Evaluation of Genetic Diversity in Chickpea (*Cicer arietinum* L.) Germplasm in PrayagrajAgro-Climatic Conditions using Metroglyph Analysis

Abstract

The present investigation consists of 25 genotypes of chick pea genotypes.The experiment was conducted during *Rabi*-2022 in RBD having three replications. The datawere recorded on 12 characters to study the variability, heritability, genetic advance, metroglyph analysis. Analysis of variance revealed that there was considerable genetic variabilityin the available germplasm for most of the characters studied. Performance of grain yield and itscomponentsdepictedthatUDAY wasfoundbestfollowedbyNBEG-3andNBEG-47.A close perusal of variability coefficients revealed that the difference between PCV and GCV wassmall indicating little influence of environment on the expression of characters studied. HighestimatesofPCVandGCVwererecordedforHarvestingindex. The highest heritability was observed for Harvesting index (92.17 %),followed by Seed yield (91.76%) and Number of pods per plant (85.61%). In the present study a perusal of genetic advance showed that it was highfor Harvesting index (14.10) Among 29 genotypes these genotypes UDAY, NBEG-3, NBEG-47, ICC-313,FLIP-09-162, RVG-202, IPC-11-85were observedashigheryielderandidentifiedforhigherindexscore.

Keywords: Chick pea, Genetic variability, PCV, GCV, Heritability, Genetic advance, Metroglyph analysis.

Introduction

The chickpea (*Cicer arietinum* L.), out of more than a dozen legumes, is the most significant edible legume in India. The legume, or chickpea, is a diploid agricultural species with 16 chromosomes that is a cool-season crop and has a genome size of 738 megabytes. It is self-pollinated. Desi chickpeas contain tiny grains with a thick seed coat that range in color from pale to dark brown. Bulki chickpeas contain larger grains, a thin seed coat, and a pale cream tint. The desi variety is more common and produces up to 80% of the chickpeas produced worldwide. Whereas kabuli varieties lack anthocyanin pigments, desi chickpeas have anthocyanin pigmentation in one or more areas(**Thudi*et al.*, 2017**). At around 11.6 million tons produced year, chickpeas come in third place in the world's pulse output; 80 percent are desi and the remaining 20 percent are kabuli (**Merga and Haji, 2019)**. Grain yield and chickpea growth and development are influenced by a range of climatic and environmental factors. Climate extremes include drought, extremely high and low temperatures, and irregular rainfall might hinder the production of chickpeas. Environmental elements that affect chickpea productivity worldwide include salt and nutritional deficiency. *Fusarium oxysporum*f.sp. ciceris seriously reduces chickpea yields annually. Ascochyta blight and Botrytis grey mold are examples of foliar diseases, whereas root diseases like as collar rot and dry root rot are also potent biotic stressors **(Dürdane,2022**)

In order to determine the extent of chickpea rust disease in nine districts of Western Maharashtra State—Ahmednagar, Solapur, Sangali, Satara Kolhapur, Pune, Nasik, Jalgaon, and Dhule—a roving survey was carried out during Rabi 2021–2022. The findings of the survey showed that, among the nine districts in Western Maharashtra, Ahmednagar, Solapur, Sangali, Satara

Kolhapur, and Pune had the highest prevalence of chickpea rust disease. The chickpea rust disease's overall severity varied from 13.77 to 60.22%. The highest percentage of illness severity, 60.22%, was found in the Satara district's Thakurki village of Phaltan tehsil, while the lowest percentage, 13.77%, was found in the Pune district's Lamjewadi village of tehsil Indapur. At every survey location from the districts of Nasik, Dhule, and Jalgaon, no sickness was found. But save from a few spots in the districts of Ahmednagar (Rahuri, 29.44%) and Pune (Baramati, 12.44%), no illness was found during the Rabi 2022–2023 survey. The degree of the disease varied depending on the farming system and climate at each area (**Mukund Dawale*et al.*, 2023**). **Punitha *et al.* (2010)** also showed in their findings of metroglyph analysis in sorghum that group VI having three genotypes with high yield an moderate test weight. Similarly**Bhargava *et al.*(2009)** reported in Chenopodium species that group IV had three genotypes exhibiting high grain yield and medium to high primary branches/plant and plant height. **Laiju*et al.* (2002)** reported Index score ranging from 12 to 23 in Hordeum species while **Ghafoor and Ahmad (2005)** in blackgram.

