

**Genetic Assessment for Quantitative and
Physiological Traits of *desi* Chickpea**

THESIS

Submitted to

**Jawaharlal Nehru Krishi Vishwa Vidhyalaya,
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**In partial fulfillment of the requirements for
The Degree of**

MASTER OF SCIENCE

In

AGRICULTURE

(GENETICS AND PLANT BREEDING)

By

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2021

CERTIFICATE - I

This is to certify that the thesis entitled “**Genetic Assessment for Quantitative and Physiological Traits of *desi* Chickpea**” submitted in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE in Agriculture (Genetics and Plant Breeding)** of Jawaharlal Nehru Krishi Vishwa Vidhyalaya, Jabalpur is a record of the bonafide research work carried out by **Mr. Akash Khandelwal** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instruction.

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Place: Jabalpur

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Date:

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LIST OF ABBREVIATIONS

S.No.	Abbreviations and Symbol	Stand for
1.	No.	Number
2.	MP	Madhya Pradesh
3.	<i>et al.</i>	<i>Et alia</i> (and others)
4.	Min	Minimum
5.	Max	Maximum
6.	<i>viz.</i>	Namely
7.	<i>i.e.</i>	<i>id est</i> (that is)
8.	etc.	<i>Et cetera</i> (and the rest)
9.	e.g.	For example
10.	Fig.	Figure
11.	@	At the rate of
12.	/	Per
13.	%	Percentage
14.	°	Degree
15.	√	Square root
16.	Σ	Summation
17.	DTF	Days to 50% flowering
18.	DTM	Days to maturity
19.	PH	Plant height
20.	HFFN	Stem height at first fruiting node
21.	ST	Stem thickness
22.	PB	Number of primary branches per Plant
23.	SB	Number of secondary branches per plant
24.	TNPPP	Total number of pods per plant
25.	NEPP	Number of effective pods per Plant
26.	NSPP	Number of seeds per pod
27.	100SW	100 seeds weight
28.	BY	Biological yield
29.	HI	Harvest index
30.	SYPP	Seed yield per plant
31.	mt/ha	Million tonnes per hectare

32.	Ha ⁻¹	Per hectare
33.	Cm	Centimeters
34.	m ²	Square meter
35.	Mm	Millimeter
36.	N	North
37.	E	East
38.	S	South
39.	W	West
40.	T	Tonnes
41.	ml	Milliliter
42.	Kg	Kilogram
43.	G	Gram
44.	PC	Principal component
45.	d.f.	Degree of freedom
46.	CV	Coefficient of variation
47.	GCV	Genotypic coefficient of variation
48.	PCV	Phenotypic coefficient of variation
49.	h ²	Heritability
50.	Bs	Broad sense
51.	GA	Genetic advance
52.	CD	Critical difference
53.	SE	Standard error
53.	SE _±	Standard error of mean

CHAPTER 1:

INTRODUCTION

CHAPTER 1: INTRODUCTION

Chickpea is one of the most important grain legume grown in all over India in cool season, mostly under dryland situations. Chickpea (*Cicer arietinum* L.) is an annual plant belongs to family Fabaceae (Leguminosae), sub family Papilionaceae with chromosome number $2n=2x=16$, originated at South East Turkey.

Legumes are considered as the second most important family after grasses which contribute nearly 27% of the global food grain production. Chickpea is considered as the third most important pulse in world, grown in many tropical and warm temperate regions. Genus *Cicer* having 9 annual and 34 perennial type of wild species. Out of 9 annual species, *Cicer arietinum* is the only cultivated one and used for its edible seeds. It is of two types called as *desi* and *kabuli*. *Desi* chana is of light brown in color and *Kabuli* contains white color seed coat. Both seeds are having rich source of protein, carbohydrate, minerals and vitamins.

It is self-pollinated crop having genome size of 738 Mbp, grown in more than 50 countries (89.7% in Asia; 4.3% in Africa; 2.6% in Oceania; 2.9% in America and 0.4% in Europe) (Phytojournal, 2017), It Improves soil fertility by fixing atmospheric nitrogen up to 140 kg/ha.

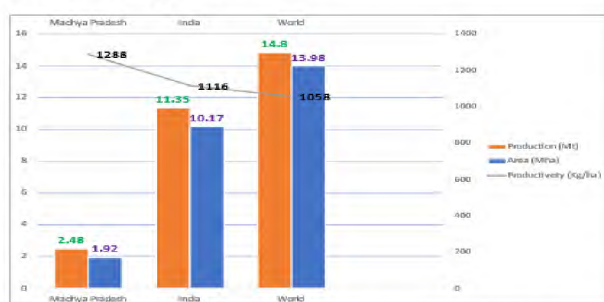


Fig.1.1: Area, Production with Productivity of Chickpea

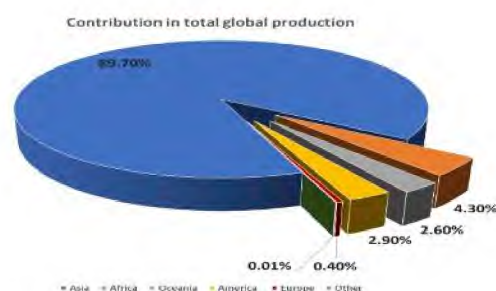


Fig. 1.2: Contributions of Different Continents in Global Chickpea Production

World chickpea production in 2017 was 14.8 Mt, led by India with 67% of the global total (FAO STAT, 2017). In India it covers 9.68 Mha area and 11.08 Mt production with an average productivity of 1142 kg/ha. In Madhya Pradesh it covers 1.92 Mha area with a production of 2.72 Mt and an average productivity of 1417 kg/ha which is the highest among different pulse crops (PC report 2019-20, IIPR, Kanpur)

Mechanical harvesting of Chickpea is desired by the farmers for saving labor cost and time. Chickpea genotypes with the upright - tall growth habit having fruiting

zone starting at about 25-30 cm from the ground are considered suitable for this and needs to be developed through breeding programme. It reduces the possibilities of damage to the crop plants due to rains, winds etc. that may occur during the additional period required in manual harvesting. In biotic stresses soil borne fungal diseases like collar rot, *Fusarium* wilt and dry root rot are the major diseases of chickpea in central India, which play crucial role to decrease yield and nutritional aspects of chickpea grain.

Morphological characterization of genotypes is useful in classification and evaluation of various germplasm, which further create base to identify and select traits of interest to transfer in desirable genotypes. The possibility of improvement in any crop depends on variability exists in the available breeding materials/ genotypes. Estimation of genetic variability parameters helps in improvement of quantitative traits inheritance and selection of best traits for crop improvement also efficient when it is having high heritability coupled with genetic advance. Since, seed yield exhibits low heritability, it creates the challenges for study of direct selection of parents based on the yield component alone, is often misleading. Hence, knowledge about relationship between yield and contributing characters of yield is essential for an efficient selection to evolve an economically superior variety. D² statistics and Principal component analysis also helps in efficient evaluation of genetic diversity related to agro-morphological traits of chickpea genotypes. By determining morpho-physiological nature of chickpea genotypes, can also be an important tool to enhance yield of chickpea genotypes through better understanding of various lines. Keeping in view the immense value of above aspects the present investigation is planned with following objective:

Objectives of Investigation:

- Characterization of genotypes on the basis of morpho-physiological traits
- To assess the extent of genetic variability, pattern of correlation, direct and indirect effect on seed yield
- To judge the extent of genetic divergence through D² statistics and rank superior lines based on Principal Component Analysis
- To identify high yielding lines suitable for mechanical harvesting

CHAPTER 2:
REVIEW OF LITERATURE

CHAPTER 2: REVIEW OF LITERATURE

The available related literatures pertaining to different aspects of present study on “**Genetic Assessment for Quantitative and Physiological Traits of *desi* Chickpea**” has been reviewed here in order to better understanding of subject and are described under the following subheads: -

2.1 Morphological Characterization

2.2 Genetic Variability Parameters

2.1.1 Analysis of Variance

2.1.2 Mean and Range

2.1.3 Genotypic and Phenotypic Coefficient of Variation

2.1.4 Heritability (%)

2.1.5 Genetic Advance as Percentage of Mean (%)

2.3 Correlation analysis

2.4 Path coefficient analysis

2.6 Genetic divergence (D^2) analysis

2.6 Principal component analysis

2.7 Selection of Lines Suitable for Mechanical Harvesting

2.8 Assessment of Physiological traits

2.1 Morphological characterization of traits: -

Characterization of traits is essential for identification of genotypes with traits of interest individually and in various combinations, where chickpea genotypes show a wide range of variation. Characterization of several agro-morphological traits is helpful to reveal their free and potential variability, which can be quite useful in utilizing germplasm in genetic improvement of the chickpea varieties/lines. The concept of distinctness, uniformity and stability (DUS) is cardinal to the characterization of a variety as a unique creation.

Shrivastava et al. (2011) reported large variation in seed coat color, Rajas variety had reddish brown; JG 11, GCP 105, Vaibhav and ICCV 07111 had brown,

whereas DCP 92-3 had yellow seed coat color. JAKI 9218, ICCV 05106 and ICCV 07111 had light brown seed coat color. Vaibhav and Rajas were early, high yielding and disease resistance found suitable for rice fallow situation.

Parmeshwarappa et al. (2012) observed ICC 13124 was the only top yielder in all the three environments *viz.*, *Khariff*, *Rabi* and *Zaid*. The genotype ICC 13124 was found promising for earliness, large seed size and high yield per plant in all the environments suggesting that this accession is best suited for both rainfed and irrigated condition during the *rabi* season.

Kaouthar (2015) reported that two lines 6 and 5 proved to be the best of the collection for most of all studied characters such as, size of pods, size of grains, the duration of the cycle of maturation and in more for number of pods of two grains per plant, number of grains per plant and yield of grain. They have also tall plants, favouring them for a mechanized harvest. These results allow line 6 and line 5 to be selected as lines of the highest capacity of yield, growth and adaptability and can also be used in other genetic programs of improvement.

Archak et al. (2016) observed high variation for eight quantitative and 12 qualitative agro-morphological traits. Allelic richness procedure was employed to assemble a core set comprising 1103 accessions, 70.0% of which were of Indian origin.

Shakaya (2017) recorded huge variation in plant height, days to flowering, growth habit, seed coat color and seed size. Considering these traits make easy identification of the genotypes in seed production programme.

Gediya et al. (2018) found that the genotypes of chickpea can be distinguished and identified by plant and seed morphological characters. These differences in morphological traits were useful in identification of individual chickpea genotypes.

Solanki et al. (2019) found that 26 *desi* indigenous lines showing anthocyanin pigmentation and the remaining 69 exotic lines including *desi* and *kabuli* absence of anthocyanin pigmentation. No variation was found among the genotypes for leaf pattern and all genotypes had pinnate type of leaf pattern. Plant growth habit is a distinguishing feature in plant characterization. Large variation observed in growth habit 44 lines were semi spreading, 36 lines were semi-erect, while 15 lines were spreading type. Erect growth habit was not found in any line under study.

Janghel (2020) observed 13 DUS traits; out of that 7 traits were found tri-morphic, four traits di-morphic and two traits polymorphic among 60 chickpea

genotypes indicated the existence of remarkable amount of genetic variability that have great potential to assign distinctive morphological profiles.

Jayalakshmi *et al.* (2021) found that among eight *desi* lines tested, NBeG 857 was superior with yield advantage of 24.5 % (2412 kg/ha) over check variety JG11 (1937 kg/ha). Among four *kabuli* lines, NBeG 810 was the best performer with 100 seed weight of 36 g and yield advantage of 57.7 % (2098 kg/ha) over popular check variety KAK-2 (1330 kg/ha). In extra-large seeded types, NBeG 833 has 100 seed weight of 45.3 g and was the most promising entry with yield advantage of 8.19 % (2021 kg/ha) over check variety MNK-1 (1868 kg/ha).

2.2 Genetic Parameters Variability: -

Genetic variability may be defined as: measure of the tendency of individual genotypes in any population to vary from one another. The genetic variabilities of characters, in the population reveals that how much that trait tends to be vary in response to environmental and genetic influences. Agro-morphological variability in any trait of a crop plant population is the basic for initiation of any crop improvement programme and for broadening gene pool.

2.2.1 Coefficient of Variation: -

Coefficient of Variation is a kind of simple measure of the variability. It partitions the total variation into genotypic, phenotypic and the environmental components. The study of genetic variance component, helps in further partitioning of genetic variance into the additive, dominance and epistatic components. A magnitude of these components is a measure of the type of genes action involved in the expression of various traits. Information about gene action helps in deciding a breeding procedure for the genetic improvement of any character.

Akhtar *et al.* (2011) reported that high phenotypic coefficient of variation (PCV) for days to flowering, days to maturity, plant height and seed yield than genotypic coefficient of variation, which means that the expression of these traits is more influenced by environmental effects. It is suggested that the grain yield could be improved by using the 100-seed weight and number of pods per plant as selection criterion in chickpea.

Dhuria and Babbar (2016) observed that high GCV and PCV for height of first fruiting node, number of effective pods per plant, number of seeds per plant and seed yield per plant.

Shakya (2017) reported high genotypic and phenotypic coefficient of variation for seed yield per plant, harvest index, biological yield per plant, number of effective pods per plant, 100 seed weight, total number of pods per plant, number of primary branches per plant and number of secondary branches per plant results indicated the presence of considerable amount of genetic variability in the existing material.

Babbar and Tiwari (2018) observed the phenotypic coefficient of variation (PCV) was higher in magnitude than its corresponding genotypic coefficient of variation for all the characters studied under three environments.

Jayamani *et al.* (2019) recorded significant variation for all the traits. High GCV and PCV were found for single plant yield followed by number of secondary branches, number of pods per plant and hundred seed weight.

Mohibullah *et al.* (2020) reported that values for PCV found greater than GCV which depicted primary presence of environment in the performance of chickpea genotypes for the traits under consideration. Overall, the GCV and PCV were low to moderate for majority of the parameters. Highest amount of GCV and PCV were recorded for seed yield per plant (30.48 and 32.00%) and secondary branches per plant (20.47 and 24.29%), respectively.

Kumar *et al.* (2021) noticed maximum phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for 100-seed weight, biological yield per plant, grain yield per plant and number of primary branches per plant. High heritability was recorded by 100 seed weight, biological yield per plant, primary branches per plant, grain yield per plant, effective pods per plant, total number of pods per plant, secondary branches per plant, plant height, days to 50% flowering and days to maturity.

2.2.2 Heritability (%) and Genetic Advance as Percentage of Mean (%): -

Heritability in broad sense is the ratio of genotypic variance to phenotypic variance or total variance. It is calculated from total genetic variance which consists of additive, dominance and epistatic variances. It is good index of the transmission of characters from parents to their off spring (Falconer 1981).

Genetic advance may be defined as the improvement in genetic value of the selected single plants, over the base population and is the measure of genetic gain under selection (Falconer 1981). Heritability estimates combined with genetic advance, are normally more useful in the prediction of gain under selection process, than the heritability estimates alone.

Khan *et al.* (2011) revealed that highest heritability was recorded for days to 50% flowering followed by biological yield per plant, plant height, 100 seed weight, grain yield per plant and days to maturity.

Waldia and Ramesh (2012) observed that high heritability with moderate estimate of genetic advance as percent of mean for most of the traits except pods per plant, 100-grain weight and plant height, where it was low (<15%).

Gul *et al.* (2013) recorded that high heritability for pods per plant, primary branches plant per plant, 100 seed weight, seed yield plant per plant and secondary branches plant per plant. Genetic advance was higher for pods per plant, seed yield plant per plant, primary branches per plant and secondary branches per plant.

Jhakar *et al.* (2017) showed high heritability for 100 seed weight followed by seed yield per plant, number of pods per plant, days to 50 per cent flowering and number of secondary branches. Seed yield per plant was exhibited highest genetic advance as per cent of mean followed by number of pods per plant and 100 seed weight.

Pezeshkpour *et al.* (2018) found high heritability for seed yield (0.84) and 100-seed weight (0.84), whereas high heritability combined with high genetic advance was observed for biological yield. Hence, selection of parental line on the basis of biological yield can be better criteria as compared to other in any breeding programme.

Yasin *et al.* (2018) recoded that out of seven studied traits seed yield, biological yield, 100-seed weight and harvest index showed high genotypic coefficient of variation (GCV) and Heritability (bs) coupled with high genetic advance as percent of mean.

Solanki *et al.* (2019) observed that GCV and PCV found high for seed yield per plant, number of effective pods per plant, biological yield, number of primary and secondary branches. High heritability coupled with high genetic advance as percent

of mean was found for seed yield per plant followed by biological yield, number of effective pods per plant and total number of pods per plant.

Kumar *et al.* (2021) noted high heritability for 100 seed weight (96.4%) followed by seed yield per plant (84.1%) and number of pods per plant (66.2%) and high degree of genetic advance was found for number of pods per plant (26.2%) followed by biological (15.2%) and seed yield per plant (6.9%). High heritability coupled with high genetic advance was found in seed yield per plant followed by biological yield per plant indicating that crop improvement for these traits should be possible through simple selection.

Srivastava *et al.* (2021) revealed that all the yield and component traits exhibited high heritability, hence higher genetic advance due to selection is expected for no. of seeds per plant, no. of pods per plant, 100 seed weight and yield per plant. The yield/ha exhibited significant positive correlation with pod filling (%), no. of pods per plant, no. of seeds per pods in both *desi* and *kabuli* varieties. However, correlation between days to 50% flowering and yield per plant was negative among *desi* varieties and positive among *kabuli* varieties.

2.3 Correlation analysis: -

It is a statistical measure which is used to find out the degree and direction of relationship between two or more than two variables. (Galton, 1988). A positive value of correlation coefficient indicates: changes of any of the two variables are in same direction, whereas in the negative correlation movements of any two variables are in opposite direction. There are three types of correlations *viz.*, phenotypic, genotypic and environmental correlations. Phenotypic correlation is the observable correlation between two variables. It includes both genotypic effects and environmental effects. Genotypic correlation measures the inherent association between the two different variables. Which may be either because of pleiotropic action of genes or linkage, more likely both or developmentally induced relationships. The need of correlation coefficients was suggested by Galton in 1988. He also described the degree of association between different variables.

Jha *et al.* (2012) reported that significant-negative genotypic correlation between primary branches per plant and plant height; primary branches per plant and plant width; primary branches per plant and days to 50% flowering; primary branches per plant and days to maturity; plant height and plant width; plant height and pods per

plant; seeds per pod and 100 seed weight; days to 50% flowering and 100 seed weight.

Ramanappa et al. (2013) reported that grain yield had highly significant and positive association with number of pods per plant, harvest index, number of primary branches, plant height and number of seeds per pod at phenotypic level. However, days to maturity was negatively correlated with grain yield.

Mohammadi and Talebi (2015) revealed that the seed yield had highly significant positive correlation with number of seeds per plant and harvest index, suggesting that these traits may be important yield predictors and perhaps it is the most important for yield improvement in chickpea. Number of primary branches had significant negative correlation with yield. Strong positive correlation was observed between number of seeds per plant and harvest index, plant biomass with plant height, while negative significant correlations were observed between number of seeds per plant with 100 seed weight, harvest index with plant height.

Tadesse et al. (2016) recorded that seed yield was significantly and positively correlated with days to flowering, days to maturity, number of pods per plant, number of seeds per pod, plant height and biomass.

Srivastava et al. (2017) observed by correlation coefficient analysis that seed yield per plant showed significant positive correlation at both phenotypic and genotypic level with harvest-index, biological yield per plant and number of pods per plant.

Qaiser et al. (2019) observed that days to flowering was associated positively and significantly at genotypic and phenotypic levels with secondary branches per plant, while negative and non-significant with seeds per plant, seeds per pod, 100-grain weight and seed yield per plant. Positive and significant correlation was observed between days to flowering with plant height at genotypic level, while positive and non-significant at phenotypic level. Negative and significant correlation was observed between days to flowering with pods per plant at genotypic level.

Sayilgan (2020) found significant correlations between the yield and the number of the days to 50% emergence, the number of days to 50% flowering, number of days to maturity, plant height, first pod height, number of pods per plant and number of seeds per pod.

Srivastava et al. (2021) observed the yield per plant exhibited significant positive correlation with days to first flowering, days to 50% flowering, days to pod

initiation, number of pods per plant, number of seeds per plant and significant negative correlation with 100 seed weight. Among component traits, all the phenological traits except days to maturity showed significant and positive correlation with each other and with plant height, number of pods per plant and yield per plant, while significant negative correlation was observed with 100 seed weight. Thus, indirect selection for early type genotypes with higher number of seeds and pods per plants may lead to improvement in yield per plant with an associated reduction in seed size.

2.4 Path coefficient analysis: -

The path coefficient analysis is the standardized partial regression coefficient, which use to splits the correlation coefficients into the measure of direct-indirect effects. Path analysis measures the cause of association of two variables. It is based on all possible simple correlation between different characters. It helps in determining yield contributing characters and useful in indirect selection. Path coefficients analysis is an extension of the regression model, which used to test the fit of the correlation matrix against two or more causal models which are being compared. The concept of path coefficient was developed by Wright in 1921. Path coefficient analysis is applied for assessment by Dewey and Lu in 1959 in crested wheat grass. The literatures available on path analysis in chickpea are as follow:

Kumar *et al.* (2012) found that direct selection for number of pods and 100 seed weight could be useful in future crop improvement programmes. Path analysis revealed that days to 50% flowering, plant height and number of pods per plant had high direct effect on seed yield at both genotypic and phenotypic levels.

Aycicek and Babagil (2013) performed path coefficients analysis and found that seed yield positively and significantly correlated with all characters except 100 kernel weight. Plant height and pod number per plant positively correlated with seed yield suggested that these yield components may be good selection criteria to improve chickpea cultivar.

Sarker *et al.* (2014) observed that the path-coefficient analysis exhibited the highest positive direct effect for number of seeds per plant followed by pod weight per plant and 100 seed weight at genotypic level and at phenotypic level number of seeds per plant followed by 100 seed weight and number of secondary branches per plant on seed yield.

Joshi and Yasin (2015) revealed that biological yield, plant height and harvest index is directly contributing to seed yield but delayed flowering and long days to maturity showed negative indirect effect on seed yield.

Agrawal *et al.* (2018) observed that biological yield, effective pods per plant, harvest index, primary branches per plant and secondary branches per plant had high positive direct effect on grain yield per plant under normal condition, while chlorophyll index, effective pods per plant and 100 -seed weight would be quite effective in improving chickpea under late condition.

Manikanteswara *et al.* (2019) revealed that biological yield and days to maturity exhibited high direct positive effect on seed yield per plant at phenotypic and genotypic levels.

Rathod *et al.* (2020) showed that pods per plant and test weight exerted high positive direct effect and had positive correlation on seed yield, suggesting, that the prime importance to selection of these characters for improving seed yield in chickpea.

Kumar *et al.* (2021) path analysis revealed that days to 50% flowering, primary branches per plant, secondary branches per plant, total number of pods per plant, biological yield per plant, harvest index and seed index had direct positive effects on seed yield at both genotypic and phenotypic levels.

2.5 Genetic divergence (D^2) analysis: -

The concept of D^2 statistics was originally developed by P.C. Mahalanobis in 1928 for Anthropometry and Psychometrical studies but Rao in 1952 suggested to use this technique first in Plant Breeding. Genetic divergence analysis helps in the selection of genetically divergent parents for their exploitation in hybridization programmes. It measures the degree of diversification and determines the relative proportion of each component characters to the total available divergence. The forces of differentiation are measured at two levels *i.e.*, inter-cluster and intra-cluster levels. This technique provides reliable estimates of divergence and a large number of germplasm lines can be evaluated at a time for genetic diversity by this technique. It is depicted by cluster diagram. (Mahalanobis, 1928 and Rao, 1952)

Babbar and Thakur (2012) evaluated eleven clusters and found that the cluster II showed largest cluster with 27 genotypes. Highest inter cluster distance was observed between cluster V and cluster IX followed by cluster V and cluster XI and cluster V and cluster VI respectively. 100 seed weight showed high percent

contribution towards genetic divergence. Maximum intra cluster distance was observed in cluster V followed by cluster II and cluster III. Maximum inter cluster distance was found between cluster V and cluster IX.

Jain and Indapurker (2013) observed the nature and magnitude of genetic divergence, which grouped into six clusters. The cluster I shows largest cluster with eight genotypes. Highest inter cluster distance was observed between cluster IV and cluster V followed by cluster V and cluster VI.

Gaikwad et al. (2014) reported that pods per plant, number of secondary branches per plant, 100-seed weight and days to 50% flowering contributed maximum to the divergence.

Naveed et al. (2015) classified the genotypes into 3 clusters with maximum 33 genotypes in cluster II. Cluster I comprised of drought tolerant accessions based on canopy temperature, while cluster III consisted of bold seeded genotypes regarding 100-seed weight. Cluster II incorporated wilt resistant, early flowering yet late maturing genotypes having highest pods per plant, grain yield and harvest index. D² statistics further confirmed the versatility of cluster II genotypes over cluster I and cluster III for most of the studied characters.

Dhuria and Babbar (2016) reported genetic divergence and grouped into 11 clusters. Maximum intra-cluster distance was observed in cluster X, followed by cluster VII, cluster II and cluster III, whereas maximum inter-cluster distance was noticed between cluster III and cluster IX. Crossing between genotypes from the cluster III and cluster IX may lead to maximum diversity in the segregating populations and development of high yielding genotype.

Saha et al. (2018) found that maximum percentage contribution towards the divergence for total number of pods per plant followed by height of first fruiting node, harvest index and biological yield. These characters were responsible for expressing maximum diversity between the clusters should be considered prime during selection. The inter cluster divergence was observed maximum between genotypes of cluster VII and VIII followed by cluster V and VIII, cluster VI and X, cluster VI and VIII, cluster V and X. Cluster VI showed maximum mean value for 100 seed weight, biological yield plant-1 had high mean value in cluster VIII, harvest index were recorded maximum in cluster V, seed yield plant-1 showed maximum value in cluster VI. Divergence elite lines viz., SAGL 152210, ICCX-090021-P19, IPC 2012-31, JG 14,

JG 2016-141611, N BeG 873, Phule G 0805-17-5 and JAKI 9218 grouped in different clusters.

Tamvar et al. (2019) observed that 100-seed weight, number of secondary branches per plant, seed yield per plant, height at first pod, days to 50% flowering and number of primary branches per plant contributed very much towards genetic divergence. Based on inter-cluster distance, clusters III and IV followed by IV and V, and II and IV had maximum inter-cluster distance.

Dar et al. (2020) recorded 959.33 to 8477.71 range of inter cluster distance. Highest inter cluster distance (8477.71) was found between the clusters, VI and VII followed by the clusters, IV and VII (5814.62), IV and V (5807.441), V and VI (4659.34). The minimum inter-cluster distance (959.33) possessed by clusters, II and III. Found IV has highest intra cluster distance (637.07) then cluster I (459.16). At last reported that plant height registered higher divergence (49.25%) then pods per plant (36.12%), days to 50% flowering (4.13%) and days to maturity (2.7%), secondary branches per plant (3.24%), seed yield per plant (1.28%) and primary branches per plant (1.14%). The 100-seed weight (1.12%) and seeds per pod (1.02%) possesses less divergence.

Boparai et al. (2021) grouped 8 main clusters by divergence analysis. Among eight clusters, cluster I was the largest cluster among all including 46 derivatives. The cluster IV showed maximum cluster mean values for maximum number of traits. Maximum inter-cluster distance was observed between cluster IV and cluster VI and maximum intra-cluster distance was showed by cluster IV. Therefore, a hybridization programme involving 17 lines (Cross 1: R-23, 7, 6, 46, 36; Cross 2: R- 6, 7, 16, 19, 29, 31, 32, 35, 43 and Cross 4: R- 7, 9, 17) from cluster IV and 13 lines (Cross 1: R- 43, 25, 31; Cross 2: R- 33, 36, 38, 13, 51, 52; Cross 3: R- 8 and Cross 4: R- 1, 15, 6) from cluster VI can be devised to yield desirable transgressive segregants.

Babbar and Jain (2021) partitioned 4 clusters on the basis of D^2 value, cluster I was the largest among all the clusters comprising of 26 genotypes followed by cluster II had 2 genotypes, while cluster III and cluster IV each had 1 genotype. Maximum percentage contribution towards genetic divergence observed for biological yield per plant followed by total number of pods per plant and 100 seed weight. Cluster I showed highest intra cluster value followed by cluster II, whereas Cluster III and IV were mono genotypic. The highest inter cluster divergence was observed between genotypes of cluster II and cluster IV, followed by cluster I and

cluster IV and cluster II and cluster III. High heterotic combinations will be obtained when genotypes of these distinctly placed clusters were crossed and would give high heterosis/ heterotic segregants. Cluster III and cluster IV had highest mean value maximum number of characters. Based on result JG 2016 – 1614, JG 11 × JG 14 and ICC 552241 × JG 11 are recommended for hybridization, as these were grouped in diverse clusters.

2.6 Principal component analysis: -

It is multivariate statistical technique for exploration and simplification of any complex data set. The ability of such method is to transform a number of possibly correlated variables into a smaller number of variable is called Principal component (Everitt and Dunn, 1992). Each Principal component is the linear combination of the original variables. In Chickpea more PCA studies are made on pure breeding lines, while these are not reported in segregating populations.

Muniraja *et al.* (2011) showed that the first two PC axes explained 44.2% of total multivariate variation with first five PC axes explaining 74.2%. The PC 1 separates genotypes on number of pods per plant, seed yield per plant, plant height and number of secondary branches per plant, while PC2 separated on days to maturity, days to 50 per cent flowering and percent pod damage.

Malik *et al.* (2014) found that in evaluation first 4 principal components accounted for 71.99(%) of the total variation. Seed yield, biological yield, pods per plant, secondary branches and plant height in chickpea reported positive relation with the first component (PC1). Days to flowering, days to maturity, 100 seed weight reported positive correlation with the second component (PC2). The grouping of genotypes would be of practical value to chickpea breeders in identifying the genotype with desired trait for utilization in breeding program for genetic improvement.

