Genetic variability and diversity analysis for yield and its associated traits in chickpea (*Cicer arietinum* L.)

Abstract

Chickpea (*Cicer arietinum* L.) is a leguminous self-pollinating crop belongs to family-Leguminosae (Fabaceae). The aim of a plant breeder is to identify or develop high yielding cultivars (indicate the study site). In the present investigation, 83 genotypes grown during *Rabi* 2021-22 to investigate genetic variability, heritability and genetic advance, correlation, direct and indirect effects and genetic divergence (D^2 analysis) among yield and its attributing traits. High GCV and PCV recorded for the numbers of pods per plant and biological yield indicating the presence of substantial amount of genetic variability in the experimenting material. High heritability coupled with high genetic advance was shown for seed yield per plant, hundred seed weight. Selection based on these traits may be proved worthwhile. Significant and positive correlation was documented for seed yield per plant with numbers of pods per plant and biological yield and path analysis signified that biological yield had the highest positive direct effect on seed yield per plant. Conclusion missingThe data obtained from the present investigation may be proved helpful in the selection of high yielding superior genotype (s) of chickpea. Recommendations missing

Keywords: Chickpea, genetic variability, heritability, genetic advance, correlation and path coefficient analysis, genetic divergence

Introduction

Chickpea, also known as gram, Bengal gram, Egyptian pea, Garbanzo or Garbanzo bean, is a self-pollinated, annual diploid ($2n = 2x = 16$) species (Cobos *et al*., 2007) with a genome size of 738 Mb (Varshney *et al*., 2013). It helps to increase soil fertility by biological nitrogen fixation. The taxonomic hierarchy of chickpea is family Fabaceae (Leguminoseae), sub-family Faboideae (Papilionaceae) and tribe *Cicereae*. According to the seed morphology, chickpeas can be separated into: *desi* type, which has small seeds with a brown coat colour, and *kabuli* type, which has big seeds with a cream- or beige-colored coat (Asati *et al*., Solanki *et al*., 2022; Yadav *et al*., 2023). The nutritional value of chickpeas is very high (Sahu *et al.*, 2020a; Sahu *et al.*, 2020b; