113.3	1.11	0.2			
		(38) NC Ac 7790	U.S.	8.4	0.73	-0.1	68.1	0.50	-0.3	113.4	0.66*	-0.2			
		(39) PI 268782	Zimbabwe	13.9	3.19	10.7*	67.0	0.92	-0.2	113.1	0.80*	-0.4			
		(40) PI 268829	Zimbabwe	13.1	2.67	5.6*	70.0	0.84	-0.3	114.1	1.10	0.5			
		(41) PI 268642	Zimbabwe	8.0	0.86	-0.1	70.4	0.77	-0.4	111.5	1.09	0.3			
		(42) Pearl	U.S.	11.0	1.09	1.3*	63.3	1.07	0.1	114.6	1.07	2.8*			
		(47) Teja Amra local	India	13.2	1.85	0.6	70.0	0.38	-0.2	112.8	0.60*	1.0			
		(48) U 1-1-1	Sudan	12.9	2.42	2.9*	63.4	1.38*	-0.4	115.1	0.66*	-0.5			
		Mean		11.9	1.17	3.1	68.9	0.77	0.3	113.2	0.97	0.5			
II	8	(6) GAUG 1	Gujarat	12.3	0.95	0.5	60.2	1.90	0.1	113.4	0.41*	1.4*			
		(11) JL 24	M.S.	8.1	2.37	0.9*	69.2	0.60	1.9*	114.6	1.23*	0.6			
		(19) Spanish Improved	M.S. and Karnataka	12.5	0.71	1.3*	69.1	0.35	0.7	115.8	0.90	3.4*			
		(22) TG 17	M.S.	11.4	1.05	0.6	65.3	0.63	-0.1	117.6	0.94	1.4*			
		(26) Ah 4104-2	India	9.6	0.68	-0.1	70.2	0.42	-0.3	109.6	1.25*	0.5			
		(28) Ah 6649	Tanzania	14.4	1.87	1.1*	67.2	0.58	-0.4	117.2	1.25*	0.2			
		(34) NC Ac 7782	U.S.	10.4	1.36	1.0*	71.5	0.71	-0.3	115.8	1.37	3.4*			
		(46) Taiwan selection	Taiwan	9.7	0.61	-0.1	64.5	1.81	3.37*	118.6	0.92	0.0			
		Mean		11.0	1.20	0.7	67.1	0.88	0.62	115.3	1.03	1.4			

Table 5.5: Continued:

Cluster formed in pooled over seasons (E ₁ +E ₂ +E ₃ +E ₄)	Total No. of genotypes	Genotypes included	Origin	(5) Mature pods per plant			(6) Shelling per cent			(7) Days to maturity		
				$\bar{X}_i$	bi	S ² di	$\bar{X}_i$	bi	S ² di	$\bar{X}_i$	bi	S ² di
III	11	(2) AK 159	M.S.	16.5	4.91	11.5*	67.8	1.02	1.0*	113.7	1.06	-0.1
		(3) ALR 3	T.N.	12.9	2.83	4.5*	58.9	1.93	2.6*	124.8	1.22*	0.2
		(7) GG 2	Gujarat	11.8	1.24	6.3*	70.6	1.00	-0.3	113.1	0.90	-0.2
		(8) Gimar 1	Entire country	14.2	-0.09	2.0*	62.4	2.24	0.5	113.1	0.76*	0.8
		(9) ICG (FDRS) 10	M.S.	11.8	-0.47	6.3*	63.9	1.31	0.9	118.5	0.94	0.3
		(16) POL 2	Karnataka	10.9	-0.19	2.0*	61.4	1.31*	-0.4	112.2	0.81*	-0.4
		(20) TAG 24	M.S.	17.2	-0.71	9.2*	69.0	1.77	-0.1	107.4	0.91	0.1
		(23) TG 26	M.S., Gujarat & AP	14.0	-0.92	4.9*	71.5	0.44	-0.1	111.4	1.11	1.5*
		(30) NC Ac 7776	U.S.	11.3	2.81	4.8*	63.5	0.72	0.0	113.7	1.27*	0.7
		(35) NC Ac 7783	U.S.	9.2	1.36	1.2*	63.6	0.78	-0.1	110.8	1.08	1.9*
		(49) U 2-4-5	Sudan	13.6	1.80*	-0.2	61.0	-1.80	17.6*	114.6	0.97	-0.5
		Mean		13.0	1.14	4.8	64.8	0.97	2.0	113.9	1.00	0.4
		(4) CO 1	T.N.	10.7	0.02	2.2*	55.0	3.26	2.2*	112.1	0.82*	-0.4
IV	8	(5) CO 2	T.N.	10.8	-0.39	2.9*	57.5	2.23	1.3*	114.4	0.67*	1.5*
		(12) JL 220	M.S.	7.4	-0.49	3.3*	59.5	1.44	-0.3	116.1	0.93	-0.1
		(21) TKG 19A	M.S.	10.0	1.16	-0.2	55.5	3.20	3.9*	121.8	1.12	0.0
		(31) NC Ac 7777	U.S.	8.6	0.98	-0.1	55.4	1.83*	-0.3	117.7	0.88	-0.1
		(33) NC Ac 7780	U.S.	9.0	0.57	2.8*	65.3	0.17	1.0*	113.3	1.29	5.2*
		(37) NC Ac 7787	U.S.	6.1	-0.04	1.5*	57.6	1.46	0.9*	113.9	0.99	4.2*
		(45) Span white	U.S.	8.6	-0.19	0.3	61.3	1.25	-0.1	112.4	0.89	1.9*
		Mean		8.8	0.20	1.6	58.3	1.86	1.1	115.2	0.95	1.5
		(43) Starr	U.S.	11.0	-0.56	1.6*	71.2	0.78	-0.3	110.0	0.93	0.6
		(44) Span cross	U.S.	14.7	3.91	10.6*	78.5	0.04	0.0	112.1	1.40*	1.2*
V	1	(50) U 2-12-1	Sudan	13.3	0.50	0.0	69.8	0.94	-0.1	111.5	1.12	0.8
VII	1	(25) Ah 1	India	13.5	2.67	7.7*	64.2	1.04	-0.2	113.4	1.32*	-0.5
VIII	1	General mean		11.6	1.05	3.0	66.18	1.00	0.8	113.9	1.00	0.8

5.4. Selection of parents based on inter-cluster distance and general adaptability

Genotypes grouped into the same cluster should diverge very little from one another on the basis of aggregate of the 13 clusters measured in the present study. Crossing programme should be planned in such a way that the parents to be used should belong to different clusters because the crossing of genotypes belonging to the same cluster is not expected to give desirable segregates. Therefore, crosses between genotypes belonging to the clusters having highest average inter-cluster distance and at the same time they should have general adaptability for maximum number of desirable traits are expected to yield better segregates having stability over environments.

From present investigation, the possible combinations beyond mean statistical distance for environment 1 ($\bar{D}=25.18$), environment 2 ($\bar{D}=24.95$), pooled over *kharif* environments 1 and 2 ($\bar{D}=20.66$), environment 3 ($\bar{D}=22.85$), environment 4 ($\bar{D}=22.91$), pooled over summer environments 3 and 4 ($\bar{D}=16.39$) and pooled over *Kharif* (environments 1 and 2) and summer (environments 3 and 4) seasons ($\bar{D}=13.03$) are arranged in descending order of magnitude of genetic distance in Table 5.6 to 5.12.

There are considerable evidences in both self and cross pollinated crops that genetic divergence and stability analysis help in selecting the parents for hybridization programme. However, this concept has not been practically utilized in selection of parents for hybridization programme in groundnut. Therefore, in the present study, phenotypic stability of the genotype for maximum characters was one of the parameters for selecting parents.

In E_1 (Table 5.6), the maximum inter-cluster distance (38.84) existed between cluster VI (TG 26) and cluster VII (Ah 1). The variety, TG 26 was specifically adapted to unfavourable environment for height of main axis, for dwarfness and for shelling. The germplasm line Ah 1 has got general

**Table 5.6: Average inter-cluster distance and cross combinations in E₁
(Kharif 2002)**

Sr. No.	Cluster combinations	Average inter cluster distance	Cross combinations based on genetic divergence and adaptability
1.	VI x VII	38.84	(23) TG 26 x (25) Ah 1
2.	VII x VIII	38.31	(25) Ah 1 x (44) Span cross
3.	IV x VIII	35.00	(21) TKG 19 A x (44) Span cross
4.	V x VII	34.09	(43) Starr x (25) Ah 1
5.	III x VIII	33.24	(22) TG 17 x (44) Span cross
6.	VII x IX	32.03	(25) Ah 1 x (20) TAG 24
7.	II x VII	30.70	(11) JL 24 x (25) Ah 1
8.	IV x VI	28.96	(21) TKG 19A x (23) TG 26
9.	IV x VII	27.76	(21) TKG 19A x (25) Ah 1
10.	V x IX	27.46	(43) Starr x (20) TAG 24
11.	V x VIII	27.12	(43) Starr x (44) Span cross
12.	I x VII	27.14	(49) U 2-4-5 x (25) Ah 1 (10) J 11 x (25) Ah 1 (18) SB XI x (25) Ah 1 (38) NC Ac 7790 x (25) Ah 1 (7) GG 2 x (25) Ah 1 (8) Girnar 1 x (25) Ah 1 (15) MH 1 x (25) Ah 1 (41) PI 268642 x (25) Ah 1 (13) Jyoti x (25) Ah 1 (34) NC Ac 7782 x (25) Ah 1 (50) U 2-12-1 x (25) Ah 1
13.	VIII x IX	26.90	(44) Span cross x (20) TAG 24
14.	III x VI	26.48	(22) TG 17 x (23) TG 26
15.	II x VI	26.18	(11) JL 24 x (23) TG 26
16.	IV x V	25.91	(21) TKG 19A x (43) Starr
17.	III x V	25.51	(22) TG 17 x (43) Starr
18.	II x V	25.47	(11) JL 24 x (43) Starr

Table 5.7: Average inter-cluster distance and cross combinations in E₂ (Kharif 2000)