Naveed *et al.* (2015) categorized chickpea genotypes into 10 PCs based on principal component analysis. First four PCs out of total ten achieved eigen values >1 and explained 75.5(%) of overall variability. Days to 50% flowering, 100 seed weight and grain yield contributed highest weight on PC1 that described 31.80(%) of total variation. PC2 reported 21.60(%) of digression and was mainly related to pods per plant, plant height and canopy temperature.

Nyende and Rao (2015) observed that first principal component was positively associated with days to flowering, plant height, number of primary and secondary branches plant per plant, days to maturity, pods plant per plant, pod length, biomass and seed yield. The second principal component was positively related with plant height, pod filling period, pods per plant, seed yield and 100 seed weight.

Shivwanshi and Babbar (2017) found that the first eight PCs out of thirteen components accounted for 77.7 (%) of the total variation. The PC1 explained total variation 26.6 (%). The maximum PC value was found in genotype IC 84037 (9.79) followed by, IC 83812(8.46), EC 489919(7.70), IC 83387 (6.42), IC 83813 (6.24).

Mahmood et al. (2018) observed results regarding PCA revealed that first three PCs showed more than 1 Eigen values accounting for 50.5(%), 19.99(%) and 15.86(%) respectively in total variation and collectively share 86.15(%) of total variation. Principle component analysis extracted higher loadings for grain yield, harvest index, pods plant per plant, 100 seed weight (g), days to 50% flowering and plant height which exhibited most significant contributions to genetic variability among chickpea genotypes in this study.

Tsehaye et al. (2020) found that the first four principal components, whose Eigenvalues greater than one, accounted more than 81.5% of the total variation. Hence, the existence of huge variability infers, exploiting the existing variation is enough to improve chickpea grain yield only thorough simple selection by giving due attention for above ground biomass, number of secondary branch per plant, number of pod per plant and harvest index.

Biswal and Babbar (2021) observed that out of 14, only 5 principal components (PCs) exhibited more than 1 eigen value and showed about 75.95% variability among the traits studied. The PC1 had the highest variability (22.2%), followed by PC2 (19.5%), PC3 (14.3%), PC4 (11.7%) and PC5 (8.04%) for traits under study. Principal component revealed that the PC1 which accounted for the highest variability (22.2%) was mostly related to harvest index and seed yield per plant. PC 2 was dominated by phenological traits viz., days to flower initiation, days to 50% flowering, days to pod initiation and days to maturity. PC 3 considered for yield attributing traits i.e. total number of pods per plant and number of effective pod per plant. PC 4 was dominated by traits i.e., number of seeds per pod, number of primary branches per plant, number of secondary branches per plant and plant height, while PC5 related the trait plant height.

2.7 Selection of Lines Suitable for Mechanical Harvesting: -

Mechanization of chickpea harvesting is desired by the farmers for saving cost and time. Mechanical harvesting will also reduce the chances of damage to the matured crop due to untimely rains, winds, shattering etc. that may occur during the additional period required in manual harvestings. It is very important to identify lines suitable for the mechanical harvesting in chickpea.

Patil (2013) observed that total harvest losses were less in mechanical harvesting of tall genotypes (2.64 to 4.96%) compared to semi-erect genotype JG 11 (20.03%). Planting tall chickpea genotype ICCV-11604 at 40 per cent higher density under irrigated ecosystem recorded significantly higher seed yield and net return compared to JG 11 at normal density by minimizing the harvesting losses and harvesting cost under mechanical harvesting.

Daheriya (2014) revealed that genotypes C121, ICCV 13107, ICCV 13106, ICCV 13101, GBT 9, PG 100, PG 099, JG 37, ICCV 13111, IPC 2011- 81, ICCV 13114, JGK 27, IPC 2006-11 and NBeG 47-1 were suitable for mechanical harvesting.

Basha et al. (2018) observed significantly higher number of branches (8.8) under 30 x 10 cm (33 plants/ m²) as compared to 22.5 x 10 cm (44 plants/ m²) (7.7). Higher plant height (46.9 cm) lower days to 50% flowering observed with NBeG 47. Higher test weight (30.9 gm) was observed in NBeG 47. Higher seed yield was observed in GBM 2 (1474 kg/ha) and is at par with NBeG 47 (1346 kg/ha), Phule G 08108 (1374 kg/ha) and BRC 1(1348 kg/ha).

Singh et al. (2019) reported that high-density planting increased the plant height (erectness) and ground clearance of cv. HC 5 (height of first pod) (~ 30 cm), an essential prerequisite for mechanical harvesting, but not in cv. JAKI 9218. Hence, cv. HC 5 requires a dense planting for higher yield and appropriate plant structure for mechanical harvesting. Therefore, it is recommended to work out the optimum planting geometry per plant population to realize the potential yield of cultivars bred for mechanical harvesting.

Ravula (2020) showed that the shortage of agricultural laborers and subsequent wage increase incentivized farmers to adopt NBeG47 (first mechanically harvestable chickpea variety) for its mechanically-harvestable characteristics. While ease of harvesting after the introduction of NBeG47 largely improved in three out of

the four villages studied, mechanized harvesting was hindered by inadequate training and limited equipment access.

Reddy et al. (2021) through analysis of variance studies revealed significant differences among the genotypes for all the characters. Variability studies revealed high PCV and GCV for seed yield; moderate for 100 seed weight and low for height of first pod and angle of primary branches. High heritability was noted for days to 50 % flowering (0.988) followed by grain yield (0.932) and test weight (0.923). High genetic advance was noticed for seed yield per plant (67.92) followed by test weight (36.81) and number of primary branches (36.11). High heritability coupled with high genetic advance was noted for seed yield, test weight and height of first pod. Chickpea genotypes GL 14049 (125.7 g per pl) and GL 14050 (120.7 g per pl) recorded highest seed yield compared to checks, NBeG 47 (29.3 g per pl) and JAKI 9218 (24.7 g per pl) apart from their suitability to mechanical harvesting.

2.8 Assessment of Physiological traits: -

Physiological study helps in understanding of any crop in better way by determining chlorophyll in leaves, leaf size, crop growth rate, net assimilation rate, plant biomass etc. And by dealing with physio-morphological nature of genotypes, can also be a crucial tool to enhance yield of chickpea genotypes. Available literature related to present study is listed below:

Ali et al. (2011) found positive effect of application of Nitrogen and Rhizobium inoculation on growth indices and yield components of chickpea. Lower levels of nitrogen application and non-inoculated plants showed less growth indices including total dry matter (TDM), leaf area index (LAI), crop growth rate (CGR), relative growth rate (RGR) and net assimilation rate (NAR) while the highest values of these indices were observed at the high levels of nitrogen application (100 kg urea ha⁻¹) and inoculated plants.

Bodake et al. (2014) studies on leaf area revealed a good indicator for increasing photosynthetic efficiency of plant. The photosynthetic rate, transpiration rate and stomatal conductance were highest at 50 per cent flowering and decreased after 15 days of 50 per cent flowering. The highest yield was recorded by the genotypes, Digvijay, Vijay, ICC-13219, ICC-15868, ICC-1579 and ICC-4593.

Kumar et al. (2017) analyze different chickpea genotypes on their morphological (plant height, 100 seed weight, days to maturity, days to flowering, yield per plant) and physiological characters (Relative Water Content, Membrane Stability Index, plant biomass) to investigate response of different genotypes under stress condition and observed 10-57% yield reduction due to stresses.

Rani et al. (2020) evaluated effect of high temperature and water deficit condition i.e., drought on chickpea plant growth and production. In both the situation, physiology of plant affects adversely like reduction in the relative leaf water content, chlorophyll loss, membrane damage, decreased root water conductivity, reduced net assimilation rate etc.

Sinha et al. (2020) took observations at fortnight intervals from 15 DAS to 60 DAS of parameters viz. leaf area, leaf number, leaf dry weight, plant height, shoot dry weight and total plant dry weight. As a result, a huge increment found in dry matter production in shoot, leaf and total plant at post flowering stage and moreover than these, Correlation analysis exhibited that parameters leaf dry weight, leaf area, shoot dry weight and total plant dry weight were strongly associated with the seed yield.

Gaurav et al. (2020) observed the effect of Plant growth promoting rhizobacteria (PGPR) usually found in rhizosphere at root surfaces, on the physiology of the plant. This PGPR are reported to affect the growth, nutrient uptake and finally yield of chickpea plant through enhancing leaf area and chlorophyll content, root mechanism, light transmission ratio, plant biomass etc.

CHAPTER 3:
MATERIAL AND METHOD

CHAPTER 3: MATERIAL AND METHOD

The current investigation entitled “**Genetic Assessment for Quantitative and Physiological Traits of *desi* Chickpea**” was carried out during the *rabi* 2020-21. The techniques followed and materials used, during the investigation are presented in this chapter as follow:

3.1 Climate and Weather:

The Geographical location of Jabalpur is at 79.58°E longitudes and at 23.90°N latitude with altitude of 411.87 meter from sea level. Climate of this region is semi humid and sub-tropical with intense summer and winter season. Jabalpur region traditionally follows the rice - wheat cropping pattern and grouped as "Kymore plateau and Satpura hills agro-climatic zone". The minimum temperature goes below 7°C in December -January, whereas maximum temperature reported in May-June reaches up to 46°C. The average rainfall precipitation is nearly **1107.1 mm** which take place mostly from mid of June to end of October month with some occasional showers, which are because of western disturbance in other seasons.

3.2 Experimental Material and Methods:

Location of work: The experiment was conducted at Seed Breeding Farm of Department of Plant Breeding and Genetics department in College of Agriculture, JNKVV, Jabalpur (M.P.) during the *rabi* season of 2020-21.

Treatment Details: The experimental material consisted of 40 elite chickpea lines including 4 checks, received from International Crop Research Institute for Semi-arid Tropics (ICRISAT), Hyderabad, INDIA and 2 local checks from AICRP on Chickpea, Department of PBG, JNKVV, Jabalpur. The experiment was performed under RCBD (Randomized Complete Block Design), used the recommended practices of agronomy for normal crop growth and occupied experimental area was quite uniform in respect of its fertility and topography of soil.

Table 3.1: Experimental Details

Season	<i>Rabi</i> , 2020-21
Experimental Design	Randomized Complete Block Design
Number of genotypes	40 (included 4 checks)
Replications	2
Rows/plot	4
Row length	4.0 m
Row to row distance	30.0 cm
Plant to plant distance	6.0-8.0 cm

Table 3.2: List of the Genotypes Used in Investigation

Serial No.	Entries	Pedigree
1	ICCV 201201	GG 2/ICC 1205
2	ICCV 201202	ICCV 93954///ICCV 93954//ICCV 96029/ICCV 93954
3	ICCV 201203	ICCV 93954///ICCV 93954//ICCV 96029/ICCV 93954
4	ICCV 201204	ICCV 93954///ICCV 93954//ICCV 96029/ICCV 93954
5	ICCV 201205	ICCV 93954///ICCV 93954//ICCV 96029/ICCV 93954
6	ICCV 201206	ICCV 93954///ICCV 93954//ICCV 96029/ICCV 93954
7	ICCV 201207	ICCV 93954///ICCV 93954//ICCV 96029/ICCV 93954
8	ICCV 201208	ICCV 93954///ICCV 93954//ICCV 96029/ICCV 93954
9	ICCV 201209	ICCV 93954///ICCV 93954//Harigantars/ICCV 93954
10	ICCV 201210	ICCV 93954///ICCV 93954//ICC 16641/ICCV 93954
11	ICCV 201211	ICCV 93954///ICCV 93954//ICC 16641/ICCV 93954
12	ICCV 201212	ICCV 93954///ICCV 93954//ICC 16641/ICCV 93954
13	ICCV 201213	ICCV 92944/ICC 5912
14	ICCV 201214	ICCV 92944/ICCV 11601
15	ICCV 201215	ICCV 92944/ICCV 11601

16	ICCV 201216	ICCV 92944/ICCV 96836
17	ICCV 201217	ICCV 96970/ICCV 96836
18	ICCV 201218	ICCV 93952/ICCV 96836
19	ICCV 201101	ICCV 97105/ICC 5912
20	ICCV 201102	ICCV 93954/ICCV 11601
21	ICCV 201103	ICCV 93952/ICCV 11601
22	ICCV 201104	ICCV 94954/ICCV 11601
23	ICCV 201105	ICCV 96970/ICCV 11601
24	ICCV 201106	ICCV 97105/ICCV 11601
25	ICCV 201107	ICCV 10/ICCV 11601
26	ICCV 201108	ICCV 96970/ICCV 96836
27	ICCV 201109	ICCV 92318/ICC 16644
28	ICCV 201110	ICCV 96836/ICCV 93954//ICC 4958TM/ICCV 93952
29	ICCV 201111	ICCV 96836/ICCV 97105//ICC 4958TM/GG 2
30	ICCV 201112	ICCV 93954/ICCV 96836
31	ICCV 201113	NBeG 3/ICCV 96836
32	ICCV 201114	ICCV 10/ICCV 96836
33	ICCV 201115	ICCV 96836/ICCV 05113
34	ICCV 201116	ICCV 10/ICCV 05113
35	ICCV 201117	ICCV 93954/ICCV 05103
36	ICCV 201118	ICCV 10/ICCV 05103
37	ICCV 08102	ICCV10 x ICCL 87322
38	RVG 204	ICCV10 x ICCL 87322
39	JG 36	JG 12 x JG 16
40	JG 24	JG 74 x ICC 4958

3.3 Observations recorded:

Observations were noticed on five randomly selected plants from each replication and plot, on the following traits-

3.3.1 Morphological traits (as per DUS guidelines):

Characters showing discrete variation were analyzed and percentage frequencies of different classes were plotted, to know which particular character was dominant between the genotypes. The genotypes were characterized as per DUS guidelines of chickpea.

3.3.1.1 Stem: Anthocyanin Coloration

Stem anthocyanin coloration recorded before flowering stage.

Status	Scale
Absent	1
Present	9

3.3.1.2 Stem: Height at the Initiation of first flower

Stage of observation is first flowering.

Status	Scale
Low (<8 nodes)	3
Medium (8-15 nodes)	5
High (>15 nodes)	7

3.3.1.3 Plant: Growth Habit

Stage of observation 50% flowering.

Status	Scale
Erect (0- 15 ° from vertical)	3
Semi-erect (16- 60° from vertical)	5
Spreading (61-80° from vertical)	7

3.3.1.4 Plant: Color of Foliage

Stage of observation 50% flowering.

Status	Scale
Light green	1
Medium green	2
Dark green	3
Greenish purple	4

3.3.1.5 Leaflet: Size (mm) (middle of the plant and middle of the leaf)

Stage of observation 50% flowering.

Status	Scale
Small (<10mm)	3
Medium(10-15mm)	5
Large (>15mm)	7

3.3.1.6 Leaf: Pattern

Stage of observation 50% flowering.

Status	Scale
Simple	1
Compound	2
Pinnate	3

3.3.17 Flower: Number per peduncle

Stage of observation 50% flowering.

Status	Scale
Single	1
Twin	3

3.3.1.8 Flower: Color

Stage of observation 50% flowering.

Status	Scale
White	1
Pink	2
Blue	3

3.3.1.9 Flower: Stripes on standard

Stage of observation is 50% flowering.

Status	Scale
Absent	1
Present	9

3.3.1.10 Peduncle: Length(mm)

Stage of observation pod development

Status	Scale
Short (<5 mm)	3
Medium (5-10 mm)	5
Long (>10 mm)	7

3.3.1.11 Plant: Height(cm)

Stage of observation fully developed green pod.

Status	Scale
Short (<45 cm)	3
Medium (45-65 cm)	5
Tall (>65 cm)	7

3.3.1.12 Pod: Size (length)(cm)

Stage of observation: at the time of maturity suitable for harvesting.

Status	Scale
Short (<15 mm)	3
Medium (15-20 mm)	5
Large (>20 mm)	7

3.3.1.13 Seed: Type

Stage of observation 30 days after harvesting.

Status	Scale
<i>Desi</i>	1
<i>Kabuli</i>	3

3.3.1.14 Seed: Shape

Stage of observation 30 days after harvesting.

Status	Scale
Owl 's head	2
Angular	3

3.3.1.15 Seed: Testa texture

Stage of observation 30 days after harvesting.

Status	Scale
Rough	1
Smooth	2
Tuberculated	3

3.3.1.16 Seed: Color

Observed took based on The Royal Horticulture Society, London (2001) color chart and stage of observation was 30 days after harvesting.

Status	Color	Scale
164(A)	Brownish Orange	1
164(B)	Dark Orange-Yellow	2
164(C)	Moderate Orange-Yellow	3
165(A)	Moderate Brown	4
165(B)	Brownish Orange	5
166(B)	Moderate Reddish-Brown	6
166(C)	Grayish Reddish-Orange	7

3.3.1.17 Seed: Ribbing

Stage of observation 30 days after harvesting.

Status	Scale
Absent	1
Present	9

3.3.1.18 Seed: Size (weight of 100 seeds at 10% moisture content)

Stage of observation 30 days after harvesting.

Status	Scale
Very small (<15 g)	1
Small (15-18 g)	3
Medium (19-24 g)	5
Large (25-30 g)	7
Very large (>30 g)	9

3.3.1.19 Lodging Resistance:

Expressed in percentage of lodged plants per plot. It is reported by visual assessment of plants in a single plot.

Status	Scale	Lodging (%)
Highly Resistant	0	No lodging
Resistant	1	1-10
Moderately resistant	3	11-20
Moderately Susceptible	5	21- 30
Susceptible	7	31-50
Highly Susceptible	9	51-100

3.3.1.20 Shattering resistance:

Expressed in percentage of shattered pods per plant at maturity suitable for harvesting.

Status	Scale	Shattering (%)
Highly Resistant	0	No shattering
Resistant	1	1-10
Moderately resistant	3	11-20
Moderately Susceptible	5	21- 30
Susceptible	7	31-50
Highly Susceptible	9	51-100

3.3.2 Quantitative Characters:

Observations were noticed based on single on randomly selected five plants from each plot and replication.

3.3.2.1 Days to 50% flowering

Expresses in days at stage when 50% of flowering get completed.

3.3.2.2 Days to maturity

Physiological maturity was noticed from sowing to the stage when about 90% of pods have matured and the plants turned yellow.

3.3.2.3 Plant height (cm)

Measured in cm from the bottom of the plant (ground level)

3.3.2.4 Height of the first fruiting node (cm)

It was recorded in cm at the time of maturity from the ground.

3.3.2.5 Stem thickness (mm)

The thickness of the stem is measured in mm at the time of harvest maturity using vernier caliper.

3.3.2.6 Number of primary branches per plant

It was counted at maturity, which born on the ground level.

3.3.2.7 Number of secondary branches per plant

It was counted at maturity, which born on the ground level.

3.3.2.8 Total number of pods per plant

At the time of maturity is had been calculated.

3.3.2.9 Number of effective pods per plant

At the time of maturity is had been calculated.

3.3.2.10 Number of seeds per pod

It was obtained by the following formula:

$$\text{Number of seeds per pod} = \frac{\text{Total number of seeds per plant}}{\text{Total number of effective pods per plant}}$$

3.3.2.11 100 Seed weight (g)

100 seed weight was counted from the seed lot and it was weighted in gram.

3.3.2.12 Biological yield per plant (g)

Each plant was harvested from the ground level and after sun drying weighted in gram.

3.3.2.13 Harvest index (%)

Harvest index was calculated by the division of total seed yield per plant by biological yield per plant.

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

3.3.2.14 Seed yield per plant (g)

Seed yield per plant was weighted in gram at the time of harvesting.

3.3.3 Physiological Traits

Following physiological characters were recorded, based on the single plant on randomly selected five plants from each plot and replication.

3.3.3.1 Leaf area (cm²/plant)

Leaf area is the area of photosynthetic surface produced by individual plant over a period of time interval and express in cm²/plant. It was observed at 30, 60 and 90 DAS stages by using an optical instrument called Leaf area meter.

3.3.3.2 Plant biomass (g)

Measured at 30, 60 and 90 DAS stages, plants were kept in an electric oven at 80°C for 48 hours till constant weight is achieved. After this their weight was recorded on electronic balance. Later mean was worked out and presented as mean dry weight per plant in gram.

3.3.3.3 Biomass duration (g * day)

This is the parameter which represent dry weight losses or gains during a unit time period. Unit is g * day.

$$\text{BMD} = \{(W_2 + W_1)/2\} * (T_2 - T_1)$$

3.3.3.4 SPAD for Chlorophyll (mg)

Chlorophyll content was defined as the milligrams of chlorophyll per unit ground area and was determined at flowering stage by using a non-destructive method that

uses an optical instrument, called The Soil Plant Analysis Development (SPAD) Chlorophyll meter.

3.3.3.5 Leaf Area Index (LAI) (%)

It expresses the ratio of the leaf surface (One side only) to the ground area occupied by the plant or a crop stand worked out as per specifications of Gardner *et al.*, (1985). It expresses in percentage.

$$\text{LAI} = \text{Total leaf area} / \text{Land area}$$

3.3.3.6 Leaf Area Duration (LAD) (cm² * days)

Leaf area duration expresses the magnitude and persistence of leaf area or leafiness during the period of crop growth. It reflects the extent of seasonal integral of light interaction and correlated with yield, LAD was computed as follows: (Watson, 1952).

$$\text{LAD} = \{(\text{LA}_2 + \text{LA}_1) \times (t_2 - t_1)\} / 2$$

Where the LA₁ and LA₂ represents the leaf area at two successive time intervals is (t₁ and t₂). It expressed in cm² * days.

3.3.3.7 Leaf Area Index Duration (LAID) (days)

Leaf area index duration is calculated as follows:

$$\text{LAID} = \{(\text{LAI}_1 + \text{LAI}_2) \times (T_2 - T_1)\} / 2$$

Where the LAI₁ and LAI₂ represents the leaf area index at two successive time intervals is (t₁ and t₂). It expressed in days.

3.3.3.8 Leaf Area Ratio (LAR) (cm² * g⁻¹)

Leaf area ratio used to determine increase or decrease in leaf area at particular period of time as compared to biomass at same time. It can be calculated by the following formula:

$$\text{LAR} = (\text{LA}_2/\text{W}_2 + \text{LA}_1/\text{W}_1)/2$$

Where the LA represents the leaf area and W represents biomass. It expressed in cm² * g⁻¹.

3.3.3.9 Crop Growth Rate (CGR) (g * cm⁻¹ * day⁻¹)

The daily increment in plant biomass is termed as crop growth rate or rate of dry matter production. It was determined as per the following formula suggested by Watson (1952). It expresses with unit g * cm⁻¹ * day⁻¹.

$$\text{CGR} = 1/P * W_2 - W_1 * (t_2 - t_1)$$

Where,

p = ground area (cm²)

W₁ = dry weight per unit area at t₁

W₂ = dry weight per unit area at t₂

t₁ = first sampling and

t₂ = second sampling

3.3.3.10 Relative Growth Rate (RGR) (g * g⁻¹ * day⁻¹)

The Relative Growth Rate expresses the dry weight increase in time interval in relation to initial weight. In practical situations, the mean relative growth rate is calculated from measurements at t₁ and t₂. It was calculated as per formula given by Watson (1952). Unit is g * g⁻¹ * day⁻¹.

$$\text{RGR} = \text{Ln } W_2 - \text{Ln } W_1 / t_2 - t_1$$

Where,

W₁ = dry weight per unit area at t₁,

W₂ = dry weight per unit area at t₂,

t₁ = first sampling, and

t₂ = second sampling.

3.3.3.11 Net Assimilation Rate (NAR) (g * cm⁻¹ * day⁻¹)

NAR is the ratio of rate of dry matter accumulation and leaf area index and a mean ratio should take into account the rate of change of each of its components. It expresses with unit g * cm⁻¹ * day⁻¹.

$$\text{NAR mean} = [(W_2 - W_1) / (t_2 - t_1)] * [\text{Ln } (LA_2) - \text{Ln } (LA_1)] / (LA_2 - LA_1)$$

Where NAR mean is the mean net assimilation rate during a period from t₂ to t₁

W₁ = dry weight per unit area at t₁,

W₂ = dry weight per unit area at t₂,

t₁ = first sampling, t₂ = second sampling,

LA₁ = Leaf Area at t₁, LA₂ = Leaf Area at t₂.

3.3.3.12 Days to Physiological Maturity (days)

It is noted as taken the number of days from the date of sowing to taken day, on which the plants showed the field maturity appearance in the plot.

3.4 Statistical analysis

The obtained data were subjected to the following statistical analysis.

3.4.1 Mean

Mean was calculated by following formula:

$$\bar{x} = \sum x_i / N$$

Where,

$\sum x_i$ = Sum of all the observations of i^{th} traits

N = Total number of observations

3.4.2 Range

Range is the difference between the smallest and the greatest value of a series of observation and thus, it provides the information about the present variability in the genotypes.

3.4.3 Analysis of variance

The mean data on five/three plants were subjected to variance analysis and the test of significance as per method of Fisher (1935).

Table 3.3 ANOVA table for Randomized Complete Block Design (RCBD)

Source of variation	d.f.	Mean squares	Expected mean squares
Replication	(r-1)	Mr	$\sigma^2 e + g \sigma^2 r$
Treatments	(t-1)	Mt	$\sigma^2 e + r \sigma^2 g$
Error	(r-1) (t-1)	Me	$\sigma^2 e$
Total	(rt-1)		

r = Number of replications; t = Number of treatment

3.4.4 Coefficient of variation

The coefficient of variation at genotypic levels and phenotypic levels, was calculated as per formula proposed by Burton, (1952). The phenotypic variances and

genotypic variances were also estimated according to the method suggested by Burton (1952) using the formula, (a) and (b).

(a) Phenotypic coefficient of variation (PCV)

$$\sigma^2_p = \sigma^2_g + \sigma^2_e \quad \text{..... (a)}$$

$$\text{PCV} = (\sigma_p / \bar{X}) \times 100$$

$$\text{Where,} \quad \sigma_p = \sqrt{\sigma^2_p}$$

(b) Genotypic coefficient of variation (GCV)

$$\sigma^2_g = \text{MS}_g - \text{MS}_e / r \quad \text{..... (b)}$$

$$\text{GCV} = (\sigma_g / \bar{X}) \times 100$$

MS_g	=	Mean square due to genotypes or accessions;	σ^2_p	=	Phenotypic variance;
MS_e	=	Error mean square;	σ_p	=	Phenotypic standard deviation;
r	=	Number of replications;	σ^2_g	=	Genotypic variance;
σ_g	=	Genotypic standard deviation;	σ^2_e	=	Environmental variance;
$\bar{X}$	=	General mean			

3.4.5 Heritability

It was calculated in the broad sense by the formula proposed by Hanson *et al.*, (1956).

$$\text{Heritability (h}^2\text{)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 (bs) = heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The range of heritability was categorized as low (< 50 per cent), moderate (50-70 per cent) and high (> 70 per cent) as followed by Johnson *et al.* (1955).

3.4.6 Genetic advance (GA):

Genetic advance is calculated by the formula suggested by Johnson *et al.*, (1955).

$$GA = h^2 (bs) \times \sigma_p \times K$$

Here,

GA = Genetic advance

σ_p = Phenotypic standard deviation

h^2 (bs) = Heritability of the character

K = Selection intensity at 5% level of significance *i.e.*, 2.06

3.4.5 Genetic advance as percentage of mean

It was calculated by following formula:

$$GA \text{ as percentage of mean} = 1 + \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

GA was categorized as-

> 35 per cent = high

25-35 per cent = moderate

< 25 per cent = low

3.4.6 Estimation of correlation coefficients

All correlation coefficients were calculated at both genotypic levels and phenotypic levels using formula suggested by Miller *et al.*, (1958).

$$r_{X_i X_j} = \frac{\text{Cov } X_i X_j}{\sqrt{(\text{Var } X_i) \cdot (\text{Var } X_j)}}$$

Where,

$r_{X_i X_j}$ = Coefficient of correlation between characters X_i and X_j

$\text{Cov } (X_i X_j)$ = Covariance between characters X_i and X_j

$\text{Var } (X_i)$ = Variance of character X_i

Var (X_j) = Variance of character X_j

Genotypic correlation coefficients and phenotypic correlation coefficients were compared by substituting the corresponding covariance and variance for all the observed traits.

$$\text{Genotypic } r(X_j Y_j) = \frac{\text{Genotypic cov } X_i Y_i}{\sqrt{\sigma_g^2(X_i) \sigma_g^2(Y_i)}}$$

$$\text{Phenotypic } r(X_j Y_j) = \frac{\text{Genotypic cov } X_i Y_i}{\sqrt{\sigma_p^2(X_i) \sigma_p^2(Y_i)}}$$

Where,

$\sigma_g^2(x_i)$ = Genotypic variance of character x_i

$\sigma_g^2(y_i)$ = Genotypic variance of character y_i

$\sigma_p^2(x_i)$ = Phenotypic variance of character x_i

$\sigma_p^2(y_i)$ = Phenotypic variance of character y_i

Testing of correlation coefficient for significance: In order to test the significance of correlation coefficient, the t-value was estimated and compared with the 't' tabulated value at (n-2) degree of freedom at both 5% and 1% level of significance.

$$t_c = \frac{r}{\sqrt{1-r^2}} \sqrt{n-2}$$

Where,

t_c = Calculated value of t

r = Estimated value of correlation coefficient

n = Number of paired observations

3.4.7 Path coefficient analysis

Path coefficient is the standardized partial regression coefficients and as such provide the means to direct influence of one character upon another character. It also permits partitioning of the correlation coefficient into direct - indirect effects *via* other traits. For the path coefficient analysis the method originally proposed by Wright

(1921), which was further modified by Dewey and Lu (1959). The cause-and-effect relationship is well defined in path coefficient analysis. It is possible to represent the whole system of variables in the form of diagram, known as path diagram.

