Agric Res J **61** (1): 70-74, *February* 2024
DOI: 10.5958/2395-146X.2024.00010.7

ASSESSMENT OF GENETIC DIVERSITY IN INTERSPECIFIC DERIVATIVES OF CHICKPEA (*Cicer arietinum* L.)

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ABSTRACT

In the present investigation, a set of 90 genotypes, derived from 4 different crosses *viz*., I: PBG5 × ILWC229; II: BGD72 × ILWC229; III: PBG5 × ILWC246 and IV: BGD72 × ILWC246 were evaluated to estimate the genetic diversity for productivity traits during 2020-21 and 2021-22 at Punjab Agricultural University, Ludhiana. The genetic diversity analysis grouped 90 genotypes into 5 clusters. Cluster I had the maximum number of genotypes, followed by cluster II. The maximum inter-cluster distance was observed between clusters II and V and the traits like seed yield plot^{-1}, 100-seed weight, and biological yield plot^{-1} in cluster II were having maximum cluster mean. The derivatives from cluster II were superior with respect to traits like seed yield plot^{-1}, biological yield plot^{-1}, 100-seed weight, days to 50% flowering and can serve as potential donors to obtain transgressive segregants.

Keywords: Genetic diversity**,** Productivity traits, Seed weight, Transgressive segregants

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Chickpea (*Cicer arietinum* L.) is the world's second most important food legume crop species that evolved from its wild ancestor, *Cicer reticulatum*. Genus '*Cicer*', includes 36 perennial and 10 annual species; of which, *Cicer arietinum* is the only species domesticated and under cultivation (Toker *et al.,* 2021). It is a 'self-pollinated' true diploid species (2n = 16) with a genome size of roughly '750 Mbp' (Varshney *et al.,* 2013). Being a C_3 plant, chickpea grows best in cool areas, as the winter season is most favourable. It serves as a major source of protein in the human diet and also adds nitrogen to the soil through root nodules leading to soil health improvement. In recent years, the global area and production of chickpea have increased to 14.84 million hectares and 15.08 million tonnes, respectively. In India, the area and production are 10.94 million hectares and 11.08 million tonnes, respectively. India is the largest producer of chickpea in the world accounting for about 73 percent of the total annual production from 10.94 million hectares area during the year 2020 (FAOSTAT, 2020). It is cultivated in over 59 countries where India, Pakistan, Iran, Myanmar, Canada, Turkey, Ethiopia, Mexico, Australia, and the United States are major chickpea-growing countries. As reported by Dixit *et al.* (2019), there is a need to produce approximately 16.0 to 17.5 million tonnes of chickpea with an average productivity of 1.5 to 1.7 tonnes per hectare by the year 2050. In Punjab, the area under the chickpea crop was about 2000 hectares and production was 2600 tonnes with an average yield of 1322 kg/ha during 2020-21 (Anonymous, 2022). The major constraints affecting chickpea productivity are its narrow genetic base, higher self-fertilization rate, and 'single domestication' event (Abbo *et al.,* 2003). Moreover, there is a lack of sources of resistance to various stresses as well as productivity traits in cultivated germplasm. Due to this variability depletion, there has been limited success in genetic improvement through classical breeding with inter-varietal crosses (Singh and Ocampo, 1993). Van Rheenen *et al.* (1993) and Mallikarjuna *et al.* (2007) advocated that interspecific hybridization involving wild relatives should be followed for expanding the genetic base of 'cultivated' chickpea. To fulfil the needs of the increasing human population, sustained efforts are required to increase the yield potential of chickpea by introducing un-adapted genes from distantly related *Cicer* species **(**Meena *et al.,* 2017; Kumar *et al.,* 2019). To create new genetic variation, the assessment of genetic diversity helps the breeders to select suitable and diverse parents for hybridization to get desirable segregants. Keeping all these facts in view, the present study has been planned to evaluate the 90 interspecific derivatives derived from the crossing of elite chickpea cultivars (PBG5 and BGD72) and accessions of wild species *Cicer reticulatum* (ILWC229) and *C. echinospermum* (ILWC246) to estimate the genetic diversity for yield and productivity traits.

