



Diversity Analysis in Chickpea (*Cicer arietinum* L.) Genotypes under Temperate Conditions

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Authors' contributions

This work was carried out in collaboration among all authors. Authors MAD and NUSK designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript.

Authors RURM, ZAD, PAS, SAD, BAL, FAS and URB managed the analyses of the study. Author ZAD managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Genetic diversity study was conducted in 38 chickpea (*Cicer arietinum* L.) genotypes using Mahalanobis D² Statistics. The current research performed at FoA, Wadura Sopore, SKUAST-Kashmir in the rabi 2017-18. In the present study, total seven clusters have been formed and range of D² values is from 301.78 to 8477.71, cluster II includes maximum 12 genotypes after that cluster I having 9 genotypes, cluster IV having 6 genotypes, cluster III and V having 4 genotypes, cluster VI having 2 genotypes and cluster VII with 1 genotype. 959.33 to 8477.71 is the range of inter cluster distance. Highest inter cluster distance (8477.71) was found between the clusters, VI and VII

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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. After comprehending the intra cluster divergence it has been found that cluster IV has highest intra cluster distance (637.07) then cluster I (459.16). Since cluster VII includes only one genotype which indicates that there is no intra cluster divergence. Total nine traits have been evaluated, plant height registered higher divergence (49.25%) then pods plant⁻¹ (36.12%), days to 50% flowering (4.13%) and days to maturity (2.7%), secondary branches plant⁻¹ (3.24%), seed yield plant⁻¹ (1.28%) and primary branches plant⁻¹ (1.14%). The 100-seed weight (1.12%) and seeds pod⁻¹ (1.02%) possesses less divergence. By considering above results the nine genotypes viz., IR-1, IR-3, IR-30, IR-20, IR-21, IR-10, IR-2, IR-7 and IR-31 have been recognized as desired genotypes for use in future breeding programme.

Keywords: Chickpea; cluster analysis; D² statistics; inter and intra cluster distance.

1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a self-pollinated crop belongs to the family *Leguminaceae*. Gram, Chana, Bengal gram and Garbanzo bean are common names of Chickpea which is generally grown in arid and semiarid regions of Ethiopia. The somatic chromosome number in chickpea is 2n = 16. 'Desi' (=microsperma) and 'Kabuli' (=macrosperma) are the two cultivars found during domestication. Desi chickpeas generally are small and angular having rough brown to yellow testas, in case of Kabuli chickpeas are relatively large, plump and having smooth cream colored testas. As Kabuli types considered highly advanced, possesses reduced pigmentation along with large seed size gained by conscious selection [1]. Chickpea (*Cicer arietinum* L.) is grown about 45 countries around world and is third important food legume. 75% of total world production is being shared by India.

Chickpea possesses quality protein and is being considered healthy food in the developed countries. Chickpea grain contains 18-24% protein, 2.0-7.0% fats, 64% total carbohydrates (47% starch, 6% soluble sugar) and 6% crude fiber. Being a legume crop it takes care of soil fertility by fixing 41-65 kg atmospheric nitrogen per hectare through *Rhizobium* spp. Out of total production in India about 75% is being consumed as 'Dal'. Chickpea (*Cicer arietinum* L.) being utmost pulse crop, cultivated in diverse agro-climatic conditions and grown both in rainfed and irrigated conditions of Indian subcontinent. Low productivity in the country is generally because maximum area is under rainfed farming.

As crossing genetically diverse parents, high heterotic effects being produced and high variability in segregating generations, which can

be exploited for the improvement. Generally, plant breeders use phenotypic divergence for the selection of parents, but for effective breeding, one should know parents genetic diversity in respective characters which are to be improved. For quantification of divergence between two populations, the [2] D² statistic is powerful tool. By virtue of this technique many studies recognized that geographical diversity is not necessarily related to genetic diversity. It, thus, is independent of size of sample and gives better idea about the magnitude of divergence and provides the basis for selection of parental lines for future breeding programme.