Following set of simultaneously equations were formed and solved for estimating direct - indirect effects. Genotypic path coefficients were calculated separately for yield and its components. The dependent variable was seed yield per plant. The unexplained variation in the dependent variable was obtained as the residual factor from the following equation. (Wright, 1921 and Dewey and Lu, 1959).

$$r_1Y = P_1Y + r_{12} P_2Y + r_{13} P_3 Y + \dots + r_{1i} P_iY.$$

$$r_2Y = r_{21} P_1Y + P_2 Y + r_{23} P_3Y + \dots + r_{2i} p_iY.$$

$$r_kY = r_{k1} P_1Y + r_{k2} P_2Y + r_{k3}P_3Y + \dots + r_k P_kY.$$

Where,

r_1Y to r_kY = Coefficient of correlation between causal factors 1 to i and dependent character Y.

P_1Y to P_kY = Direct effect of characters 1 to i on character Y.

r_{12} to r_{k-1} , = Coefficient of correlation among causal factors.

The above equations were written in a matrix form as under:

$$\begin{array}{ccc}
 \text{A} & & \text{C} \\
 \begin{bmatrix} r_1Y \\ r_2Y \\ \vdots \\ r_kY \end{bmatrix} & & \begin{bmatrix} 1 & r_{12} & r_{13} \dots r_{1i} \\ r_{21} & 1 & r_{23} \dots r_{2i} \\ \vdots & \vdots & \vdots \\ r_{k1} & r_{k2} & r_{k3} \dots 1 \end{bmatrix} & & \begin{bmatrix} P_1Y \\ P_2Y \\ \vdots \\ P_kY \end{bmatrix}
 \end{array}$$

Then, $B = [C]^{-1} A$

Where,

$$[C]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} \dots C_{1i} \\ C_{21} & C_{22} & C_{23} & C_{2i} \\ \vdots & \vdots & \vdots & \vdots \\ C_{i1} & C_{i2} & C_{i3} & C_{ii} \end{bmatrix}$$

Then the direct effects were calculated as follows-

$$P_1Y = \sum_{i=1}^k C_{1i} r_{iy}$$

$$P_2Y = \sum_{i=1}^k C_{2i} r_{iy}$$

$$P_kY = \sum_{i=1}^k C_{ki} r_{iy}$$

Residual effect: Residual effect was obtained as per the formula given below

$$R = \sqrt{1 - E_{di} r_{ji}}$$

Where,

d_i = Direct effect of character

r_{ij} = Correlation coefficient of i^{th} character with j^{th} character

Later the path coefficients were scored based on the scales given below: (Lenka and Mishra, 1973).

>1.00	=	Very high
0.3-0.99	=	High
0.2-0.29	=	Moderate
0.1-0.19	=	Low
0.0-0.09	=	Negligible

3.4.8 Genetic divergence

Mahalanobis (1928) defines D^2 analysis as follows:

$$D^2P = b_1d_1 + b_2d_2 + \dots + b_pd_p$$

A resource for group distance based on multiple characters with $X_1, X_2, X_3, \dots, X_p$ as the multiple measurements available on each individual and $d_1, d_2, \dots, d_p$ as $\bar{x}_1 - \bar{x}_1', \bar{x}_2 - \bar{x}_2', \dots, \bar{x}_p - \bar{x}_p'$ respectively is the difference in the means of two populations. The 'P' values are to be estimated that the ratio of variance between the populations to the variance within the populations is maximized. Taking variance and covariance under consideration, the D^2 value may be estimated by this formula.

$$D^2 = \sum_{i,j} w_{ij} \left(\bar{x}_i^2 - \bar{x}_i \bar{x}_j \right) \left(\bar{x}_j^2 - \bar{x}_j \bar{x}_i \right)$$

Where,

W_{ij} is the inverse of estimated variance and covariance matrix. Step to estimate D^2 value: (Mahalanobis, 1928)

I. Collection of data

Data were collected considering "V" population and "P" characters which have been measured on each individual.

II. Test of significance

According to Wilk's criteria, a simultaneous test of difference between mean values of number of correlated variance is completed.

Using pivotal condensation method the determinant of error and error variety matrix was calculated.

$$A = \left| \frac{W}{S} \right| = \frac{\text{Determination of error matrix}}{\text{Determination of error + Variety Matrix}}$$

$$V(\text{State}) = -m \log e = - \left[n \frac{(p+g+1)}{2} \right] \log e$$

Where,

$$M = n - (p+q+1)/2$$

P = number of variance or character

Q = degree of freedom for population

N = degree of freedom for error + variety

E = constant (2.7183)

V (state) is distributed as X^2 with Pq degree of freedom.

The tabulated value of X^2 for Pq degree of freedom at 5% level is compared with the X^2 value for testing the significance.

III. Transformation of correlated values

Transformation was done by using the pivotal consideration method. The correlated variables first transformed into uncorrelated once and then D^2 values were calculated.

IV. Computation of D^2 values

The obtained D^2 value for a pair of population was taken as the calculated value of X^2 and then tested against the tabulated value of X^2 at P degree of freedom, where “P” was considered as the number of traits.

V. Contribution of individual characters towards divergence

In all combinations, each trait was ranked on the basis of $d_i = Y_{ij} - Y_{ik}$ values and rank 1 was given to highest mean difference, where “P” was considered as the number of traits.

VI. Grouping of genotypes into various clusters: Tocher's method

Populations are categorized in order to their relative genetic distance from each other. In first step grouping of various varieties into distinct clusters. The two populations having the least distance from each other from the first two populations is added, then comes the fourth population and so on. There is disrupt increase in the average D^2 at certain stage by adding a particular population, and then this population is not added in the cluster.

Similarly, second cluster is formed. The process is continuing till all the populations are included into one or other cluster.

VII. Average intra cluster distance

The formula was used for measuring the intra cluster distance as follows:

$$\sum D_i^2/n$$

Where,

$\sum D_i^2/n$ is the sum of distance between all possible contributions (n) of the population included in the cluster.

VIII. Average inter cluster distance

At first, the distance clusters were measured. The clusters were taken one by

one and their distances from another cluster were calculated.

IX. Determination of group constellation or clusters

Categorization of the population into different clusters was done by using Tocher's method, as described by Rao (1948). The criterion used in this clustering method is that any two variables belonging to the same cluster should at least on average, show a smaller D^2 value than those belonging to the different cluster. For this purpose D^2 values of the combinations of each genotypes were arranged in ascending order of their magnitudes in tabular form. To start with, two populations having the smallest distance from each other were considered to which a third population having the smaller D^2 value from the first two populations was added. Similarly, next the nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2 , that population was not considered for, in that cluster. The groups of the first cluster were then omitted and the rest were treated in a similar way. This process was continuing till all the populations were included in to one of the other cluster. After the formation of the clusters, the average inter cluster and intra cluster divergences (distance) were calculated. The square root of the D^2 value obtained from the above, represent the D-values between and within clusters.

X. Average intra-cluster distance

For the measurement of intra cluster distances, the formula used was $\sum_i D_i^2/n$ where $\sum_i D_i^2/n$ was the sum of distance between all possible combination (n) of the populations included in a cluster.

XI. Average inter-cluster distances

Clusters are taken one by one and their distances from other clusters were calculated. The distance between the two clusters was the sum of the D^2 values between the members of the other, divided by the product of number of genotypes in both the clusters under consideration.

3.8.9 Principal Components Analysis

It is the multivariate statistical analysis to reduce data size with large number of correlated variables into a comparatively smaller set of new variables through linear combination of variables, that accounts most of variation present in the original variables. Principal components are usually estimated either from correlation or covariance matrix. When the variables are measured in various units, scale effects

can influence the composition of the derived components. In such conditions it becomes desirable to standardize the different variables. In the present study, correlation matrix was used to extract principal components.

Principal Component Analysis is a well-known method of dimension reduction (Massey, 1965; Jolliffe, 1986), which seeks linear combinations of the columns of X with maximal variance or equivalently, high information. It is routinely applied in chemometrics with the goal of providing the most compact representation of the data. The original p variables $X = [x_1 \dots x_p]$ are transformed in a new predictor set $T = [t_1 \dots t_k]$, with $k \leq \min(n-1, p)$. The new variables t_j , called scores, are a weighted average of the original X variables. The principal components are the eigenvectors, u_j from the Eigen decomposition of $X'X$ (and of the sample covariance matrix S , up to a constant). PCA sequentially maximizes the variance of a linear combination of the original predictor variables.

$$U_j = \arg \max_{u=1} \text{Var}(Xu),$$

Subject to the constraint that $u' u_i = 0$ for all $1 \leq i < j$. This ensures that $t_j = Xu_j$ is uncorrelated with all the previous linear combinations $t_i = Xu_i$. The principal components are ordered in terms of the amount of variation of the original data they account for. The first principal component direction has the property that $t_1 = Xu_1$ has the largest sample variance among all normalized linear combinations of the columns of X . Each subsequent component gives combinations with the largest possible variance which is uncorrelated with those that have been taken earlier.

This is because the number of required components is usually much less than the total possible number ($k \ll p$). In fact, the NIPALS algorithm does not calculate all the principal components at once, but it first calculates t_1 and u_1 from the X matrix. Then the outer product $t_1 u_1'$ is subtracted from X and the residual X_2 is calculated. In turn, this residual can be used to calculate t_2 and u_2 .

CHAPTER 4:
RESULT

CHAPTER 4: RESULT

The present investigation entitled “**Genetic Assessment for Quantitative and Physiological Traits of *desi* Chickpea**” was carried out with 40 *desi* Chickpea genotypes, grown under RCBD (Randomized Complete Block Design) in two replications at Seed Breeding Farm of Department of Plant Breeding and Genetic, JNKVV, Jabalpur during *Rabi* 2020-21.

To understand variability in better way, experiment was conducted on genetic variability parameters. Performed correlation analysis to get an idea about degree of association among various characters. Conducted path coefficient analysis, to determine the direct - indirect effects of various types of independent traits on the dependent one. Divergence (D^2) analysis was conducted to measure diversity at the inter and intra cluster levels between diverse chickpea genotypes, which give an idea to select genotypes for future crop improvement programmes. Studying chickpea genotypes on the basis of principal component analysis (PCA), informed type and magnitude of the variation available in selected plant population. The quantitative and qualitative data of various traits under experimentation were analyzed with the help of some standard statistical procedures. The experiment results obtained from present investigation are presented under the following headings:

4.1 Morphological characterization of traits

4.2 Genetic variability parameters

4.2.1 Analysis of Variance

4.2.2 Mean and Range

4.2.3 Genotypic and Phenotypic Coefficient of Variation

4.2.4 Heritability (%)

4.2.5 Genetic Advance as Percentage of Mean (%)

4.3 Correlation analysis

4.4 Path coefficient analysis

4.5 Genetic divergence (D^2) analysis

4.6 Principal component analysis

4.1 Morphological characterization of traits

40 *desi* Chickpea genotypes (including 4 checks) in two replications were evaluated and scored on the basis of morphological characters at both plant level and seed level, as per DUS guideline and result of the current study are revealed in table 4.1: -

4.1.1 At Plant level

4.1.1.1 Stem: Anthocyanin Coloration

Stem anthocyanin coloration was recorded before the flowering stage with various scoring point of 1, for absent and 9, for presence of anthocyanin coloration, in all studied 40 chickpea genotypes.

4.1.1.2 Stem: Height at initiation of first flower

To measure stem height at initiation of first flower, number of nodes was counted at first flowering of the plant. As per DUS guidelines of chickpea, there are three types of number of nodes noticed in chickpea. In present investigation out of 40 genotypes, 15 genotypes had low (<8 nodes), 18 genotypes had medium (8-15 nodes), while 7 genotypes had high (>15 nodes).

4.1.1.3 Growth habit

In relation to plant growth habit, out of studied 40 genotypes, ICCV 201201, ICCV 201205, ICCV 201207, ICCV 201208, ICCV 201101 and ICCV 201112 observed as spreading (61-80° from vertical) type growth habit. Thirty-four genotypes had semi-erect (16- 60° from vertical) growth habit.

4.1.1.4 Foliage color

Out of 40 genotypes, 14 genotypes light green, 12 genotypes medium green and 14 genotypes contained dark green type of foliage color.

4.1.1.5 Leaflet size (mm)

Leaflet size observed small (<10mm) in 8 genotypes, while two genotypes *i.e.* ICCV 201117 and JG 24 noticed large (>15mm) leaflet size, whereas remaining 30 genotypes had medium type of leaflet size.

4.1.1.6 Leaf pattern

In chickpea plant, there are majorly three types of leaf patterns *viz.*, simple, compound and pinnate. In the present experimentation, all of the 40 genotypes had pinnate type of leaf pattern.

4.1.1.7 Flower: Number per peduncle

All the investigated *desi* chickpea genotypes had single flower per peduncle.

4.1.1.8 Flower color

In Chickpea plant usually three types of flower color are predominant *i.e.* white, pink and blue color flower. Although in this experiment all the 40 *desi* chickpea genotypes had pink color of flower.

4.1.1.9 Flower: Stripes on standard

In current investigation all the *desi* chickpea genotypes were having stripes on standard, which further scored 1 means absence and 9 presence of stripes on standard.

4.1.1.10 Peduncle length (mm)

In the current study out of 40 *desi* Chickpea genotypes, 25 genotypes had medium (5-10 mm) peduncle length, whereas 15 genotypes had large long (>10 mm) peduncle length.

4.1.1.11 Pod size (mm)

Out of investigated 40 genotypes, ICCV 201202, ICCV 201208 and ICCV 201209 had short (<15 mm) pod size, whereas 15 genotypes were of large (>20 mm) pod size, while remaining 22 genotypes had medium pod size.

4.1.1.12 Lodging resistance (%)

Lodging resistance was estimated in percentage of the total lodged plants per plot. It was observed by visual evaluation of plants per plot basis and categorized into six groups. Eighteen genotypes showed highly resistant (no lodging), 14 genotypes resistant (1-10%), 5 genotypes moderately resistant (11-20%) , 2 genotypes moderately susceptible (21- 30%) genotypes, while only one genotype were susceptible (31-50%) for lodging.

4.1.1.13 Shattering resistance (%)

Investigated all the chickpea genotypes were resistance for shattering.

4.1.2 At seed level

4.1.2.1 Seed type

All the 40 genotypes under investigation were *desi* type of chickpea genotypes.

4.1.2.2 Seed coat color

Seed coat color observed after harvesting at fully dried seed stage with the help of Fan 4 (Greyed Orange Group) according to the Royal Horticulture Society, London (2001) color chart. As a result 5 genotypes had 164(A) - Brownish Orange type color, 2 genotypes had 164(B) - Dark Orange-Yellow type color, 4 genotypes had 164(C) - Moderate Orange-Yellow type color, 5 genotypes had 165(A) - Moderate Brown type color, 21 genotypes had 165(B) - Brownish Orange type color, only 1 genotypes had 166(B) - Moderate Reddish-Brown type color and 2 genotypes had 166(C) - Grayish Reddish-Orange type of color.

4.1.2.3 Seed shape

All the investigated *desi* chickpea genotypes had seed shape of angular type.

4.1.2.4 Seed Texture

All the investigated *desi* chickpea genotypes had smooth type of seed texture.

4.1.2.5 Seed ribbing

In all of the 40 chickpea genotypes under experimentation had presence of ribbing on seed surface.

4.1.2.6 Seed size

Out of investigated 40 genotypes, only one genotype had very small (<15 g) seed size, 3 genotypes had small (15-18 g) seed size, 22 genotypes had medium (19-24 g) seed size, 12 genotypes had large (25-30 g) seed size and only two genotypes *i.e.* ICCV 201210 and JG 24 had very large (>30 g) type of seed size.

Table 4.1 Frequency Distributions of Different Morphological and Seed Characters of Studied *desi* Chickpea Genotypes

S. No.	Characters	Score	Genotype frequency	Percentage contribution (%)
1.	Stem: Anthocyanin Coloration			
	Absent	1	-	-
	Present	9	40	100.0
2.	Stem: Height at the initiation of first flower			
	Low (<8 nodes)	3	15	37.5
	Medium (8-15 nodes)	5	18	45.0
	High (>15 nodes)	7	7	17.5
3.	Plant: Growth habit			
	Erect (0- 15 ° from vertical)	3	-	-
	Semi-erect (16- 60° from vertical)	5	34	85.0
	Spreading (61-80° from vertical)	7	6	15.0
4.	Plant: Color of foliage			
	Light green	1	14	35.0
	Medium green	2	12	30.0
	Dark green	3	14	35.0
	Greenish purple	4	-	-
5.	Leaflet: Size (mm)			
	Small (<10mm)	3	8	20.0
	Medium(10-15mm)	5	30	75.0
	Large (>15mm)	7	2	5.0
6.	Leaf: Pattern			
	Simple	1	-	-
	Compound	2	-	-
	Pinnate	3	40	100.0
7.	Flower: Number per peduncle			
	Single	1	40	100.0
	Twin	3	-	-
8.	Flower: Color			
	White	1	-	-
	Pink	2	40	100.0
	Blue	3	-	-
9.	Flower: Stripes on standard			
	Absent	1	-	-
	Present	9	40	100.0
10.	Peduncle: Length			
	Short (<5 mm)	3	-	-
	Medium (5-10 mm)	5	25	62.5
	Long (>10 mm)	7	15	37.5
11.	Plant: Height			
	Short (<45 cm)	3	3	7.5
	Medium (45-65 cm)	5	34	85.0

	Tall (>65 cm)	7	3	7.5
12.	Pod: Size (length)			
	Short (<15 mm)	3	3	7.5
	Medium (15-20 mm)	5	22	55.0
	Large (>20 mm)	7	15	37.5
13.	Seed: Type			
	<i>Desi</i>	1	40	100.0
	<i>Kabuli</i>	3	-	-
14.	Seed: Shape			
	Owl 's head	2	-	-
	Angular	3	40	100.0
15.	Seed: Color {according to The Royal Horticulture Society, London (2001) color chart}			
	164(A) – Brownish Orange	1	5	12.5
	164(B) – Dark Orange-Yellow	2	2	5.0
	164(C) - Moderate Orange-Yellow	3	4	10.0
	165(A) – Moderate Brown	4	5	12.5
	165(B) – Brownish Orange	5	21	52.5
	166(B) – Moderate Reddish-Brown	6	1	2.5
	166(C) – Grayish Reddish-Orange	7	2	5.0
16.	Seed: Testa texture			
	Rough	1	-	-
	Smooth	2	40	100.0
	Tuberculated	3	-	-
17.	Seed: Ribbing			
	Absent	1	-	-
	Present	9	40	100.0
18.	Seed: Size			
	Very small (<15 g)	1	1	2.5
	Small (13-18 g)	3	3	7.5
	Medium (19-24 g)	5	22	55
	Large (25-30 g)	7	12	30
	Very large (>30 g)	9	2	5.0
19.	Lodging Resistance (%)			
	Highly Resistant	No lodging	18	45
	Resistant	1-10	14	35
	Moderately resistant	11-20	5	12.5
	Moderately Susceptible	21- 30	2	5.0
	Susceptible	31-50	1	2.5
	Highly Susceptible	51-100	-	-
20.	Shattering resistance (%)			
	Highly Resistant	No shattering	40	100.0
	Resistant	1-10	-	-
	Moderately resistant	11-20	-	-
	Moderately Susceptible	21- 30	-	-
	Susceptible	31-50	-	-
	Highly Susceptible	51-100	-	-

Fig. 4.1: Anthocyanin Coloration

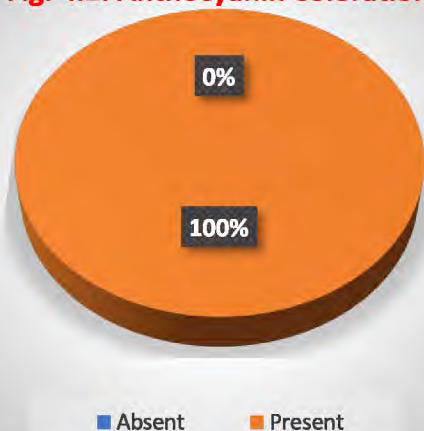


Fig. 4.2: Stem: Height at the initiation of first flower

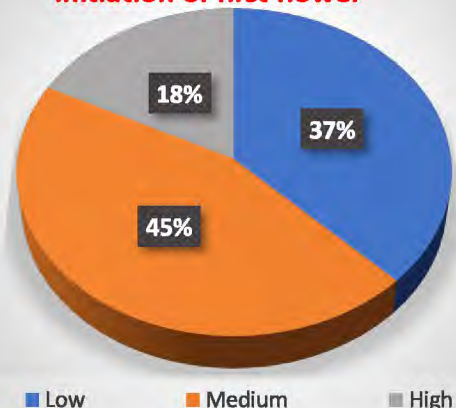


Fig. 4.3: Plant: Growth habit

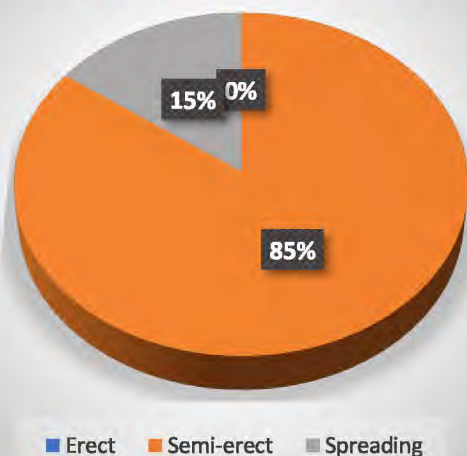


Fig. 4.4: Plant: Color of foliage

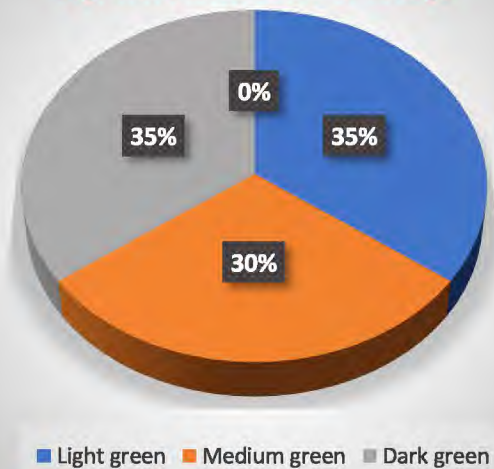


Fig. 4.5: Leaf: Pattern



Fig. 4.6: Leaflet: Size

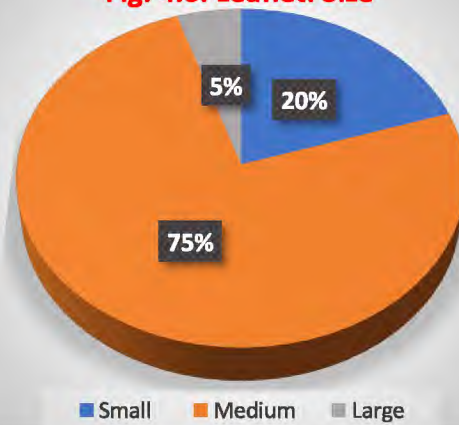


Fig. 4.7: Flower: Number per peduncle

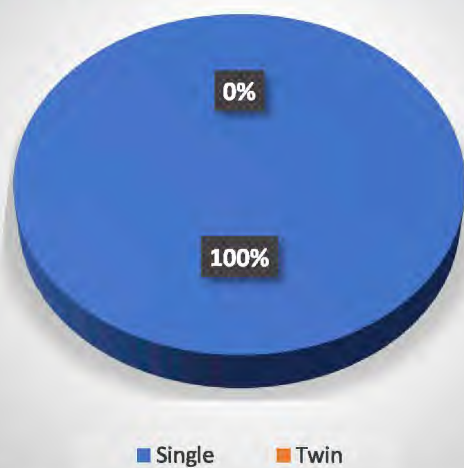


Fig. 4.8: Flower: Color

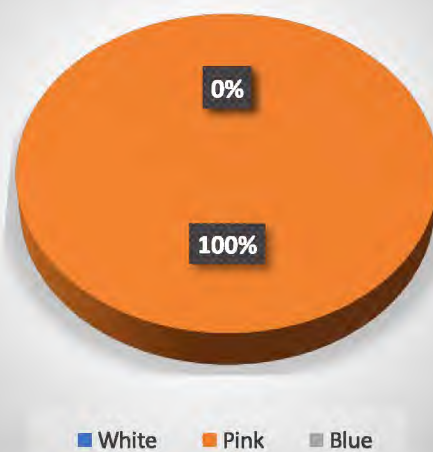


Fig. 4.9: Flower: Stripes on standard

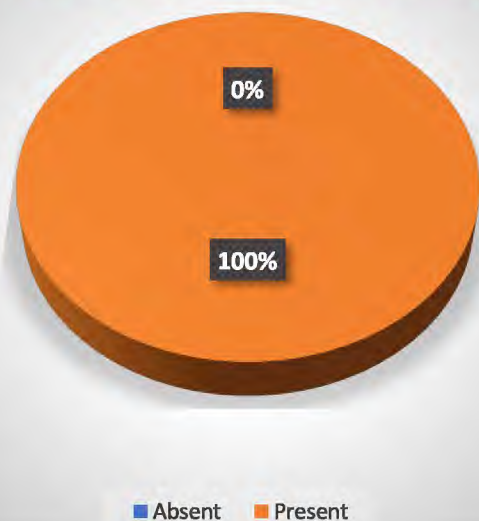


Fig. 4.10: Peduncle: Length

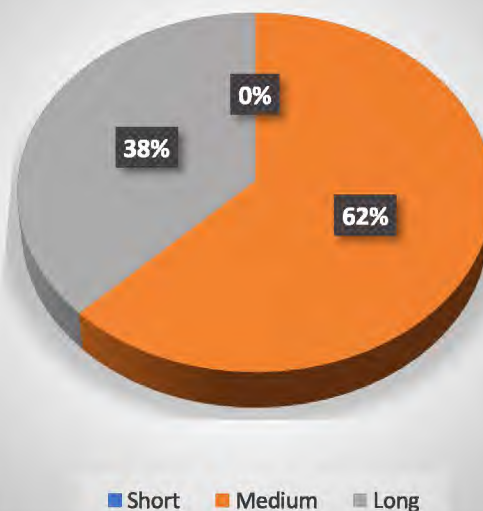


Fig. 4.11: Plant: Height

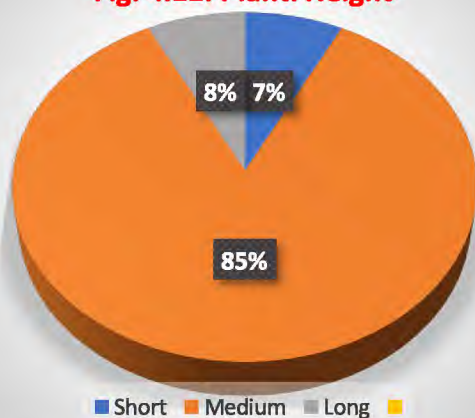


Fig. 4.12: Pod: Size (length)