Sr. No.	Cluster combinations	Average inter cluster distance	Cross combinations based on genetic divergence and adaptability
1.	V x VI	34.74	(44) Span cross x (25) Ah 1
2.	IV x VI	33.03	(43) Starr x (25) Ah 1
3.	III x VI	31.44	(21) TKG 19A x (25) Ah 1
4.	V x VII	31.21	(44) Span cross x (5) CO 2
5.	III x V	29.28	(21) TKG 19A x (44) Span cross
6.	IV x VII	28.32	(43) Starr x (5) CO.2
7.	II x V	27.99	(45) Span white x (44) Span cross
8.	II x VI	27.90	(45) Span white x (25) Ah 1
9.	VI x VII	27.69	(25) Ah 1 x (5) CO.2
10.	I x VI	26.13	(10) J 11 X (25) Ah 1 (13) Jyoti x (25) Ah 1 (18) SB XI x (25) Ah 1 (41) PI 268642 x (25) Ah 1 (15) MH 1 x (25) Ah 1 (38) NC Ac 7790 x (25) Ah 1 (49) U 2-4-5 x (25) Ah 1 (34) NC Ac 7782 x (25) Ah 1 (8) Girnar 1 x (25) Ah 1 (7) GG 2 x (25) Ah 1 (50) U 2-12-1 x (25) Ah 1
11.	IV x V	25.52	(43) Starr x (44) Span cross

adaptability for days to 50 per cent flowering. Thus, the hybridization programme involving parents from these two clusters is expected to give high frequency of better segregates. This was followed by distance 38.31 exhibited between cluster VII (Ah 1) and cluster VIII (Span cross). The germplasm line, Span cross was generally adapted for days to 50 per cent flowering, specifically adapted to favourable environment for primary branches per plant and secondary branches per plant and specifically adapted to unfavourable environments for shelling per cent. Thus, crossing among

parents of these clusters would also give the desirable transgrates. In E_2 (Table 5.7), the maximum inter-cluster distance (34.74) existed between cluster V (Span cross) and cluster VI (Ah 1), followed by distance 33.03 exhibited between cluster IV (Starr) and cluster VI (Ah 1). The genotype, Starr had below average stability for secondary branches per plant, general adaptability for shelling per cent above average stability for days to maturity. Thus, the hybridization programme involving parents from these clusters is expected to give higher frequency of better segregates.

In pooled analysis of *kharif* environment (E_1+E_2) (Table 5.8), the maximum inter-cluster distance (33.94) existed between cluster VI (TG 26) and cluster X (Ah 1), followed by distance 33.73 exhibited between cluster IX (Span cross) and cluster X (Ah 1) and distance 31.62 exhibited between cluster IV (U 2-12-1) and cluster X (Ah 1). The germplasm line U 2-12-1 registered above average stability for days to 50 per cent flowering, average stability for mature pods per plant and for shelling per cent and below average stability for days to maturity. Thus, crossing among parents from these clusters would also give the desirable transgrates.

In E_3 (Table 5.9), the maximum inter-cluster distance (35.41) existed between cluster V (U 2-12-1 and GG 2) and cluster IX (TKG 19A). The released variety, GG 2 had average stability for height of main axis for dwarfness and for shelling per cent, below average stability for secondary branches per plant and above average stability for days to maturity. The variety TKG 19A had average stability for height of main axis for dwarfness. Thus, the hybridization programme involving parents from these two clusters is expected to give higher frequency of better segregates. This was followed by distance 34.19 exhibited between cluster V (U 2-12-1 and GG 2) and cluster VIII (Ah 1). Thus, crossing among parents from these clusters would also give the desirable transgrates. In E_4 (Table 5.10), the maximum inter-cluster distance (37.50) existed between cluster VIII (U 2-12-1) and cluster IX (Ah 1), followed by distance 35.62 exhibited between cluster IV (TG 26) and cluster IX (Ah 1). Thus, the hybridization programme involving parents from these clusters is expected to give higher frequency of better segregates.

Table 5.8: Average inter-cluster distance and cross combinations in pooled E_1+E_2 (Kharif 2002)

Sr. No.	Cluster combinations	Average inter cluster distance	Cross combinations based on genetic divergence and adaptability
1.	VI x X	33.94	(23) TG 26 x (25) Ah 1
2.	IX x X	33.73	(44) Span cross x (25) Ah 1
3.	IV x X	31.62	(50) U 2-12-1 x (25) Ah 1
4.	VIII x X	30.91	(43) Starr x (25) Ah 1
5.	V x IX	27.17	(20) TAG 24 x (44) Span cross
6.	V x X	26.82	(20) TAG 24 x (25) Ah 1
7.	II x IX	25.72	(34) NC Ac 7782 x (44) Span cross
8.	VII x VIII	25.26	(2) AK 159 x (43) Starr
9.	I x X	24.94	(49) U 2-4-5 x (25) Ah 1 (10) J 11 x (25) Ah 1 (38) NC Ac 7790 x (25) Ah 1 (7) GG 2 X (25) Ah 1 (18) SB XI x (25) Ah 1 (41) PI 268642 x (25) Ah 1 (15) MH 1 x (25) Ah 1 (13) Jyoti x (25) Ah 1 (8) Girnar 1 x (25) Ah 1
10.	III x X	24.48	(27) Ah 4515 x (25) Ah 1
11.	VIII x IX	24.35	(43) Starr x (44) Span cross
12.	VII x X	23.71	(2) AK 159 x (25) Ah 1
13.	V x VIII	22.87	(20) TAG 24 x (43) Starr
14.	V x VI	22.66	(20) TAG 24 x (23) TG 26
15.	II x IV	22.36	(34) NC Ac 7782 x (50) U 2-12-1
16.	II x VI	22.26	(34) NC Ac 7782 x (23) TG 26
17.	III x V	21.67	(27) Ah 4515 x (20) TAG 24
18.	II x VIII	21.04	(34) NC Ac 7782 x (43) Starr

Table 5.9: Average inter-cluster distance and cross combinations in E₃ (Summer 2003)

Sr. No.	Cluster combinations	Average inter cluster distance	Cross combinations based on genetic divergence and adaptability
1.	V x IX	34.41	(50) U 2-12-1 x (21) TKG 19A (7) GG 2 x (21) TKG 19A
2.	V x VIII	34.19	(50) U 2-12-1 x (25) Ah 1 (7) GG 2 x (25) Ah 1
3.	II x VIII	33.98	(49) U 2-4-5 x (25) Ah 1
4.	II x IX	33.07	(49) U 2-4-5 x (21) TKG 19A
5.	I x IX	30.08	(10) J 11 x (21) TKG 19A (38) NC Ac 7790 x (21) TKG 19A (13) Jyoti x (21) TKG 19A (8) Girnar 1 x (21) TKG 19A (15) MH 1 x (21) TKG 19A (18) SB XI x (21) TKG 19A
6.	VII x IX	29.38	(3) ALR 3 x (21) TKG 19A
7.	VII x VIII	28.78	(3) ALR 3 x (25) Ah 1
8.	I x VIII	27.79	(10) J 11 x (25) Ah 1 (38) NC Ac 7790 x (25) Ah 1 (13) Jyoti x (25) Ah 1 (8) Girnar 1 x (25) Ah 1 (15) MH 1 x (25) Ah 1 (18) SB 11 x (25) Ah 1
9.	VI x IX	27.36	(28) Ah 6649 x (21) TKG 19A
10.	III x IX	26.80	(2) AK 159 x (21) TKG 19A
11.	II x VI	25.86	(49) U 2-4-5 x (28) Ah 6649
12.	IV x V	24.06	(34) NC Ac 7782 x (50) U 2-12-1 (41) PI 268642 x (50) U 2-12-1 (34) NC Ac 7782 x (7) GG 2 (41) PI 268642 x (7) GG 2
13.	V x VI	23.33	(50) U 2-12-1 x (28) Ah 6649 (7) GG 2 x (28) Ah 6649
14.	II x IV	22.94	(49) U 2-4-5 x (34) NC Ac 7782 (49) U 2-4-5 x (7) GG 2
15.	V x VII	22.85	(50) U 2-12-1 x (3) ALR 3 (7) GG 2 x (3) ALR 3

**Table 5.10: Average inter-cluster distance and cross combinations in E₄
(Summer 2003)**

Sr. No.	Cluster combinations	Average inter cluster distance	Cross combinations based on genetic divergence and adaptability
1.	VIII x IX	37.50	(50) U 2-12-1 x (25) Ah 1
2.	IV x IX	35.62	(23) TG 26 x (25) Ah 1
3.	VII x IX	34.87	(44) Span cross x (25) Ah 1
4.	V x IX	34.36	(35) NC Ac 7783 x (25) Ah 1
5.	VII x X	29.49	(44) Span cross x (5) CO.2
6.	V x X	28.22	(35) NC Ac 7783 x (5) CO.2
7.	II x VIII	28.03	(34) NC Ac 7782 x (50) U, 2-12-1
8.	IV x X	27.64	(23) TG 26 x (5) CO.2
9.	III x VII	27.53	(49) U 2-4-5 x (44) Span cross (8) Girnar 1 x (44) span cross
10.	I x IX	27.30	(10) J 11 x (25) Ah 1 (13) Jyoti x (25) Ah 1 (38) NC Ac 7790 x (25) Ah 1 (15) MH 1 x (25) Ah 1 (18) SB XI x (25) Ah 1 (7) GG 2 x (25) Ah 1 (41) PI 268642 x (25) Ah 1
11.	III x IX	27.15	(49) U 2-4-5 x (25) Ah 1 (8) Girnar 1 x (25) Ah 1
12.	VIII x X	26.32	(50) U 2-12-1 x (5) CO.2
13.	II x IV	24.48	(34) NC Ac 7782 x (23) TG 26
14.	VI x VII	24.20	(20) TAG 24 x (44) Span cross
15.	VI x IX	24.18	(20) TAG 24 x (25) Ah 1
16.	II x V	23.69	(34) NC Ac 7782 x (35) NC Ac 7783
17.	II x VII	23.66	(34) NC Ac 7782 x (44) Span cross
18.	III x IV	23.29	(49) U 2-4-5 x (23) TG 26 (8) Girnar 1 x (23) TG 26