Identifying various genotypes beneficial for hybridization programs to generate improved recombinants and classifying the chick pea germplasm into distinct groups based on genetic diversity were the primary objectives of this work.The present investigation was undertaken to estimate the variability parameters for quantitative characters of chickpea and to classify the genotypes by metroglyph analysis. Apart from this, estimation of the genetic divergence for the identification of divergent parents for future hybridization programme was also studied.

Materials and Methods

The experiment was carried out to assess at Field Experimentation Centre, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj during *Rabi* 2022-2023. The genotypes were planted in a randomized block design with three replications.The spacing between two row is 30 cm and distance between plant to plant is 10 cm. Five plants are randomly selected from each block of genotypes for recording observation.Data of 12 quantitative characters*viz*., Days to 50% flowering, Days to 50% pod setting,Plant height,Number of primary branches per plant, Number of secondary branches per plant, Number of pods per plant, Number of seeds per pod,Biological yield per plant (g), Days to maturity, Seed index (g), Harvesting index (%), Seed yield per plant (g).The analysis of variance for all the characters of genotypes was carried out following RBD design.Metroglyph and index score method advocated by **Anderson (1957)** were used for analysis of morphological characters in different crop species.

The two most important characters, Harvesting index and Days to maturity, were plotted on the x-axis and y-axis, respectively. A scatter diagram was generated in which each genotype was represented by a circle for the interval of the characters. The range of variability of a trait was represented by ray length. Observed traits were represented by the various positions of rays on the glyph (Figure 1). The index values were divided into three classes i.e., 1- no ray, 2 -short ray and 3-long ray. The total index values were taken by adding up the index scores of all the twelve characters studied.

The statistical analysis was done by using replication mean values based on the observations recorded. The data recorded on above characters were subjected to following statistical analysis.

1. Analysis of Variance(ANOVA) (**Fisher, 1936**)
2. Variability (**Burton, 1952**)

(a) Genotypic coefficient of variation (GCV)

(b) Phenotypic coefficient of variation (PCV)

3. Heritability (**Burton and Daevane, 1953**)
4. Genetic advance (**Johnson *et al.*, 1955**)
5. Metroglyph Analysis (**Anderson, 1957**)

RESULTS AND DISCUSSION

Among 25 genotypes, UDAY, NBEG-3, NBEG-47 was found to be superior in seed yield /plant. The analysis of variance revealed significant variance among genotypes for all character's studies, indicating the existence of wide genetic divergence among them. Environment plays an important role in the expression of Phenotype and Genotype, in present investigation Phenotypic coefficient of variance is higher than Genotypic coefficient of variance indicating that characters are influenced by Environment. Hence, variability can be observed through parameters like GCV, PCV, Heritability (broad sense), genetic advance. **Sivasubramanian and Madhava Menon (1973)** classified variability as Low (0 – 10%) and Moderate (10 – 20%) and High (>20%). High magnitude of GCV, for Harvesting index, seed yield, number of pods per plant and number of seeds per pod and for high magnitude of PCV recored Harvesting index, Seed yield , number of seeds per pod and numbers of pod per plant provide sufficient variation.**Johnson *et al.* (1955)** classified Heritability as Low (60%). The highest heritability was observed for Harvesting index followed by Seed yield, Number of pod per plant , Number of seed per pod . The lowest heritability was observed for Plant height and Days to 50% flowering .A higher value for heritability indicates that it may be due to higher contribution of genotypic components. **Johnson *et al.* (1955)** classified "Genetic advance as % mean Low (20%).