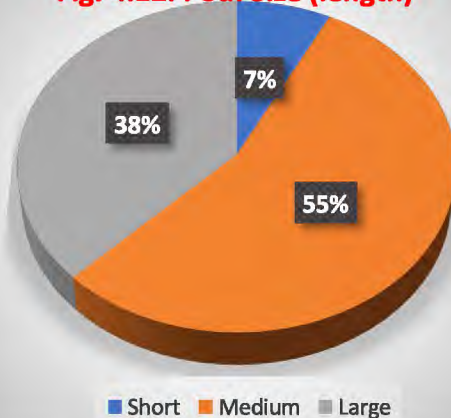


Fig. 4.13: Seed: Type

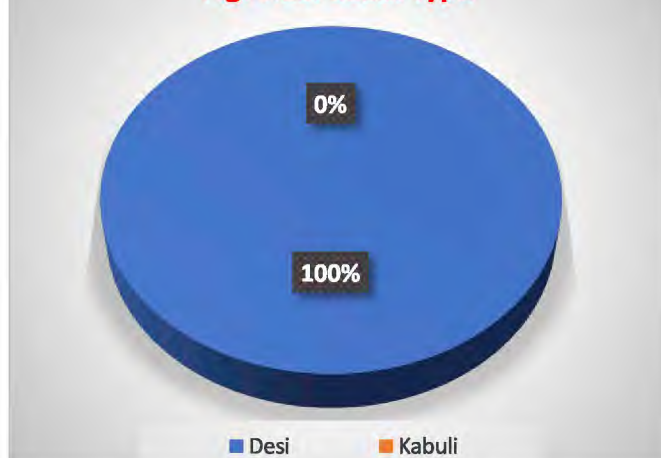


Fig. 4.14: Seed: Shape



Fig. 4.15: Seed: Color

{according to The Royal Horticulture Society, London (2001) color chart}

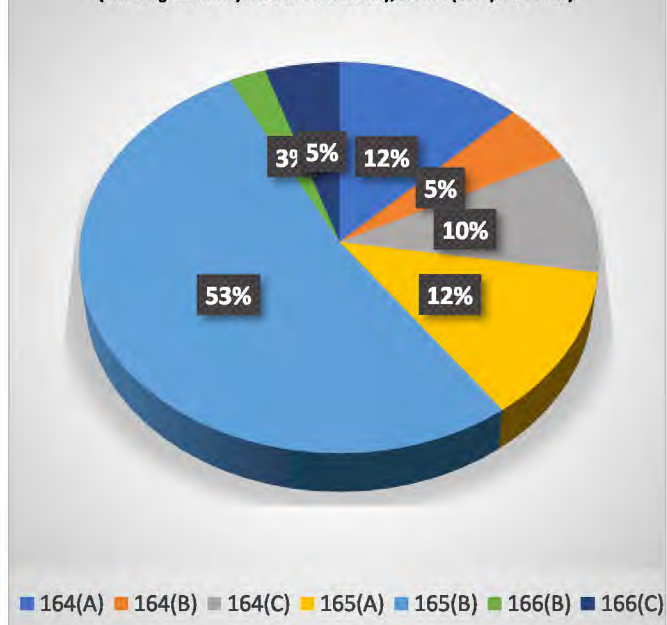


Fig. 4.16: Seed: Testa texture

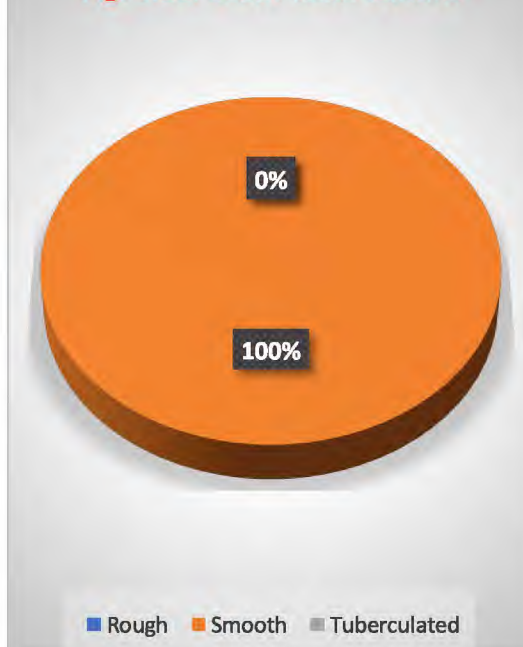


Fig. 4.17: Seed: Size

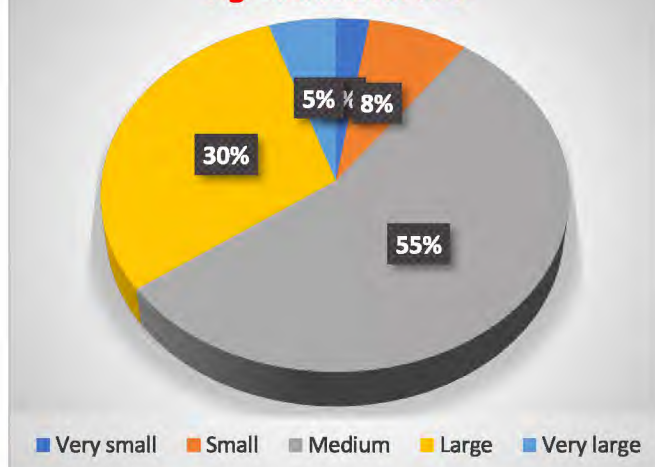


Fig. 4.18: Seed: Ribbing



Fig. 4.19: Lodging Resistance

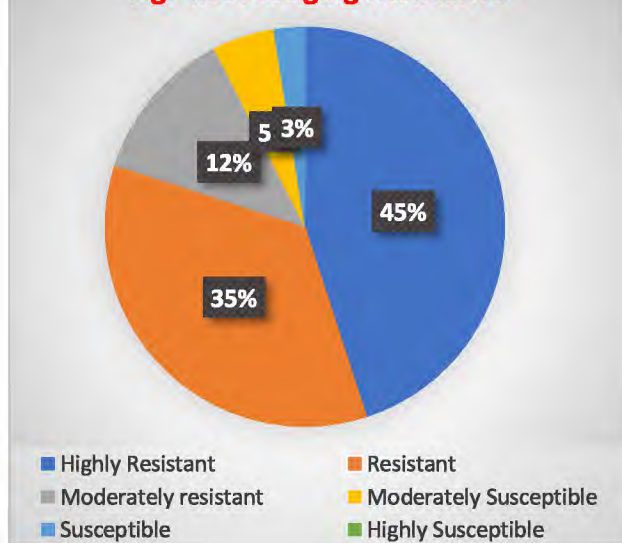
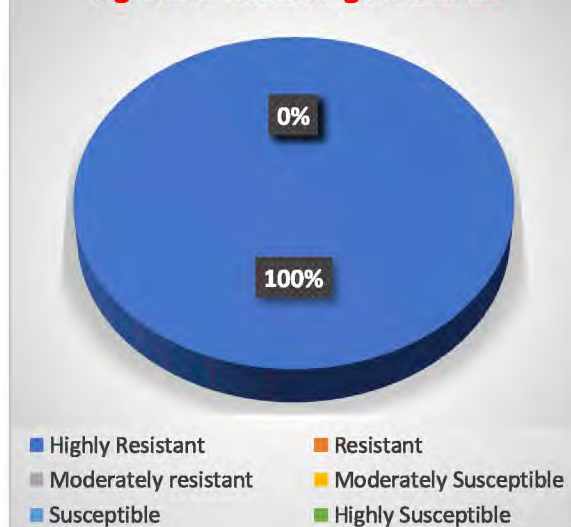


Fig. 4.20: Shattering resistance



4.2 Genetic variability parameters

The Genetic variability parameters *i.e.* range, mean, genotypic coefficient of variation %, phenotypic coefficient of variation %, heritability %, genetic advance and genetic advance as a percentage of mean %, were calculated for all the studied traits and are exhibited the in table 4.2

4.2.1 Analysis of Variance

Analysis of variance used to define observable differences in individuals for a particular trait and it partitioned the total variation into various available sources of variations. The ANOVA study indicated that mean sum of square (MSS) due to various genotypes showed significance for all the investigated traits *viz.*, days to 50% flowering, days to maturity, plant height, height of first fruiting node, total number of pods per plant, number of effective pods per plant, 100 seed weight, biological yield per plant, harvest index and seed yield per plant. In order to know the variation extent of observed traits among 40 *desi* chickpea genotypes, analysis of variance study was performed and presented in table 4.3

4.2.2 Mean and Range

Performance of different characters on basis of their mean and range, have presented in table 4.2. Days to 50% flowering ranged from 66 days to 83 days with mean 74 days. Days to maturity showed mean value of 120 days and varied from 110 days to 131 days. Plant height varied from 38.3 cm to 68.1 cm with 53.09 cm mean value. The degree of dispersion for height of first fruiting node varied from 15.3 cm to 36.9 cm with 24.8 cm mean value. Stem thickness ranged from 1.93 mm to 3.19 mm with 2.6 mm mean value. Number of primary branches per plant showed 2.97 mean value and varied from 2.26 to 3.67. Number of secondary branches per plant was dispersed from 6.33 to 12.99 with 10.29 mean value. Total number of pods per plant was observed in range from 41.0 to 96.3 with an average of 58.5. Number of effective pods per plant had a mean value of 55.1 and ranged from 39.0 to 94.4. Number of seeds per pod varied from 1.03 to 1.82 with the mean value of 1.23. The dispersion of 100 seed weight ranged from 15.4 to 39.6 with 23.5 mean value. Biological yield per plant was recorded with mean 32.4 g and ranged from 22.6 g to 54.0 g. Harvest index had an average of 41.5% with the range of 25.7% minimum and 64.7% maximum. Seed yield per plant showed range from 10.0 g to 22.6 g with an average performance of 13.3 g.

4.2.3 Genotypic and Phenotypic Coefficient of Variation (GCV% and PCV%)

Genotypic coefficient of variation and Phenotypic coefficient of variation for the yield and contributing traits are presented in table 4.2. Usually, phenotypic variance must be higher than the genotypic variance. The same kind of pattern was recorded in the present investigation of all the traits.

The highest value of PCV% and GCV% recorded respectively for number of effective pods per plant (28.5% and 28.3%), total number of pods per plant (27.4% and 27.3%), seed yield per plant (22.6% and 20.2%), biological yield per plant (21.8% and 20.2%), height of first fruiting node (20.6% and 19.4%), harvest index (18.7% and 17.8%), 100 seed weight (17.9% and 17.4%), number of secondary branches per plant (14.6% and 12.3%), plant height (13.9% and 13.2%), stem thickness (12.8% and 11.9%), number of primary branches per plant (12.5% and 10.7%), number of seeds per pod (11.3% and 10.3%), days to 50% flowering (6.2% and 5.9%), days to maturity (4.7% and 4.6%).

Table 4.2: Genetic Variability Parameters for Yield with Component Traits of Yield

S.No.	Traits	Range		Grand Mean	Coefficient of Variation		h ² (bs) %	Genetic Advance as % of Mean
		Minimum	Maximum		GCV %	PCV %		
1.	DTF	66	83	74	5.9	6.2	88.8	11.4
2.	DTM	110	131	120	4.6	4.7	94.4	9.2
3.	PH	38.3	68.1	53.0	13.2	13.9	89.9	25.8
4.	HFFN	15.3	36.9	24.8	19.4	20.6	88.4	37.6
5.	ST	1.93	3.19	2.6	11.9	12.8	86.7	22.9
6.	PB	2.26	3.67	2.97	10.7	12.5	73.1	18.9
7.	SB	6.33	12.99	10.2	12.3	14.6	70.9	21.4
8.	TNPPP	41.0	96.3	58.5	27.3	27.4	98.7	55.8
9.	NEPP	39.0	94.4	55.1	28.3	28.5	98.8	58.0
10	NSPP	1.03	1.82	1.2	10.3	11.3	83.3	19.5
11.	100SW	15.4	39.6	23.5	17.4	17.9	95.1	35.1
12.	BY	22.6	54.0	32.4	20.2	21.8	85.6	38.5
13.	HI%	25.7	64.7	41.5	17.8	18.7	90.2	34.8
14.	SYPP	10.04	22.6	13.3	20.2	22.6	79.7	37.1

Table 4.3 Analysis of Variance

Source of variation	d.f	Mean sum of squares						
		DTF	DTM	PH	HFFN	ST	PB	SB
Replication	1	7.81	14.45	14.02	6.10	0.00	0.01	1.52
Treatment	39	40.84**	63.89**	103.78**	49.37**	0.21	0.24	3.88
Error	39	2.40	1.83	5.46	3.01	0.01	0.03	0.66
Source of variation	d.f	Mean sum of squares						
		TNPPP	NEPP	NSPP	100SW	BY	HI%	SYPP
Replication	1	0.01	1.74	0.02	0.36	2.34	10.02	6.30
Treatment	39	514.48**	491.21**	0.03	34.92**	93.64**	115.49**	16.39**
Error	39	3.30	2.79	0.03	0.86	7.24	5.89	1.84

*Means Significance 5% and ** means Significance at 1%

Where,

DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), HFFN: Height of first fruiting node (cm), ST: Stem thickness (mm), PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPP: Number of effective pods per plant, NSPP: Number of seeds per pod, 100SW: 100 Seed weight, BY: Biological yield per plant (g), HI: Harvest index (%) and SYPP: Seed yield per plant (g)

4.2.4 Heritability (%)

Heritability (broad sense) has been classified as low (<50%), moderate (50% - 70%) and high (>70%) heritability of trait. The recorded observations of heritability (bs) for the yield and it's contributing traits shown in table 4.2.

Highest heritability (bs) was recorded for number of effective pods per plant (98.8%), total number of pods per plant (98.7%), 100 seed weight (95.1%), days to maturity (94.4%), harvest index (90.2%), plant height (89.9%), days to 50% flowering (88.8%), height of first fruiting node (88.4%), stem thickness (86.7%), biological yield per plant (85.6%), number of seed per pod (83.3%), seed yield per plant (79.7%), number of primary branches per plant (73.1%) and number of secondary branches per plant (70.9%).

4.2.5 Genetic Advance as Percentage of Mean

Genetic advance (as % of means) was extended from 9.2% to 58.0%. The maximum was obtained for number of effective pods per plant (58.0%) then total number of pods per plant (55.8%), biological yield per plant (38.5%), height of first fruiting node (37.6%), seed yield per plant (37.1%), 100 seed weight (35.1%), harvest index (34.8%), plant height (25.8%), stem thickness (22.9%), number of secondary branches per plant (21.4%), number of seeds per pod (19.5%), number of primary branches per plant (18.9%), days to 50% flowering (11.4%) and days to maturity (9.2%) recorded with minimum genetic advance as % of mean in current investigation.

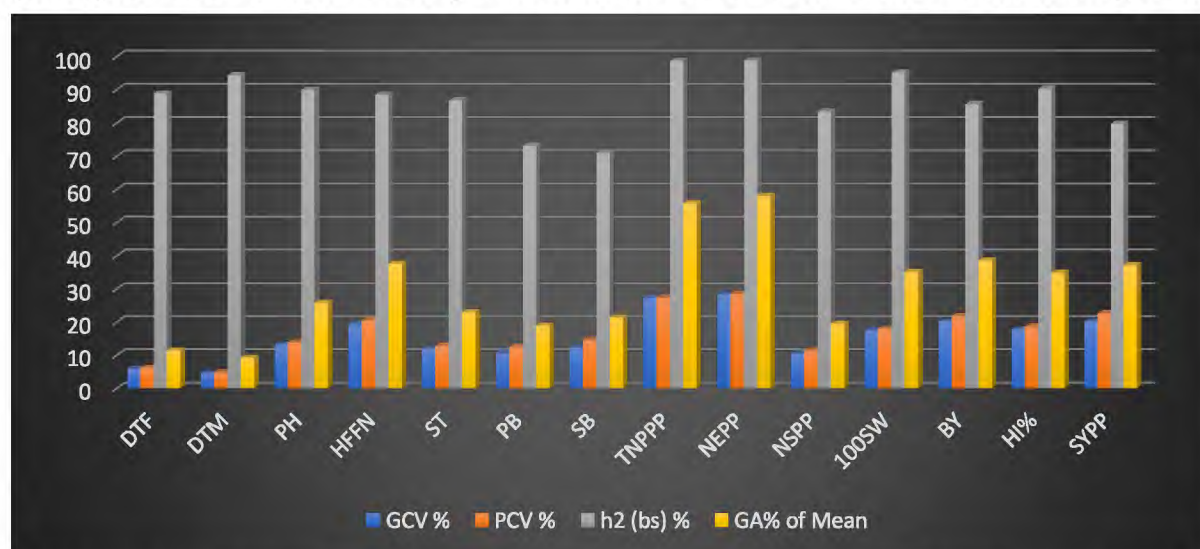


Fig. 4.21: Graphical Representation of GCV %, PCV %, Heritability % and Genetic Advance as % of Mean

4.3 Correlation Coefficient Analysis

Correlation coefficient analysis is one of important the statistical tool, which provides direction and degree of relationship between the variables at phenotypic, genotypic and environmental levels. It gives information about nature, direction and extent of selection pressure to be applied for practical consideration. Phenotypic and genotypic correlation coefficients for various yield and contributing traits of yield were estimated, by taking seed yield per plant as dependent variable in the correlation analysis. Phenotypic correlation can be defined as the association between two variables, which estimated using phenotypic variance and covariance. It provides direction and degree of relationship between different variables at phenotypic level, whereas the genotypic correlation indicates heritable association between traits.

4.3.1 Correlation Coefficient Analysis of Quantitative – Yield Attributing Traits: -

4.3.1.1 Days to 50% flowering

Days to 50% flowering exposed positive-significant association with the days to maturity (0.816), height of first fruiting node (0.596) and hundred seed weight (0.403). whereas, negative-significant correlation was rcordeed for number of effective pods per plant (-0.471), total number of pods per plant (-0.465) and stem thickness (-0.299).

4.3.1.2 Days to maturity

It showed positive, significant correlation with character height of first fruiting node (0.590) , whereas negative-significant correlation was noticed for number of effective pods per plant (-0.496), total number of pods per plant (-0.482) and stem thickness (-0.290).

4.3.1.3 Plant height

Plant height exhibited positive, significant correlation with height of first fruiting node (0.545), number of seeds per pod (0.410), stem thickness (0.269) and hundred seed weight (0.255). However, total number of pods per plant (-0.273) and number of effective pods per plant (-0.260) demonstrated significant and negative correlation.

4.3.1.4 Height of first fruiting node

Height of first fruiting node revealed positive, significant correlation with trait number of seed per plant(0.559), hundred seed weight (0.326), harvest index (0.224),

whereas, trait total number of pods per pod (-0.355) and number of effective pods per plant (-0.349) had significant, negative correlation.

4.3.1.5 Stem thickness

It expressed positive, significant correlation with harvest index (0.336). however, had negative-significant association with the number of secondary branches per plant (-0.237).

4.3.1.6 Number of primary branches per plant

Number of primary branches per plant exposed positive association with the character number of secondary branches per plant (0.564). However, it revealed the non-significant correlation with the other traits.

4.3.1.7 Number of secondary branches per plant

Number of secondary branches per plant had the positive, significant correlation with trait biological yield per plant (0.499) and seed yield per plant (0.308). whereas, it showed negative, significant correlation with trait harvest index (-0.264).

4.3.1.8 Total number of pods per plant

Number of effective pods per plant (0.994), seed yield per plant (0.441) and trait biological yield per plant (0.330) showed positive-significant correlation. Although, hundred seed weight (-0.295) had negative, significant correlation with trait total number of pods per plant.

4.3.1.9 Number of effective pods per plant

Seed yield per plant (0.443) followed by trait biological yield per plant (0.338) exhibited positive, significant correlation, whereas 100 seed weight (-0.288) showed negative, significant correlation with trait number of effective pods per plant.

4.3.1.10 Number of seeds per pod

Number of seeds per pod found with positive-significant association with the trait seed yield per plant (0.594), harvest index (0.447) and with biological yield (0.284).

4.3.1.11 Hundred Seed weight

Hundred seed weight showed non-significant correlation with different characters.

4.3.1.12 Biological yield per plant

Biological yield per plant expressed positive-significant relation with seed yield per plant (0.639). However, showed negative, significant correlation with harvest index (-0.375).

4.3.1.13 Harvest index

Harvest index reported with positive, significant correlation with the trait seed yield per plant (0.442).

Table 4.4: Phenotypic Correlations Coefficient for the Yield and Attributing Traits of Yield in *desi* Chickpea Genotypes

	DTF	DTM	PH	HFFN	ST	PB	SB	TNPPP	NEPP	NSPP	100SW	BY	HI%	SYPP
DTF	1.000	0.816**	0.181	0.596**	-0.299**	-0.126	0.018	-0.465**	-0.471**	0.180	0.403**	0.004	-0.141	-0.163
DTM		1.000	0.151	0.590**	-0.290**	-0.166	-0.046	-0.482**	-0.496**	0.197	0.218	-0.159	0.007	-0.173
PH			1.000	0.545**	0.269*	-0.043	-0.042	-0.273*	-0.260*	0.410**	0.255*	-0.059	0.193	0.080
HFFN				1.000	0.157	-0.096	-0.000	-0.355**	-0.349**	0.559**	0.326**	-0.037	0.224*	0.096
ST					1.000	-0.107	-0.237*	-0.073	-0.061	0.206	0.056	-0.084	0.336**	0.152
PB						1.000	0.564**	0.103	0.132	-0.089	0.105	0.198	-0.100	0.133
SB							1.000	0.112	0.139	0.202	0.017	0.499**	-0.264*	0.308**
TNPPP								1.000	0.994**	-0.067	-0.295**	0.330**	0.091	0.441**
NEPP									1.000	-0.073	-0.288**	0.338**	0.083	0.443**
NSPP										1.000	0.127	0.284*	0.447**	0.594**
100SW											1.000	0.062	-0.056	-0.006
BY												1.000	-0.375**	0.639**
HI%													1.000	0.442**
SYPP														1.000

* Means Significant at 5% and ** means significant at 1%

Where,

DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), HFFN: Height of first fruiting node (cm), ST: Stem thickness (mm), PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPP: Number of effective pods per plant, NSPP: Number of seeds per pod, 100SW: 100 Seed weight, BY: Biological yield per plant (g), HI: Harvest index (%) and SYPP: Seed yield per plant (g).

Table 4.5: Genotypic Correlations Coefficient for the Yield and Attributing Traits of Yield in *desi* Chickpea Genotypes

	DTF	DTM	PH	HFFN	ST	PB	SB	TNPPP	NEPP	NSPP	100SW	BY	HI%	SYPP
DTF	1.000	0.883	0.203	0.641	-0.355	-0.115	0.026	-0.490	-0.502	0.192	0.439	-0.020	-0.142	-0.192
DTM		1.000	0.179	0.635	-0.345	-0.221	-0.049	-0.497	-0.512	0.228	0.222	-0.160	-0.006	-0.195
PH			1.000	0.568	0.310	-0.062	-0.020	-0.284	-0.271	0.519	0.273	-0.059	0.225	0.113
HFFN				1.000	0.163	-0.121	-0.008	-0.383	-0.372	0.625	0.374	-0.061	0.257	0.136
ST					1.000	-0.170	-0.307	-0.083	-0.064	0.319	0.055	-0.070	0.382	0.222
PB						1.000	0.745	0.123	0.161	-0.076	0.128	0.235	-0.164	0.163
SB							1.000	0.104	0.133	0.119	0.038	0.539	-0.450	0.172
TNPPP								1.000	0.997	-0.086	-0.305	0.360	0.079	0.475
NEPP									1.000	-0.095	-0.299	0.363	0.068	0.471
NSPP										1.000	0.156	0.281	0.481	0.640
100SW											1.000	0.089	-0.069	-0.003
BY												1.000	-0.422	0.640
HI													1.000	0.420
SYPP														1.000

Where,

DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), HFFN: Height of first fruiting node (cm), ST: Stem thickness (mm), PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPP: Number of effective pods per plant, NSPP: Number of seeds per pod, 100SW: 100 Seed weight, BY: Biological yield per plant (g), HI: Harvest index (%) and SYPP: Seed yield per plant (g).

4.3.2 Correlation Coefficient Analysis of Physiological-Yield Attributing Traits: -

4.3.2.1 Relative growth rate

It showed significant, positive correlation with trait crop growth rate (0.967), biomass duration (0.963), leaf area index (0.536), leaf area duration (0.518), leaf area index duration (0.518), leaf area ratio (0.419), seed yield per plant (0.357) and chlorophyll content (0.265). While, net assimilation rate (-0.857) exhibited significant negative association with relative growth rate.

4.3.2.2 Leaf area ratio

LAR exhibited positive, significant correlation with the physiological trait leaf area index (0.474), leaf area duration (0.341), leaf area index duration (0.341) and chlorophyll content (0.263). However, LAR revealed negative, significant correlation with biomass duration (-0.441), net assimilation rate (-0.405) and crop growth rate (-0.384).

4.3.2.3 Leaf area index

LAI exhibited positive significant correlation with leaf area duration (0.976), leaf area index duration (0.975), biomass duration (0.798), crop growth rate (0.783) and chlorophyll content (0.410) and showed negative significant correlation with net assimilation rate (-0.276).

4.3.2.4 Net assimilation rate

It revealed significant, positive association with the trait crop growth rate (0.912) and biomass duration (0.818) while, negative significant correlation with leaf area duration (-0.280), leaf area index duration (-0.280) and trait seed yield (-0.277).

4.3.2.5 Crop growth rate

CGR exhibited positive, significant correlation with biomass duration (0.991), leaf area duration (0.770), leaf area index duration (0.770), seed yield per plant (0.351) and chlorophyll content (0.324).

4.3.2.6 Leaf area duration

It expressed positive, significant correlation with character leaf area index duration (1.00), biomass duration (0.786) and chlorophyll content (0.381).

4.3.2.7 Leaf area index duration

It showed positive, significant association with biomass duration (0.775) and chlorophyll content (0.381).

4.3.2.8 Biomass duration

It expressed positive, significant correlation with chlorophyll content (0.317) and with seed yield per plant (0.283).

4.3.2.9 Chlorophyll content

It showed positive, significant association with physiological maturity (0.248).

4.3.2.10 Physiological maturity

Expressed significant-negative relation with the number of effective plant per plant (-0.496).

4.3.2.11 Number of effective pods per plant

It exhibited significant, positive correlation with trait seed yield per plant (0.443).

4.3.2.12 Harvest index

It showed significant, positive association with trait seed yield per plant (0.442).

Table 4.6: Phenotypic Correlation Coefficient for Physiological and Attributing Characters of Yield in *desi* Chickpea Genotype

	RGR 1	RGR 2	LAR 1	LAR 2	LAI 1	LAI 2	LAI 3	NAR 1	NAR 2	CGR 1	CGR 2	LAD 1	LAD 2	LAID 1	LAID 2	BMD 1	BMD 2	CHL	PM	NEPP	HI%	SYPP
RGR 1	1.000	0.057	0.251*	0.260*	0.103	0.536**	0.476**	-0.355*	-0.205	0.682**	-0.031	0.498**	0.518**	0.498**	0.518**	0.684**	0.134	0.265*	-0.038	-0.122	0.104	0.254*
RGR 2		1.000	0.020	0.419**	0.091	0.180	0.178	0.022	-0.857**	0.067	0.967**	0.179	0.183	0.179	0.183	0.075	0.963**	0.120	-0.038	-0.182	0.038	0.357**
LAR 1			1.000	-0.059	0.474**	0.215	0.121	0.013	-0.073	0.214	-0.010	0.341*	0.172	0.341*	0.172	0.217	0.040	0.263*	-0.139	0.078	-0.027	0.113
LAR 2				1.000	-0.047	0.210	0.194	0.047	-0.405**	-0.280*	-0.384**	0.183	0.207	0.183	0.207	-0.275*	-0.441**	-0.104	-0.002	0.094	-0.081	0.205
LAI 1					1.000	0.218	0.193	0.164	-0.028	0.173	0.047	0.457**	0.211	0.457**	0.211	0.209	0.093	0.410**	0.163	-0.090	-0.053	-0.045
LAI 2						1.000	0.902**	0.215	-0.276*	0.783**	0.072	0.959**	0.975**	0.959**	0.975**	0.798**	0.258*	0.291*	-0.043	-0.126	0.161	0.203
LAI 3							1.000	0.231	-0.270*	0.720**	0.094	0.866**	0.976**	0.866**	0.976**	0.736**	0.265*	0.254*	-0.106	-0.134	0.079	0.102
NAR 1								1.000	-0.103	0.183	0.003	0.234	0.229	0.234	0.229	0.183	0.042	-0.004	-0.263	0.101	-0.037	0.001
NAR 2									1.000	0.318*	0.912**	-0.261*	-0.280*	-0.261*	-0.280*	0.317*	0.818**	-0.021	-0.025	-0.132	-0.060	-0.277*
CGR 1										1.000	-0.035	0.752**	0.770**	0.752**	0.770**	0.991**	0.200	0.324*	-0.053	-0.136	0.189	0.252*
CGR 2											1.000	0.070	0.085	0.070	0.085	-0.027	0.972**	0.085	-0.058	-0.170	0.012	0.351*
LAD 1												1.000	0.935**	1.000**	0.935**	0.775**	0.250*	0.381**	0.016	-0.132	0.131	0.177
LAD 2													1.000	0.935**	1.000**	0.786**	0.268*	0.279*	-0.077	-0.133	0.123	0.156
LAID 1														1.000	0.935**	0.775**	0.250*	0.381**	0.016	-0.132	0.131	0.177
LAID 2															1.000	0.786**	0.268*	0.279*	-0.077	-0.133	0.123	0.156
BMD 1																1.000	0.210	0.317*	-0.034	-0.128	0.212	0.251*
BMD 2																	1.000	0.155	-0.065	-0.200	0.061	0.283*
CHL																		1.000	0.248*	-0.225	0.116	-0.079
PM																			1.000	-0.496**	0.007	-0.173
NEPP																				1.000	0.083	0.443**
HI%																					1.000	0.442**
SYPP																						1.000

*Significant at 5% and ** means significant at 1%

RGR 1: Relative growth rate (30-60 days interval), RGR 2: Relative growth rate (60-90 days interval), LAR 1: Leaf area ratio (30-60 days interval), LAR 2: Leaf area ratio (60-90 days interval), LAI 1: Leaf area index (30 days), LAI 2: Leaf area index (60 days), LAI 3: Leaf area index (90 days), NAR 1: Net assimilation rate (30-60 days interval), NAR 2: Net assimilation rate (60-90 days interval), CGR 1: Crop growth rate (30-60 days interval), CGR 2: Crop growth rate (60-90 days interval), LAD 1: Leaf area duration (30-60 days interval), LAD 2: Leaf area duration (60-90 days interval), LAID 1: Leaf area index duration (30-60 days interval), LAID 2: Leaf area index duration (60-90 days interval), BMD 1: Biomass duration (30-60 days interval), BMD 2: Biomass duration (60-90 days interval), CHL: Chlorophyll, PM: Physiological maturity, NEPP: Number of effective pods per plant, HI: Harvest index, SYPP: Seed yield per plant

4.4 Path Coefficient Analysis

Path coefficient is the standardized partial regression coefficients and it provide the means to direct influence of one character upon another character. It also permits partitioning of correlation coefficient into direct - indirect effects *via* other characters. In the present investigation, during path coefficients analysis, seed yield per plant was kept as dependent variable, whereas remaining were independent variables. The analyzed estimates of genotypic path coefficient presented in table 4.7.

4.4.1 Path Coefficient Analysis of Quantitative – Yield Attributing Traits: -

4.4.1.1 Direct and Indirect effects

4.4.1.1.1 Days to 50% flowering

The direct contribution of trait days to 50% flowering on dependent variable seed yield per plant estimated negative (-0.2650) and it exhibited positive, indirect effect through number of effective pod per plant (0.4586), height of first fruiting node (0.1306), days to maturity (0.1035), stem thickness (0.0227) and plant height (0.0050). However, trait total number of pod per plant (-0.4453), harvest index (-0.1174), number of seed per pod (-0.0256), number of primary branches per plant (-0.0218), biological yield per plant (-0.0217), number of secondary branches per plant (-0.0039) and 100 seed weight (-0.0112) expressed negative, indirect effect on the seed yield per plant.

4.4.1.1.2 Days to maturity

Showed positive direct effect (0.1172) and positive, indirect effect with number of effective pod per plant (0.4674) then height of first fruiting node (0.1294), stem thickness (0.0220), plant height (0.0048) on the seed yield per plant. However, it exhibited negative, indirect effect on dependent variable seed yield per plant with traits total number of pod per plant (-0.4514) then days to 50% flowering (-0.2339), biological yield per plant (-0.1748) and number of seed per pod (-0.0304).