2. MATERIALS AND METHODS

The present investigation was conducted at Regional Research Station, Faculty of Agriculture, Wadura Sopore during rabi season of 2017-18. The experimental material used for the study consisted of 38 genotypes which were obtained from the ICARDA-BIGMP. Thirty five genotypes and 3 varieties of chickpea as checks were evaluated in a Randomized Block Design (RBD) with three replications during Rabi 2017-2018. Each genotype was sown in three rows of 2m length with spacing 30 cm between rows and 10 cm within rows. Standard agronomic practices were adopted. Observations were recorded on days to flowering and maturity (50%), plant height (cm), number of primary and secondary branches, pods plant⁻¹, 100-seed weight (g), seeds pod⁻¹ and yield plant⁻¹ (g). Data were calculated by [2] and the genotypes were grouped into different clusters according to Tocher's method as described by [3]. Contribution of individual characters towards divergence was estimated according to the method described by [4]. Grouping of variety into

various clusters was done and average intra and inter cluster distance were estimated.

3. RESULTS AND DISCUSSION

The values of D^2 ranged from 301.78 to 8477.71, refers adequate diversity between genotypes studied. [5,6,7 and 8] reported wide genetic diversity in chickpea germplasm. Table 1 shows clustering pattern based on magnitude of D^2 values. 38 genotypes have been grouped into seven clusters. Largest cluster II having 12 genotypes, 9 genotypes in cluster I, 6 genotypes in cluster IV, 4 genotypes in cluster III and V, 2 genotypes in cluster VI and 1 genotype in cluster VII (Fig. 1). Table 2 represents the average intra and inter cluster D^2 values. Cluster VI and VII (8477.71) possessed maximum statistical distance then cluster IV and VII (5814.62). Genotypes from these clusters leads the successful production of hybrids and desirable segregants in future generations. Cluster IV (637.08) having highest intra cluster value shows more heterogeneous nature of the cluster. Similar findings have been reported by [9,10,11,12 and 8]. In order to select parents for hybridization programme, cluster formation and intra and inter cluster divergence plays utmost role. Theoretically clustering, genotypes

belonging to different clusters are much diverse than genotypes of same cluster [3]. Thus crossing of genotypes from different clusters give high heterosis in comparison of crossing of genotypes belonging to the same clusters. Heterosis decline also occurs if crosses involving the parents having extreme divergence [13]. Therefore, crop improvement programme requires parents selection with desired characters on the basis of genetic diversity, their per se performance and cluster mean.

The cluster mean for the nine characters are presented in Table 3. Most of the characters varied considerably in clusters II, III, IV and VI from other clusters which is being revealed by cluster mean. Genotypes belonging to such clusters possesses different genetic architecture as compared to genotypes of other clusters. Traits, days to 50% flowering, days to maturity, 100 seed weight, seed yield plant⁻¹, pods plant⁻¹ and plant height possesses high variability among the clusters as indicated by cluster means. Inter-cluster variation have been marked within the cluster means for the traits studied viz., plant height, pods plant⁻¹, 100seed weight, and seed yield plant⁻¹. Highest cluster mean for pods plant⁻¹ have been recognized in cluster VI (62.03) and lowest in cluster VII (24.20). D^2 analysis is

Table 1. Composition of 38 chickpea genotypes into different clusters by Tocher’s method

Cluster No.	No. of genotypes	Genotypes
I	9	IR-18, IR-28, IR-27, IR-19, IR-23, IR-29, IR-17, IR-11, Y8
II	12	IR-12, IR-35, IR-8, IR-6, IR-32, IR-25, IR-16, IR-15, IR-9, IR-26, IR-14, SC-1
III	4	IR-5, IR-13, IR-22, Y10
IV	6	IR-2, IR-7, IR-4, IR-24, IR-33, IR-34
V	4	IR-20, IR-31, IR-21, IR-10
VI	2	IR-1, IR-3
VII	1	IR-30

Table 2. Average intra cluster (diagonal) and inter cluster (above diagonal) distance values in chickpea [*Cicer arietinum* L.]