The range of variability for characters, their values for index score and signs with rays are presented in Table. It was observed that maximum variability was in Days to maturity (129-150.67) followed by Days to 50% pod setting (85.33-94.67), Days to 50% flowering (72.67-80.67), plant height (51.27-66.33). These traits thus were most variable for classificatory analysis in chick pea. The range of mean values were utilized to assess the index score 1, 2 and 3 for all the characters studied. The simple circle without rays represents index score 1, while other with values for index score 2 and 3 have short and long rays on respective circle in different directions, respectively.

Based on Metroglyph analysis 25 genotypes were grouped into four clusters based on the genotypes within different characters. Cluster I (FLIP-09-162, RVG-202, IPC-11-85, ICC2211, IPCK-9-40, RATILA,ICC-2300, IPC-12-100, CSJ-515, RSG-931, FLIP-97-53c, IPC-11-09, IPC-10-134, JG-36, IPC-2000-17, ICC-495, ICC-4968, BG-212, ICC-313, IPC-12-211) is the largest cluster with twenty genotypes with low number of pods per plant with early maturity is followed by cluster ll (NBEG-3, NBEG-47) with two genotypes with high number of pods per plant with early maturity , cluster lll (RSG-963, ILC-0) with 2 genotypes with low number of pods per plant with late maturity followed by cluster lv (UDAY (CHECK))with one genotypes with high number of pods plant with early maturity and it showed high seed yield and Harvesting index.

A study was carried out by using 45 genotypes of sesame at Seed Research and Technology Centre, Hyderabad during 2018 to evaluate the genetic variability, morphological clustering using Metroglyph and to identify the principle components having a major contribution to the total variation. Analysis of variance indicated appreciable variation among the genotypes for the traits. The genotypes Julang Sesame and NI8-8316 recorded the highest average performance

for seed yield per plant and other yield components. The trait, seed yield per plant recorded the highest value for GCV and PCV followed by test weight. High heritability together with high values of genetic advance was showed by 1000 seed weight and seeds per individual pod. Principal component analysis (PCA) indicated three principle components with eigenvalue more than one and contributing 78 % towards the total variability of the population. Metroglyph analysis clustered the genotypes into six groups and group IV being the largest with 20 genotypes. Cluster VI characterized with high seed yield and number of seeds per pod comprised of three genotypes including Julang Sesame and NI8- 8316. The overall study indicated that genotypes Julang Sesame and NI8-8316 were superior in performance and could be utilized as parents in hybridization programs (**Sasipriya*et al.*,2022**).

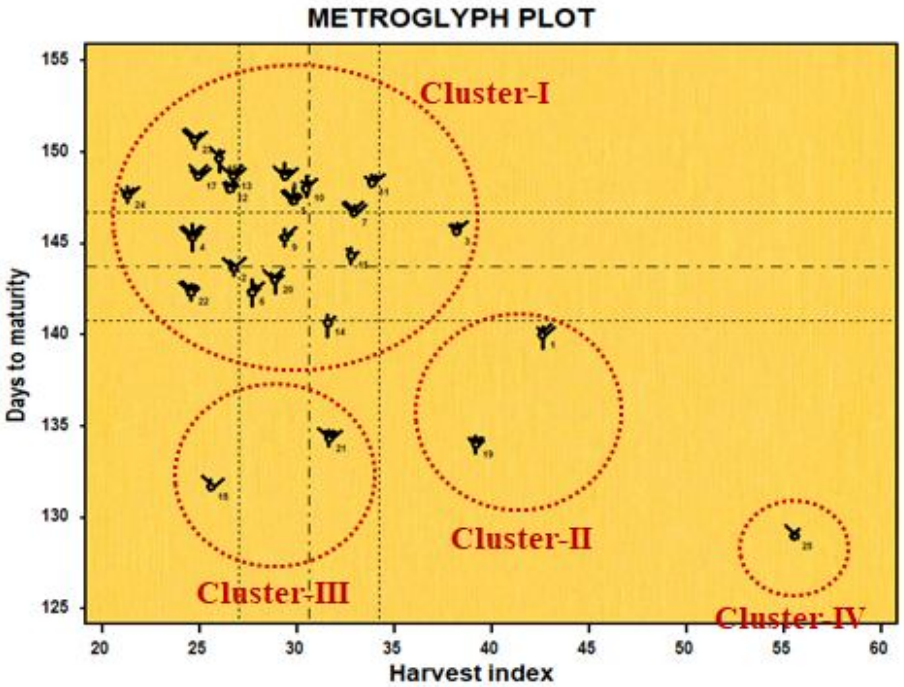

Figure 1 : Distribution of chick pea genotypes into different clusters following metroglyph analysis

