Evaluation of Chickpea (*Cicer arietinum* L.) Genetic Diversity Germplasm in Prayagraj Agro-climatic Conditions Using Metroglyph Analysis

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

Total 25 genotypes of chick pea were investigated during current study. The experiment was conducted during *Rabi*-2022 in RBD having three replications and the data were recorded on 12 characters to study the variability, heritability, genetic advance, metroglyph analysis. Analysis of variance revealed that there was considerable genetic variability in the available germplasm for most of the characters studied for 12 different quantitative characters and analysed on the basis of heredity, Genetic advance and metroglyph analysis. Performance of grain yield and its components depicted that UDAY was found best followed by NBEG-3 and NBEG-47. A close perusal of variability coefficients revealed that the difference between PCV and GCV was small indicating little influence of environment on the expression of characters studied. High estimates of PCV and GCV

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were recorded for Harvesting index. 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 high for Harvesting index (14.10). We have noticed that among selected 25 genotypes, UDAY, NBEG-3, NBEG-47, ICC-313, FLIP-09-162, RVG-202, IPC-11-85 were observed as higher yielder and identified for higher index score.

1. INTRODUCTION

The chickpea (*Cicer arietinum* L.), out of more than a dozen legumes, is the most significant edible legume in India. The legume, 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 [1]. Chickpeas come in third place in the world's pulse output with 11.6 million tons/year where 80% are desi while the remaining 20% are kabuli [2]. 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 [3].

In order to determine the extent of chickpea rust disease in nine districts of Western Maharashtra State—Ahmednagar, Solapur, Sangali, Satara Kolhapur, Pune, Nashik, 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 showed or exhibited the highest prevalence. 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 [4].

Punitha et al. [5] 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. [6] 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. [7] reported "Index score ranging from 12 to 23 in Hordeum species while Ghafoor and Ahmad [8] 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.

Metroglyph analysis, also known as metrological analysis, often focuses on one season's data because it allows for a more comprehensive understanding of seasonal patterns and trends. By analyzing data from one season allows for a more targeted investigation into the effects and dynamics specific to that particular time of the year. Different seasons bring distinct

environmental conditions, such as temperature, precipitation, and daylight duration, which can significantly influence various phenomena, from biological processes to human behavior. Focusing on one season helps researchers control for these variables and draw more precise conclusions about the relationships of study. It also enables them to detect seasonal patterns, trends, and anomalies more effectively. Additionally, studying data from one season can be more manageable in terms of data collection, analysis, and interpretation compared to analyzing data across multiple seasons. Researchers to assess the performance of plants under specific environmental conditions. This helps in understanding how genetics interact with environmental factors, aiding in the selection of traits that are stable across different conditions. It also allows for focused analysis and comparison between different genotypes within the same environmental context.

2. 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 [9] 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 (Fig. 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. Following statistical analysis were used to record various characters.

1. Analysis of Variance(ANOVA) [10]
2. Variability [11]
(a) Genotypic coefficient of variation (GCV)
(b) Phenotypic coefficient of variation (PCV)
3. Heritability [12]
4. Genetic advance [Johnson et al., 1955]
5. Metroglyph Analysis [9]

3. 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 [13] 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 1. 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 cm). 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 II (NBEG-3, NBEG-47) with two genotypes with high number of pods per plant with early maturity , cluster III (RSG-963, ILC-0) with 2 genotypes with low number of pods per plant with late maturity followed by cluster Iv (UDAY (CHECK))with one genotypes with high number of pods plant with early maturity and it showed high seed yield and Harvesting index.
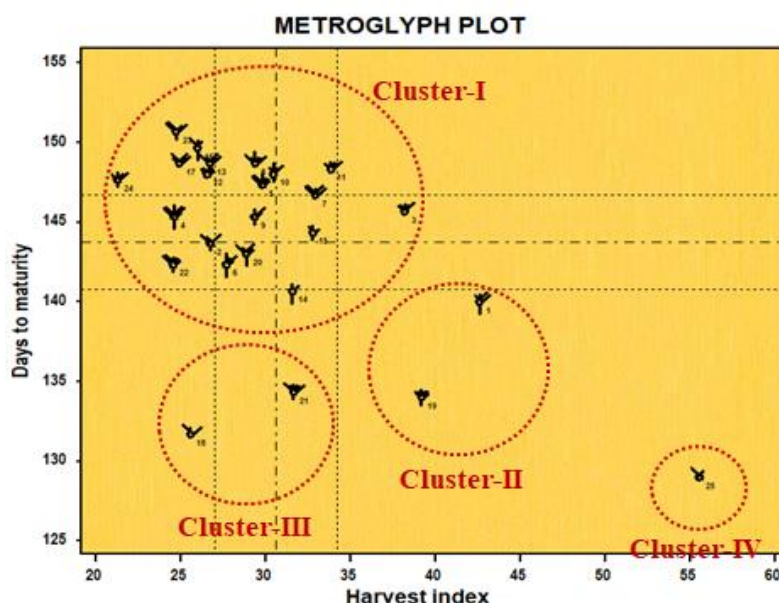

Fig. 1. Distribution of chick pea genotypes into different clusters following metroglyph analysis

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

SI.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

* Significant at 0.01 level of probability, ** Significance 1%

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

Sl.No	Characters	GCV	PCV	H²(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 height (cm)	3.878	8.361	21.513	2.066	3.705
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 3. 25 genotypes into different complexes in scattered diagram

Sl.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

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" [14].

"Seed yield per plant and Seed Index showed high GCV and plotted a graph on their mean values which represented as a glyph. Remaining

eight characters were depicted by a ray, the ray for anyone trait having the same position on each glyph. Thirty germplasms of groundnut were grouped into eight clusters, out of these group IV has the highest number of genotypes. Highly diverse germplasms on the basis of their total index score were ICMS-25, ICMS-97, ICMS-26, ICMS-20, and ICMS-82. The scoring procedure would be utilized in the preliminary screening of a large number of germplasm for selection with a desirable combination" [15].

"Analysis of variance indicated high significant differences among the genotypes for all the traits. Considerable variability existed in the genotypes for all the characters studied. These were the genotypes with high mean values in desirable direction i.e., From the present investigation it is concluded that among 31 genotypes of rice, VASUMATHI showed Early flowering (80 days), and had characters like Early maturity (113days), DRR DHAN-38 showed high Plant height (155.8 cm), PUSA BASMATHI-1 showed high Panicle length (28.8 cm), NAGARJUNA is showing both high Biomass (69.3 g), and Grain Yield per Plant (39.7 g). A scatter diagram was created for 31 genotypes that formed five complexes with 13,9,4,4 and 1 genotype in each complex. The genotypes Nagarjuna, Jarva and NDR-359, which have a high index score and fall into various clusters, can be utilized as parents in hybridization to get the most variety in character combinations. This character should be given due consideration during selection for crop improvement" [16].

"In this classification analysis made based on biological yield and harvest index for all the 20 genotypes formed 4 complexes. Out of 20 genotypes 4 genotypes like KU-99-16, KU-96-8, KU48 and KU-303 were recorded highest index score and fell into different complex, hence used as parents for getting good combinations for future hybridization programmers" (Putta et al.,2022) [17-18].

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.

4. 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.

5. 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.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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