S. No.	Cluster	I	II	III	IV	V	VI	VII
1	I	459.16	994.68	1524.32	2687.02	1303.92	4305.40	1366.92
2	II		450.88	959.33	1302.31	2459.03	2304.97	3324.80
3	III			428.17	2902.09	1923.34	1365.51	4309.72
4	IV				637.08	5807.44	3717.75	5814.62
5	V					368.36	4659.34	1423.95
6	VI						301.78	8477.71
7	VII							0.00

also being used to know the the relative contribution of the various plant traits towards genetic divergence. Table 4, shows percent contribution of nine traits. Trait, plant height contributed highest percent towards diversity then pods plant⁻¹, days to 50% flowering, days to maturity, 100 seed weight, whereas the trait seeds pod⁻¹ possesses least percent which refers that very less variability within the genotypes, because of this trait. [8] indicated

highest genetic divergence due to traits plant height and 100 seed weight. [14] marked the traits like days to 50% flowering, effective branches, seed size contributed high to divergence. [5] examined that the traits like seed yield plant⁻¹, pods plant⁻¹, and 100 seed weight contributed to diversity. [15] noticed the contribution of 100 seed weight, seed yield plant⁻¹ and days to 50% flowering to the total divergence.

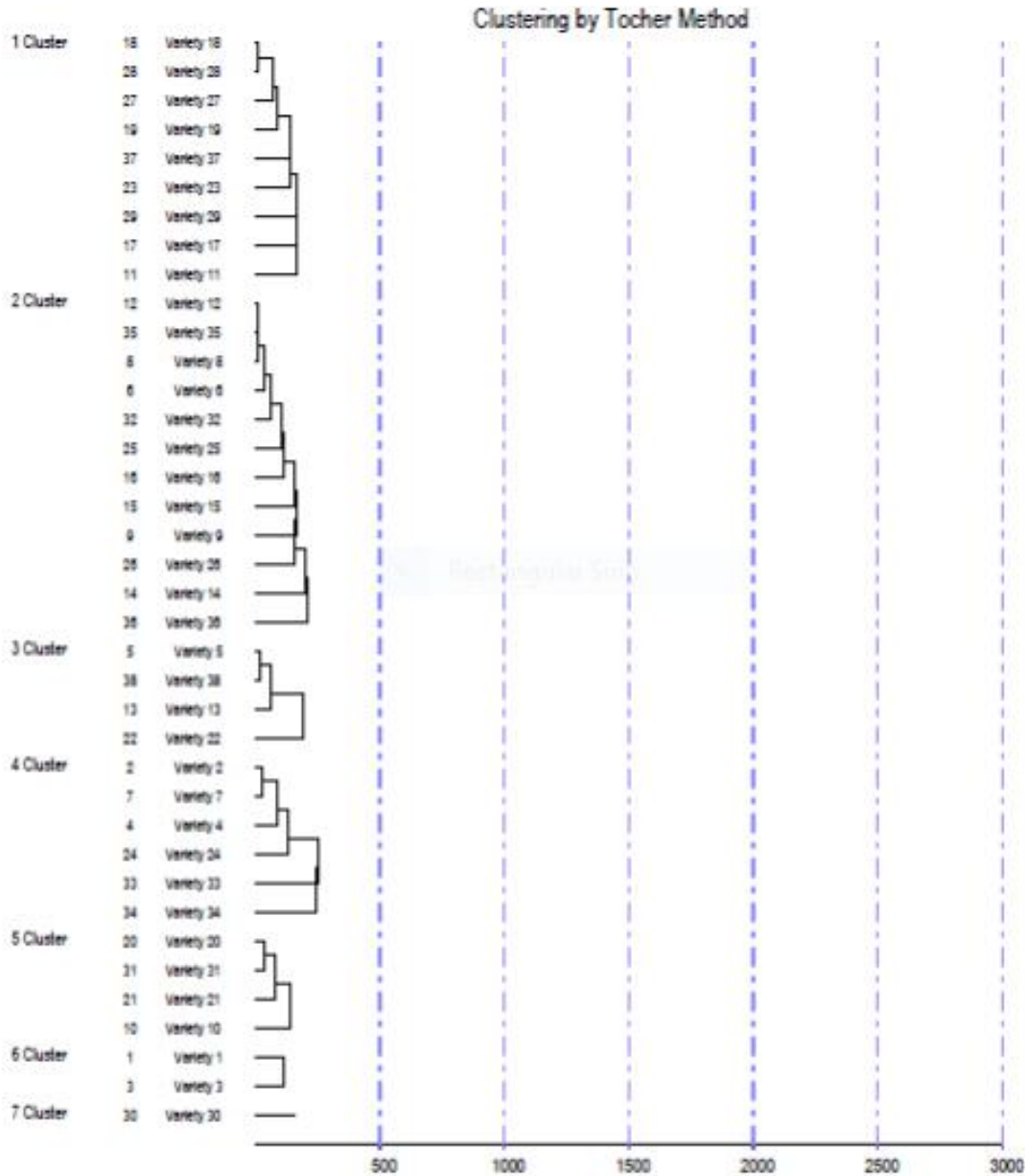


Fig. 1. Grouping of 38 genotypes into 7 clusters by Tocher's method

Table 3. Clusters means for various traits in chickpea [*Cicer arietinum* L.] genotypes

Clusters	DF	DM	NPB	NSB	PH	NPP	NSP	100-SW	SYP
I	147.67	186.30	3.29	7.57	54.34	33.08	1.21	22.51	8.97
II	146.53	182.03	3.43	8.72	68.47	38.35	1.31	23.28	11.48
III	148.83	187.17	3.18	11.14	63.43	50.47	1.28	21.74	13.87
IV	144.83	181.06	3.35	7.71	85.32	31.28	1.21	24.30	8.98