The total index score was varied from 27 (ICC-313) to 21 (RSG-963) It indicates that germplasm lines were having variations. In the present investigation, that high yield genotypes were found with highest index score. Among the 25 genotypes these genotypes UDAY, NBEG-3, NBEG-47, RVG-202, CSJ-515 were observed as high yielder and identified for higher index score.

Table 1. Analysis of variance of 12 quantitative characters of 25 chick pea genotypes during *Rabi* 2022-23

Sl.No.	Source	Replication	Treatment	Error
	Degrees of freedom	**2**	**24**	**48**
1	Days to 50% flowering	3.453	9.164	4.648
2	Days to 50% pod setting	3.72	12.553	5.553
3	Plant height (cm)	3.639	31.097	17.065
4	Number of pods per plant	2.474	74.294	3.94
5	Numbers of seeds per pod	0.015	0.166	0.015
6	Days to maturity	46.84	104.209	23.271
7	Number of primary branches	0.085	0.221	0.037

8	Number of secondary branches	0.357	4.849	0.474
9	Seed yield	0.02	4.089	0.119
10	Biological yield (g)	1.008	8.286	1.265
11	Harvest Index (%)	12.474	156.824	4.317
12	Seed Index	0.903	16.984	1.634

* Significance at 0.05 level of significance

** Significance at 0.01 level of significance

SI.No	**Characters**	**GCV**	**PCV**	**H^2(Broad scence)**	**Genetic Advancement 5%**	**Gen.Adv as % of Mean 5%**
1.	**Days to 50% flowering**	1.559	3.152	24.467	1.25	11.589
2.	**Days to 50% pod setting**	1.667	3.065	29.586	1.712	1.868
3.	**Plant**	3.878	8.361	21.513	2.066	3.705

	height (cm)					
4.	**Number of pods per plant**	15.951	17.239	85.615	9.231	30.404
5.	**Numbers of seeds per pod**	15.393	17.604	76.457	0.403	27.727
6.	**Days to maturity**	3.613	4.931	53.69	7.84	5.454
7.	**Number of primary branches**	9.985	12.625	62.555	0.404	16.269
8.	**Number of secondary branches**	14.454	16.637	75.485	2.161	25.87
9.	**Seed yield**	18.626	19.444	91.762	2.27	36.755
10.	**Biological yield (g)**	7.386	9.167	64.921	2.539	12.26
11.	**Harvest Index (%)**	23.298	24.267	92.172	14.101	46.077
12.	**Seed Index**	12.087	13.884	75.791	4.057	21.676

Table 2 .Estimation of variability and Genetic parameters for 12quantitative characters of 25 genotypes

Table-3 25 genotypes into different complexes in scattered diagram

SI.NO	COMPLEX	No. of lines	Name of lines	Range and average score
1.	Low Number of pods per plant with Early maturity	20	FLIP-09-162, RVG-202, IPC-11-85, ICC2211, IPCK-9-40, RATILA ICC-2300, IPC-12-100, CSJ-515, RSG-931, FLIP-97-53c, IPC-11-09, IPC-10-134, JG-36, IPC-2000-17, ICC-495, ICC-4968, BG-212, ICC-313, IPC-12-211	21.00-27.00(23.75)
2.	High Number of pods per plant with Early maturity	2	NBEG-3, NBEG-47	24.00-26.00(25.00)

3.	Low Number of pods per plant with Late maturity	2	RSG-963, ILC-0	21.00-24.00(22.50)
4.	High Number of pods per plant with Early maturity	1	UDAY (CHECK)	23