4.4.1.1.3 Plant height

Plant height exhibited positive (0.0250) direct effect and showed positive, indirect effect with number of effective pod per plant (0.2470) followed by harvest index (0.1862), height of first fruiting node (0.1157), days to maturity (0.02101). However plant height expressed negative, indirect effect on seed yield per plant with characters

total number of pod per plant (-0.2582), number of seed per pod (-0.0693), biological yield per plant (-0.0647) and days to 50% flowering (-0.0537).

4.4.1.1.4 Height of first fruiting node

Height of the first fruiting node had positive (0.2038) direct effect and positive indirect effect with the trait number of effective pod per plant (0.3398) followed by character harvest index (0.2128), days to maturity (0.0744). Although, Negative indirect effects reported with total number of pod per plant (-0.3478), days to 50% flowering (-0.1698), number of seed per pod (-0.0835) and biological yield per plant (-0.0662) on dependent variable seed yield per plant.

4.4.1.1.5 Stem thickness

Stem thickness exhibited negative (-0.0638) direct effect and positive indirect effects with harvest index (0.3161) then days to 50% flowering (0.0942), number of effective pod per plant (0.0581), number of secondary branch per plant (0.0452), height of first fruiting node (0.0332) and trait plant height (0.0077). Although stem thickness showed negative, indirect effects on the trait seed yield per plant with biological yield per plant (-0.0770), total number of pods per plant (-0.0753), number of seed per pod (-0.0426) and days to maturity (-0.0404).

4.4.1.1.6 Number of primary branches per plant

Expressed positive direct effect (0.1902) on seed yield, with positive indirect effect with the trait biological yield per plant (0.2565) then total number of pod per plant (0.1121), days to 50% flowering (0.0304), stem thickness (0.0108). However negative indirect effects observed with number of effective pod per plant (-0.1498), harvest index (-0.1355), number of secondary branch per plant (-0.1098) and days to maturity (-0.0259).

4.1.1.7 Number of secondary branches per plant

Number of secondary branches on per plant basis noticed with negative, direct effect (-0.1474). Whereas, positive indirect effects with traits biological yield per plant (0.5887) followed by number of primary branches per plant (0.1417), total number of pods per plant (0.0945), stem thickness (0.0196). Negative indirect effects on dependent trait seed yield per plant were recorded with traits viz. harvest index (-0.3723), number of effective pod per plant (-0.1214), number of seed per pod (-0.0159)

and negligible negative indirect effects of days to 50% flowering, stem thickness, days to maturity and with plant height.

4.4.1.1.8 Total number of pods per plant

It showed positive direct effect (0.9080) and had positive, indirect effects with trait biological yield per plant (0.3927), days to 50% flowering (0.1300), harvest index (0.06568), number of primary branch per plant (0.0234) and with number of seeds per pod (0.0114). However, negative- indirect effects on seed yield per plant of total number of pod per plant recorded with number of effective pod per plant (-0.9102).

4.4.1.1.9 Number of effective pods per plant

Exhibited negative direct effect (-0.9132) and exhibited positive indirect effects with total number of pods per plant (0.9050) followed by biological yield per plant (0.3967), coupled with negligible positive indirect effects of plant height, stem thickness and number of primary branches per plant . Negative, indirect effects were noticed with height of first fruiting node (-0.0758) on trait seed yield per plant.

4.4.1.1.10 Number of seeds per pod

This trait showed negative direct effect (-0.1337) on the trait seed yield per plant. However, positive- indirect effects were of number of seed per pod observed with harvest index (0.3980) followed by trait biological yield per plant (0.3070), height of first fruiting node (0.1273), number of effective pods per plant (0.0868), days to maturity (0.0267) and plant height (0.0129). Negative, indirect effects were noticed with total number of pods per plant (-0.0777) followed by trait days to 50% flowering (-0.0508) and negligible effect of remaining traits.

4.4.1.1.11 Hundred Seed weight

Hundred seed weight reported with negative, direct effect (-0.0255), whereas positive, indirect effects with traits number of effective pod per plant (0.2732), biological yield per plant (0.0971), height of the first fruiting node (0.0762) and number of primary branches per plant (0.0243). However, negative- indirect effect of 100 seed weight observed on the trait seed yield, with total number of pod per plant (-0.2772) followed by days to 50% flowering (-0.1162). Stem thickness, number of seeds per pod and number of secondary branches per plant had negative, indirect minor effect.

4.4.1.1.12 Biological yield per plant

This character exhibited positive, direct effect (1.0922) and positive- indirect effects with total number of pod per plant (0.3264), number of primary branches per plant (0.0446) coupled with negligible positive, indirect effects of days to 50% flowering and stem thickness. However, negative- indirect effect of biological yield per plant on seed yield per plant reported with trait harvest index (-0.3495) and with number of effective pod per plant (-0.3317).

4.4.1.1.13 Harvest index

Harvest index showed positive direct effect (0.8277) on the dependent trait seed yield per plant. Although, it exhibited positive indirect effects with trait total number of pods per plant (0.0720) then number of secondary branches per plant (0.0663), height of first fruiting node (0.0524), days to 50% flowering (0.0376). However indirect negative effects of harvest index on the seed yield per plant reported with biological yield per plant (-0.4612).

4.4.1.2 Residual effects

The path analysis of current investigation showed minor (0.0144) residual effect on the trait seed yield per plant.

Table 4.7: Phenotypic Path Coefficient for Yield and Component Traits of Yield in *desi* Chickpea Genotypes

	DTF	DTM	PH	HFFN	ST	PB	SB	TNPPP	NEPP	NSPP	100SW	BY	HI%
DTF	-0.1014	0.0546	0.0047	-0.0062	0.0091	0.0041	0.0016	-0.0569	0.0319	-0.0076	0.0130	0.0035	-0.1140
DTM	-0.0827	0.0669	0.0039	-0.0061	0.0088	0.0054	-0.0041	-0.0590	0.0336	-0.0083	0.0070	-0.1438	0.0057
PH	-0.0183	0.0101	0.0262	-0.0056	-0.0082	0.0014	-0.0038	-0.0334	0.0176	-0.0173	0.0082	-0.0534	0.1566
HFFN	-0.0604	0.0394	0.0142	-0.0104	-0.0048	0.0031	-0.0000	-0.0435	0.0237	-0.0236	0.0105	-0.0332	0.1814
ST	0.0302	-0.0194	0.0070	-0.0016	-0.0305	0.0035	-0.0215	-0.0089	0.0041	-0.0086	0.0018	-0.0762	0.2720
PB	0.0127	-0.0111	-0.0011	0.0010	0.0032	-0.0327	0.0512	0.0126	-0.0089	0.0037	0.0034	0.1792	-0.0807
SB	-0.0018	-0.0030	-0.0011	0.0000	0.0072	-0.0184	0.0909	0.0137	-0.0094	-0.0085	0.0005	0.4522	-0.2139
TNPPP	0.0471	-0.0322	-0.0071	0.0037	0.0022	-0.0033	0.0102	0.1225	-0.0675	0.0028	-0.0095	0.2988	0.0734
NEPP	0.0477	-0.0331	-0.0068	0.0036	0.0018	-0.0043	0.0126	0.1218	-0.0679	0.0030	-0.0093	0.3065	0.0674
NSPP	-0.0182	0.0131	0.0107	-0.0058	-0.0062	0.0029	0.0183	-0.0081	0.0049	-0.0422	0.0041	0.2573	0.3627
100SW	-0.0408	0.0145	0.0066	-0.0034	-0.0017	-0.0034	0.0015	-0.0361	0.0195	-0.0053	0.0323	0.0560	-0.0456
BY	-0.0004	-0.0106	-0.0015	0.0003	0.0025	-0.0064	0.0453	0.0404	-0.0229	-0.0120	0.0020	0.9060	-0.3039
HI%	0.0142	0.0004	0.0050	-0.0023	-0.0102	0.0032	-0.0240	0.0111	-0.0056	-0.0189	-0.0018	-0.3397	0.8105

Where,

DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), HFFN: Height of first fruiting node (cm), ST: Stem thickness (mm), PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPP: Number of effective pods per plant, NSPP: Number of seeds per pod, 100SW: 100 Seed weight, BY: Biological yield per plant (g), HI: Harvest index (%), SYPP: Seed yield per plant (g).

Table 4.8: Genotypic Path Coefficient for Yield and Component Traits of Yield in *desi* Chickpea Genotypes

	DTF	DTM	PH	HFFN	ST	PB	SB	TNPPP	NEPP	NSPP	100SW	BY	HI%
DTF	-0.2650	0.1035	0.0050	0.1306	0.0227	-0.0218	-0.0039	-0.4453	0.4586	-0.0256	-0.0112	-0.0217	-0.1174
DTM	-0.2339	0.1172	0.0044	0.1294	0.0220	-0.0421	0.0072	-0.4514	0.4674	-0.0304	-0.0056	-0.1748	-0.0048
PH	-0.0537	0.0210	0.0250	0.1157	-0.0198	-0.0118	0.0029	-0.2582	0.2470	-0.0693	-0.0069	-0.0647	0.1862
HFFN	-0.1698	0.0744	0.0142	0.2038	-0.0104	-0.0231	0.0011	-0.3478	0.3398	-0.0835	-0.0095	-0.0662	0.2128
ST	0.0942	-0.0404	0.0077	0.0332	-0.0638	-0.0323	0.0452	-0.0753	0.0581	-0.0426	-0.0014	-0.0770	0.3161
PB	0.0304	-0.0259	-0.0015	-0.0247	0.0108	0.1902	-0.1098	0.1121	-0.1468	0.0101	-0.0032	0.2565	-0.1355
SB	-0.0070	-0.0057	-0.0005	-0.0016	0.0196	0.1417	-0.1474	0.0945	-0.1214	-0.0159	-0.0009	0.5887	-0.3723
TNPPP	0.1300	-0.0583	-0.0071	-0.0781	0.0053	0.0234	-0.0153	0.9080	-0.9102	0.0114	0.0077	0.3927	0.0656
NEPP	0.1331	-0.0600	-0.0067	-0.0758	0.0040	0.0306	-0.0196	0.9050	-0.9132	0.0127	0.0076	0.3967	0.0563
NSPP	-0.0508	0.0267	0.0129	0.1273	-0.0203	-0.0144	-0.0175	-0.0777	0.0868	-0.1337	-0.0039	0.3070	0.3980
100SW	-0.1162	0.0260	0.0068	0.0762	-0.0035	0.0243	-0.0055	-0.2772	0.2732	-0.0208	-0.0255	0.0971	-0.0573
BY	0.0052	-0.0187	-0.0014	-0.0123	0.0045	0.0446	-0.0794	0.3264	-0.3317	-0.0375	-0.0022	1.0922	-0.3495
HI%	0.0376	-0.0006	0.0056	0.0524	-0.0243	-0.0311	0.0663	0.0720	-0.0621	-0.0643	0.0017	-0.4612	0.8277

Where,

DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), HFFN: Height of first fruiting node (cm), ST: Stem thickness (mm), PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPP: Number of effective pods per plant, NSPP: Number of seeds per pod, 100SW: 100 Seed weight, BY: Biological yield per plant (g), HI: Harvest index (%), SYPP: Seed yield per plant (g).

4.4.2 Path Coefficient Analysis of Quantitative – Yield Attributing Traits: -

4.4.2.1 Direct and Indirect effects

4.4.2.1.1 Relative growth rate

RGR showed positive direct effect (0.37) on trait seed yield and had positive-indirect effect *via* trait biomass duration (7.19), leaf area index (6.19), leaf area duration (5.44), net assimilation rate (0.87), chlorophyll content (0.30) and harvest index (0.28). However, crop growth rate (-8.37), leaf area index duration (-7.52), leaf area ratio (-0.90) and with number of effective pods per plant (-0.36) had negative, indirect effect with relative growth rate on the seed yield per plant.

4.4.2.1.2 Leaf area ratio

LAR expressed positive, direct effect (0.528) coupled with indirect, positive effects with crop growth rate (4.78), leaf area index duration (0.731), leaf area duration (0.529), leaf area index (0.32) and negative, indirect effects with biomass duration (-4.649), net assimilation rate (-0.465) and relative growth rate (-0.23).

4.4.2.1.3 Leaf area index

It had positive direct effect (2.63) and positive, indirect effects with leaf area duration (2.14), biomass duration (1.88), crop growth rate (0.857) and chlorophyll content (0.11). While, negative-indirect effects observed with leaf area index duration (-3.19), leaf area ratio (-0.22), net assimilation rate (-0.16) and number of effective pods per plant (-0.12).

4.4.2.1.4 Net assimilation rate

NAR showed positive direct effect (0.952) on trait seed yield per plant, coupled with positive, indirect effects with leaf area duration (2.19), leaf area duration (3.17) and biomass duration (7.43). However, negative-indirect effects exhibited with relative growth rate (-0.37), leaf area ratio (-0.52), leaf area index (-2.63), crop growth rate (-8.25), number of effective pods per plant (-0.57) and harvest index (-0.39).

4.4.2.1.5 Crop growth rate

It exhibited negative-direct effect (-8.61). While, it showed positive indirect effects with biomass duration (7.29), leaf area index (2.15), leaf area duration (1.89), net assimilation rate (0.91), relative growth rate (0.36), harvest index (0.11) and indirect

negative effects with leaf area index duration (-2.70), leaf area ratio (-0.29) and with number of effective pods per plant (-0.11) on seed yield.

4.4.2.1.6 Leaf area duration

It had negative- direct effect (-2.19) on the seed yield. While, positive- indirect effects were found with leaf area index (2.64), biomass duration (1.79), crop growth rate (0.82) and chlorophyll content (0.10). However, leaf area index duration (-3.17), net assimilation rate (-0.15) and trait number of effective pods per plant (-0.12) had negative, indirect effect on seed yield.

4.4.2.1.7 Leaf area index duration

LAIID revealed negative indirect effect (-3.17). However, it showed positive, indirect effects with leaf area index (2.64), leaf area duration (2.19), biomass duration (1.79), crop growth rate (0.81) and chlorophyll content (0.10). While, net assimilation rate (-0.16), number of effective pods per plant (-0.12) and leaf area index (-0.10) exhibited negative, indirect effect on the seed yield.

4.4.2.1.8 Biomass duration

It had positive direct effect (7.43) on the trait seed yield and exhibited positive, indirect effects with trait leaf area index (2.20), leaf area duration (1.93), net assimilation rate (0.85), relative growth rate (0.36) and harvest index (0.11). While, negative- indirect effects crop growth rate (-8.46), leaf area index duration (-2.75) and with leaf area ratio (-0.19).

4.4.2.1.9 Chlorophyll content

In chickpea plant it showed positive direct effect (0.19) and positive- indirect effects with leaf area duration (1.55), biomass duration (1.41), leaf area index (1.24), crop growth rate (0.91) and harvest index. However, negative- indirect effects showed with traits leaf area index duration (-2.15), leaf area ratio (-0.15) and number of effective pods per plant (-0.13) on seed yield per plant.

4.4.2.1.10 Physiological maturity

It had negative- direct effect (-0.07) on the seed yield. While, positive indirect effects observed with crop growth rate (0.59), leaf area index duration (0.49) and negative- indirect effects with biomass duration (-0.62), leaf area index (-0.44), number of effective pods per plant (-0.29) and leaf area duration (-0.12) on seed yield per plant.

4.4.2.1.11 Number of effective pods per plant

It exhibited positive direct effect (0.57) and indirect, positive effects with crop growth rate (1.52), leaf area index duration (0.71) and number of effective pods per plant (0.57). While, biomass duration (-1.58), leaf area index (-0.63), leaf area duration (-0.48) and net assimilation rate (-0.13) had negative- indirect effects.

4.4.2.1.12 Harvest index

It revealed positive direct effect (0.39) on the trait seed yield per plant and showed positive, indirect effects with biomass duration (0.43), leaf area duration (0.32) and leaf area index (0.21). While, leaf area index duration (-0.50) had negative- indirect effect on seed yield.

4.2.2.2 Residual effect

Performed path analysis of present investigation for physiological and yield attributing traits exhibited minor (0.7389) residual effect on the seed yield per plant.

Table 4.9: Genotypic Path Coefficients for Physiological and Component Traits of Yield in Chickpea Genotypes

	RGR 1	RGR 2	LAR 1	LAR 2	LAI 1	LAI 2	LAI 3	NAR 1	NAR 2	CGR 1	CGR 2	LAD 1	LAD 2	LAID 1	LAID 2	BMD 1	BMD 2	CHL	PM	NEPP	HI%
RGR 1	0.017	0.026	-0.482	-0.905	0.499	0.702	6.197	0.012	-0.693	2.938	1.374	5.445	-0.087	-7.521	-7.365	-2.229	3.025	0.307	0.025	-0.368	0.287
RGR 2	0.001	0.377	0.018	-0.327	0.039	0.047	0.415	0.010	0.874	-0.022	-8.373	0.339	-0.005	-0.469	-0.494	0.008	7.190	0.029	0.004	-0.110	0.013
LAR 1	0.029	-0.025	0.283	-0.307	0.321	0.020	-0.045	0.010	-0.113	0.406	0.678	0.529	-0.009	-0.731	0.073	-0.288	-0.069	0.107	0.027	0.089	-0.026
LAR 2	-0.030	-0.234	0.165	0.528	-0.107	-0.058	-0.188	0.010	-0.465	-0.362	4.780	-0.448	0.005	0.619	0.412	0.277	-4.649	-0.018	-0.003	0.077	-0.072
LAI 1	0.021	0.036	-0.222	-0.137	0.411	0.063	0.386	0.012	0.016	0.216	-0.406	1.026	-0.006	-1.418	-0.559	-0.195	0.709	0.110	-0.013	-0.071	-0.045
LAI 2	0.040	0.058	-0.018	-0.101	0.085	0.304	2.690	0.010	-0.168	0.857	-0.523	2.141	-0.038	-2.959	-3.193	0.671	1.728	0.117	0.011	-0.123	0.096
LAI 3	0.041	0.059	0.004	-0.037	0.060	0.310	2.634	0.010	-0.161	0.777	0.806	2.105	-0.038	-2.908	-3.192	-0.617	1.885	0.940	0.013	-0.137	0.032
NAR 1	-0.017	-0.377	0.283	-0.528	-0.411	-0.304	-2.634	0.010	-0.952	-0.953	8.616	2.197	0.037	3.035	3.175	0.738	7.430	-0.198	0.078	-0.574	-0.397
NAR 2	-0.012	0.346	0.033	-0.287	0.007	-0.053	-0.446	0.010	0.952	-0.283	-8.255	-0.368	0.006	0.508	0.547	0.215	6.694	-0.006	0.001	-0.079	-0.025
CGR 1	0.054	-0.008	-0.121	-0.200	0.093	0.273	2.150	0.010	0.283	-0.953	0.848	1.891	-0.032	-2.612	-2.708	-0.737	0.681	0.095	0.008	-0.111	0.112
CGR 2	-0.002	0.367	0.022	-0.292	0.019	0.018	0.246	0.012	0.912	-0.093	-8.616	0.127	-0.002	-0.176	-0.244	0.063	7.296	0.021	0.005	-0.101	0.002
LAD 1	0.043	0.058	-0.068	-0.107	0.192	0.296	2.524	0.010	-0.159	0.820	-0.509	-2.197	-0.236	-3.035	-3.052	-0.649	1.662	0.140	0.004	-0.126	0.058
LAD 2	0.040	0.058	-0.006	-0.068	0.072	0.305	2.648	0.012	-0.164	0.812	0.663	2.112	-0.037	-2.917	-3.175	-0.640	1.798	0.104	0.012	-0.130	0.063
LAID 1	0.043	0.058	-0.068	-0.107	0.192	0.296	2.524	0.010	-0.159	0.820	-0.509	2.197	-0.036	-3.035	-3.052	-0.649	1.662	0.140	0.004	-0.126	0.058
LAID 2	0.040	0.058	-0.006	-0.068	0.072	0.305	2.648	0.012	-0.164	0.812	0.663	2.112	-0.037	-2.917	-3.175	-0.640	1.798	0.104	0.012	-0.130	0.064
BMD 1	0.053	-0.004	-0.110	-0.198	0.109	0.276	2.203	0.012	-0.278	0.951	0.735	1.933	-0.032	-2.671	-2.755	-0.738	0.778	0.092	0.006	-0.101	0.115
BMD 2	0.007	0.365	0.002	-0.330	0.039	0.070	0.668	0.010	0.857	0.087	-8.460	0.491	-0.009	-0.679	-0.768	-0.077	7.430	0.037	0.006	-0.122	0.023
CHL	0.027	0.056	-0.153	-0.048	0.228	0.179	1.248	0.012	-0.031	0.457	0.916	1.556	-0.020	-2.150	-1.677	-0.342	1.419	0.198	-0.021	-0.132	0.063
PM	-0.005	-0.019	0.097	0.002	0.072	-0.044	-0.444	0.010	-0.023	-0.099	0.595	-0.124	0.005	0.171	0.496	0.061	-0.625	0.053	-0.078	-0.293	-0.002
NEPP	-0.011	-0.072	-0.040	0.071	-0.050	-0.065	-0.632	0.010	-0.131	-0.184	1.520	-0.483	0.008	0.667	0.719	0.130	-1.580	-0.045	0.040	0.574	0.027
HI%	0.012	0.015	0.019	-0.095	-0.047	0.073	0.216	0.012	-0.059	0.270	-0.049	0.323	-0.006	-0.446	-0.507	0.214	0.439	0.031	0.005	0.039	0.397

RGR 1: Relative growth rate (30-60 days interval), RGR 2: Relative growth rate (60-90 days interval), LAR 1: Leaf area ratio (30-60 days interval), LAR 2: Leaf area ratio (60-90 days interval), LAI 1: Leaf area index (30 days), LAI 2: Leaf area index (60 days), LAI 3: Leaf area index (90 days), NAR 1: Net assimilation rate (30-60 days interval), NAR 2: Net assimilation rate (60-90 days interval), CGR 1: Crop growth rate (30-60 days interval), CGR 2: Crop growth rate (60-90 days interval), LAD 1: Leaf area duration (30-60 days interval), LAD 2: Leaf area duration (60-90 days interval), LAID 1: Leaf area index duration (30-60 days interval), LAID 2: Leaf area index duration (60-90 days interval), BMD 1: Biomass duration (30-60 days interval), BMD 2: Biomass duration (60-90 days interval), CHL: Chlorophyll, PM: Physiological maturity, NEPP: Number of effective pods per plant, HI: Harvest index

4.5 Genetic divergence

In order to perform genetic divergence analysis on 40 *desi* chickpea genotypes, the correlated means of various characters had transformed to the standard uncorrelated means through Tocher's method. The statistical distance (estimated through Mahalanobis D^2 statistics) between pair of different genotypes were calculated as sum of square of different between pairs of the corresponding uncorrelated values of any of the two genotypes, considered at a time.

4.5.1 Contribution of individual characters toward genetic divergence

The contributions of studied fourteen quantitative traits in percentage toward genetic divergence are shown in table 4.8. The percentage contribution of the individual character towards divergence was recorded highest for total number of pods per plant (39.3%) followed by harvest index (20.1%), 100 seed weight (13.5%), number of seeds per pod (11.4%), number of effective pods per plant (4.6%), days to maturity (3.5%) and plant height (2.3%). Stem thickness (1.7%), seed yield per plant (1.1%), biological yield per plant (0.89%), days to 50% flowering (0.38%), number of primary branches per plant (0.38%), stem height of first fruiting node (0.25%) and number of secondary branches per plant (0.12%) exhibited very low contribution toward the divergence.

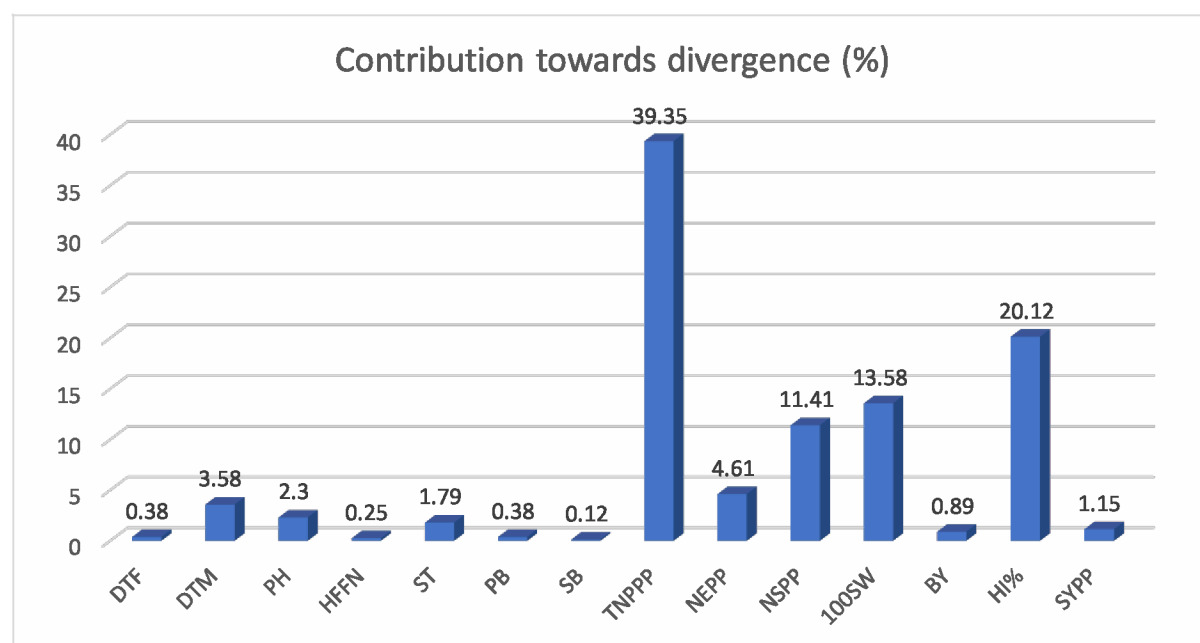


Fig.22: Contribution of different characters towards the divergence

4.5.2 Intra and inter cluster divergence

Through D^2 values, 40 *desi* chickpea genotypes were categorized into 8 clusters. The intra cluster distance was varied from 215.1 to 291.8. Cluster II expressed highest intra cluster distance (291.8) followed by cluster I (259.0), cluster IV (245.5), whereas cluster III had lowest intra cluster distance (215.1). However, cluster V, cluster VI, cluster VII and cluster VIII showed zero value of intra cluster distance.

The highest inter- cluster distance was reported between cluster II and cluster V (2305.1) followed by cluster V and cluster VI (2151.2), cluster V and cluster VII (1719.9), cluster I and cluster V (1687.0), cluster III and cluster VI (1528.2), cluster II and cluster III (1519.6), cluster VII and cluster VIII (1456.0), cluster VI and cluster VII (1267.1), cluster II and cluster VII (1221.5), cluster I and cluster VIII (1087.3), cluster V and cluster VIII (1001.7), cluster II and cluster VIII (915.2), cluster III and cluster VIII (893.3), cluster I and cluster III (866.3) and lowest inter cluster distance was observed between cluster III and cluster V (351.2). The D^2 mean values of inter and intra clusters are presented in the table 4.9.

4.5.3 Cluster mean

The cluster means for various traits are presented in the table 4.10. For trait days to 50% flowering cluster VI showed minimum (67 days) means value, whereas cluster I exhibited maximum (76 days) cluster mean. For days to maturity cluster VI had lowest means value (113 days) and cluster I showed highest mean value (123 days). Plant height exhibited minimum mean in cluster V (44.6 cm) and the maximum in cluster VIII (66.4 cm). Trait height of the first fruiting node exhibited minimum cluster mean in cluster V (20.2 cm), whereas maximum in cluster VIII (35.9 cm). For stem thickness cluster VII showed minimum mean values (2.37 mm) and cluster VI showed maximum cluster mean value (3.01 mm). Cluster II expressed lowest cluster mean value (2.57), whereas cluster VII showed the highest (3.16) for number of primary branches per plant. Although, number of secondary branches per plant cluster II showed minimum (8.33) and cluster VI showed maximum (12.0) mean value. Total number of pod per plant had minimum cluster mean value in cluster II (44.1) and maximum in cluster V (94.4). Number of effective pods per plant cluster II (40.48) exhibited lowest and cluster V (92.85) showed highest cluster mean value. Cluster V showed minimum (1.16) mean value and cluster VIII (1.75) highest cluster mean value for number of seeds per pod. However, cluster V expressed minimum (18.0 g), whereas cluster VII showed maximum (38.1 g) cluster mean value for trait 100 seed

weight. Biological yield per plant cluster II (25.0 g) showed lowest and cluster VI showed highest (53.1 g) mean value. Cluster VII (33.8%) reported with minimum and the cluster VIII with maximum (64.1%) cluster mean value for harvest index. Seed yield per plant cluster VII showed minimum (11.35 g), whereas cluster VI exhibited maximum (21.38 g) cluster mean value.

Table 4.10: Contribution of Various Traits Toward Clustering in *desi* Chickpea Genotypes

S.No.	Traits	Times ranked 1st	Contribution towards divergence (%)
1	Days to 50% flowering	3	0.38
2	Days to maturity	28	3.58
3	Plant height	18	2.30
4	Stem height of first fruiting node	2	0.25
5	Stem thickness	14	1.79
6	No. of primary branches per plant	3	0.38
7	No. of secondary branches per plant	1	0.12
8	Total number of pods per plant	307	39.35
9	No. of effective pods per plant	36	4.61
10	No. of seeds per pod	89	11.41
11	100 seed weight	106	13.58
12	Biological yield per plant	7	0.89
13	Harvest index	157	20.12
14	Seed yield per plant	9	1.15

Total rank: 780

Torcher cut off Value: 395.58

Table 4.11: Inter-Cluster and Intra-Cluster D² Values for Various Clusters

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	259.0	560.8	866.3	493.6	1687.0	733.9	538.8	1087.3
Cluster II		291.8	1519.6	678.3	2305.1	454.9	1221.5	915.2
Cluster III			215.1	473.1	351.2	1528.2	882.7	893.3
Cluster IV				245.5	818.5	668.1	771.7	567.4
Cluster V					0.0	2151.2	1719.9	1001.7
Cluster VI						0.00	1267.1	836.6
Cluster VII							0.00	1456.0
Cluster VIII								0.00

Where,

DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), HFFN: Height of first fruiting node (cm), ST: Stem thickness (mm), PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPP: Number of effective pods per plant, NSPP: Number of seeds per pod, 100SW: 100 Seed weight, BY: Biological yield per plant (g), HI: Harvest index (%), SYPP: Seed yield per plant (g).