MATERIALS AND METHODS

The material used for conducting this experiment includes a total of 90 genotypes, derived from four different crosses *viz.*, I: PBG5 (*Cicer arietinum*) × ILWC229 (*Cicer reticulatum*); II: BGD72 (*Cicer*

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Date of receipt: 22.12.2022, Date of acceptance: 27.02.2024

arietinum) × ILWC229 (*Cicer reticulatum*); III: PBG5 (*Cicer arietinum*) × ILWC246 (*Cicer echinospermum*) and IV: BGD72 (*Cicer arietinum*) × ILWC246 (*Cicer echinospermum*) (Table 1). All the 90 genotypes and their parents were planted in paired rows of 2-meter length with a row-to-row spacing of 30 cm in alpha lattice design with two replications during *rabi* 2020-21 and 2021-22 in the experimental area of Pulses Section, Punjab Agricultural University, Ludhiana. Data from five randomly selected plants were recorded for various productivity traits viz., DFF (Days to 50% flowering), DTM (Days to maturity), PH (Plant height), PBPP (Primary branches per plant), SBPP (Secondary branches per plant), NPP (No. of pods per plant), SPTP (Seeds per ten pods), HSW (100-seed weight), SYPP (Seed yield per plot), BYPP (Biological yield per plot), and HI (Harvest index). Genetic diversity was estimated using the D^2 statistics proposed by Mahalanobis (1936) and the clustering of genotypes was done according to Tocher's method (Rao, 1952) with the help of R software biotools package (Version 4.2.1) and the method suggested by Singh and Choudhary (1979) was used to estimate the amount, each character contributed to the divergence.

Table 1. List of derivatives used for diversity analysis based on Mahalonobis D^2

Derivative(s)	Number	Parentage
PAU21-1 to PAU21-33	33	PBG5 × ILWC229
PAU21-34 to PAU21-63	30	BGD72 × ILWC229
PAU 21-64 to PAU21-71	08	PBG5 × ILWC246
PAU21-72 to PAU21-90	19	BGD72 × ILWC246

RESULTS AND DISCUSSION

The assessment of genetic diversity is important in any crop breeding programme. D^2 analysis categorized the 90 genotypes into five clusters (Table 2 and Fig 1) based on their D^2 values. The inclusion of derivatives into different clusters revealed that interspecific hybridization is useful for generating a significant amount of variability, which can be used to broaden the genetic base of cultivated chickpea for crop improvement. Cluster I had the maximum number of genotypes (66), followed by cluster II (18 genotypes), cluster IV (3 genotypes), cluster III (2 genotypes), and cluster V (1 genotype). The maximum number of genotypes found in Cluster I, indicates that there was narrow genetic variation amongst the genotypes. Therefore, genetic similarity may be caused by the resemblance in the ancestral population, from which they had originated. Similar findings have been reported in many other diversity studies of chickpea (Salaria *et al.,* 2021; Dwevedi and Lal, 2009; Kumar *et al.,* 1998; Samal and Jagadev, 1996; Anilkumar *et al*., 1993). Kumar (1997) reported the grouping of 60 genotypes into five clusters. Similarly, Sharma *et al.* (2004) grouped 83 genotypes and Lokare *et al.* (2007) grouped 60 genotypes into ten clusters based on yield and productivity traits.

The formation of 5 distinct clusters from 90 genotypes indicated that the material under study contains a significant amount of genetic variability. However, this distribution does not reveal how much variability exists between them. Therefore, intra and inter-cluster distances, in addition to the mean values for the various observed traits, help to identify the diverse genotypes. The intra and inter-cluster distances are presented in Table 3 and Fig 2. The intra-cluster distances ranged from 0.00 (cluster III) to 195.24 (cluster II). This intra-cluster distance reveals the variation in morphological traits among the genotypes within the same cluster. The maximum inter-cluster distance was observed between

Table 2. Cluster information of 90 interspecific derivatives based on D^2 analysis

Cluster No	No. of Genotypes	Genotypes
Cluster I	66	PAU21-43, PAU21-77, PAU21-86, PAU21-68, PAU21-62, PAU21-83, PAU21-4, PAU21-30, PAU21-56, PAU21-17, PAU21-89, PAU21-26, PAU21-24, PAU21-7, PAU21-85, PAU21-9, PAU21-5, PAU21-65, PAU21-76, PAU21-27, PAU21-3, PAU21-18, PAU21-55, PAU21-6, PAU21-28, PAU21-20, PAU21-45, PAU21-13, PAU21-71, PAU21-16, PAU21-29, PAU21-75, PAU21-12, PAU21-25, PAU21-53, PAU21-19, PAU21-80, PAU21-74, PAU21-10, PAU21-23, PAU21-31, PAU21-14, PAU21-69, PAU21-57, PAU21-67, PAU21-64, PAU21-72, PAU21-37, PAU21-49, PAU21-73, PAU21-78, PAU21-90, PAU21-40, PAU21-8, PAU21-39, PAU21-58, PAU21-87, PAU21-47, PAU21-21, PAU21-70, PAU21-66, PAU21-32, PAU21-88, PAU21-60, PAU21-22, PAU21-81
Cluster II	18	PAU21-41, PAU21-44, PAU21-52, PAU21-38, PAU21-42, PAU21-61, PAU21-1, PAU21-50, PAU21-34, PAU21-63, PAU21-48, PAU21-46, PAU21-54, PAU21-79, PAU21-59, PAU21-36, PAU21-51, PAU21-82
Cluster III	2	PAU21-15, PAU21-84
Cluster IV	3	PAU21-33, PAU21-35, PAU21-11
Cluster V	1	PAU21-2