V	142.00	177.50	3.42	9.71	37.52	43.31	1.40	20.51	11.90
VI	137.17	171.50	3.83	13.70	76.02	62.03	1.20	23.68	17.32
VII	139.67	175.67	3.93	6.07	35.13	24.20	1.07	22.87	5.83

DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), NPB = Number of primary branches, NSB = Number of secondary branches, NPP = Number of pods per plant, NSP = Number of seeds per pod, SW = Seed weight, SYP = Seed yield per plant

Table 4. Percent contribution of nine traits towards total genetic divergence in chickpea [*Cicer arietinum* L.]

S. No.	Characters	Contribution %
1.	Days to 50% Flowering	4.13
2.	Days to Maturity	2.7
3.	Number of Primary branches plant ⁻¹	1.12
4.	Number of Secondary branches plant ⁻¹	3.24
5.	Plant Height (cm)	49.25
6.	Number of Pods plant ⁻¹	36.12
7.	Number of Seeds Pod ⁻¹	1.02
8.	100- Seed Weight (g)	1.16
9.	Seed yield plant ⁻¹ (g)	1.26
Total		100.00

4. CONCLUSION

Genetic diversity is being indicated by the D^2 values within the genotypes studied. Seven clusters with different number of genotypes have been formed with the help of D^2 values. In case of cluster formation of genotypes geographical distribution in not being followed. Clusters VI and VII with highest genetic distance of 8477.71 implies the genotypes in these clusters are much diverse. On the basis of cluster means for utmost yield components and inter-cluster distance of different clusters the below mentioned parents can be used in future hybridization programme, in order to improve yield.

IR-1, IR-3, IR-30, IR-20, IR-31, IR-2, IR-7, IR-10, IR-21

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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