Table 5.11: Average inter-cluster distance and cross combinations in pooled E₃+E₄ (Summer 2003)

Sr. No.	Cluster combinations	Average inter cluster distance	Cross combinations based on genetic divergence and adaptability
1.	III x V	22.69	(50) U 2-12-1 x (21) TKG 19 A (7) GG 2 x (21) TKG 19A
2.	III x VII	21.65	(50) U 2-12-1 x (25) Ah 1 (7) GG 2 x (25) Ah 1
3.	V x VI	20.86	(21) TKG 19A x (28) Ah 6649
4.	III x IX	20.80	(50) U 2-12-1 x (33) NC Ac 7780 (7) GG 2 x (33) NC Ac 7780
5.	III x VIII	19.97	(50) U 2-12-1 x (3) ALR 3 (7) GG 2 x (3) ALR 3
6.	VI x IX	18.74	(28) Ah 6649 x (33) NC Ac 7780
7.	VI x VIII	18.36	(28) Ah 6649 x (3) ALR 3
8.	I x V	18.24	(10) J 11 x (21) TKG 19A (13) Jyoti x (21) TKG 19A (38) NC Ac 7790 x (21) TKG 19A (34) NC Ac 7782 x (21) TKG 19A (15) MH 1 x (21) TKG 19A (41) PI 268642 x (21) TKG 19A (18) SB XI x (21) TKG 19A
9.	I x IX	18.10	(10) J 11 x (33) NC Ac 7780 (13) Jyoti x (33) NC Ac 7780 (38) NC Ac 7790 x (33) NC Ac 7780 (34) NC Ac 7782 x (33) NC Ac 7780 (15) MH 1 x (33) NC Ac 7780 (41) PI 268642 x (33) NC Ac 7780 (18) SB XI x (33) NC Ac 7780
10.	V x IX	18.03	(21) TKG 19A x (33) NC Ac 7780
11.	II x VI	18.02	(49) U 2-4-5 x (28) Ah 6649 (8) Gimar 1 x (28) Ah 6649
12.	III x VI	17.81	(50) U 2-12-1 x (28) Ah 6649 (7) GG 2 x (28) Ah 6649
13.	IV x VI	17.64	(22) TG 17 x (28) Ah 6649
14.	III x IV	17.60	(50) U 2-12-1 x (22) TG 17 (7) GG 2 x (22) TG 17
15.	II x V	17.57	(49) U 2-4-5 x (21) TKG 19A (8) Gimar 1 x (21) TKG 19A
16.	II x VII	17.35	(49) U 2-4-5 x (25) Ah 1 (8) Gimar 1 x (25) Ah 1
17.	VI x VII	16.81	(28) Ah 6649 x (25) Ah 1
18.	VIII x IX	16.76	(3) ALR 3 x (33) NC Ac 7780
19.	II x III	16.49	(49) U 2-4-5 x (50) U 2-12-1 (8) Gimar 1 x (50) U 2-12-1 (49) U 2-4-5 x (7) GG 2 (8) Gimar 1 x (7) GG 2

Table 5.12: Average inter-cluster distance and cross combinations in pooled over seasons E₁+E₂+E₃+E₄ (Kharif 2002 and Summer 2003)

Sr. No.	Cluster combinations	Average inter cluster distance	Cross combinations based on genetic divergence and adaptability
1.	VI x VIII	20.74	(44) Span cross x (25) Ah 1*
2.	VII x VIII	20.53	(50) U 2-12-1 x (25) Ah 1
3.	IV x VI	18.44	(21) TKG 19A x (44) Span cross*
4.	V x VIII	17.48	(43) Starr x (25) Ah 1*
5.	III x VIII	15.68	(49) U 2-4-5 x (25) Ah 1 (8) Girnar 1 x (25) Ah 1
6.	II x VII	15.33	(34) NC Ac 7782 x (50) U 2-12-1*
7.	I x VIII	14.93	(10) J 11 x (25) Ah 1 (13) Jyoti x (25) Ah 1 (38) NC Ac 7790 x (25) Ah 1 (41) PI 268642 x (25) Ah 1 (18) SB XI x (25) Ah 1 (15) MH 1 x (25) Ah 1
8.	IV x VII	14.37	(21) TKG 19A x (50) U 2-12-1*
9.	II x VI	14.36	(34) NC Ac 7782 x (44) Span cross*
10.	V x VI	13.84	(43) Starr x (44) Span cross
11.	IV x VIII	13.61	(21) TKG 19A x (25) Ah 1*
12.	IV x V	13.55	(21) TKG 19A x (43) Starr*

* Remaining cross combinations

In pooled analysis of summer environments (E₃+E₄) (Table 5.11), the maximum inter-cluster distance (22.69) existed between cluster III (U 2-12-1 and GG 2) and cluster V (TKG 19A), followed by distance 21.65 exhibited between cluster III (U 2-12-1 and GG 2) and cluster VII (Ah 1). Thus, the hybridization programme involving parents from these clusters is expected to give higher frequency of better segregates.

In pooled analysis over seasons (E₁+E₂+E₃+E₄) (Table 5.12), the maximum inter-cluster distance (20.74) existed between cluster VI (Span cross) and cluster VIII (Ah 1), followed by distance (20.53) exhibited between

cluster VII (U 2-12-1) and cluster VIII (Ah 1). Thus, crossing among parents from these clusters would also give the desirable transgrates.

Table 5.13: Selected cross combinations in *kharif* (E_1 , E_2 and $E_1 + E_2$) and in summer (E_3 , E_4 and $E_3 + E_4$)

Season	Total	Cross combinations
<i>Kharif</i>	13	(25) Ah 1 x (44) Span cross (43) Starr x (25) Ah 1 (43) Starr x (44) Span cross (49) U 2-4-5 x (25) Ah 1* (10) J 11 x (25) Ah 1 (18) SB XI x (25) Ah 1 (38) NC Ac 7790 x (25) Ah 1 (7) GG 2 x (25) Ah 1* (8) Girnar 1 x (25) Ah 1* (15) MH 1 x (25) Ah 1 (41) PI 268642 x (25) Ah 1 (13) Jyoti x (25) Ah 1 (50) U 2-12-1 x (25) Ah 1*
Summer	4	(50) U 2-12-1 x (25) Ah 1* (7) GG 2 x (25) Ah 1* (49) U 2-4-5 x (25) Ah 1* (8) Girnar 1 x (25) Ah 1*

* appeared in both seasons

On the basis of results obtained in the present study, some cross combinations were similar over *Kharif* (13) and over summer (4) Table 5.13. These crosses may show relatively good amount of heterosis in F_1 and high frequency of transgressive segregates. Similarly, remaining cross combinations from pooled analysis over seasons (Table 5.12) should be attempted for wider adaptability, i.e., Span cross x Ah 1, TKG 19A x Span cross, Starr x Ah 1, NC Ac 7782 x U 2-12-1, TKG 19A x U 2-12-1, NC Ac 7782 x Span cross, TKG 19A x Ah 1, TKG 19A x Starr. Table 5.13 also revealed that the four cross combinations, viz., U 2-4-5 x Ah 1, GG 2 x Ah 1, Girnar 1 x Ah 1 and U 2-12-1 x Ah 1 have repeatedly occurred in both seasons, need to be concentrated first. The transgrates isolated from such crosses would be useful for *Kharif* and *summer* adaptations.

CHAPTER VI

SUMMARY

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CHAPTER VI

SUMMARY

In the present investigations entitled “Genetic diversity in relation to seasonal adaptability in groundnut (*Arachis hypogaea* L.)” in all 50 genotypes consisting of 24 released varieties in seven different states of India, including four standard checks (SB XI, JL 24, TAG 24 and AK 159) and 26 germplasm lines originated from six different countries belonging to Spanish Bunch (*Spp. fastigiata*, var. *vulgaris*) botanical group have been evaluated under *Kharif* and summer seasons on two dates of sowing in each season with an objectives, to estimate genetic divergence for grouping, to estimate $g \times e$ interaction and stability parameters of some of the components of yield for adaptability and to identify the superior genotypes on the basis of genetic diversity and phenotypic stability for their use in future groundnut breeding programme.

The experiment was laid out during *kharif* 2002 and summer 2003 on research farm of Crop Research Unit (Oilseeds) at Central Research Station, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The experiment was raised in a randomized complete block design with four replications. Plot size was 2.00 x 0.90 m with spacing of 30 x 10 cm. Data on 13 quantitative characters were recorded on the basis of five plants.

D^2 analysis was carried out separately for each date (four environments), pooled over dates of each season and pooled over seasons using model of Mahalanobis’ D^2 -Statistic (1936) and grouping was done by Tocher’s method (Rao, 1952). Phenotypic stability of an individual genotype was estimated using the model of Eberhart and Russell (1966). While selecting the parents from diverse clusters, general adaptability or average stability of genotypes was considered. It is expected that the crossing between genotypes from diverse clusters and having different means and regression coefficients can bring together diverse gene groups and therefore may provide a mechanism for the stability.

Higher significant differences were existed among genotypes and environments for all characters. Analysis of dispersion was highly significant for aggregate effect of all characters under separate as well as pooled environments, justifying, thereby, the need to calculate D^2 values.

Fifty genotypes were grouped into 9, 7, 10, 9, 10, 9 and 8 clusters in E_1 , E_2 , pooled E_1 , E_2 , E_3 , E_4 , pooled $E_3 + E_4$ and pooled $E_1 + E_2 + E_3 + E_4$ respectively. Distribution of genotypes into different clusters were comparatively good in pooled analysis of four environments as indicated by in cluster I 38 per cent, in cluster II 16 per cent, in cluster III 22 per cent in cluster IV 16 per cent genotypes were grouped. Therefore, a combined analysis over years or over seasons for assessing divergence would appear to be useful. In spite of variation in mean and D^2 values some varieties viz., J 11, Jyoti, MH 1, SB XI and TMV 2 and some germplasm lines viz., NC Ac 7790, PI 268782, PI 268829, Pearl and U 1-1-1 consistently occupied cluster I in pooled analysis over dates of each season, over both seasons and separately for each season indicating seasonal adaptability. However, none of the genotypes in other clusters were consistent except JL 220 which was present in cluster II of pooled analysis over $E_1 + E_2$ and $E_3 + E_4$, indicating differential response of genotypes for their grouping in separate and pooled analysis. It was observed that the magnitude of intra and inter cluster distance were least in pooled analysis. It was also observed that environment played a significant role in the expression of genetic diversity between genotypes. Hundred pod weight, shelling per cent and sound mature kernel per cent contributed maximum towards genetic divergence. The canonical analysis showed good agreement with the D^2 analysis.

