Genetic Diversity Analysis for Yield and Yield Attributing Triats in Chickpea (*Cicer arietinum* L.)

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Abstract: ***The present investigation on Genetic diversity analysis were studied in a set of 30 genotypes of Chick pea (Cicer arietinum L.) using Mahalanobis D^2 Statistics, at field experimentation centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U. P. The experiment was conducted during rabi 2020 - 21 in a randomized block design with three replications. Observations on five randomly selected plants were recorded for days to fifty percent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, total number of pods per plant, total number of effective pods per plant, biological yield per plant (gm), 100 - seed weight (gm), harvest index (%) and seed yield per plant. The cluster I and cluster VI was with the highest number of genotypes (8) followed by cluster V (06), clusters VI (04), cluster II (03) cluster III had single genotype. Inter cluster values varied from 5.47 to 16.01. However, the maximum inter - cluster distance was noticed between clusters VI (16.01), followed by cluster V (11.83), cluster IV (11.57), cluster I (5.47) and Cluster II (4.19). Whereas, seed yield per plant contributed highest (20%), followed by harvest index (15%), number of effective pods per plant (14%), 100 seed weight (12%), Biological yield per plant (10 %) to the divergence, followed by total number of pods per plant (10%), number of secondary branches (8%), number of primary branches (5%), Plant height (3%), days to maturity (2%) and days to 50% flowering (1.15%) contributed maximum towards diversity. Based on inter cluster distances and Per se performance ICC 11334, ICC 4568, ICC 11163, ICC 6058, ICC 5138, ICC 6058, ICC 7365A were identified for inclusion in hybridization programme for realizing desirable transgressive segregates.***

Keywords: Chickpea, Cluster analysis, Mahalnobis D^2 statistics, Inter cluster distance and Intra cluster distance.

1. Introduction

Pulse crops are considered as the gift of nature to human being because of its high nutritive value and the ability to enrich the soil fertility, by fixing atmospheric nitrogen through symbiotic association with *Rhizobium* present in then root nodules. Chickpea occupies a prime position among the pulses in the country with a maximum acreage, production and its high nutritive value. It is known to have originated in Western Asia. It belongs to genus *Cicer* and tribe *Cicereae* and subfamily papilionaceae of family leguminaceae with a chromosome number of 2n=16 and it is self - pollinated crop. In Pulses, chickpea occupies first position in the world and in India the area under chickpea was 9.51 million ha. With production of 8.88 million tons and productivity 934 kg/ha (ICAR - Directorate of Pulses Development - Annual Report). Genetic diversity among parents, which is heritable, is a pre - requisite for any successful breeding programme. The proper choice of parents in the breeding programme is of paramount importance. Genetic divergence among the parents plays a vital role in cultivar improvement because crosses involving genetically diverse parents are likely to produce high heterotic effects and also more variability in segregating generations, which can be exploited for the desired improvement. The Mahalanobis's (1936) D^2 statistics is a powerful tool for estimating the divergence betweentwo populations.

2. Materials and Methods

The experimental material for the present study comprised of 30 genotypes of chickpea. All 30 genotypes were from IIPR (Indian Institute of Pulses Research, Kanpur) for evaluating their genetic variability and divergence with respect to yield, yield contributing traits. Thirty genotypes were sown in randomized block design with three replications during *rabi* 2020 - 21. Each genotype was sown in single row of 3 m length with spacing 30 cm between row and 10 cm within plant. Observations were recorded on the various morpho - agronomic, yield and quality traits in order to study the magnitude of genetic variability and level of genetic divergence in the material. Five competitive representative plants were selected at random from each experimental plot in each replication and tagged for recording the biometrical observations. Observations on five randomly selected plants were recorded for days to fifty percent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, total number of pods per plant, total number of effective pods per plant, biological yield per plant (gm), 100 - seed weight (gm), harvest index (%) and seed yield per plant. The data for days to 50 per cent flowering and days to maturity were recorded on whole plot basis. Mean values for all the characters and median values for days to 50 per cent flowering and maturity were worked out. Observations were recorded in the field at the appropriate developmental stages of plant growth and morphological characters.

3. Results and Discussion

Analysis of variance showed highly significant differences were present among the genotypes studied for all the characters at 5% level of significance. This indicated the existence of sufficient variation for effective selection for all the characters in the material studied. The presence of considerable phenotype variability in the present set of materials should enable their use in future chickpea breeding programmes. The estimates of genotypic as well as phenotypic coefficients of variation in the present study were highest for number of effective pods per plant followed by total number of pods per plant, seed yield per plant, biological yield per plant, seed index, plant height, days to 50% flowering and days to maturity. For days to maturity both the genotypic and phenotypic coefficient of variation was lowest. Number of pods per plant (92.2) followed by number of effective pods per plant (89.3), seed yield per plant (83.3), number of primary branches (78.9), seed index (63.1), plant height (53.1) all characters showed high estimates of heritability (bs) of all attributes. High heritability coupled with high genetic advance as percent of mean total number of pods per plant followed by number of effective pods per plant, seed yield per plant, biological yield per plant, seed index indicating that these traits are under control of additive gene action and potential possibilities exist for the improvement of these characters through simple selection. The estimates of D^2 values ranged from 4.19 to 57.61 this clearly indicates the presence of adequate diversity between genotypes studied. The highest D^2 value was between a pair of genotype viz., ICC 6058 and ICC 3020 (57.61), while lowest (4.19) was between ICC 5429 and ICC 10911.