Table 4.12: Cluster Mean for Yield and Component Traits of Yield in *desi* Chickpea Genotypes: Tocher's Method

Cluster	DTF	DTM	PH	HFFN	ST	PB	SB	TNPPP	NEPP	NSPP	100SW	BY	HI%	SYPP
Cluster I	76	123	53.83	25.66	2.51	3.03	10.54	47.70	44.58	1.20	24.72	31.54	38.80	12.11
Cluster II	76	122	56.56	29.17	2.85	2.57	8.33	44.19	40.48	1.35	22.89	25.06	53.12	13.36
Cluster III	71	117	48.96	21.81	2.42	2.97	10.54	79.12	74.81	1.18	21.53	36.45	39.21	14.35
Cluster IV	69	115	54.28	23.02	2.91	3.00	9.66	63.54	60.50	1.18	21.79	28.50	43.30	12.30
Cluster V	70	115	44.65	20.25	2.92	3.10	10.67	94.45	92.85	1.16	18.00	40.65	43.87	17.84
Cluster VI	67	113	59.10	22.70	3.01	3.05	12.04	45.60	41.30	1.56	22.30	53.15	40.26	21.38
Cluster VII	73	117	46.30	23.20	2.37	3.16	10.99	57.30	53.80	1.19	38.15	33.60	33.84	11.35
Cluster VIII	74	123	66.45	35.90	2.98	3.03	11.66	79.66	76.45	1.75	25.47	32.75	64.19	21.01

Table 4.13: Wilks Test

Determinant of Error Matrix	0.000054029
Determinant of Error +Variety Matrix	%381212581473.15
Wilk's Criterion	0.00
M	50.0
V statistics	1824.63
Degree of Freedom	546

4.5.4 Grouping of different genotypes into various clusters

On basis of D² analysis, 40 *desi* chickpea genotypes were categorized into 8 clusters and distribution of different genotypes into various clusters are presented in the table 4.13. Cluster I was reported as largest cluster among all, as it had 18 genotypes, which is 45% of total genotypes. Cluster II had 04 genotypes, cluster III consisted 09 genotypes, cluster IV contained 05 genotypes and remaining 04 clusters *i.e.* cluster V, cluster VI, cluster VII, cluster VIII were comprising of only one genotype each.

Table 4.14: Distribution of *desi* Chickpea Genotypes into Different Clusters

Cluster no.	No. of genotypes	Name of the Genotypes
Cluster I	18	ICCV 201101, ICCV 201102, ICCV 201103, ICCV 201104, ICCV 201105, ICCV 201106, ICCV 201108, ICCV 201110, ICCV 201111, ICCV 201112, ICCV 201113, ICCV 201116, ICCV 201201, ICCV 201213, ICCV 201215, ICCV 201216, RVG 204, JG 24
Cluster II	04	ICCV 201114, ICCV 201117, ICCV 201118, ICCV 201217
Cluster III	09	ICCV 201107, ICCV 201203, ICCV 201204, ICCV 201205, ICCV 201206, ICCV 201209, ICCV 201214, ICCV 08102, JG 36
Cluster IV	05	ICCV 201109, ICCV 201207, ICCV 201208, ICCV 201212, ICCV 201218
Cluster V	01	ICCV 201202
Cluster VI	01	ICCV 201211
Cluster VII	01	ICCV 201210
Cluster VIII	01	ICCV 201115

4.6 Principal component analysis

It is the multivariate-statistical analysis for reducing various available data with large number of the correlated variables into comparatively substantially smaller collection of new variables, through the linear combinations of variables which accounts most of variation, present in original variables. Principal components (PCs) are generally analyzed either from the correlation matrix or the covariance matrix. When variables are measured in various types of units-scale, effects can affect the composition of the derived components. In such of the situations, it becomes needful to standardize variables. In the present experimentation, the correlation matrix had been used to estimate the various principal components.

Out of 14 principal components (PC), only 4 PC reported with more than 1 Eigen value and exhibited 73.79% variability among investigated traits. Hence, only 4 PC were given importance for further explanation. Principal component 1 showed highest variability (25.71%) followed by principal component 2 (20.11%), principal component 3 (18.58%) and principal component 4 (9.38%) for the traits studied. Scree plot (Fig.4) exposed percentage of variance associated between principal component and eigen value with each principal component obtained by drawing the graph. After 4 PC semi-curved line obtained with slight variation found in each of the PCs, which revealed that maximum variation was noticed in PC1 along with PC2. Hence, selection of genotypes for various types of traits under PC1 and PC2 can be effective and desirable.

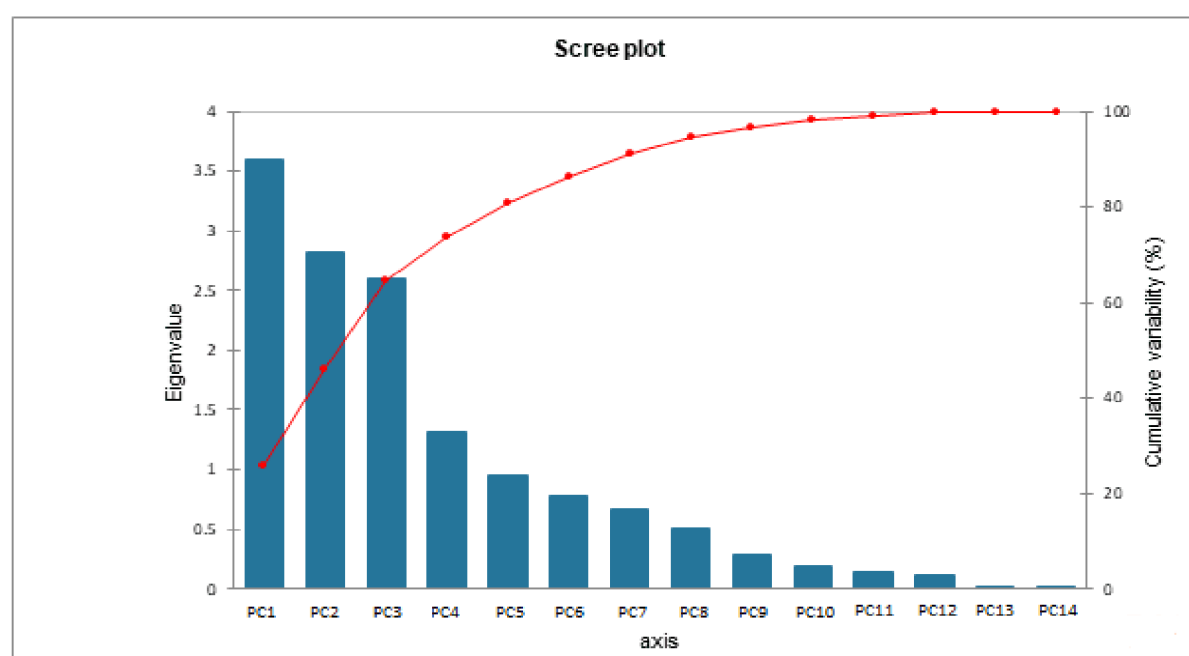


Fig. 4.23: Scree Plot between Eigen Value and Principal Component

Table 4.15: Principal Components of *desi* Chickpea Genotypes for Different Characters

Traits	Principal Component (PC)	Eigen value	Variability (%)	Cumulative (%)
Days to 50% flowering	PC1	3.60	25.71	25.71
Days to maturity	PC2	2.81	20.11	45.82
Plant height	PC3	2.60	18.58	64.41
Stem height at first fruiting node	PC4	1.31	9.38	73.79
Stem thickness	PC5	0.95	6.83	80.63
No. of primary branches per plant	PC6	0.78	5.61	86.25
No. of secondary branches per plant	PC7	0.66	4.76	91.01
Total number of pods per plant	PC8	0.50	3.60	94.62
No. of effective pods per plant	PC9	0.29	2.09	96.71
No. of seeds per pod	PC10	0.19	1.36	98.07
100 seed weight	PC11	0.14	1.04	99.12
Biological yield per plant	PC12	0.11	0.78	99.91
Harvest index%	PC13	0.01	0.06	99.97
Seed yield per plant	PC14	0.03	0.02	100.00

Rotated component matrix showed that first 4 principal component represented maximum variability (73.7%), so that the traits presented in these 4 PC can be useful and important in future chickpea crop improvement programme. It exposed that PC1 showed maximum variation (25.7%) and was related with pod concerned traits *viz.*, total number of pod per plant and number of effective pod per plant. The PC 2 was dominated for plant height, stem thickness, number of seeds per pod, harvest index and seed yield per plant. PC 3 related with days to 50% flowering, number of secondary branches per plant and with biological yield per plant. Although, PC 4 were dominating for number of primary branches per plant.

Table 4.16: Principal Component Values of the Rotation Component Matrix of *desi* Chickpea Genotypes

Traits	Principal components			
	PC 1	PC 2	PC 3	PC 4
Days to 50% flowering	-0.40	-0.41	0.61	-0.33
Days to maturity	-0.74	-0.09	0.27	-0.43
Plant height	-0.45	0.53	0.07	0.25
Stem height at first fruiting node	-0.69	0.45	0.29	-0.15
Stem thickness	-0.04	0.56	-0.36	0.36
No. of primary branches per plant	0.28	-0.06	0.45	0.61
No. of secondary branches per plant	0.22	-0.09	0.80	0.27
Total number of pods per plant	0.86	0.17	0.04	-0.29
No. of effective pods per plant	0.86	0.17	0.05	-0.26
No. of seeds per pod	-0.24	0.80	0.33	-0.13
100 seed weight	-0.40	0.11	0.27	0.35
Biological yield per plant	0.40	0.16	0.73	-0.05
Harvest index%	-0.04	0.72	-0.41	-0.12
Seed yield per plant	0.41	0.74	0.37	-0.15

Table: 4.17: Rotated Component Matrix Results of Different Characters (>0.500)

Traits	PC1	PC2	PC3	PC4
	Total number of pods per plant	Plant height	Days to 50% flowering	Number of primary branches per plant
	Number of effective pods per plant	Stem thickness	Number of secondary branches per plant	
		Number of seeds per pod	Biological yield per plant	
		Harvest index		
		Seed yield per plant		

4.6.1 PC scores of various genotypes

The PC scores of each principal component (PC1, PC2, PC3 and PC4) had both positive and negative values (Table 4.14, 4.15, 4.16 and Table 4.17). In PC1, the positive score varied from 0.12 to 4.27, whereas negative values varied from -2.98 to -0.15. In PC2 the positive value ranged from 0.01 to 6.23 and negative value ranged from -2.17 to -0.01. For PC3 positive values were ranged from 0.02 to 3.45, whereas negative values were ranged from -3.57 to -0.08. However, PC4 showed positive values of the components varied from 0.02 to 2.45, while negative values were varied from -2.08 to -0.03.

Table: 4.18: List of Different PC-Scores of *desi* Chickpea Genotypes

Genotype	PC1	PC 2	PC3	PC4
ICCV 201201	1.68	-0.38	0.33	0.70
ICCV 201202	4.27	0.96	0.02	-0.83
ICCV 201203	4.12	-0.39	1.31	-0.93
ICCV 201204	2.68	-1.27	0.75	-0.03
ICCV 201205	2.31	0.30	0.43	1.22
ICCV 201206	2.42	-0.57	-0.99	-2.08
ICCV 201207	0.94	0.01	-3.57	-0.21
ICCV 201208	1.47	-0.56	-0.70	1.81
ICCV 201209	1.86	-0.01	-0.57	-1.52
ICCV 201210	-0.18	-1.33	1.11	1.55
ICCV 201211	1.09	3.34	2.19	1.41
ICCV 201212	0.99	1.43	-1.05	2.27
ICCV 201213	0.24	-1.36	-0.65	1.36
ICCV 201214	1.83	-0.73	-0.08	-0.15
ICCV 201215	-0.76	-0.45	-1.40	2.02
ICCV 201216	-0.29	0.34	-0.44	2.45
ICCV 201217	-0.26	0.12	-3.09	0.48
ICCV 201218	1.30	0.21	-1.79	0.35
ICCV 201101	-1.30	-1.64	1.96	-0.21
ICCV 201102	-2.52	-1.72	0.57	-1.10
ICCV 201103	-2.35	0.23	2.55	0.08
ICCV 201104	-1.16	-2.17	0.80	-0.26
ICCV 201105	-1.16	-1.60	3.45	-0.69
ICCV 201106	-2.30	-1.09	1.17	0.45
ICCV 201107	0.52	-1.67	0.40	-0.36
ICCV 201108	-0.48	-1.13	0.06	-0.53
ICCV 201109	-0.99	0.25	-0.09	-0.96
ICCV 201110	-0.97	-0.88	1.58	0.45

ICCV 201111	-2.86	-0.20	2.93	-0.42
ICCV 201112	-1.31	0.47	-1.70	-1.06
ICCV 201113	-2.50	-0.23	-1.86	-0.84
ICCV 201114	-1.88	-0.23	-2.31	-2.08
ICCV 201115	-0.15	6.23	1.63	-1.00
ICCV 201116	0.12	-1.11	-0.18	0.16
ICCV 201117	-2.87	3.51	-1.50	-0.83
ICCV 201118	-2.98	3.30	-1.11	0.35
ICCV 08102	2.60	2.28	2.70	-0.96
RVG 204	-1.21	-1.37	-0.91	0.02
JG 36	1.31	-1.10	-1.41	-1.50
JG 24	-1.29	0.24	-0.56	1.42

Based on PC scores eminent genotypes were grouped in table 4.18. Here, genotype ICCV 201202 reported with maximum PC score followed by ICCV 201203, ICCV 201204, ICCV 08102 and ICCV 201205 in PC1. In PC2 highest PC score showed by ICCV 201115 followed by ICCV 201117, ICCV 201211 and ICCV 201118, which were mainly related with traits plant height, stem thickness, number of seeds per pod, harvest index and with seed yield per plant. PC score in PC3 were maximum for traits *i.e.* days to 50% flowering, number of secondary branch per plant and with biological yield per plant by genotypes ICCV 201105, ICCV 201111, ICCV 08102 and ICCV 201103. Genotype ICCV 201216 followed by ICCV 201212, ICCV 201215 and ICCV 201208 obtained the maximum PC score in PC4 related with trait number of primary branches per plant.

Genotype exhibited maximum positive PC score and was common in various principal components is ICCV 201211 which is common in all PC *viz.* PC1, PC2, PC3 and PC4. Genotype ICCV 08102 was common in PC1, PC2 and PC3. Genotype ICCV 201205 and ICCV 201208 in PC1 and PC4. Genotype ICCV 201203, in PC1 and PC3. However, genotype ICCV 201115 was common in PC2 and PC3.

Table: 4.19: Categorization of Promising Genotypes Based on PC Scores

PC 1	PC 2	PC 3	PC 4
ICCV 201202	ICCV 201115	ICCV 201105	ICCV 201216
ICCV 201203	ICCV 201117	ICCV 201111	ICCV 201212
ICCV 201204	ICCV 201211	ICCV 08102	ICCV 201215
ICCV 08102	ICCV 201118	ICCV 201103	ICCV 201208
ICCV 201206	ICCV 08102	ICCV 201211	ICCV 201210
ICCV 201205	ICCV 201212	ICCV 201101	JG 24
ICCV 201209		ICCV 201115	ICCV 201211
ICCV 201214		ICCV 201110	ICCV 201213
ICCV 201201		ICCV 201203	ICCV 201205
ICCV 201208		ICCV 201106	
JG 36		ICCV 201210	
ICCV 201218			
ICCV 201211			

CHAPTER 5:

DISCUSSION

CHAPTER 5: DISCUSSION

Success of any crop improvement programme mainly depends upon the free variability, present in the genotypes of any of the crop by which plant breeder can achieve their ultimate goal *i.e.* increment in yield. When more yield per unit area combine with high quality product, resistance/tolerance to biotic or abiotic stresses, it convert particular improved genotypes into long lasting future cultivar and developing this type of elite cultivar is every breeder's dream, basically which can achieve through identifying various traits of interest to initiate future breeding programme.

Through the current investigation entitled “**Genetic Assessment for Quantitative and Physiological Traits of *desi* Chickpea**” an attempt has been done in order to understand available genetic variability among investigated genotypes, nature of correlation among yield contributing components with determination of their direct-indirect effects on seed yield. This information obtained by present investigations can play an important role for any breeder of chickpea crop to develop new elite cultivars by their future crop improvement breeding works. The important points of obtained experimental result are arranged and discussed as follow:

5.1 Morphological characterization of traits

5.2 Genetic variability parameters

5.2.1 Analysis of Variance

5.2.2 Mean and Range

5.2.3 Genotypic and Phenotypic Coefficient of Variation

5.2.4 Heritability (%)

5.2.5 Genetic Advance as Percentage of Mean (%)

5.3 Correlation analysis

5.4 Path coefficient analysis

5.5 Genetic divergence (D^2) analysis

5.6 Principal component analysis

5.7 Identification of promising genotypes based on some priority trait

5.1 Morphological characterization of traits

Morphological characterization of genotypes plays a very important role in any of the varietal development programme because this kind of identification of traits can provide strong idea for breeder to select genotype for any specific traitor combinations of traits for crop improvement. In present investigation, large variation was found for different agro-morphological traits in different *desi* chickpea genotypes.

In present investigation the traits which were usually observed in all the genotypes were presence of stem anthocyanin coloration, pinnate leaf pattern, single flower per peduncle, pink flower, presence of stripes on standard of flower, seed type, seed shape, seed testa texture and seed ribbing. On the basis of plant growth habit chickpea genotypes were of two types, 6 genotypes had spreading type growth habit, while remaining 34 genotypes had semi-erect type of plant growth habit. Based on nature of plant growth habits, genotypes can be selected for various agro-climatic zones as spreading genotypes having profuse branching, which can reduce transpiration water loss with survival in deficit water, suitable for dryland areas. Whereas semi-erect genotypes can be used for mechanical harvesting, which can save harvesting cost and time of farmers. Most of the genotypes showed resistance against lodging, while all genotypes showed shattering resistance and both of the qualities enhance yield through lowering harvesting time losses.

It was noticed that the tall genotypes having lodging resistant and semi erect growth habit JG 24, ICCV 201212, ICCV 201103, ICCV 201115 and ICCV 201118 were suitable for mechanical harvesting. Significant variation was reported in seed coat color, foliage color and leaflet size. Out of 40 genotypes, 14 light green, 12 medium green and 14 had dark green foliage color, whereas leaflet size revealed that 8 genotypes had small, two genotypes *i.e.* ICCV 201117 and JG 24 exhibited with large and remaining 30 genotypes had medium type of leaflet size. Investigated all the genotypes were *desi* type of chickpea. Large variation found in seed size of various genotype *viz.*, only one genotype had very small seed size, 3 genotypes showed small seed size, 22 genotypes had medium seed size, 12 genotypes had large seed size, whereas only two genotypes *i.e.* ICCV 201210 and JG 24 had very large seed size. For marketing purpose seed size is important, which can increase or decrease the price of product. Smooth type of seed surface is having high consumer preference, whereas rough seed surface is having non-preference by stored-grain pest. Visually observable phenotypic traits exhibited overlapping expression of different

combinations and degree, but at last they perform a critical role to identify various genotypes of the different origin. The investigated results are in the agreement with finding of Shrivastava *et al.* (2011), Parmeshwarappa *et al.* (2012), Kaouthar (2015), Archak *et al.* (2016), Shakaya (2017), Gediya *et al.* (2018), Solanki *et al.* (2019), Janghel (2020) and Jayalakshmi *et al.* (2021).

5.2 Genetic variability parameters

In order to start a judicious crop improvement programme, presence of high magnitude genetic variability is one of the key factor to a plant breeder. The analysis of variance (ANOVA) indicated that genotypes were significantly differ for all the investigated characters, suggesting the presence of much amount of variation between all genotypes for all the traits. Quantitative inherited traits also play a crucial role in crop improvement, which directly affect the yield and its attributing traits. Hence, in order to improve quantitative inherited traits estimation and evaluation of various genetic variability parameters *i.e.* mean, range, coefficient of variation, heritability, genetic advance as percentage of mean is also important, which were calculated in the present investigation .

5.2.1 Genotypic and phenotypic coefficient of variation

Expression of genotypes along with environment and their interaction determine phenotypic coefficient of variation, which was higher than genotypic variation coefficient for all the investigated traits. However, in some genotypes and traits reported little influence of environment. Closeness between PCV and GCV values showed weak level of environmental influences on the studied traits. In present investigation number of effective pod per plant exhibited highest PCV and GCV. Similar kind of findings were also observed by Dhuria and Babbar (2016), Kumar *et al.* (2021), Shakya (2017), Babbar and Tiwari (2018). High GCV and PCV for days to flowering was reported by Akhtar *et al.* (2011). Seeds yield per plant with maximum PCV and GCV were noticed by Jayamani *et al.* (2019) and Mohibullah *et al.* (2020). The magnitude of the PCV and GCV were higher for traits total number of pods per plant, seed yield per plant, biological yield per plant, height of first fruiting node, harvest index, 100 seed weight, plant height, number of secondary branches per plant, stem thickness, number of primary branches per plant, number of seed per pod, days to 50% flowering and days to maturity. This shows that substantial variation is present in

traits in various genotypes and can use to exploit variability for further crop improvement. These findings are in accordance with earlier findings of Shakya (2017), Babbar and Tiwari (2018), Mohibullah *et al.* (2020), Kumar *et al.* (2021).

Phenological traits *i.e.* days to 50% flowering and days to maturity observed with low PCV and GCV, means showed very less variation as compared to all other traits under study. That's why there is very less scope to improve these phenological traits in investigated genotypes by selection. Stem thickness, number of primary branches per plant and number of seed per pod showed moderate PCV and GCV, similar findings found by the earlier workers *viz.*, Akhtar *et al.* (2011) and Dhuria and Babbar (2016) but contradictory to Shakya (2017), Jayamani *et al.* (2019) and Mohibullah *et al.* (2020).

5.2.2 Heritability (broad sense) and genetic advance as percentage of mean

Heritability may be defined as ratio of the genotypic variance and total (phenotypic) variance. Heritability (bs) comprise both additive and the non-additive types of gene actions. It helps the breeder to select promising genotypes from the available total genotypes. Although, heritability of same trait may differ significantly for one and for any other populations. Alone heritability (bs) is not that much reliable source for selection criteria because it interacts with environment. Hence, selection of traits based on heritability (bs) together with genetic advance as % of mean give more accurate result.

High heritability combined with high genetic advance as % of mean was observed for trait number of effective pods per plant followed by total number of pods per plant, biological yield per plant, height of first fruiting node, seed yield per plant, and hundred seed weight, which showed that these traits were influenced by the additive genes action. Hence, direct selection for such traits can be quite useful. High heritability together with moderate genetic advance exhibited by traits harvest index and plant height. High heritability along with low genetic advance was reported by stem thickness, number of secondary branches per plant, number of seeds per pod, number of primary branches per plant, days to 50% flowering and days to maturity. No low heritable traits were observed, which means no significant influences of the environmental factors had been found on genotypes. And selection for low heritable traits may not be effective in further crop improvement. The findings of the results are in line with earlier outcomes Waldia and Ramesh (2012) for number of effective pod

per plant and total number of pod per plant, Gul *et al.* (2013) observed for pods per plant and trait seed yield plant per plant, Jhakar *et al.* (2017) for pods per plant and 100 seed weight, Pezeshkpour *et al.* (2018) for biological yield, Yasin *et al.* (2018) observed for the seed yield per plant, biological yield per plant, 100-seed weight and harvest index, Solanki *et al.* (2019) for seed yield followed by biological yield per plant, number of effective pod per plant and total number of pod per plant, Kumar *et al.* (2021) noted high heritability for hundred seed weight, whereas high heritability coupled with higher genetic advance was found in trait seed yield per plant then biological yield per plant and Srivastava *et al.* (2021) observed high heritability with high genetic advance for number of seed per pod, Number of pods per plant, hundred seed weight and seed yield per plant. The above findings revealed, that in order to improve crop yield, the selection will be effective if it is based on traits like number of effective pods per plant, total number of pods per plant, biological yield per plant, hundred seed weight, seed yield per plant and number of seeds per pod.

In current investigation, the results are unsupportive of Khan *et al.* (2011) observed high heritability together with higher genetic advance for days to 50% flowering, Gul *et al.* (2013) for number of primary branches per plant, Waldia and Ramesh (2012) found low heritability with traits plant height and 100 seed weight. Jhakar *et al.* (2017) recorded high heritability of number of secondary branches per plant.

5.3 Correlation analysis

Correlation analysis provide the magnitude of linear association among pairs of various traits and use to form basis of any selection index. Hence, traits association analysis known to be inevitable in the evaluation of association of contributing traits over yield, which helps breeder a lot to choose superior genotype in any breeding programme. Genotypic correlation between traits can be a result of either pleiotropy or linkage, that's why it use to plays a critical role in indirect selection. Knowledge of phenotypic correlation among various components contributing to yield leads to the most effective method of selecting superior genotypes by using favorable pair of traits. Investigation regarding to nature and magnitude of association between various traits is basic and effective way for yield improvement.

It was noticed from the analyzed result that for most of the traits, genotypic correlation coefficients were higher than the phenotypic correlation coefficients, which

showed a strong inherent association was present their, between various traits and that traits were influenced less by external environmental factors.

In current investigation, phenological traits *viz.*, days to 50% flowering and days to maturity indicated a positive-association toward each other. Days to 50% flowering exhibited strong positive, significant correlation with traits days to maturity, height of first fruiting node and hundred seeds weight, whereas highly negative, significant correlation was noticed for number of effective pod per plant, total number of pod per plant and stem thickness. Phenological character days to maturity showed positive, significant correlation with height of the first fruiting node ,while negative, significant correlation was recorded for trait number of effective pod per plant, total number of pods per plant and with stem thickness. Through above associations of phenological traits with others, it can be observed that any changes in these phenological traits are in the same direction because of presence of strong genotypic and phenotypic correlation between them. Above results are in the findings of Tadesse *et al.* (2016), Kaiser *et al.* (2019) and Mohammadi and Talebi (2015).

Plant height exposed the positive-significant association with the height of the first fruiting node, number of seed per plant, stem thickness and with hundred seed weight. However, total number of pods per plant and number of effective pods per plant demonstrated significant, negative correlation with it. The correlation of plant height with other traits revealed that selection of tall plants finally increases height of the first fruiting node of genotype, thickness of stem with hundred seed weight means seed size. Height of first fruiting node noticed with positive, significant association with trait number of seed per pod, hundred seed weight, harvest index, whereas traits total number of pod per plant and number of effective pods per plant had significant-negative correlation. Trait stem thickness expressed positive-significant correlation with harvest index, however showed negative-significant correlation with number of secondary branches per plant. It means this positive type of correlation can help in selection of traits *i.e.* plant height, height of the first fruiting node of stem and stem thickness desired for genotypes found suitable for mechanical harvesting with enhanced seed traits *viz.*, number of seed per pod, hundred seeds weight and with harvest index, which ultimately leads to the yield improvement.

Number of primary branch per plant found with positive-significant relation with trait number of secondary branch per plant. However, it showed non-significant correlation with other traits. Number of secondary branches per plant, showed

positive-significant association with both biological yield per plant and the seed yield per plant, whereas it showed negative-significant correlation with trait harvest index. This correlation revealed that selection of different genotypes, based on a greater number of primary and secondary branches per plant, can enhance seed yield.

With trait total number of pods per plant, trait number of effective pods per plant followed by seed yield per plant and biological yield per plant, exhibited positive-significant correlation, whereas hundred seed weight showed negative significant correlation. Number of effective pods per plant had the positive, significant associations with the seed yield per plant then biological yield per plant, although hundred seed weight revealed negative, significant relation with it. Number of seeds per pod exhibited positive-significant correlation with trait seed yield per plant, harvest index and with biological yield. The above correlation showed that selection based on pod per plant and seed per pod criteria leads to increased crop yield. Biological yield per plant expressed positive-significant correlation with the seed yield per plant however, harvest index showed negative-significant correlation with character biological yield per plant. Trait harvest index exhibited positive-significant correlation with the seed yield per plant. It showed, rise in biological yield per plant together with harvest index leads to increment in seed yield.

Seed yield per plant recorded with significant-positive correlation with most of the yield attributing traits in present experimentation. Some traits, had high association are number of seed per pod, biological yield per plant, number of effective pod per plant, harvest index, total number of pod per plant and number of secondary branches per plant. Therefore, with respect to improve yield potential, chickpea plant should be selected on basis of above-mentioned traits.

In the current investigation, significant and positively associated traits can be suggested to enhance simultaneously and increment of one trait will lead automatic enhancement of another correlated one. Although, such kind of simultaneous modifications are not possible for negatively correlated traits.