G x E interactions were significant only for seven characters, out of 13 characters under study, suggesting that the analysis should proceed further for estimating stability parameters in these seven characters viz., days to 50 per cent flowering, height of main axis, primary branches per plant, secondary branches per plant, mature pods per plant, shelling per cent and days to maturity. The linear components of g x e were significant for these seven characters only suggesting the genotypes differed from each

other in respect to their linear response for these characters only and there were no linear response for remaining six characters viz., 100 pod weight, 100 kernel weight, sound mature kernel per cent, oil content, pod yield and kernel yield. The pooled deviations were non significant for all the characters, indicating the large part of $g \times e$ interactions were accounted by linear component and thus, predictable. Magnitudes of linear component of $g \times e$ interactions were higher than non-linear components indicating the possibility of prediction across the environments and prediction will be more reliable.

General adaptability of genotype for component characters of yield is equally important when it has to be used as parent. Stability analysis made it possible to identify the genotypes having average stability, below average stability or above average stability. For days to 50 per cent (earliness) flowering none of the released varieties were found stable. However, germplasm lines viz., Ah 1, NC Ac 7785, NC Ac 7790, Span cross and U 2-4-5 were having average stability. For height of main axis, released varieties viz., GG 2, Girnar 1, J 11, TKG 19A, TG 17 (Dwarfness) and ALR 3 (Tallness) and germplasm lines viz., NC Ac 7782, NC Ac 7790, PI 268642 and Pearl (Dwarfness) were having average stability. For primary branches and secondary branches per plant, the release varieties, Pol. 2 and Girnar 1 were found generally adaptable respectively. For mature pods per plant, none of the released varieties were found stable. However, germplasm lines viz., Teja Amra Local, U 2-4-5 and U 2-12-1 were found generally adaptable. For shelling per cent, released varieties, viz., GG2, Jyoti, MH 1, SB XI and TMV 2 and germplasm lines Ah 4515, Ah 6649, NC Ac 7782, PI 268782, PI 268829, PI 268642, Starr and U 2-12-1 were found to be generally adaptable. For days to maturity (Earliness), released varieties, viz., J 11, Jyoti, MH 1 and SB XI were having average stability.

On the basis of inter-cluster distance and phenotypic stability with special reference to average stability, 13 cross combination viz., Ah 1 x Span cross, Starr x Ah 1, Starr x Span cross, U 2-4-1, J 11, SB XI, NC Ac 7790, GG 2, Girnar 1, MH 1, PI 268642, Jyoti and U 2-11-1 x Ah 1 have

been suggested for *Kharif* season. Similarly four cross combinations, viz., U 2-12-1, GG 2, U 2-4-5 and Girnar 1 x Ah 1 were suggested for summer season. These four crosses have appeared in both the seasons and therefore are expected to perform well for the seasonal adaptation. Therefore, the transgrates isolated from such crosses would be useful for *Kharif* and summer adaptation. In addition, remaining eight cross combinations from pooled analysis over seasons should also be attempted for wider adaptability i.e., Span cross x Ah 1, TKG 19 A x Span cross, Starr x Ah 1, NC Ac 7782 x U 2-12-1, TKG 19 A x U 2-12-1, NC Ac 7782 x Span cross, TKG 19 A x Ah 1 and TKG 19 A x Starr.

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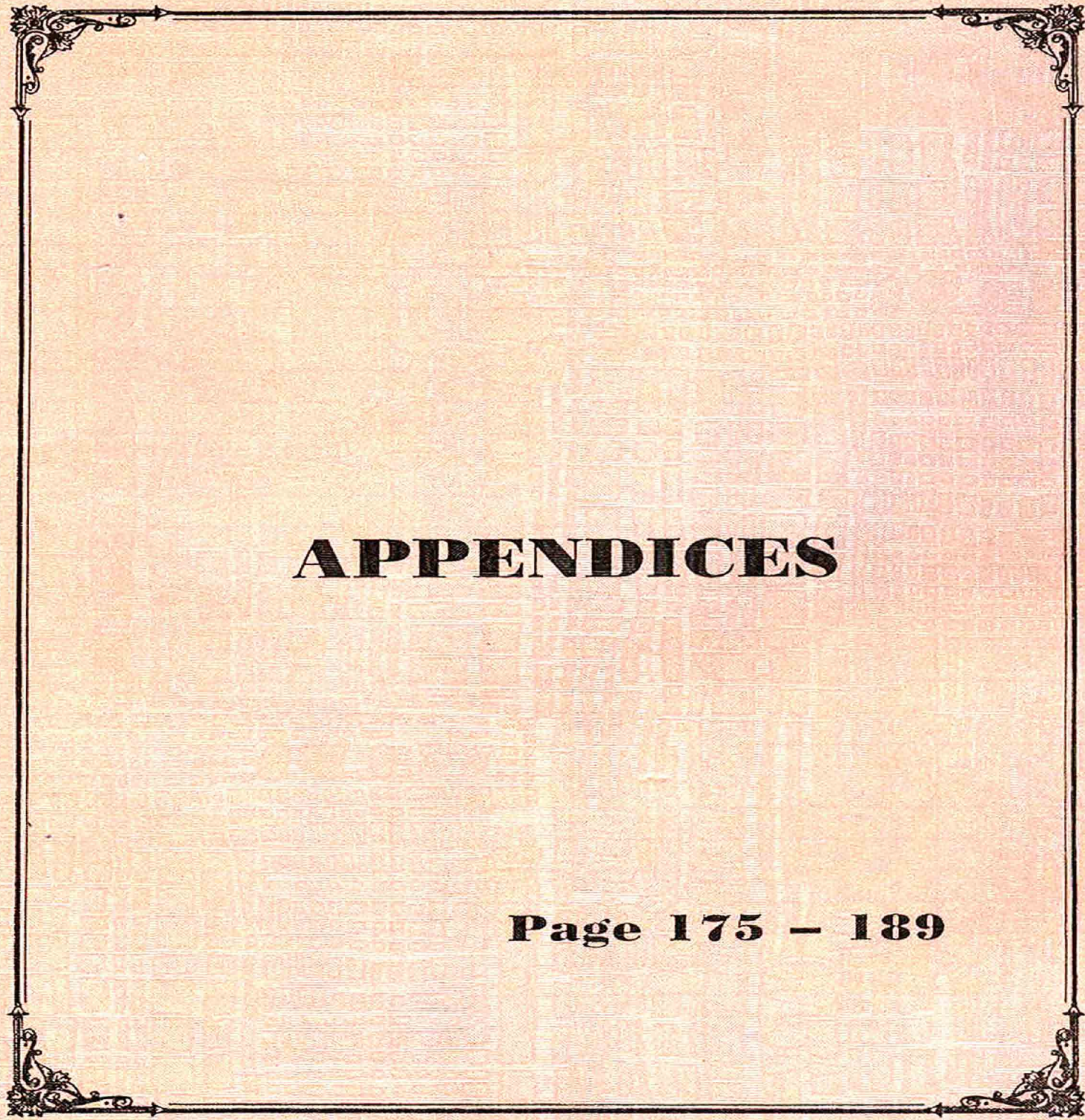
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*Original not seen



APPENDICES

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Appendix-I

Mean performance for 100-pods weight (g)

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
1.	AK 12-24	67.48	65.35	71.68	76.68	70.29
2.	AK 159	67.40	65.33	68.35	76.10	69.29
3.	ALR 3	71.15	69.05	73.58	71.20	71.24
4.	CO 1	73.70	72.28	73.55	80.73	75.06
5.	CO 2	76.50	73.28	75.30	79.38	76.11
6.	GAUG 1	65.95	63.98	65.78	68.75	66.11
7.	GG 2	55.50	52.68	50.93	56.30	53.85
8.	Girnar 1	60.90	58.10	68.20	65.40	63.15
9.	ICG (FDRS) 10	68.35	66.28	63.50	68.88	66.75
10.	J 11	63.78	63.08	60.50	66.73	63.52
11.	JL 24 (Phule Pragati)	86.13	76.65	70.50	78.78	78.01
12.	JL 220 (Vyas)	70.35	66.25	75.53	71.35	70.87
13.	Jyoti	73.90	69.90	63.13	68.10	68.76
14.	KRG 1	56.85	54.63	52.58	57.00	55.26
15.	MH 1	69.05	66.95	65.15	66.83	66.99
16.	POL 2	70.35	69.45	67.35	69.60	69.19
17.	S 206	62.98	60.98	60.08	63.58	61.90
18.	SB 11	68.40	63.95	63.60	69.75	66.43
19.	Spanish Improved	78.15	76.70	75.15	78.70	77.18
20.	TAG 24	72.15	70.05	69.28	71.38	70.71
21.	TKG 19A	80.23	76.55	85.55	83.65	81.49
22.	TG 17	79.40	80.68	81.10	80.50	80.42
23.	TG 26	55.18	53.98	57.23	57.08	55.86
24.	TMV 2	67.68	65.00	64.68	67.60	66.24
25.	Ah 1	95.35	94.23	92.83	96.78	94.79
26.	Ah 4104-2	82.68	79.70	80.05	82.13	81.14
27.	Ah 4515	64.15	62.35	62.23	65.50	63.56
28.	Ah 6649	76.35	75.05	71.90	74.43	74.43
29.	Comet	63.68	62.65	62.55	65.43	63.58
30.	NC Ac 7776	62.98	60.78	60.73	62.75	61.81