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Table 3. The intra (bold) and inter cluster distances among 90 interspecific derivatives

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	97.08	333.01	216.37	242.44	338.97
Cluster II		122.31	440.08	460.14	735.90
Cluster III			70.35	527.41	404.03
Cluster IV				185.43	340.32
Cluster V					0.00

Table 4. Mean performance of different clusters for productivity traits of 90 interspecific derivatives

Cluster No	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	Secondary branches plant^{-1}	Number of pods plant^{-1}	Seeds per ten pods	100-seed weight (g)	Seed yield plot^{-1} (g/plot)	Biological yield plot^{-1} (g/plot)	Harvest index (%)
I	103.27	149.79	66.99	3.74	5.41	40.64	17.69	18.49	490.22	1193.93	41.17
II	95.83	149.18	60.95	3.80	6.02	51.46	16.23	27.33	522.06	1226.18	42.56
III	104.62	152.37	73.03	3.76	6.57	70.51	16.87	18.38	447.12	1018.75	43.60
IV	101.25	148.66	61.50	3.35	4.77	30.85	17.66	20.04	412.83	1241.66	33.41
V	96.25	149.00	42.33	3.82	5.49	56.24	18.00	13.42	392.50	1158.75	33.87

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cluster II and cluster V (735.90), followed by cluster III and cluster IV (527.41). As a result, hybridization between genotypes of various clusters with more inter-cluster distance can produce combinations with a high heterotic response and superior recombinants (Murty and Arunachalam, 1986). There is a lot of genetic diversity among derivatives grouped into different clusters, as evidenced by the fact that the values of the inter-cluster distances are higher than the intra-cluster distances.

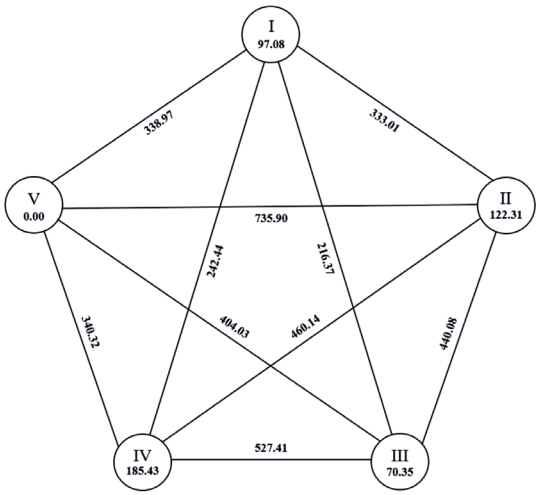


Fig. 2. Dendrogram of intra and inter cluster distances among 90 interspecific derivatives

The mean value of clusters for all the eleven characters is presented in Table 4. The traits like seed yield per plot (522.06g), 100-seed weight (27.33g), and biological yield per plot (1216.18g) belonging to cluster II were having the maximum cluster mean. Also, cluster II was found to be better for traits like early flowering, seed yield per plot and 100-seed weight, whereas cluster III was better for traits like plant height, secondary branches per plant, and the number of pods per plant. Therefore, genotypes from the clusters with high mean for desirable traits can be inter-crossed to produce offspring with the desired trait combinations according to the breeding objectives.

Genotype expression towards diversity (Table 5) is maximum for the 100-seed weight (31.00%) followed by harvest index (25.30%), days to 50% flowering (13.50%), number of pods per plant (12.50%) and seed yield per plant (4.00%). Thakur *et al*. (2018) reported that days to 50% flowering followed by 100-seed weight contributed the maximum towards the genetic divergence. Similar contributions toward genetic diversity were reported by

Table 5. Contribution of productivity traits towards diversity

Trait	Contribution %
Days to 50 % flowering	13.50
Days to maturity	3.20
Plant height (cm)	2.20
Primary branches plant^{-1}	2.00
Secondary branches plant^{-1}	1.50
Number of pods plant^{-1}	12.50
Seeds ten pods^{-1}	1.90
100-seed weight (g)	31.00
Seed yield plot^{-1} (g/plot)	4.00
Biological yield plot^{-1} (g/plot)	3.10
Harvest index (%)	25.30