The findings presented by Jha *et al.* (2012) reported significant and positive genotypic correlation between the plant height and seeds per pod and with 100 seed weight and 100 seed weight, Ramanappa *et al.* (2013) for grain yield with number of pod per plant, harvest index and number of seed per pod at phenotypic level however, days to maturity was negatively-correlated with grain yield, Mohammadi and Talebi (2015) for the seed yield and number of seed per pod and harvest index. Tadesse *et*

al. (2016) recorded for seed yield with number of pods per plant, number of seed per pod and biomass. Srivastava *et al.* (2017) observed for trait seed yield per plant showed significant-positive correlation at both phenotypic and genotypic level with the harvest index, biological yield per plant and number of pods per plant. Qaiser *et al.* (2019) found negative-significant correlation was observed between days to flowering with pods per plant at genotypic level. Sayilgan (2020) for trait number of pods per plant and number of seeds per pod and seed yield, Srivastava *et al.* (2021) observed the yield per plant number of pod per plant, number of seed per pod and significant negative correlation with 100 seed weight were agreement with the current findings.

Contradictory findings were reported by Tadesse *et al.* (2016) for days to flowering and for days to maturity with seed yield, Sayilgan (2020) found significant correlations between the yield and days to 50% flowering and days to maturity, Srivastava *et al.* (2021) observed for yield/plant with trait days to 50% flowering.

In present study, relative growth rate showed significant and positive correlation with crop growth rate, biomass duration, leaf area index, leaf area duration, leaf area index duration, leaf area ratio, seed yield/plant and trait chlorophyll content, which means increment in relative growth rate (RGR) will lead to enhancement of correlated traits including the seed yield per plant. Leaf area ratio exhibited positive significant correlation with leaf area index, leaf area duration, leaf area index duration and chlorophyll content. However, it showed negative significant correlation with biomass duration, net assimilation rate and crop growth rate. So, improvement in the leaf area ratio leads to reduction in biomass duration, net assimilation rate and crop growth rate.

Leaf area index had positive-significant correlation with leaf area duration, leaf area index duration, biomass duration, crop growth rate and with chlorophyll content and showed negative-significant correlation with trait net assimilation rate. Net assimilation rate revealed significant-positive association with crop growth rate and biomass duration, While negative significant correlation with leaf area duration, leaf area index duration and seed yield. Hence, enhanced net assimilation rate can reduce seed yield. Crop growth rate exhibited positive-significant correlation with biomass duration, leaf area duration, leaf area index duration, seeds yield per plant and chlorophyll content. So, genotypes showing more crop growth rate can lead to contribute in improved yield also.

Leaf area duration expressed positive-significant correlation with the leaf area index duration, biomass duration and chlorophyll content. Here it should be notable

that leaf area index duration is very strongly associated with trait leaf area duration. Leaf area index duration showed positive-significant association with biomass duration and chlorophyll content. Biomass duration expressed positive-significant correlation with chlorophyll content and the seed yield per plant. It means chlorophyll content along with biomass duration contribute positively for seed yield per plant. Chlorophyll content showed positive-significant association with physiological maturity. It shows that increment in chlorophyll content can increase physiological maturity of crop plant. Physiological maturity expressed significant-negative correlation with trait number of effective pod plant per plant, which indicate that as duration of the physiological maturity increases, that much number of effective pod plant per plant may reduce. Number of effective pod per plant and harvest index both revealed with significant, positive associations with the trait seed yield per plant.

Above correlation study indicated that selection based on traits *viz.*, relative growth rate, crop growth rate, biomass duration, number of effective pod per plant and harvest index can be effectively and contribute directly to increase yield component. The correlation coefficient analysis between various traits exhibits the existing association between pairs of the traits. But change in one dependent or independent trait can change whole arrangement of cause-and-effect association. Path coefficient analysis permits to divide the estimated correlation coefficient into two unitless components and therefore, are easy to interpret. The similar kind of results were noted by Ali *et al.* (2011), Bodakeet *al.* (2014) and Gaurav *et al.* (2020) in their investigations.

5.4 Path coefficient analysis

The correlation coefficient analysis between traits shows the existing association between pairs of various traits. But change in one dependent or independent character can change whole arrangement of cause-and-effect association. Path coefficient analysis permits to divide the estimated correlation coefficient into two unitless components and therefore, are easy to interpret. In present experimentation, the path analysis was performed at both phenotypic level and genotypic level by taking seed yield as dependent variable. Usually, genotypic direct and indirect effects were of higher in magnitude than phenotypic effects.

Genotypic path analysis revealed that positive, high direct effect was reported for trait days to maturity, plant height, height of the first fruiting node, number of primary branch per plant, total number of pod per plant, biological yield per plant and for

harvest index on the seed yield per plant. Thus, these are direct yield influencing traits and selection based on such characters would be useful in yield improvement. Similar kind of result were noted by Aycicek and Babagil (2013) for number of pods, Joshi and Yasin (2015) revealed that biological yield/plant and harvest index direct effect on seed yield, Agrawal *et al.* (2018) for biological yield, Manikanteswara *et al.* (2019) found direct effect of biological yield/plant, Rathod *et al.* (2020) for pods/plant and Kumar *et al.* (2021) observed for trait primary branches per plant, total number of pod per plant, biological yield/plant and harvest index on seed yield/plant.

The maximum negative, direct effect had been exhibited by trait number of effective pod per plant followed by days to 50% flowering, number of secondary branch per plant and number of seeds per pod, which supported by findings of Kumar *et al.* (2012) and Joshi and Yasin (2015). Whereas, contradictory findings were of Agrawal *et al.* (2018) observed that effective pod per plant and secondary branch per plant had high positive direct effect.

On the basis of the path coefficients analysis, traits like days to maturity, plant height, height of the first fruiting node, number of primary branches per plant, total number of pods per plant, biological yield per plant and trait harvest index found most effective to enhance the seed yield per plant. These contributing traits of yield can be used during formulation of selection strategies and a plant type to develop high yielding cultivars of chickpea.

Genotypic path analysis revealed that positive, high direct effect was reported for physiological trait biomass duration then leaf area index, net assimilation rate, number of effective pod per plant, leaf area ratio, harvest index, relative growth rate and chlorophyll content. These all are direct yield influencing traits hence, selection rooted on such characters, would be useful in the yield improvement of *desi* chickpea genotypes. The highest negative-direct effect was exhibited by crop growth rate followed by leaf area duration, leaf area index duration and physiological maturity.

On the basis of the path coefficients analysis, traits such as biomass duration followed by leaf area index, net assimilation rate, number of effective pod per plant, leaf area ratio, harvest index, relative growth rate found to be most effective to enhance the seed yield per plant. These contributing traits of yield can be used during formulation strategy for any crop improvement programme.

The similar kind of results were noted by Ali *et al.* (2011), Bodakeet *et al.* (2014), Kumar *et al.* (2017), Rani *et al.* (2020), Sinha *et al.* (2020) and Gaurav *et al.* (2020) in their investigations.

5.5 Genetic divergence (D^2) analysis

Divergence analysis helps in evaluating nature and magnitude of diversity exist in various genotypes in order to their use in future breeding programme. The current investigation aimed at estimating the genetic divergence among 40 *desi* chickpea genotypes to determine their free and potential variability. Mahalanobis (D^2 statistics) divergence analysis is an important and reliable tool to measure degree of genetic divergence widely used by breeders.

Characters, which exhibited more contribution to the divergence, should be considered as an important trait during selection. Through D^2 statistics it was expressed that total number of pod per plant contributed maximum toward divergence at genetic level followed by traits harvest index, hundred seed weight and number of seeds per pod. Thus, above traits showed maximum diversity into the cluster whereas, traits days to 50% flowering, number of primary branch per plant, stem height of the first fruiting node and number of secondary branch per plant exhibited negligible contribution toward the genetic divergence. Above findings showed similarities to findings of Babbar and Thakur (2012) for hundred seeds weight, Gaikwad *et al.* (2014) reported that pod per plant and hundred seeds weight contributed maximum to the divergence, Saha *et al.* (2018) found that maximum percentage contribution towards the divergence for total number of pod per plant, Tamvar *et al.* (2019) observed for 100-seed weight and Dar *et al.* (2020) for pods per plant. However, some findings were in disagreement with the findings of Gaikwad *et al.* (2014) observed for number of secondary branch per plant and days to 50% flowering and Dar *et al.* (2020) for plant height.

Forty *desi* chickpea genotypes, which were evaluated for magnitude and nature of existing genetic divergence, categorized into 8 groups. Cluster V, cluster VI, cluster VII and cluster VIII were having single genotype in group, whereas remaining 04 clusters were poly genotypic. Cluster I had highest 18 genotypes followed by cluster III had 09 genotypes, cluster IV had 05 genotypes and cluster II had 04 genotypes. The divergence analysis showed that the investigated material was highly diverse and had no relationship between geographical diversity and the genetic diversity, although

there was presence of some homologous correspondence between the closely established clusters.

The maximum distance at inter-cluster level was noticed between the cluster II and the cluster V followed by the cluster V and cluster VI. High heterotic combination will derive, when genotypes of such distinctly situated clusters crossed to one other and would give rise to higher heterotic segregation. Inter-cluster distance observed minimum between the cluster III and cluster V. The estimated results indicated that inclusion of genotypes of cluster II (ICCV 201101, ICCV 201102, ICCV 201103, ICCV 201104, ICCV 201105, ICCV 201106, ICCV 201108, ICCV 201110, ICCV 201111, ICCV 201112, ICCV 201113, ICCV 201116, ICCV 201201, ICCV 201213, ICCV 201215, ICCV 201216, RVG 204 and JG 24), while cluster V (ICCV 201202) and cluster VI (ICCV 201211) in any of the future crossing programme, is expected to give effective and useful recombinants in the subsequent generation as genetic diverse parents could exhibit large amount of variability. Highest mean of cluster was observed for trait days to 50% flowering and of days to maturity in cluster I. Cluster V had high mean value for total number of pod per plant and number of effective pod per plant. Traits stem thickness, number of secondary branch per plant, biological yield/plant and seed yield/plant showed maximum mean value in cluster VI, while hundred seed weight and number of primary branch per plant exhibited highest cluster mean value in cluster VII. Cluster VIII showed maximum mean value for plant height, stem height at the first fruiting node, number of seeds per pod and harvest index. Above findings were approved in earlier studies of Babbar and Thakur (2012), Jain and Indapurker (2013), Gaikwad *et al.* (2014), Naveed *et al.* (2015), Dhuria and Babbar (2016), Saha *et al.* (2018), Tamvar *et al.* (2019), Dar *et al.* (2020), Boparai *et al.* (2021) and Babbar *et al.* (2021).

5.6 Principal component analysis

Principal component analysis the type of multivariate analysis, which initially described by Pearson in 1901 and later modified by Hotelling in 1933 for simplification and evaluation of complex data sets. Principal components analysis (PCA) is a non-parametric and simple method for squeezing relevant information. PCA can transform a big number of different correlated variables into a smaller number of the uncorrelated variables, which called principal component. Each of the principal component show a linear combination of original variables. Principal component analysis had been

conducted in order to identify and rank various genotypes on the basis of their combinations of phenotypic traits.

Principal components analysis indicated that out of 14 principal component (PC), only 4 PC showed Eigen value more than 1 and they accounted for 73.79% variability out of total variability. It exposed that PC1 showed maximum variation (25.71%) and was related with pod concerned traits *viz.*, total number of pod per plant and number of effective pod per plant. The PC 2 was dominated for height of plant, stem thickness, number of seed per pod, harvest index and the seed yield per plant. PC 3 was associated with traits days to 50% flowering, number of secondary branch per plant and biological yield per plant. Although, PC 4 were dominating for number of primary branch per plant.

The PC scores of each principal component (PC1, PC2, PC3 and PC4) had both positive as well as the negative values. These score can be effective for the propose of making precision selection indices, whose intensity decided by variation showed by each PC. High PC score for any of the particular genotype in any of the particular principal component informs high value for variable in the particular genotype. Genotype ICCV 201202 reported with maximum PC score followed by ICCV 201203, ICCV 201204, ICCV 08102 and ICCV 201205 in PC1, which indicated that these genotypes contain high value of pods traits *viz.* total number of pod per plant and number of effective pod per plant. In PC 2 highest PC score showed by genotypes ICCV 201115 followed by ICCV 201117, ICCV 201211 and ICCV 201118, which were mainly associated with traits height of plant, stem thickness, number of seed per pod, harvest index and the seed yield per plant. PC score in PC 3 were maximum for traits *i.e.* days to 50% flowering, number of secondary branch per plant and biological yield per plant by genotypes ICCV 201105, ICCV 201111, ICCV 08102 and ICCV 201103. Genotype ICCV 201216 followed by ICCV 201212, ICCV 201215 and ICCV 201208 obtained the maximum PC score in PC 4 related with trait number of primary branch per plant. Since most of the contributing traits of yield are presented in PC 1 and PC 2, which contain nearly half of the variability also of total variation, selection of various genotypes from PC 1 along with PC 2, would be useful and effective in the future crop yield improvement programme.

Above findings confirmed in earlier findings of Muniraja *et al.* (2011) for number of pod per plant, seed yield per plant and plant height, Malik *et al.* (2014) for Seed yield, pod per plant and plant height, Naveed *et al.* (2015) for grain yield, Nyende and

Rao (2015) for plant height, pod plant per plant and seed yield, Shivwanshi and Babbar (2017) and Mahmood *et al.* (2018) found for grain yield, harvest index and pods plant per plant, Tsehaye *et al.* (2020) for number of pods per plant and harvest index and Biswal (2021) reported for harvest index and the seed yield per plant.

5.7 Identification of promising genotypes based on some priority traits

The ultimate goal of any plant breeding programme is to enhance yield. Although, apart from yield improvement, each breeding programme has some other priority traits also according to need of particular crop and cultivated area. Usually main focus would be on developing early maturing, high yielding, biotic-abiotic stress resistance genotypes. Increment in cost of cultivation and non-availability of labors for harvesting create a demand for developing varieties suitable for mechanical harvesting in chickpea. In the current investigation, following promising genotypes have been identified on the basis of some priority traits:

1. Short-Medium Duration (<115 days) genotypes were ICCV 201204, ICCV 201207, ICCV 201208, ICCV 201211, ICCV 201212, ICCV 201214, ICCV 201216 and ICCV 201217.

2. High yielding genotypes were ICCV 201201, ICCV 201216, ICCV 201101, ICCV 201114, ICCV 201115, ICCV 08102, ICCV 201211, JG 36 and JG 24 in local investigation condition on the basis of plot yield.

3. Suitable for mechanical harvesting were having plant height more than 65 cm, height of the first fruiting node were more than 20.0 cm, semi-erect type of growth habit, high stem thickness with lodging and shattering resistance qualities. In present investigation 5 genotypes found with such merits namely JG 24, ICCV 201212, ICCV 201103, ICCV 201115 and ICCV 201118.

4. Genotypes, reported with high eminent physiological attributes should be related with traits such as biomass duration, leaf area index, net assimilation rate, number of effective pod per plant, leaf area ratio, harvest index, relative growth rate, which found to be most effective to enhance the seed yield per plant in current study. So based on these traits, genotypes ICCV 201201, ICCV 201207, ICCV 201210, ICCV 201102, ICCV 201103, ICCV 201104, ICCV 201105, ICCV 201118, JG 24 and JG 36 recorded as eminent genotypes.

5. Categorization of studied genotypes based on their 50% flowering and maturity time: -

S.No.	Criteria	Genotypes Name
1.	Early Flowering and Early-Medium Maturity	ICCV 201207, ICCV 201211, ICCV 201212, ICCV 201216, ICCV 201217
2.	Early Flowering and Late Maturity	ICCV 201116
3.	Late Flowering and Late Maturity	ICCV 201105, ICCV 201111

Where,

Early Flowering – Genotypes showed 50% flowering in less than 70 DAS

Late Flowering - Genotypes showed 50% flowering after 80 DAS

Early-Medium Maturity – Genotypes had physiological maturity at less than 115 DAS

Late Maturity – Genotypes which exhibited physiological maturity after 125 DAS

6. Ideal genotype: In the present investigation it was found that genotype ICCV 201211 contained variation for most of the economical useful traits like total number of pod per plant, number of effective pod per plant, seed yield per plant, biological yield per plant, harvest index, biomass duration, leaf area index, net assimilation rate and leaf area ratio. Genotype ICCV 201211 performed well in divergence analysis and presented in all first 4 PC's, it is noticed as short-medium duration genotype with the higher yield. Hence, based on above qualities, genotype ICCV 201211 can be identify as ideal genotype of present study.

CHAPTER 6
SUMMARY, CONCLUSIONS AND
SUGGESTIONS FOR FUTURE WORKS

CHAPTER – 6

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER WORK

6.1 Summary

The current investigation entitled “**Genetic Assessment for Quantitative and Physiological Traits of *desi* Chickpea**” was aimed to identify the phenological, morphological, quantitative and physiological traits, which influence disease-insect resistance attributes and seed yield of Chickpea. Experimental material consisted of 40 *desi* Chickpea genotypes grown under Randomized Completely Block Design in two replications in All India Coordinated Research Project on Chickpea at Seed Breeding Farm of Department of Plant Breeding and Genetics, College of Agriculture, Jabalpur (M.P.), during *Rabi* 2020-21.

Based on 2 phenological traits *viz.*, days to 50% flowering and days to maturity coupled with 12 quantitative traits *viz.*, plant height (cm), height of first fruiting node (cm), stem thickness (mm), number of primary branches per plant, number of secondary branches per plant, total number of pod per plant, number of effective pod per plant, number of seed per pod, hundred seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g), observations were recorded. For physiological analysis observations of 10 traits *i.e.* relative growth rate, leaf area ratio, leaf area index, net assimilation rate, crop growth rate, leaf area duration, leaf area index duration, biomass duration, chlorophyll content, physiological maturity were recorded.

For the purpose of characterization of various genotypes, observations were recorded of visual characters: at plant level *viz.*, stem anthocyanin pigmentation, stem height at initiation of first flower, plant growth habit, colour of foliage, leaflet size, leaf pattern, flower number per peduncle, flower stripes on standard, colour of flower, length of peduncle, plant height, size of pod and at seed level were seed colour, size of seed, seed shape, seed texture, seed ribbing and type of seed were taken into consideration. With this lodging resistance and shattering resistance were also recorded for the purpose of creating better plant type of chickpea.

In order to study genetic-variability parameters: mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance

as percentage of mean, genotypic correlation coefficient, phenotypic correlation coefficient, path coefficient analysis, genetic diversity analysis and principal component analysis were performed for various characters.

The magnitude of both PCV and GCV were higher for traits total number of pod per plant, seed yield per plant, biological yield per plant, height of the first fruiting node, harvest index, hundred seed weight, plant height, number of secondary branches per plant, stem thickness, number of primary branches per plant, number of seed per pod, days to 50% flowering and days to maturity. That means in above order basis, these traits exhibited large variation.

High heritability combined with higher genetic advance as % of mean was observed for trait number of effective pods per plant followed by total number of pods per plant, biological yield per plant, height of first fruiting node, seed yield per plant, and hundred seed weight, which showed that these traits were influenced by additive genes action. Hence, direct selection for such traits can be quite effective.

Trait seed yield per plant revealed significant, positive correlation with most of the yield attributing traits in present experimentation. However, some traits had high association are number of seed per pod, biological yield per plant, number of effective pod per plant, harvest index, total number of pod per plant and number of secondary branches per plant. Therefore, in order to improve the potential of yield in chickpea plant should be selected on basis of above-mentioned traits.

Genotypic path analysis revealed that positive, high direct effects was reported for traits days to maturity, plant height, height of the first fruiting node, number of primary branches per plant, total number of pod per plant, biological yield per plant and harvest index on the seed yield per plant. Thus, these are direct yield influencing traits and selection based on such characters would be useful in yield improvement.

Based on divergence analysis, it was found that characters, which shows more contribution to the divergence were total number of pod per plant contributed maximum toward divergence at genetic level followed by harvest index, hundred seed weight and number of seed per pod and these mentioned traits should be considered as an important trait during selection. And 40 *desi* chickpea genotypes, which were evaluated for magnitude and nature of existing genetic divergence, categorized into 8 groups. Cluster V, cluster VI, cluster VII and cluster VIII were having single genotype in group, whereas remaining 04 clusters were poly genotypic. Cluster I had highest 18

genotypes then cluster III had 09 genotypes, cluster IV had 05 genotypes and cluster II had 04 genotypes.

The maximum distance at inter-cluster level was reported among the cluster II and the cluster V then by cluster V and cluster VI. Maximum cluster-mean was recorded for traits days to 50% flowering and days to maturity in cluster I. Cluster V had high mean value for total number of pod per plant and number of effective pod per plant. Traits stem thickness, number of secondary branches per plant, biological yield per plant and the seed yield per plant showed maximum mean-value in cluster VI, while hundred seed weight and trait number of primary branches per plant had highest cluster mean value in cluster VII. Cluster VIII showed the maximum mean value for plant height, stem height at first the fruiting node, number of seed per pod and harvest index.

Principal component analysis revealed that PC1 showed maximum variation (25.71%) and was related with pod concerned traits *viz.*, total number of pod per plant and number of effective pod per plant. The PC 2 was dominated for plant height, stem thickness, number of seed per pod, harvest index and the seed yield per plant. PC 3 related with days to 50% flowering, number of secondary branch per plant and biological yield per plant. Although, PC 4 were dominating for number of primary branch per plant.

High PC-score for any of the particular genotype in any of the particular principal component informs high value for variable in the particular genotype. Genotype ICCV 201202 reported with maximum PC score followed by ICCV 201203, ICCV 201204, ICCV 08102 and ICCV 201205 in PC1, which indicated that these genotypes contain high value of pods traits *viz.* total number of pod per plant and number of effective pod per plant. In PC 2 highest PC score showed by ICCV 201115 followed by ICCV 201117, ICCV 201211 and ICCV 201118, which were mainly associated with plant height, stem thickness, number of seed per pod, harvest index and the seed yield per plant. PC score in PC 3 were maximum for traits *i.e.* days to 50% flowering, number of secondary branches per plant and biological yield per plant by genotypes ICCV 201105, ICCV 201111, ICCV 08102 and ICCV 201103. Genotype ICCV 201216 followed by ICCV 201212, ICCV 201215 and ICCV 201208 obtained the maximum PC score in PC 4 related with trait number of primary branches per plant.

After evaluating 40 *desi* chickpea genotypes based on physiological traits, it was noticed that physiological attributes such as biomass duration, leaf area index,

net assimilation rate, leaf area ratio and relative growth rate found to be most effective to enhance seed yield per plant, so based on these investigation, genotypes ICCV 201201, ICCV 201207, ICCV 201210, ICCV 201102, ICCV 201103, ICCV 201104, ICCV 201105, ICCV 201118, JG 24 and JG 36 were selected as eminent chickpea genotypes.

After investigation, some genotypes categorized based on their 50% flowering and maturity days *viz.* Early Flowering and Early-Medium Maturity, Early Flowering and Late Maturity, Late Flowering and Early-Medium Maturity and Late Flowering and Late Maturity. And genotype ICCV 201211 recorded as ideal genotype based on its qualities.

6.2 Conclusions

1. Higher genotypic coefficient of variation and the heritability together with genetic advance as % of mean was found for traits total number of pod per plant, seed yield per plant, biological yield per plant, harvest index and hundred seeds weight, which showed that these traits were influenced by additive genes action. Hence, the direct selection for these traits can be quite effective.
2. Seed yield per plant revealed significant-positive correlation with the traits number of seed per pod, biological yield per plant, number of effective pod per plant, harvest index, total number of pod per plant and number of secondary branches per plant. However, biological yield and total number of pod per plant exhibited significant-negative correlation with trait harvest index. Significant, positively associated traits can be suggested to enhance simultaneously and increment of one trait will lead automatic enhancement of another correlated one. Although, such kind of simultaneous modifications are not possible for negatively correlated traits.
3. Path coefficients analysis indicated that positive-direct effects was reported for traits days to maturity, plant height, height of the first fruiting node, number of primary branches per plant, total number of pod per plant, biological yield per plant and for harvest index on the seed yield per plant. Thus, these are direct yield influencing traits and selection based on such characters would be useful in yield improvement.
4. The maximum inter-cluster distance was reported among the cluster II and cluster V, then cluster V and cluster VI. High heterotic combination will derive, when genotypes of such distinctly situated clusters crossed to each other and would give

higher heterotic segregation or heterotic progenies. Inter cluster distance observed minimum between the cluster III and cluster V.

5. Principal components analysis revealed that PC1 showed maximum variation (25.71%), which means genotypes of PC 1 should be given due importance. Genotype ICCV 201202 reported with maximum PC score followed by ICCV 201203, ICCV 201204, ICCV 08102 and ICCV 201205 in PC1 and these genotypes contain high value of pods traits *viz.* total number of pod per plant and number of effective pods per plant.

6. In present experimentation, based on physiological analysis, it was noticed that genotypes ICCV 201201, ICCV 201207, ICCV 201210, ICCV 201102, ICCV 201103, ICCV 201104, ICCV 201105, ICCV 201118, JG 24 and JG 36 were selected as eminent chickpea genotypes.

7. Genotype ICCV 201211 found as an ideal genotype because of its best performance in regarding to quantitative and physiological in the present investigation.

6.3 Suggestions for Future Work

1. Promising genotypes should be further evaluated in multilocation trails for different years in order to judge phenotypic stability.

2. Traits such as total number of pod per plant, seed yield per plant, biological yield per plant, harvest index and hundred seed weight, have to be utilized in future breeding programmes for enhancing the yield attributes.

3. Genotypes ICCV 201201, ICCV 201207, ICCV 201210, ICCV 201211, ICCV 201102, ICCV 201103, ICCV 201104, ICCV 201105, ICCV 201118, JG 24 and JG 36 can be evaluate more in relation to their physiological superiority and can be use in the sscrop improvement programme.

4. Molecular characterization of Chickpea promising genotypes should be done through various biotechnological techniques for more precision.