Continued -

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
31.	NC Ac 7777	60.65	58.40	62.30	63.58	61.23
32.	NC Ac 7778	63.68	61.35	63.48	66.43	63.73
33.	NC Ac 7780	77.83	75.10	85.23	83.60	80.44
34.	NC Ac 7782	80.15	78.18	80.38	79.08	79.44
35.	NC Ac 7783	52.45	50.55	50.75	52.05	51.45
36.	NC Ac 7785	58.05	54.58	60.55	58.18	57.84
37.	NC Ac 7787	62.25	61.00	62.38	63.00	62.16
38.	NC Ac 7790	65.80	64.48	66.93	66.70	65.98
39.	PI 268782	62.53	61.85	67.38	65.80	64.39
40.	PI 268829	62.20	59.48	65.13	63.68	62.62
41.	PI 268642	68.30	66.93	72.38	71.33	69.73
42.	Pearl	56.25	56.08	62.63	61.30	59.06
43.	Starr	60.85	59.00	68.35	65.70	63.48
44.	Span cross	54.80	52.65	56.43	54.90	54.69
45.	Span white	78.60	77.10	82.45	80.38	79.63
46.	Taiwan Selection	79.90	77.70	74.85	80.35	78.20
47.	Teja Amra Local	53.43	51.45	60.50	55.90	55.32
48.	U 1-1-1	60.78	58.88	60.53	59.50	59.92
49.	U 2-4-5	57.20	54.95	57.58	56.78	56.63
50.	U 2-12-1	55.83	53.23	55.35	53.35	54.44
	Mean	67.56	65.37	67.36	68.85	67.29
	SE (m) $\pm$	0.71	0.87	0.71	0.73	0.63
	CD at 5%	1.98	2.44	1.98	2.03	1.74
	CD at 1%	2.61	3.22	2.62	2.68	2.29

Appendix-II

Mean performance for 100-kernel weight (g)

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
1.	AK 12-24	28.75	26.93	27.45	29.90	28.26
2.	AK 159	30.35	29.30	25.35	28.33	28.33
3.	ALR 3	26.53	25.63	28.55	27.73	27.11
4.	CO 1	23.03	21.50	21.40	24.55	22.62
5.	CO 2	34.58	33.68	30.23	35.65	33.53
6.	GAUG 1	28.50	27.38	27.28	29.55	28.18
7.	GG 2	27.15	25.13	23.30	27.10	25.67
8.	Girnar 1	19.93	17.90	22.35	20.53	20.18
9.	ICG (FDRS) 10	28.35	26.40	26.60	27.63	27.24
10.	J 11	30.33	28.58	28.60	31.55	29.76
11.	JL 24 (Phule Pragati)	33.83	31.23	33.48	35.23	33.44
12.	JL 220 (Vyas)	35.20	33.35	34.40	36.18	34.78
13.	Jyoti	32.00	30.33	31.55	32.05	31.48
14.	KRG 1	29.25	27.90	26.25	29.60	28.25
15.	MH 1	30.43	29.40	28.53	30.15	29.63
16.	POL 2	24.65	21.83	21.70	21.28	22.36
17.	S 206	28.35	27.08	25.05	27.45	26.98
18.	SB 11	27.70	25.68	26.45	28.35	27.04
19.	Spanish Improved	35.35	33.03	32.18	34.73	33.82
20.	TAG 24	30.43	28.38	29.48	29.33	29.40
21.	TKG 19A	36.85	33.00	45.50	40.68	39.01
22.	TG 17	32.93	31.43	35.88	33.58	33.45
23.	TG 26	26.48	25.75	29.05	26.48	26.94
24.	TMV 2	27.63	26.48	27.55	26.63	27.07
25.	Ah 1	36.48	35.63	36.75	36.90	36.44
26.	Ah 4104-2	31.03	29.30	29.33	30.68	30.08
27.	Ah 4515	30.20	28.58	30.35	29.33	29.61
28.	Ah 6649	28.23	27.35	27.35	27.83	27.69
29.	Comet	30.08	28.35	28.48	30.50	29.35
30.	NC Ac 7776	23.98	22.38	23.00	23.63	23.24

Continued -

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
31.	NC Ac 7777	23.35	21.05	21.30	23.05	22.19
32.	NC Ac 7778	28.43	25.53	26.58	27.38	26.98
33.	NC Ac 7780	24.75	22.55	24.78	24.30	24.09
34.	NC Ac 7782	33.38	30.78	35.30	33.50	33.25
35.	NC Ac 7783	23.00	21.58	22.20	23.15	22.48
36.	NC Ac 7785	25.20	23.20	23.48	23.55	23.86
37.	NC Ac 7787	22.43	20.80	24.50	22.03	22.44
38.	NC Ac 7790	26.70	25.95	25.55	26.68	26.22
39.	PI 268782	26.20	25.38	31.60	30.38	28.39
40.	PI 268829	28.35	27.48	29.23	28.43	28.37
41.	PI 268642	28.63	28.18	30.43	30.30	29.38
42.	Pearl	24.63	23.38	25.23	24.28	24.38
43.	Starr	28.03	26.98	29.45	28.20	28.16
44.	Span cross	25.18	24.43	26.53	25.60	25.43
45.	Span white	26.95	25.80	29.38	28.33	27.61
46.	Taiwan Selection	33.65	31.40	32.33	34.60	32.99
47.	Teja Amra Local	22.63	21.53	24.33	22.10	22.64
48.	U 1-1-1	27.05	25.30	27.15	26.45	26.49
49.	U 2-4-5	26.00	23.85	26.28	25.33	25.36
50.	U 2-12-1	22.75	21.48	23.65	22.23	22.53
	Mean	28.32	26.71	28.05	28.46	27.88
	SE (m) $\pm$	0.48	0.59	0.52	0.52	0.37
	CD at 5%	1.34	1.65	1.45	1.45	1.04
	CD at 1%	1.77	2.18	1.913	1.913	1.37

Appendix-III

Mean performance for sound mature kernel per cent

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
1.	AK 12-24	92.35	90.63	89.53	90.95	90.86
2.	AK 159	91.28	88.63	86.35	87.80	88.51
3.	ALR 3	91.15	90.35	90.48	91.60	90.89
4.	CO 1	90.23	87.83	85.40	87.60	87.76
5.	CO 2	76.95	74.65	78.23	78.68	77.13
6.	GAUG 1	93.60	92.33	90.43	92.40	92.19
7.	GG 2	92.23	91.70	91.55	93.10	92.14
8.	Girnar 1	86.18	82.53	87.48	88.80	86.24
9.	ICG (FDRS) 10	80.63	77.48	79.20	80.60	79.48
10.	J 11	87.08	82.35	90.18	91.60	87.80
11.	JL 24 (Phule Pragati)	92.95	90.88	87.43	87.98	89.81
12.	JL 220 (Vyas)	85.75	83.05	82.45	85.40	84.16
13.	Jyoti	90.55	87.95	86.03	88.58	88.28
14.	KRG 1	84.50	81.10	84.73	85.70	84.01
15.	MH 1	94.78	93.03	90.50	91.78	92.52
16.	POL 2	86.63	85.65	87.03	87.60	86.73
17.	S 206	93.38	92.00	89.65	90.78	91.45
18.	SB 11	94.45	92.85	92.25	93.70	93.31
19.	Spanish Improved	93.68	92.80	91.40	92.65	92.63
20.	TAG 24	80.90	75.50	83.93	83.98	81.08
21.	TKG 19A	90.48	88.38	85.60	87.28	87.93
22.	TG 17	94.55	93.50	92.30	93.60	93.49
23.	TG 26	90.38	88.15	89.50	89.13	89.29
24.	TMV 2	96.58	95.95	91.85	93.75	94.53
25.	Ah 1	92.53	91.30	88.50	89.65	90.49
26.	Ah 4104-2	94.35	92.95	93.13	94.38	93.70
27.	Ah 4515	86.20	81.60	83.75	84.80	84.09
28.	Ah 6649	94.63	93.55	92.40	93.58	93.54
29.	Comet	83.73	81.93	72.55	85.78	80.99
30.	NC Ac 7776	92.80	93.68	92.33	93.75	93.14

Continued-

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
31.	NC Ac 7777	73.88	71.20	76.08	76.35	74.38
32.	NC Ac 7778	94.40	92.53	91.30	93.33	92.89
33.	NC Ac 7780	90.55	88.63	85.33	87.93	88.11
34.	NC Ac 7782	92.28	91.33	90.30	91.68	91.39
35.	NC Ac 7783	89.63	87.73	90.33	91.53	89.80
36.	NC Ac 7785	86.80	82.25	84.55	85.35	84.74
37.	NC Ac 7787	73.20	70.43	74.48	75.85	73.49
38.	NC Ac 7790	91.83	91.75	92.03	93.73	92.33
39.	PI 268782	84.73	83.80	84.53	85.30	84.59
40.	PI 268829	86.03	83.78	83.33	84.15	84.32
41.	PI 268642	88.38	87.33	87.18	88.95	87.96
42.	Pearl	92.23	91.15	89.23	90.95	90.89
43.	Starr	82.68	79.43	80.50	83.45	81.51
44.	Span cross	89.15	87.03	88.95	91.20	89.08
45.	Span white	73.25	71.33	73.63	74.58	73.19
46.	Taiwan Selection	86.25	84.90	87.55	88.70	86.85
47.	Teja Amra Local	88.18	87.50	87.43	88.80	87.98
48.	U 1-1-1	93.38	92.70	92.55	93.15	92.94
49.	U 2-4-5	82.90	81.88	83.50	84.65	83.23
50.	U 2-12-1	75.90	74.00	74.68	75.48	75.01
	Mean	88.22	86.30	86.47	88.04	87.26
	SE (m) $\pm$	0.67	0.73	0.71	0.63	0.47
	CD at 5%	1.88	2.03	1.97	1.76	1.31
	CD at 1%	1.52	1.68	1.63	1.73	2.17

Appendix-IV

Mean performance for oil content (%)