The aim of cluster formation and measuring inter and intra cluster divergence is to provide the basis for hybridization programme. The theoretical concept behind such grouping is that, the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to the different clusters and will not give expected desired heterotic response and segregates in further generations. Maximum genotypes (08) were included in cluster I and clusterVI followed by cluster V (06), cluster IV (04), cluster II (03), cluster III had single genotype. The highest statistical distance was found between the clusters II. And V (D = 57.61) followed by cluster II and IV (D = 48.19), cluster II and cluster III (37.17) and cluster I and cluster IV (D = 33.04). The minimum inter cluster distance (D = 12.91) was between I and II. The intra cluster value was highest for cluster VI (D = 16.01) indicating that this cluster is more heterogeneous. The cluster means revealed high variability among the clusters for the traits, days to 50 per cent flowering, days to maturity, 100 seed weight, seed yield per plant and total number of pods per plant. Among these traits, It was observed that protein content of seed contributed highest for seed yield per plant, followed by harvest index, number of effective pods per plant, 100 seed weight, Biological yield per plant to the divergence, followed by total number of pods per plant, number of secondary branches, number of primary branches, Plant height, days to maturity and days to 50% flowering.

Table 1: Analysis of Variance (ANOVA) among 30 chickpea genotypes for 11 Quantitative traits

Source of Variations	Replicate	Treatments	Error
DF	2	29	58
Days to 50% flowering	16.56	51.43 *	25.13
Days to maturity	34.54	74.87 **	29.06
Plant height (cm)	4.15	15.75 **	3.59
Number of Primary Branches	0.06	0.26 **	0.02
Number of Secondary Branches	0.74	0.99 **	0.2
Total number of pods per plant	10.43	126.93 **	3.43
Number of effective pods per plant	11.63	100.76 **	3.87
Biological yield per plant (g)	11.37	66.17 **	5.71
Seed index (g)	8.04	31.41 ***	5.12
Harvest index (%)	0.10	84.22 **	34.68
Seed yield per plant (g)	1.13	24.08 **	1.50

* 5% Level of Significance ** 1% Level of Significance

Table 2: Distribution of 30 chickpea genotypes into different clusters

Cluster	Number of genotypes	Genotypes
I	08	ICC 5439, ICC 10911, ICC 11332, ICC 11334, ICC 4568, ICC 7365A, ICC 5138, GNG 469
II	03	DCP 92, GL 88341, GNG 2226
III	01	ICC 11163
IV	04	ICC 15850, IPC 04 - 98, ICC 15562, IPC 05 - 62
V	06	ICC 12369, ICC 124106, ICC 12472, IPC 04 - 01, BG 209, ICC 15936
VI	08	BGD 72, ICC 1708, ICC 12416, ICC 14866, ICC 15487, ICC 1009, ICC 3020, ICC 6058

Table 3: Average intra and inter cluster D^2 and D (in parenthesis) values of 6 Clusters formed from 40 chickpea genotypes

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**
I	**5.47**	12.91	14.29	33.04	32.73	17.33
II		**4.19**	37.17	48.19	57.61	23.7
III			**0**	17.9	14.65	22.53
IV				**11.57**	21.67	26.41
V					**11.83**	28.99
VI						**16.01**

Table 4: Cluster mean value for 11 characters in chickpea genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of Primary Branches	Number of Secondary Branches	Total number of pods per plant	Number of effective pods per plant	Biological yield per plant (g)	Seed index (g)	Harvest index (%)	Seed yield per plant (g)
1 Cluster	81.935	120.933	36.120	2.003	5.465	12.733	10.732	22.453	19.733	48.606	10.987
2 Cluster	81.733	121.067	38.200	2.269	5.732	18.201	15.387	20.573	20.267	47.491	10.293
3 Cluster	80.721	119.278	39.248	2.058	5.611	23.556	19.378	21.933	17.333	54.529	12.138
4 Cluster	80.611	111.333	39.011	2.168	4.779	28.555	23.877	15.244	23.167	47.693	7.476
5 Cluster	80.083	118.250	37.450	2.251	5.001	17.50'0	14.167	13.417	21.583	46.197	6.216
6 Cluster	85.420	111.500	35.517	2.581	4.585	24.583	20.417	17.367	25.750	48.311	8.616

Table 5: Percent contribution of different characters to genetic diversity

S. No.	Source	Contribution %	Times ranked 1st
1	Days to 50% flowering	1.15	5
2	Days to maturity	2	9
3	Plant height (cm)	3	13
4	Number of Primary Branches	5	22
5	Number of Secondary Branches	8	35
6	Total number of pods per plant	10	43
7	Number of effective pods per plant	14	61
8	Biological yield per plant (g)	10	65
9	Seed index (g)	12	52
10	Harvest index (%)	15	65
11	Seed yield per plant (g)	20	87

4. Conclusion

It is concluded that based on mean performance of 30 genotypes of chickpea ICC 11334 (12.8967g) recorded the highest seed yield per plant followed by the genotypes ICC 4568 (12.4667g). On the basis of Analysis of variance significant difference was recorded for all the seed yield and its components indicating presence of large amount of variability in the genotypes. Maximum number of genotypes were grouped into cluster I and VI which included total of 16 genotypes. In the present study the highest inter cluster distance (57.61) was found between clusters II and V. Genotypes belongs to these clusters may use as parents to produce transgressive segregates. Based on inter cluster distances and *Per se* performance **ICC 11334, ICC 4568, ICC 11163, ICC 6058, ICC 5138, ICC 6058, ICC 7365A** were identified for inclusion in hybridization programme for realizing desirable transgressive segregates.

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