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Plate 1: Experimental Trial



Plate 2: Variation in Anthocyanin Coloration, Plant: Growth Habit
Stem: Anthocyanin Coloration

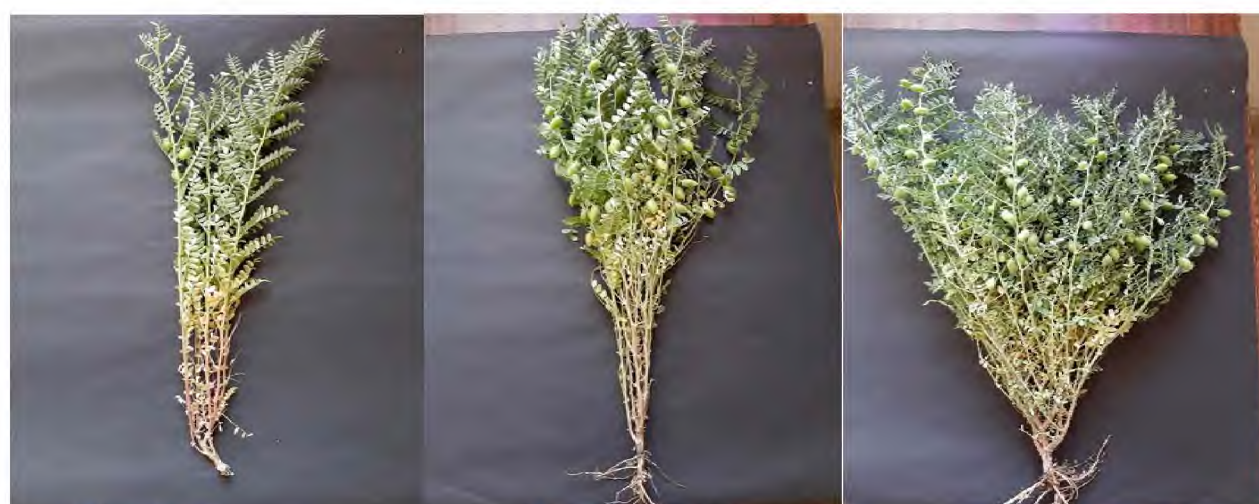


Absent

Present

Present

Plant: Growth Habit



Erect

Semi-erect

Spreading

Plate 3: Variation in Leaflet: Size (Length), Leaf: Pattern, Plant: Color of Foliage, Flower: Stripes on Standard, Flower: Color
Leaflet: Size (Length) **Leaf: Pattern**



Large Medium Small



Pinnate

Simple

Plant: Color of Foliage



Dark green

Medium green

Light green

Flower: Stripes on Standard



More

Less

Flower: Color



Pink

Blue

White

Pink

Blue

White

Plate 4: Variation in Flower: Number per Peduncle, Pods: Number per Peduncle, Peduncle: Length, Plant: Height, Pod: Size (length)

Flower: Number per Peduncle



Single

Twin

Pods: Number per Peduncle



Single

Twin

Peduncle: Length



Long

Medium

Short



Short

Medium

Long

Plant: Height



Tall

Medium

Short

Pod: Size (length)



Short

Medium

Large

**Plate 5: Lodging susceptible-resistance and plants suitable for the
Mechanical Harvesting
Lodging susceptible**



Lodging resistance



Plants suitable for Mechanical Harvesting



Plate 6: Seed: Type, Seed: Shape Seed: color Seed: Ribbing

Seed: Type



Desi

Seed: Shape



Kabuli

Angular

Seed: color



According to The Royal Horticulture Society, London

Seed: Ribbing



Absent



Present

Plate 7: Leaf Area Meter and Leaf Chlorophyll SPAD (The Soil Plant Analysis Development) Meter

Physiological Analysis

Leaf Area measurement



Leaf Area Meter

Leaf Chlorophyll measurement



SPAD (The Soil Plant Analysis Development) Meter

Appendix I: Weekly meteorological parameters during *Rabi* season (October to March 2020-21)

Month	Meteor. Weeks	Dates	Temperature (°C)		Sunshine Hours	Rainfall (mm)	R. H. (%)		Evaporation (mm)	Rainy days
			Max.	Min.			Morning	Evening		
Oct.	42	12 Oct – 18 Oct.	33.0	21.2	8.2	0	89	49	3.6	0
	43	19 Oct – 25 Oct.	32.7	16.7	8.7	0	85	33	3.3	0
	44	26 Oct – 01 Nov	30.8	12.7	8.3	0	80	25	3.1	0
Nov.	45	02 Nov-08 Nov	29.6	8.3	7.9	0	81	22	2.7	0
	46	09 Nov-15 Nov	31.2	15.5	8.2	5.2	86	41	2.4	1
	47	16 Nov-22 Nov	28.0	10.7	6.9	1.4	82	37	2.6	0
	48	23 Nov - 29 Nov	27.6	9.1	8.1	0.0	83	33	2.4	0
Dec.	49	30 Nov - 06 Dec	29.3	9.1	9.4	0.0	81	29	2.4	0
	50	07 Dec -13 Dec	26.4	14.7	3.2	2.3	88	57	1.7	0
	51	14 Dec -20 Dec	23.2	5.5	7.4	0.0	74	31	2.1	0
	52	21 Dec -27 Dec	23.8	7.2	6.2	0.0	83	43	1.8	0
Jan.	1	28 Dec – 03 Jan	26.5	12.4	4.5	0.5	87	50	1.6	0
	2	04 Jan – 10 Jan	25.0	11.8	5.7	0.4	86	49	2.1	0
	3	11 Jan – 17 Jan	25.4	8.0	8.2	0.0	75	31	2.5	0
	4	18 Jan – 24 Jan	24.6	8.6	7.4	0.0	86	49	2.1	0
	5	25 Jan – 31 Jan	21.4	4.8	6.0	0.0	73	31	2.6	0
Feb.	6	01 Feb – 07 Feb	26.4	8.9	9.1	0.0	72	34	3.0	0
	7	08 Feb – 14 Feb	27.7	11.8	7.7	12.6	83	42	2.7	1
	8	15 Feb – 21 Feb	28.6	10.6	9.3	0.0	79	28	3.1	0
	9	22 Feb – 28 Feb	32.7	12.4	9.8	0.0	74	25	4.4	0
Mar.	10	01 Mar– 07 Mar	34.8	13.0	8.9	0.0	74	20	4.6	0
	11	08 Mar – 14 Mar	32.3	15.3	7.0	6.2	78	29	4.4	1
	12	15 Mar – 21 Mar	33.9	16.7	5.0	0.0	67	27	4.6	0
	13	22 Mar – 28 Mar	36.8	16.7	8.5	0.0	57	13	6.7	0

Appendix II: Mean performance of *desi* chickpea genotypes for yield and component characters of yield

S. No.	Genotypes	DTF	DTM	PH (cm)	HFFN (cm)	ST (mm)	PB	SB	TNPPP	NEPP	NSPP	100SW (g)	BY (g)	HI %	SYPP (g)
1	ICCV 201201	72	115	47.3	19.9	2.43	3.39	10.26	61.9	58.1	1.13	24.8	36.3	44.0	15.99
2	ICCV 201202	70	115	44.6	20.2	2.92	3.10	10.67	94.4	92.8	1.16	18.0	40.6	43.8	17.84
3	ICCV 201203	72	116	40.2	16.9	2.17	3.23	12.06	90.3	82.6	1.17	21.2	40.0	44.6	17.84
4	ICCV 201204	72	114	49.8	19.5	2.15	3.28	10.98	76.0	73.8	1.16	20.2	37.9	34.8	13.27
5	ICCV 201205	69	118	45.3	22.6	3.00	3.59	11.29	73.6	71.3	1.19	23.1	36.4	40.2	14.60
6	ICCV 201206	71	119	45.1	19.6	2.42	2.49	9.28	88.8	82.1	1.19	20.7	33.4	39.6	13.31
7	ICCV 201207	68	110	47.8	20.4	3.10	2.33	7.04	64.3	58.8	1.15	22.4	27.9	41.4	11.58
8	ICCV 201208	72	114	44.1	22.7	3.12	3.66	10.16	62.8	60.8	1.11	23.0	29.8	41.0	12.19
9	ICCV 201209	72	119	50.1	20.2	2.61	2.41	9.97	79.9	73.1	1.16	21.8	36.6	40.8	14.96
10	ICCV 201210	73	117	46.3	23.2	2.37	3.16	10.99	57.3	53.8	1.19	38.1	33.6	33.8	11.35
11	ICCV 201211	67	113	59.1	22.7	3.01	3.05	12.05	45.6	41.3	1.56	22.3	53.1	40.2	21.38
12	ICCV 201212	67	114	66.6	20.7	2.90	3.38	10.93	67.8	65.8	1.21	26.5	26.1	49.6	13.00
13	ICCV 201213	72	115	53.8	22.1	2.51	3.16	11.04	53.0	52.1	1.07	24.3	26.6	40.3	10.70
14	ICCV 201214	73	114	53.2	20.1	2.48	2.93	9.14	77.8	73.3	1.17	25.4	37.4	33.8	12.66
15	ICCV 201215	72	116	58.4	21.5	3.05	3.06	9.88	43.5	41.9	1.08	26.4	27.1	41.6	11.29
16	ICCV 201216	67	114	59.8	23.2	2.86	3.33	10.83	41.9	39.8	1.27	23.2	31.6	38.5	12.21
17	ICCV 201217	68	112	54.3	21.3	3.01	2.46	9.19	44.4	42.1	1.20	17.8	24.3	45.8	11.14
18	ICCV 201218	67	115	48.4	23.4	3.03	2.82	10.06	64.6	61.3	1.19	18.7	29.8	41.2	12.30
19	ICCV 201101	79	125	45.7	24.7	2.39	2.93	12.14	43.4	40.3	1.33	25.3	35.3	32.2	11.42

20	ICCV 201102	79	129	55.0	27.8	2.58	2.41	10.06	41.8	39.9	1.12	24.9	34.4	31.4	10.83
21	ICCV 201103	82	125	65.1	32.3	3.05	2.81	10.99	47.9	44.3	1.33	25.9	44.3	27.3	12.09
22	ICCV 201104	79	126	48.3	20.2	2.33	2.93	11.82	42.9	40.3	1.17	23.4	28.9	39.2	11.39
23	ICCV 201105	82	128	47.8	26.8	2.11	3.23	12.16	44.3	41.9	1.30	24.0	42.4	32.4	13.82
24	ICCV 201106	78	127	60.9	30.4	2.48	3.23	10.63	44.6	41.1	1.14	25.5	29.4	34.0	11.79
25	ICCV 201107	74	121	48.1	27.3	2.32	3.14	11.24	65.8	63.3	1.09	20.8	29.9	36.8	11.04
26	ICCV 201108	75	122	50.5	27.3	2.37	3.05	10.89	55.1	51.6	1.20	18.7	27.4	40.6	11.18
27	ICCV 201109	75	124	64.3	27.8	2.43	2.84	10.12	58.1	55.8	1.26	18.2	28.8	43.2	12.46
28	ICCV 201110	75	124	49.6	26.0	2.35	3.28	12.13	42.4	39.9	1.24	23.9	33.4	40.1	13.45
29	ICCV 201111	82	128	55.9	35.4	2.47	2.99	11.54	46.4	44.1	1.36	30.2	35.9	34.4	12.44
30	ICCV 201112	72	129	45.6	23.0	2.79	2.78	8.11	48.1	44.8	1.25	24.3	26.4	53.6	14.19
31	ICCV 201113	70	129	56.6	28.7	2.58	2.45	7.04	47.4	43.3	1.13	28.6	27.9	40.8	11.40
32	ICCV 201114	72	127	49.2	24.1	2.33	2.44	6.97	43.6	39.8	1.30	19.9	24.7	49.1	12.17
33	ICCV 201115	72	123	66.4	35.9	2.98	3.03	11.66	79.6	76.4	1.75	25.4	32.7	64.1	21.01
34	ICCV 201116	69	126	55.6	22.6	2.20	3.40	10.64	60.4	53.8	1.20	18.4	27.8	39.2	10.93
35	ICCV 201117	71	124	57.5	35.0	3.06	2.48	8.19	44.1	40.1	1.43	27.7	26.4	61.4	16.24
36	ICCV 201118	68	125	65.1	36.2	2.99	2.92	8.99	44.4	39.9	1.46	26.0	24.7	56.0	13.88
37	ICCV 08102	72	117	58.5	28.8	2.28	3.16	11.04	87.8	85.8	1.32	24.9	49.1	41.9	20.64
38	RVG 204	72	124	47.5	25.9	2.26	3.17	9.99	44.4	39.9	1.13	22.0	23.4	46.4	10.90
39	JG 36	73	116	50.3	21.1	2.34	2.55	9.90	71.9	67.9	1.21	15.5	27.1	40.0	10.86
40	JG 24	67	121	65.1	23.8	2.40	3.05	9.68	48.4	45.1	1.22	30.3	28.9	41.5	11.93

Appendix III: Analysis of Variance (ANOVA)

SV	DTF	DTM	PH	HFFN	ST	PB	SB	TNPPP	NEPP	NSPP	100SW	BY	HI	SYPP
Mean	74.0	120.4	53.0	24.8	2.6	2.9	10.2	58.5	55.1	1.2	23.5	32.4	41.5	13.3
CV (%)	2.0	1.1	4.4	7.0	4.6	6.5	7.8	3.1	3.0	4.6	3.9	8.2	5.8	10.1
SE	1.0	0.9	1.6	1.2	0.08	0.1	0.5	1.2	1.1	0.0	0.6	1.9	1.7	0.9
CD (5%)	3.1	2.7	4.6	3.4	0.2	0.3	1.6	3.6	3.3	0.1	1.8	5.4	4.8	2.7

Where,

DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), HFFN: Height of first fruiting node (cm), ST: Stem thickness (mm), PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPP: Number of effective pods per plant, NSPP: Number of seeds per pod, 100SW: 100 Seed weight, BY: Biological yield per plant (g), HI: Harvest index (%), SYPP: Seed yield per plant (g), SV: Source of variation, CV: Coefficient of variation, SE: Standard error, CD 5% Critical difference at 5%, CD 1%: Critical difference at 1%.

Appendix IV: Scoring of morphological and seed characters of *desi* chickpea genotypes

S.NO.	Genotypes	Stem anthocyanin coloration	Stem: Height at initiation of first flower	Growth Habit	Foliage Color	Leaflet Size	Leaf Pattern	Flower per Peduncle	Flower Color	Stripes on Standard	Peduncle Length
1	ICCV 201201	9	3	7	2	5	3	1	2	5	7
2	ICCV 201202	9	3	5	1	5	3	1	2	4	5
3	ICCV 201203	9	3	5	1	3	3	1	2	6	5
4	ICCV 201204	9	5	5	1	5	3	1	2	4	5
5	ICCV 201205	9	5	7	1	5	3	1	2	5	5
6	ICCV 201206	9	3	5	2	3	3	1	2	5	5
7	ICCV 201207	9	5	7	3	5	3	1	2	4	7
8	ICCV 201208	9	3	7	3	5	3	1	2	7	5
9	ICCV 201209	9	3	5	2	5	3	1	2	4	7
10	ICCV 201210	9	3	5	3	3	3	1	2	5	5
11	ICCV 201211	9	7	5	1	5	3	1	2	4	5
12	ICCV 201212	9	5	5	3	5	3	1	2	5	7
13	ICCV 201213	9	7	5	3	3	3	1	2	4	5
14	ICCV 201214	9	5	5	1	5	3	1	2	5	7
15	ICCV 201215	9	5	5	1	3	3	1	2	4	5
16	ICCV 201216	9	5	5	3	5	3	1	2	4	5
17	ICCV 201217	9	5	5	1	5	3	1	2	4	7
18	ICCV 201218	9	3	5	2	3	3	1	2	4	7
19	ICCV 201101	9	3	7	1	5	3	1	2	6	7
20	ICCV 201102	9	5	5	2	5	3	1	2	4	7
21	ICCV 201103	9	7	5	3	5	3	1	2	6	5
22	ICCV 201104	9	5	5	2	5	3	1	2	4	5
23	ICCV 201105	9	3	5	3	5	3	1	2	7	7
24	ICCV 201106	9	5	5	2	5	3	1	2	7	7
25	ICCV 201107	9	3	5	1	5	3	1	2	6	5
26	ICCV 201108	9	5	5	1	3	3	1	2	4	5

27	ICCV 201109	9	5	5	2	3	3	1	2	7	5
28	ICCV 201110	9	5	5	1	5	3	1	2	5	5
29	ICCV 201111	9	5	5	1	5	3	1	2	6	7
30	ICCV 201112	9	3	7	3	5	3	1	2	5	5
31	ICCV 201113	9	7	5	3	5	3	1	2	6	5
32	ICCV 201114	9	3	5	2	5	3	1	2	4	5
33	ICCV 201115	9	7	5	3	5	3	1	2	4	5
34	ICCV 201116	9	5	5	2	5	3	1	2	6	5
35	ICCV 201117	9	5	5	2	7	3	1	2	5	5
36	ICCV 201118	9	7	5	3	5	3	1	2	7	5
37	ICCV 08102	9	5	5	2	5	3	1	2	5	7
38	RVG 204	9	3	5	1	5	3	1	2	4	5
39	JG 36	9	3	5	3	5	3	1	2	4	7
40	JG 24	9	7	5	3	7	3	1	2	4	7

S.No.	Genotypes	Plant Height	Pod Size	Seed Color	Seed Shape	Seed Texture	Seed Ribbing	Seed Type	Seed Size	Lodging Resistance	Shattering Resistance
1	ICCV 201201	5	7	4	3	2	9	1	5	0	0
2	ICCV 201202	3	3	3	3	2	9	1	3	0	0
3	ICCV 201203	3	5	2	3	2	9	1	5	0	0
4	ICCV 201204	5	5	3	3	2	9	1	5	0	0
5	ICCV 201205	5	5	5	3	2	9	1	5	0	0
6	ICCV 201206	5	5	1	3	2	9	1	5	1	0
7	ICCV 201207	5	5	5	3	2	9	1	5	0	0
8	ICCV 201208	3	3	5	3	2	9	1	5	0	0
9	ICCV 201209	5	3	5	3	2	9	1	5	1	0
10	ICCV 201210	5	7	5	3	2	9	1	9	3	0
11	ICCV 201211	5	5	1	3	2	9	1	5	1	0

12	ICCV 201212	7	5	3	3	2	9	1	7	3	0
13	ICCV 201213	5	7	5	3	2	9	1	5	0	0
14	ICCV 201214	5	7	4	3	2	9	1	7	5	0
15	ICCV 201215	5	7	5	3	2	9	1	7	0	0
16	ICCV 201216	5	7	5	3	2	9	1	5	5	0
17	ICCV 201217	5	5	3	3	2	9	1	3	0	0
18	ICCV 201218	5	5	5	3	2	9	1	5	0	0
19	ICCV 201101	5	7	5	3	2	9	1	7	0	0
20	ICCV 201102	5	7	5	3	2	9	1	7	1	0
21	ICCV 201103	7	7	5	3	2	9	1	7	3	0
22	ICCV 201104	5	7	1	3	2	9	1	5	1	0
23	ICCV 201105	5	5	5	3	2	9	1	5	1	0
24	ICCV 201106	5	5	4	3	2	9	1	7	1	0
25	ICCV 201107	5	5	7	3	2	9	1	5	1	0
26	ICCV 201108	5	5	5	3	2	9	1	5	1	0
27	ICCV 201109	5	5	5	3	2	9	1	5	0	0
28	ICCV 201110	5	7	5	3	2	9	1	5	3	0
29	ICCV 201111	5	7	4	3	2	9	1	7	1	0
30	ICCV 201112	5	7	7	3	2	9	1	5	1	0
31	ICCV 201113	5	5	6	3	2	9	1	7	1	0
32	ICCV 201114	5	5	5	3	2	9	1	5	0	0
33	ICCV 201115	7	7	5	3	2	9	1	7	3	0
34	ICCV 201116	5	5	5	3	2	9	1	3	1	0
35	ICCV 201117	5	5	5	3	2	9	1	7	0	0
36	ICCV 201118	5	5	4	3	2	9	1	7	0	0
37	ICCV 08102	5	7	1	3	2	9	1	5	0	0

38	RVG 204	5	5	5	3	2	9	1	5	0	0
39	JG 36	5	5	2	3	2	9	1	1	7	0
40	JG 24	7	5	1	3	2	9	1	9	1	0

Appendix V: Mean Performance of the *desi* Chickpea Genotypes for its Major Physiological Characters

S.No.	Genotypes	Leaf Area (mm)			Plant Biomass (g)			SPAD for Chlorophyll
		30 DAS	60 DAS	90 DAS	30 DAS	60 DAS	90 DAS	
1	ICCV 201201	57.1	335.355	469.995	0.0265	5.095	39.05	53.4
2	ICCV 201202	39.655	183.57	302.285	0.0206	2.505	15.245	43.6
3	ICCV 201203	70.78	250.335	330.23	0.02625	4.125	11.24	49.95
4	ICCV 201204	59.325	162.695	296.925	0.02395	2.65	18.995	47.25
5	ICCV 201205	53.59	202.545	327.515	0.0226	3.195	8.365	47.85
6	ICCV 201206	57.09	203.345	323.28	0.021	3.255	26.265	53
7	ICCV 201207	72.27	300.525	440	0.02515	3.98	20.97	56.3
8	ICCV 201208	57.73	336.625	437.165	0.02215	6.565	20.51	56.15
9	ICCV 201209	59.48	129.09	284.01	0.0318	1.67	8.105	52.7
10	ICCV 201210	73.49	232.935	312.355	0.02375	3.585	31.235	62.9
11	ICCV 201211	53.09	349.31	463.64	0.023	5.985	10.275	51.05
12	ICCV 201212	62.525	353.57	491.035	0.0289	5.175	23.67	56.85
13	ICCV 201213	65.58	199.615	340.14	0.03075	2.78	17.515	56.45
14	ICCV 201214	72.59	227.575	375.565	0.0338	3.46	10.89	50.5
15	ICCV 201215	46.575	224.995	343.105	0.01945	3.165	23.525	47.75
16	ICCV 201216	78.935	246.355	358.305	0.0221	3.7	14.565	55.45
17	ICCV 201217	55.105	223.87	375.3	0.02125	4.325	51.26	53.05
18	ICCV 201218	61.665	271.14	401	0.02485	3.69	32.39	54.85
19	ICCV 201101	45.3	163.81	293.24	0.0234	3.58	14.08	55.55
20	ICCV 201102	69.135	212.33	354.085	0.02735	4.175	10.005	57.95
21	ICCV 201103	93.295	308.42	411.74	0.0385	4.4	36.245	51.85
22	ICCV 201104	81.185	311.405	435.86	0.04275	3.995	22.1	56.7
23	ICCV 201105	81.73	327.12	454.3	0.0294	4.84	10.99	57.9
24	ICCV 201106	68.29	220.065	389.56	0.02985	3.84	27.985	53.7

25	ICCV 201107	64.38	191.595	300.855	0.03015	2.765	29.38	63.1
26	ICCV 201108	59.115	291.125	431.155	0.03225	5.2	30.665	51.7
27	ICCV 201109	42.95	199.35	313.57	0.0258	3.63	17.795	49.4
28	ICCV 201110	58.01	179.265	250.81	0.02895	2.255	30.08	47.05
29	ICCV 201111	74.215	275.04	398.715	0.0349	3.09	14.47	56.5
30	ICCV 201112	58.135	262.495	369.88	0.0314	2.85	30.745	47
31	ICCV 201113	110.605	268.255	379.305	0.04115	4.65	16.29	51.15
32	ICCV 201114	52.52	190.285	302.195	0.01745	3.73	11.915	61.7
33	ICCV 201115	92.01	308.385	395.215	0.03715	5.93	14.15	63.5
34	ICCV 201116	68.965	194.21	310.89	0.02975	2.675	36.66	53.45
35	ICCV 201117	48.83	216.545	310.245	0.0255	3.785	13.45	59.8
36	ICCV 201118	74.095	337.11	452.645	0.02565	5.785	36.805	55.1
37	ICCV 08102	79.71	262.15	360.6	0.01945	4.31	15.94	55.7
38	RVG 204	54.645	213.555	337.835	0.02685	2.73	19.075	59.8
39	JG 36	67.6	206.695	344.055	0.02945	2.49	32.295	44.95
40	JG 24	137.285	231.35	354.605	0.0335	4.295	28.29	59.55

S.No.	Genotypes	RGR		LAR		LAI			NAR		CGR		LAD		LAI D		BMD	
		30-60	60-90	30-60	60-90	30	60	90	30-60	60-90	30-60	60-90	30-60	60-90	30-60	60-90	30-60	60-90
1	ICCV 201201	0.8482	3.5769	1121.844	41.044	0.3172	1.8631	2.6111	0.6211	0.0028	0.0009	0.0063	5886.825	12080.25	32.70458	67.1125	76.822	662.175
2	ICCV 201202	0.5313	2.6482	1050.854	46.491	0.2203	1.0198	1.6794	0.6486	0.0018	0.0005	0.0024	3348.375	7287.825	18.60208	40.48792	37.884	266.25
3	ICCV 201203	0.7699	2.3322	1560.362	44.883	0.4442	1.3907	1.8346	0.4947	0.0008	0.0008	0.0013	4954.275	8708.475	27.52375	48.38042	62.268	230.475
4	ICCV 201204	0.6674	2.8628	1260.452	38.641	0.3296	0.9039	1.6496	0.6106	0.0024	0.0005	0.0030	3330.3	6894.3	18.50167	38.30167	40.109	324.675
5	ICCV 201205	0.6646	2.0405	1223.137	51.10764	0.2977	1.1252	1.8195	0.7573	0.0007	0.0006	0.0010	3842.025	7950.9	21.34458	44.17167	48.264	173.4
6	ICCV 201206	0.7852	3.1822	1412.148	37.563	0.3172	1.1297	1.7960	0.3082	0.0030	0.0006	0.0043	3906.525	7899.375	21.70292	43.88542	49.14	442.8
7	ICCV 201207	0.7979	2.9539	1511.039	48.252	0.4015	1.6696	2.4444	0.8233	0.0015	0.0007	0.0031	5591.925	11107.88	31.06625	61.71042	60.077	374.25

8	ICCV 201208	1.0843	2.9269	1358.824	36.307	0.3207	1.8701	2.4287	0.7237	0.0012	0.0012	0.0026	5915.325	11606.85	32.86292	64.4825	98.807	406.125
9	ICCV 201209	0.3501	2.0212	969.195	55.882	0.3304	0.7172	1.5778	0.4891	0.0011	0.0003	0.0012	2828.55	6196.5	15.71417	34.425	25.527	146.625
10	ICCV 201210	0.8496	3.3542	1594.196	37.408	0.4083	1.2941	1.7353	0.7489	0.0035	0.0007	0.0051	4596.375	8179.35	25.53542	45.44083	54.131	522.3
11	ICCV 201211	1.1210	2.2274	1190.016	52.151	0.2949	1.9406	2.5758	0.5536	0.0004	0.0011	0.0008	6036	12194.25	33.53333	67.74583	90.12	243.9
12	ICCV 201212	0.8985	3.0754	1174.305	44.986	0.3474	1.9643	2.7280	1.0197	0.0015	0.0010	0.0034	6241.425	12669.08	34.67458	70.38375	78.058	432.675
13	ICCV 201213	0.5910	2.7782	1097.111	45.900	0.3643	1.1090	1.8897	0.6341	0.0019	0.0005	0.0027	3977.925	8096.325	22.09958	44.97958	42.161	304.425
14	ICCV 201214	0.6947	2.3031	1122.057	49.797	0.4033	1.2643	2.0865	0.8289	0.0008	0.0006	0.0014	4502.475	9047.1	25.01375	50.26167	52.407	215.25
15	ICCV 201215	0.6235	3.0708	1235.18	42.233	0.2587	1.2500	1.9061	0.8338	0.0025	0.0006	0.0038	4073.55	8521.5	22.63083	47.34167	47.766	400.35
16	ICCV 201216	0.8235	2.5931	1998.584	45.350	0.4385	1.3686	1.9906	0.6791	0.0013	0.0007	0.0020	4879.35	9069.9	27.1075	50.38833	55.831	273.975
17	ICCV 201217	0.9231	3.8479	1346.047	29.510	0.3061	1.2437	2.0850	0.3535	0.0054	0.0008	0.0087	4184.625	8987.55	23.24792	49.93083	65.193	833.775
18	ICCV 201218	0.8330	3.3917	1276.801	43.208	0.3426	1.5063	2.2278	0.3625	0.0029	0.0007	0.0053	4992.075	10082.1	27.73375	56.01167	55.722	541.2
19	ICCV 201101	0.9084	2.5535	986.7963	33.181	0.2517	0.9101	1.6291	0.2027	0.0017	0.0007	0.0019	3136.65	6855.75	17.42583	38.0875	54.051	264.9
20	ICCV 201102	0.8091	2.2179	1297.035	42.842	0.3841	1.1796	1.9671	0.4259	0.0007	0.0008	0.0011	4221.975	8496.225	23.45542	47.20125	63.035	212.7
21	ICCV 201103	0.7620	3.5056	1261.032	40.747	0.5183	1.7134	2.2874	0.9075	0.0030	0.0008	0.0059	6025.725	10802.4	33.47625	60.01333	66.577	609.675
22	ICCV 201104	0.8843	3.0071	994.0804	48.281	0.4510	1.7300	2.4214	0.3501	0.0017	0.0007	0.0034	5888.85	11208.98	32.71583	62.27208	60.566	391.425
23	ICCV 201105	0.9859	2.3057	1417.567	55.168	0.4541	1.8173	2.5239	0.4177	0.0005	0.0009	0.0011	6132.75	11721.3	34.07083	65.11833	73.041	237.45
24	ICCV 201106	0.8656	3.2420	1170.581	35.933	0.3794	1.2226	2.1642	0.3508	0.0027	0.0007	0.0045	4325.325	9144.375	24.02958	50.80208	58.047	477.375
25	ICCV 201107	0.6856	3.2969	1125.337	39.824	0.3577	1.0644	1.6714	0.6512	0.0037	0.0005	0.0049	3839.625	7386.75	21.33125	41.0375	41.927	482.175
26	ICCV 201108	0.8819	3.3311	961.8125	34.629	0.3284	1.6174	2.3953	0.6535	0.0024	0.0010	0.0047	5253.6	10834.2	29.18667	60.19	78.483	537.975
27	ICCV 201109	0.7531	2.7943	880.1785	36.295	0.2386	1.1075	1.7421	0.4104	0.0020	0.0007	0.0026	3634.5	7693.8	20.19167	42.74333	54.837	321.375
28	ICCV 201110	0.4524	3.3302	1039.746	44.962	0.3223	0.9959	1.3934	0.4986	0.0044	0.0004	0.0052	3559.125	6451.125	19.77292	35.83958	34.259	485.025
29	ICCV 201111	0.5271	2.5943	1135.611	59.849	0.4123	1.5280	2.2151	0.6527	0.0012	0.0006	0.0021	5238.825	10106.33	29.10458	56.14625	46.873	263.4
30	ICCV 201112	0.6845	3.3436	983.5306	51.663	0.3230	1.4583	2.0549	0.2647	0.0031	0.0005	0.0052	4809.45	9485.625	26.71917	52.69792	43.221	503.925
31	ICCV 201113	0.8243	2.7030	1413.187	39.747	0.6145	1.4903	2.1072	0.5180	0.0013	0.0009	0.0022	5682.9	9713.4	31.57167	53.96333	70.367	314.1
32	ICCV 201114	0.7939	2.3899	1531.138	38.128	0.2918	1.0571	1.6789	0.4061	0.0011	0.0007	0.0015	3642.075	7387.2	20.23375	41.04	56.211	234.675
33	ICCV 201115	1.0514	2.5557	1264.682	39.995	0.5112	1.7133	2.1956	0.5869	0.0008	0.0011	0.0015	6005.925	10554	33.36625	58.63333	89.507	301.2
34	ICCV 201116	0.5252	3.5256	1231.431	41.463	0.3831	1.0789	1.7272	0.3104	0.0046	0.0005	0.0063	3947.625	7576.5	21.93125	42.09167	40.571	590.025

35	ICCV 201117	0.7627	2.5110	984.7909	39.895	0.2713	1.2030	1.7236	0.4331	0.0012	0.0007	0.0018	3980.625	7901.85	22.11458	43.89917	57.157	258.525
36	ICCV 201118	0.9492	3.5136	1540.266	35.844	0.4116	1.8728	2.5147	0.6998	0.0026	0.0011	0.0057	6168.075	11846.33	34.26708	65.81292	87.159	638.85
37	ICCV 08102	0.9596	2.6320	2212.839	42.431	0.4428	1.4564	2.0033	0.3256	0.0012	0.0008	0.0022	5127.9	9341.25	28.48833	51.89583	64.941	303.75
38	RVG 204	0.7445	2.8646	1057.997	48.790	0.3036	1.1864	1.8769	0.2181	0.0021	0.0005	0.0030	4023	8270.85	22.35	45.94917	41.352	327.075
39	JG 36	0.6687	3.3932	1196.159	47.754	0.3756	1.1483	1.9114	0.5456	0.0037	0.0005	0.0055	4114.425	8261.25	22.85792	45.89583	37.791	521.775
40	JG 24	0.8998	3.2538	1996.073	32.896	1.0405	1.2853	1.9700	0.7047	0.0029	0.0008	0.0044	5529.525	8789.325	30.71958	48.82958	64.927	488.775

Where,

RGR: Relative growth rate ($\text{g} \cdot \text{g}^{-1} \cdot \text{day}^{-1}$), LAR: Leaf area ratio ($\text{cm}^2 \cdot \text{g}^{-1}$), LAI: Leaf area index, NAR: Net assimilation rate ($\text{g} \cdot \text{cm}^{-1} \cdot \text{day}^{-1}$), CGR: Crop growth rate ($\text{g} \cdot \text{cm}^{-1} \cdot \text{day}^{-1}$), LAD: Leaf area duration ($\text{cm}^2 \cdot \text{days}$), LAID: Leaf area index duration (days), BMD: Biomass duration ($\text{g} \cdot \text{day}$).

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