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
1.	AK 12-24	48.18	46.00	48.05	49.35	47.89
2.	AK 159	51.60	50.55	49.35	50.85	50.59
3.	ALR 3	44.33	43.50	44.20	45.20	44.31
4.	CO 1	46.58	45.35	46.48	47.38	46.44
5.	CO 2	46.55	45.33	44.35	45.33	45.39
6.	GAUG 1	43.75	42.15	43.48	44.18	43.39
7.	GG 2	42.80	41.30	42.43	43.58	42.53
8.	Girnar 1	46.50	44.88	45.05	47.03	45.86
9.	ICG (FDRS) 10	45.25	44.30	45.13	46.40	45.27
10.	J 11	46.03	45.23	44.90	47.13	45.82
11.	JL 24 (Phule Pragati)	45.58	43.93	43.28	44.28	44.26
12.	JL 220 (Vyas)	43.55	41.88	43.60	44.45	43.37
13.	Jyoti	45.13	44.50	43.65	45.80	44.77
14.	KRG 1	44.70	42.95	43.08	44.58	43.83
15.	MH 1	46.73	46.43	46.65	48.08	46.97
16.	POL.2	45.65	44.33	44.05	45.40	44.86
17.	S 206	43.43	41.50	41.18	41.93	42.01
18.	SB 11	45.70	43.10	44.18	45.20	44.54
19.	Spanish Improved	43.30	42.30	43.58	44.70	43.47
20.	TAG 24	47.80	45.90	45.00	48.28	46.74
21.	TKG 19A	42.08	40.40	40.50	41.40	41.09
22.	TG 17	43.88	42.30	41.80	42.10	42.52
23.	TG 26	41.38	38.88	40.63	41.18	40.51
24.	TMV 2	45.28	44.43	43.58	45.05	44.58
25.	Ah 1	47.65	47.10	47.05	48.20	47.50
26.	Ah 4104-2	47.60	45.15	45.15	47.25	46.29
27.	Ah 4515	46.38	44.70	44.70	47.23	45.75
28.	Ah 6649	46.40	45.05	43.48	45.10	45.01
29.	Comet	41.43	40.70	40.63	41.28	41.01
30.	NC Ac 7776	46.28	44.65	43.73	45.00	44.91

Continued-

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
31.	NC Ac 7777	43.03	40.58	40.28	41.08	41.24
32.	NC Ac 7778	48.38	46.98	47.28	47.85	47.62
33.	NC Ac 7780	42.80	41.13	40.43	41.20	41.39
34.	NC Ac 7782	42.68	41.48	41.25	42.55	41.99
35.	NC Ac 7783	42.45	41.55	41.33	41.85	41.79
36.	NC Ac 7785	43.43	41.93	40.30	40.65	41.58
37.	NC Ac 7787	41.60	39.60	39.65	40.58	40.36
38.	NC Ac 7790	45.45	44.60	44.50	45.90	45.11
39.	PI 268782	46.45	45.30	45.78	47.45	46.24
40.	PI 268829	44.33	44.85	43.93	45.18	44.57
41.	PI 268642	45.35	44.38	43.33	44.20	44.31
42.	Pearl	44.53	42.50	42.40	43.33	43.19
43.	Starr	32.70	30.50	39.48	40.45	35.78
44.	Span cross	48.18	47.55	47.13	48.05	47.73
45.	Span white	44.38	43.18	43.58	44.63	43.94
46.	Taiwan Selection	41.78	40.18	40.65	42.45	41.26
47.	Teja Amra Local	42.48	41.13	40.38	42.28	41.56
48.	U 1-1-1	43.95	43.23	43.43	44.53	43.78
49.	U 2-4-5	43.63	42.03	42.33	43.58	42.89
50.	U 2-12-1	41.95	40.73	41.25	42.10	41.51
	Mean	44.62	43.24	43.43	44.65	43.99
	SE (m) $\pm$	0.42	0.47	0.55	0.53	0.30
	CD at 5%	1.18	1.30	1.55	1.47	0.83
	CD at 1%	1.55	1.72	2.05	1.94	1.09

Appendix-V

Mean performance for pod yield per plant (g)

Sr. No:	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
1.	AK 12-24	3.98	2.78	7.18	10.88	6.20
2.	AK 159	12.28	10.13	6.28	7.30	8.99
3.	ALR 3	9.40	8.48	6.35	5.53	7.44
4.	CO 1	3.93	3.50	6.50	7.98	5.48
5.	CO 2	6.03	5.48	7.25	8.55	6.83
6.	GAUG 1	7.73	7.18	6.15	7.38	7.11
7.	GG 2	3.55	2.88	5.73	7.33	4.87
8.	Girnar 1	8.13	6.63	8.63	8.10	7.87
9.	ICG (FDRS) 10	5.65	4.23	6.98	8.03	6.22
10.	J 11	8.70	7.73	5.40	6.65	7.12
11.	JL 24 (Phule Pragati)	6.93	5.00	3.55	3.05	4.63
12.	JL 220 (Vyas)	4.30	3.00	4.83	5.65	4.44
13.	Jyoti	7.28	6.25	5.78	5.90	6.30
14.	KRG 1	6.95	5.33	6.33	7.85	6.61
15.	MH 1	8.40	6.90	6.93	7.53	7.44
16.	POL.2	5.95	4.85	6.23	6.10	5.78
17.	S 206	7.53	6.63	7.40	8.28	7.46
18.	SB 11	8.15	6.78	8.18	9.05	8.04
19.	Spanish Improved	6.95	5.43	7.23	7.88	6.87
20.	TAG 24	9.95	7.70	11.90	12.98	10.63
21.	TKG 19A	7.20	6.10	7.40	5.38	6.52
22.	TG 17	8.83	7.80	8.43	6.35	7.85
23.	TG 26	6.38	4.93	8.50	7.10	6.73
24.	TMV 2	7.80	6.95	6.40	4.95	6.53
25.	Ah 1	11.15	12.43	8.05	8.15	9.94
26.	Ah 4104-2	6.08	5.70	5.70	5.73	5.80
27.	Ah 4515	11.23	9.98	5.13	6.73	8.26
28.	Ah 6649	11.30	10.20	7.98	7.05	9.13
29.	Comet	6.23	5.53	7.08	6.73	6.39
30.	NC Ac 7776	7.85	7.45	3.95	4.30	5.89

Continued-

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
31.	NC Ac 7777	5.33	3.85	3.78	4.35	4.33
32.	NC Ac 7778	7.08	6.65	3.48	3.98	5.29
33.	NC Ac 7780	7.00	5.68	8.18	4.85	6.43
34.	NC Ac 7782	8.70	8.13	6.63	5.60	7.26
35.	NC Ac 7783	5.23	4.35	4.18	3.48	4.31
36.	NC Ac 7785	6.15	5.25	4.75	4.58	5.18
37.	NC Ac 7787	3.38	3.05	3.85	3.43	3.43
38.	NC Ac 7790	5.65	4.60	4.58	4.40	4.81
39.	PI 268782	9.55	9.83	6.40	4.88	7.66
40.	PI 268829	8.90	8.45	5.73	4.93	7.00
41.	PI 268642	6.18	5.45	4.48	3.65	4.94
42.	Pearl	6.18	6.20	5.38	4.60	5.59
43.	Starr	5.60	5.10	7.58	6.58	6.21
44.	Span cross	10.28	8.93	5.13	5.05	7.34
45.	Span white	5.93	4.58	6.75	5.78	5.76
46.	Taiwan Selection	7.40	6.80	6.40	5.78	6.59
47.	Teja Amra Local	7.45	6.48	6.50	5.78	6.55
48.	U 1-1-1	8.68	8.25	5.65	5.33	6.98
49.	U 2-4-5	8.48	6.93	6.25	5.93	6.89
50.	U 2-12-1	6.93	6.45	6.33	6.55	6.56
	Mean	7.32	6.38	6.31	6.28	6.57
	SE (m) $\pm$	0.41	0.33	0.37	0.40	0.37
	CD at 5%	1.15	0.91	1.02	1.12	1.02
	CD at 1%	1.52	1.20	1.35	1.48	1.34

Appendix-VI

Mean performance for kernel yield per plant (g)

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
1.	AK 12-24	2.65	1.78	5.20	7.73	4.34
2.	AK 159	8.33	6.65	4.33	5.05	6.09
3.	ALR 3	5.38	4.73	4.08	3.33	4.38
4.	CO 1	2.13	1.70	3.88	4.55	3.06
5.	CO 2	3.40	2.93	4.38	5.08	3.94
6.	GAUG 1	4.75	4.03	3.85	4.48	4.28
7.	GG 2	2.48	1.98	4.15	5.18	3.44
8.	Girnar 1	5.03	3.85	5.65	5.18	4.93
9.	ICG (FDRS) 10	3.55	2.60	4.58	5.23	3.99
10.	J 11	6.28	5.45	3.78	4.78	5.07
11.	JL 2(Phule Pragati)	4.93	3.38	2.48	2.05	3.21
12.	JL 220 (Vyas)	2.60	1.70	2.95	3.38	2.66
13.	Jyoti	5.15	4.35	4.13	4.23	4.46
14.	KRG 1	4.78	3.60	4.33	5.28	4.49
15.	MH 1	5.88	4.70	4.85	5.23	5.16
16.	POL.2	3.70	2.88	3.95	3.75	3.57
17.	S 206	5.35	4.68	5.28	5.80	5.28
18.	SB 11	5.98	4.80	6.08	6.58	5.86
19.	Spanish Improved	4.90	3.70	4.98	5.38	4.74
20.	TAG 24	6.83	5.08	8.68	9.08	7.41
21.	TKG 19A	3.85	3.05	4.50	3.05	3.61
22.	TG 17	5.70	5.00	5.60	4.18	5.12
23.	TG 26	4.58	3.48	6.15	5.03	4.81
24.	TMV 2	5.48	4.68	4.48	3.38	4.50
25.	Ah 1	7.15	7.73	5.25	5.30	6.36
26.	Ah 4104-2	4.25	3.98	4.05	4.00	4.07
27.	Ah 4515	7.90	6.80	3.65	4.75	5.78
28.	Ah 6649	7.65	6.75	5.43	4.75	6.14
29.	Comet	4.45	3.90	5.08	4.78	4.55
30.	NC Ac 7776	5.05	4.65	2.55	2.70	3.74