Conclusion

From the present investigation it is concluded that among 25 genotypes of chick pea, UDAY(10) was found superior followed by NBEG-3(7.8) for grain yield per plant. The smaller number of days to 50 percent flowering was recorded by UDAY whereas, genotype ILC-0, ICC-4968, BG-212 was recorded a greater number of days to 50% flowering. Harvesting index, seed yield, Numbers of pods per plant had shown high genotypic coefficient variation and phenotypic coefficient variation. High heritability recorded Harvesting index, Seed yield, Numbers of pod per plant, Numbers of seed per pod. High genetic advance showed by that it was high for Harvesting index,Seed yield, and low for no of seed per pod, Days to 50% flowering and Days to 50% pod setting .Among these 25 genotypes UDAY, NBEG-3, NBEG-47 were found high yielding. ICC-313 (27), NBEG-3(26),FLIP-09- 162(26),RVG-202(26),IPC-11-85(26) identified genotypes with high index score. Whereas UDAY (CHECK) was recorded as higher Seed yield with early maturity and used as parents for future hybridization programmes.

Suggestion

Based on the finding of the present investigation the following suggestions are being made for further work. **UDAY,NBEG-3,NBEG-47** was found superior for grain yield per plant and according to metroglyph analysis we observed high yielding genotypes and **ICC-313(27), NBEG-(26),FLIP-09-162(26),IPC-11-85(26)** identified with high index scores**.**

REFERENCE

1. **Anderson E**. A semigraphical method for the analysis of complex problems. Proc. Nat Acad Sci. Washington, USA. 1957;43: 923-927
2. **Bhargava A, Shukla S, Kumar R, Ohri D.**Metroglyph Analysis of Morphological Variation in *Chenopodium spp*. World J Agric Sci. 2009; 5: 117-120.
3. **Burton GW.** Quantitative inheritance in grasses. *Proceedings of the sixth International Grassland Congress.*1952; 277-283.
4. **Burton GW, Devane.** Estimating heritability in tall fescus from replicated clonal material. J. Agronomy. 1953; 45 (3): 473-481.
5. **Dawale M, Narute TK, Thakare S, Joshi M.**Prevalence and distribution of chickpea rust disease in Western Maharashtra state during 2021-22 and 2022-23.The Pharma Innov J. 2023; 12(9): 2130-2132
6. **Dürdane MART.**Chickpea (*Cicer arietinum* L.): A Current Review. MAS J ApplSci.2022; 7(2): 372–379, 202
7. **Fisher RA, Yates F. (1963)** Statistical table for Biological Agricultural and Medical Research. *Oliver and Boyd Publishing Company Private Limited., Edinburgh.*1963. 46-63.
8. **Ghafoor A, Ahmad Z**. Diversity in black gram *(Vigna mungo* L. Hepper) for Agronomic traits and total seed proteins analysis. Acta Biol Cracov Bot. 2005*;* 47: 1-7

9. **Laiju NM, Islam MJ, Hasanuzzaman M, Mondol MAS, Kabir G**. Metroglyph analysis in two species of Hordeum. Pak J Biol Sci. 2022; 5: 1217-1219.
10. **Merga B, Haji, J.**Economic importance of chickpea: production, value,and world trade. Cogent Food Agri. 2019; 5:1615718. doi: 10.1080/ 23311932.2019.1615718
11. P**unitha D, Ganesamurthy K, Rajarathinam S.**Metroglyph analysis of morphological variations in Sorghum germplasm collections. J Plant Breed. 2010; 1: 536-541
12. **Sasipriya S, Parimala K, Eswari KB, Balram M.** Principal component analysis and metroglyph of variation among sesame (*Sesamum indicum L.)*genotypes .Elec J Plant Breed. 2022; 13(4): 1234-1242
13. **Sivasubramanian S, Madhavamenon P.** Genotypic and phenotypic variability in rice. Madras Agric J. 1973; 60:1093-1096.
14. **ThudiM,RoorkiwalM,KudapaH,ChaturvediSK,SinghNP,VarshneyRK.(2017)**.Anoverview ofchickpeaResearch*:* From Discovery to Delivery. Pulse India. 2017; 2(5).22-25.