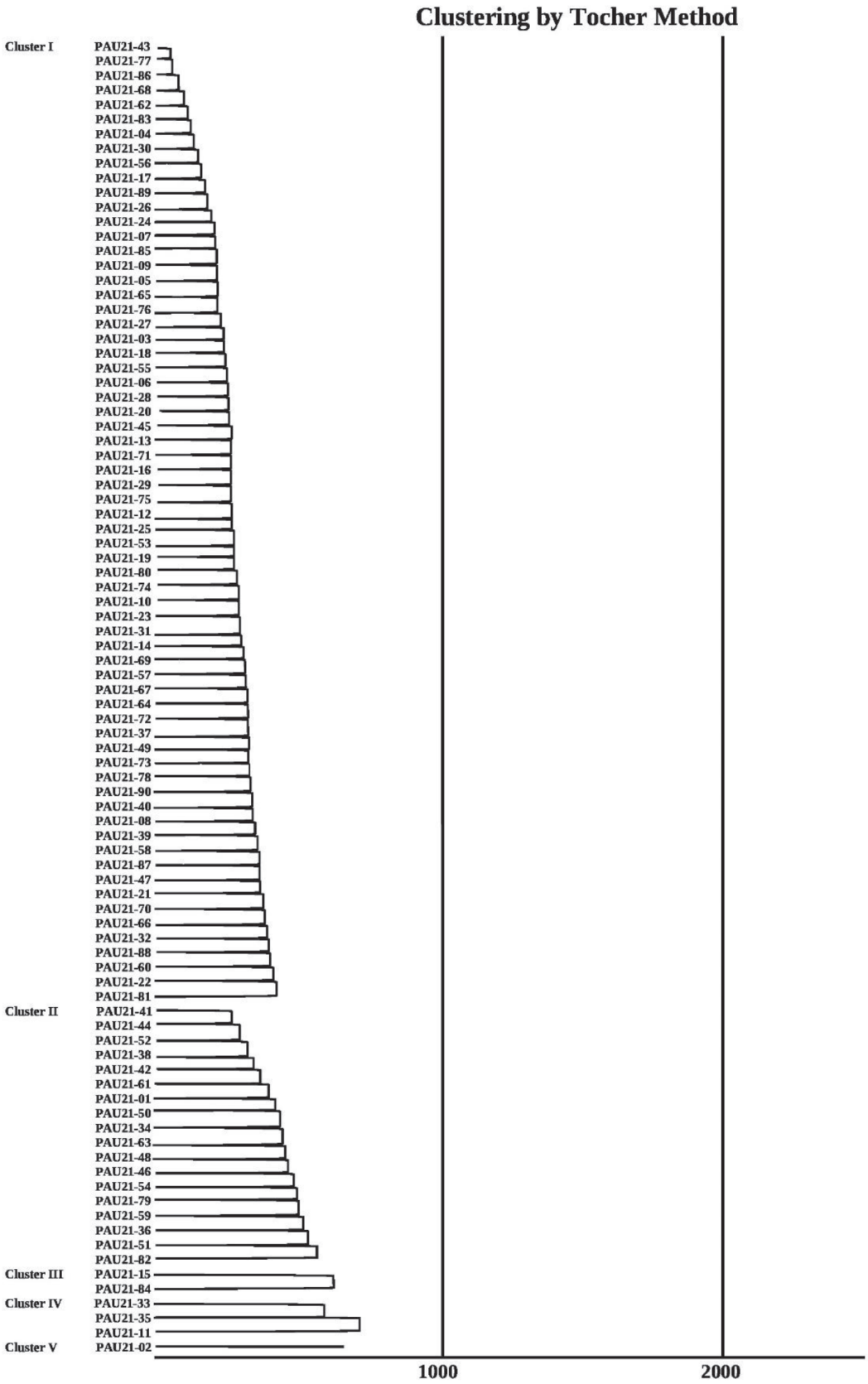


Fig. 1. Grouping of 90 interspecific derivatives into 5 clusters by Tocher's method

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Parashi *et al.* (2013); Pahre *et al.* (2014) and Kuldeep *et al.* (2015).

Overall, based on the diversity analysis, it is possible to conclude that the interspecific derivatives under study were genetically diverse for yield and productivity traits observed. The derivatives from cluster II were good with respect to traits like seed yield per plot, biological yield per plot, 100-seed weight and days to 50% flowering and maturity and cluster III for plant height, the number of pods per plant, secondary branches per plant and harvest index. The diverse genotypes can be combined in the right ways to produce more diverse material and also the genotypes of clusters with moderate to large distances should be crossed in order to create a wide range of variability and to isolate desirable recombinants in later generations.

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Authors' contribution

Conceptualization and designing of the research work (IS, SB, MS, AS); Execution of field/lab experiments and data collection (AS, IS, SB); Analysis of data and interpretation (AS, IS, PS); Preparation of manuscript (AS, IS, SB).

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