Continued-

Sr. No.	Genotypes	Environmental means				General Mean
		E ₁	E ₂	E ₃	E ₄	
31.	NC Ac 7777	2.95	2.00	2.20	2.45	2.40
32.	NC Ac 7778	4.98	4.58	2.40	2.65	3.65
33.	NC Ac 7780	4.65	3.68	5.38	3.13	4.21
34.	NC Ac 7782	6.28	5.73	4.78	3.98	5.19
35.	NC Ac 7783	3.33	2.73	2.70	2.20	2.74
36.	NC Ac 7785	4.08	3.38	3.33	3.10	3.47
37.	NC Ac 7787	1.90	1.68	2.33	2.00	1.98
38.	NC Ac 7790	3.83	3.13	3.18	2.95	3.27
39.	PI 268782	6.35	6.53	4.33	3.28	5.12
40.	PI 268829	6.30	5.80	4.10	3.45	4.91
41.	PI 268642	4.38	3.78	3.20	2.58	3.48
42.	Pearl	3.98	3.80	3.45	2.90	3.53
43.	Starr	4.00	3.58	5.50	4.65	4.43
44.	Span cross	8.13	7.00	4.05	3.93	5.78
45.	Span white	3.65	2.70	4.28	3.50	3.53
46.	Taiwan Selection	4.60	4.15	4.30	3.80	4.21
47.	Teja Amra Local	5.28	4.48	4.58	4.03	4.59
48.	U 1-1-1	5.50	5.03	3.70	3.38	4.40
49.	U 2-4-5	5.53	4.40	3.60	3.38	4.23
50.	U 2-12-1	4.90	4.40	4.45	4.55	4.58
	Mean	4.89	4.14	4.28	4.18	4.37
	SE (m) $\pm$	0.29	0.22	0.25	0.27	0.26
	CD at 5%	0.80	0.62	0.70	0.76	0.71
	CD at 1%	1.06	0.81	0.92	1.00	0.93

Appendix-VII

Variance, co-variance matrix for different characters under pooled over sowing dates and seasons ($E_1+E_2+E_3+E_4$)

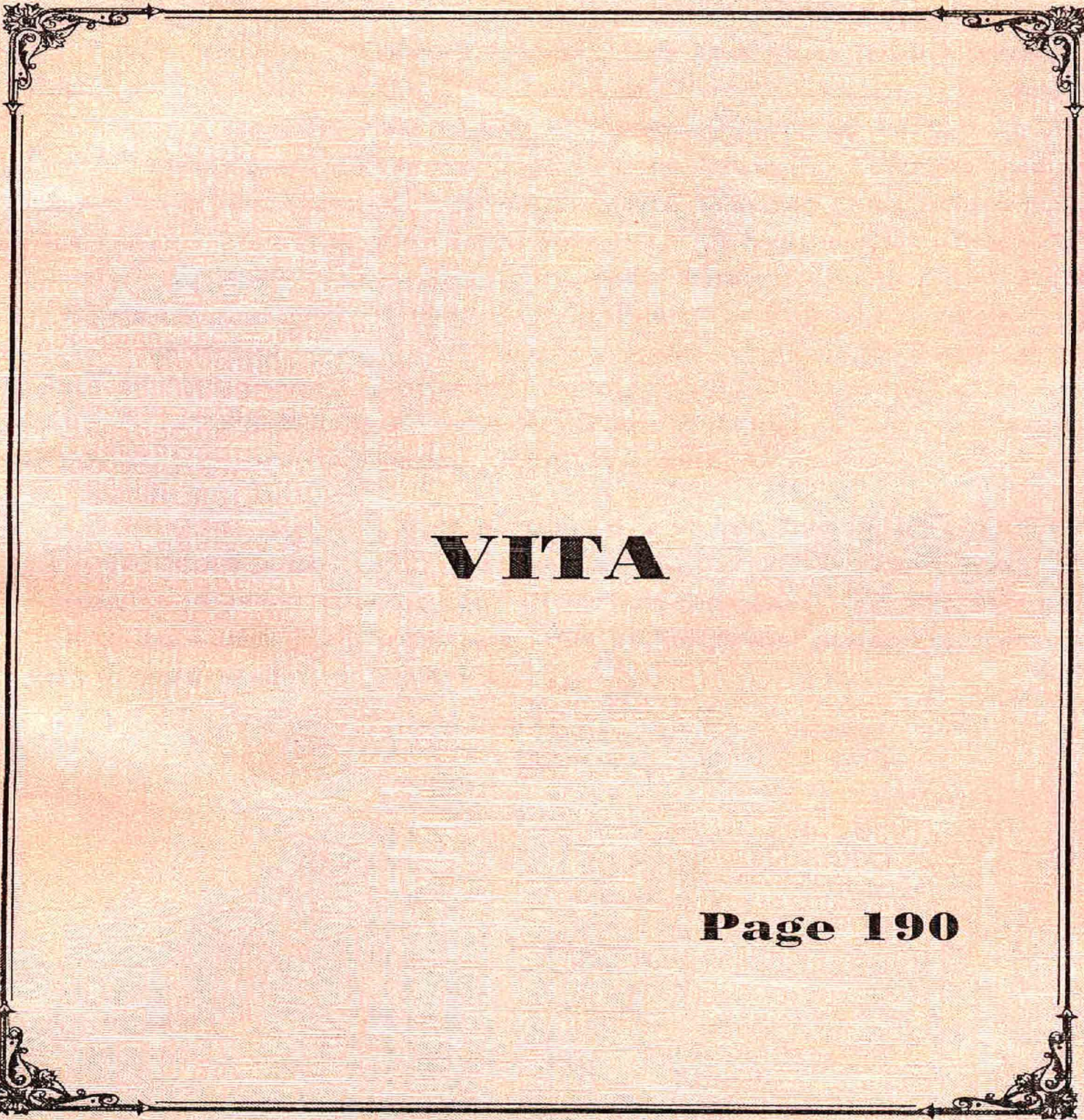
Sr. No.	Characters	Genotypical matrix												
		2	3	4	5	6	7	8	9	10	11	12	13	
1.	Days to 50%flowering													
2.	Height of main axis(cm)	15.71												
3.	Primary branches per plant	0.54	0.21											
4.	Secondary branches/plant	1.33	0.27	1.75										
5.	Mature pods/plant	1.36	0.15	0.58	5.48									
6.	100 pod weight (g)	4.65	-1.04	-1.42	-4.79	83.77								
7.	100 kernel weight (g)	2.63	-0.20	0.47	-0.44	24.68	16.59							
8.	Shelling %	2.66	-0.16	1.94	4.67	-11.38	1.37	26.69						
9.	Sound mature kernel %	6.28	-0.18	-0.54	2.07	7.20	3.94	9.63	32.34					
10.	Oil content %	1.07	0.05	0.08	2.14	4.91	0.90	1.47	4.08	6.44				
11.	Days to maturity	1.28	0.40	-0.55	-1.23	7.42	3.49	-7.00	1.63	-0.16	8.82			
12.	Pod yield/plant	0.90	0.01	0.25	2.71	3.54	1.66	1.91	1.59	1.41	-0.20	1.91		
13.	Kernel yield/plant	0.65	0.00	0.28	2.08	1.49	1.11	2.92	1.49	1.03	-0.62	1.37	1.08	

Continued-

Characters		Phenotypic matrix												
Sr. No		1	2	3	4	5	6	7	8	9	10	11	12	13
1.	Days to 50% flowering	2.70												
2.	Height of main axis (cm)	0.90	16.31											
3.	Primary branches per plant	0.05	0.54	0.22										
4.	Secondary branches per plant	0.29	1.31	0.27	1.83									
5.	Mature pods/plant	0.17	1.52	0.16	0.57	5.81								
6.	100 pod weight (g)	2.90	4.68	-1.04	-1.44	-4.77	84.17							
7.	100 kernel weight (g)	2.85	2.61	-0.20	0.47	-0.44	24.76	16.73						
8.	Shelling %	1.80	2.67	-0.16	1.92	4.70	-11.33	1.40	26.88					
9.	Sound mature kernel %	2.98	6.30	-0.18	-0.55	2.10	7.21	3.94	9.63	32.57				
10.	Oil content %	0.11	1.09	0.05	0.09	2.17	4.93	0.90	1.47	4.08	6.53			
11.	Days to maturity	0.60	1.25	0.40	-0.54	-1.35	7.38	3.51	-7.04	1.56	-0.19	9.34		
12.	Pod yield/plant	0.18	1.00	0.01	0.25	2.90	3.58	1.67	1.95	1.60	1.43	-0.29	2.04	
13.	Kernel yield/plant	0.21	0.71	0.00	0.27	2.21	1.52	1.11	2.95	1.50	1.04	-0.69	1.46	1.15

Continued-

Sr. No	Characters	Environmental matrix												
		1	2	3	4	5	6	7	8	9	10	11	12	13
1.	Days to 50% flowering	0.12												
2.	Height of main axis(cm)	0.02	0.61											
3.	Primary branches/ plant	0.00	0.01	0.01										
4.	Secondary branches/ plant	0.00	-0.02	0.00	0.08									
5.	Mature pods/plant	0.01	0.16	0.00	-0.01	0.32								
6.	100-pod weight (g)	0.00	0.03	0.00	-0.03	0.02	0.39							
7.	100-kernel weight (g)	0.01	-0.02	0.00	-0.01	0.00	0.08	0.14						
8.	Shelling %	-0.01	0.01	0.00	-0.02	0.03	0.06	0.03	0.19					
9.	Sound mature kernel %	-0.02	0.02	0.00	-0.01	0.03	0.00	0.00	0.00	0.22				
10.	Oil content %	0.00	0.02	0.00	0.01	0.03	0.03	0.00	0.00	0.00	0.09			
11.	Days to maturity	0.01	-0.02	0.00	0.01	-0.13	-0.04	0.02	-0.04	-0.07	-0.03	0.52		
12.	Pod yield/plant	0.01	0.10	0.00	-0.01	0.19	0.04	0.01	0.03	0.01	0.02	-0.09	0.14	
13.	Kernel yield/plant	0.01	0.07	0.00	-0.01	0.13	0.03	0.01	0.03	0.01	0.01	-0.06	0.09	0.07



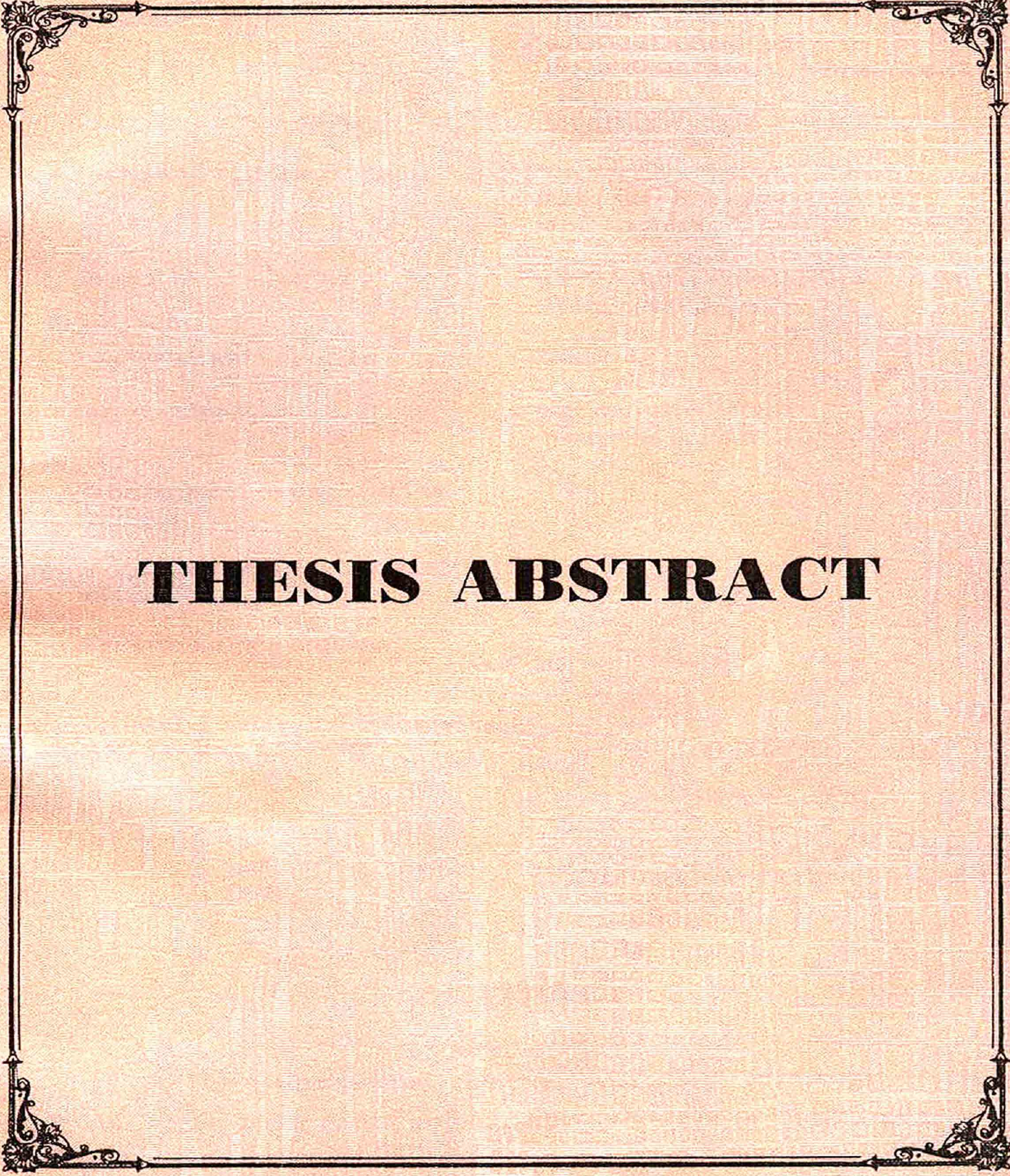
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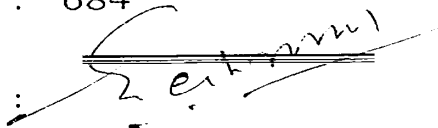
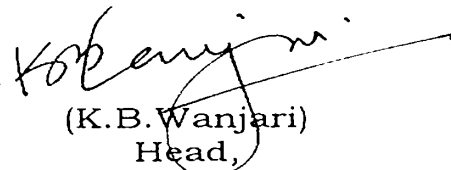
Subhash Deshmukh, son of Late Shri Narayanrao Madhoraaji Deshmukh, Takarkheda (Sambhu), Amravati District, was born on December 17th 1953 at Amravati. He passed HSSC Examination in 1970 from Shri Shivaji Multipurpose Higher Secondary School, Amravati. Later, he secured admission in Shri Shivaji College of Agriculture, Amravati and obtained B.Sc. (Agri.) degree from PKV, Akola in the year 1973. Subsequently, during 1975, he obtained M.Sc. (Agri.) degree in Agril. Botany (Genetics and Plant Breeding) in first division from Post Graduate Institute, PKV, Akola. He started his service career as SRA (Higher Grade) in PKV in 1978 and during 1982, selected as Asstt. Professor of Botany. In 2002, he sought admission for Ph.D. in Agril. Botany (Genetics and Plant Breeding) as in-service trainee in PGI, Dr.Panjabrao Deshmukh Krishi Vidyapeeth, Akola.

He involved in the released and notification of groundnut varieties, TAG 24 and TG 26. He developed AK 159 which was released and notified at national level for zone III for *kharif* season. He was awarded Dr.K.G.Joshi cash prize for the year 1994-95 jointly for outstanding research work in the field of Agriculture.



THESIS ABSTRACT

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- a) Title of the thesis : Genetic diversity in relation to seasonal adaptability in groundnut (*Arachis hypogaea* L.)
- b) Full name of the student : Subhash Narayanrao Deshmukh
- c) Name and address of major advisor : Dr.Vandan Mohod,
Associate Professor of Botany,
and Registrar, Dr.PDKV, Akola
- d) Degree to be awarded : Ph.D. (Agril. Botany) Genetics and Plant Breeding
- e) Year of award of degree : 2004
- f) Major subject : Agricultural Botany
(Genetics & Plant Breeding)
- g) Total number of pages in the thesis : 190
- h) Number of words in the thesis abstract : 684
- i) Signature of the student : 
- j) Signature, Name and address of forwarding authority : 
(K.B. Wanjari)
Head,

Univ. Dept. of Agril. Botany,
Dr.Panjabrao Deshmukh Krishi
Vidyapeeth, Akola

ABSTRACT

The experimental material comprised of 50 genotypes of Spanish bunch habit group of groundnut (24 varieties and 26 germplasm lines) was grown over 2 successive seasons i.e. *Kharif* 2002 and summer 2003 and 2 dates of sowings i.e. recommended date and 10-20 days early in each season with an objectives to estimate genetic divergence for grouping, to estimate $g \times e$ interaction and stability parameters of some of the

components of yield for adaptability and to identify the superior genotypes on the basis of genetic diversity and phenotypic stability for their use in future groundnut breeding programme. The data were recorded for 13 agronomic characters.

Differences between genotypes and environments were highly significant for all characters. Analysis of dispersion showed highly significant differences for aggregate effect of all characters under separate as well as pooled environments. D^2 analysis was carried out separately for each date, pooled over dates of each season and pooled over seasons. Fifty genotypes were grouped into 7-10 clusters in individual as well as pooled over environments D^2 analysis. Hundred pod weight, shelling percentage and sound mature kernel per cent contributed maximum toward genetic divergence. The canonical analysis showed good agreement with the D^2 analysis. Grouping on the basis of pooled over environments appeared to be more useful. Five varieties, viz., J 11, Jyoti, MH 1, SB XI and TMV 2 and five germplasm lines viz., NC Ac 7790, PI 268782, PI 268829, Pearl and U 1-1-1 ~~consistently occupied the same cluster in separate and pooled over~~ environments, i.e. E_1 , E_2 , E_3 , E_4 , E_1+E_2 , E_3+E_4 and $E_1+E_2+E_3+E_4$ indicating seasonal adaptability.

Genotype x environment interactions were significant for seven component characters of yield viz., days to 50 per cent flowering, height of main axis, primary and secondary branches per plant, mature pods per plant, shelling per cent and days to maturity. The linear components of $g \times e$ were significant for these seven characters only suggesting genotypes differed from each other in respect of their linear response for these characters. The pooled deviation (non-linear) were non significant for all characters indicating the large part of $g \times e$ interactions were accounted by linear components and thus, predictable.

Stability analysis made it possible to identify the genotypes having average stability, above average stability and below average stability. However, general adaptability or average stability is more important. In present investigation five germplasm lines viz., Ah 1, NC Ac 7785, NC Ac



7790, Span cross and U 2-4-5 (earliness) were having average stability for days to 50 per cent flowering. Six released varieties viz., GG 2, Girnar 1, J 11, TKG 19A, TG 17 (dwarfness) and ALR 3 (tallness) and four germplasm lines viz., NC Ac 7782, NC Ac 7790, PI 268642 and pearl (dwarfness) showed average stability for height of main axis. Released varieties viz., Pol. 2 and Girnar 1 were found to be generally adaptable for primary and secondary branches per plant respectively. Three germplasm lines viz., Teja Amra Local, U 2-4-5 and U 2-12-1 showed average stability for mature pods per plant. Five varieties, viz., GG 2, Jyoti, MH 1, SB XI and TMV 2 and eight germplasm lines viz., Ah 4515, Ah 6649, NC Ac 7782, PI 268782, PI 268829, PI 268642, Starr and U 2-12-1 were found to be generally adaptable for shelling per cent. Four varieties viz., J 11, Jyoti, MH 1 and SB XI (earliness) were having average stability for days to maturity.

On the basis of inter cluster distance and phenotypic stability, 13 cross combinations for *Kharif* and four for summer have been suggested. In addition remaining eight cross combinations from pooled analysis over seasons should also be attempted for wider adaptability i.e. Span cross x Ah 1, TKG 19 A x Span cross, Starr x Ah 1, NC Ac 7782 x U 2-12-1, TKG 19 A x U 2-12-1, NC Ac 7782 x Span cross, TKG 19 A x Ah 1 and TKG 19 A x Starr. Four cross combinations viz., U 2-4-5, GG 2, Girnar 1 and U 2-12-1 x Ah 1 have been particularly selected to isolate useful transgrates for *Kharif* and summer adaptations.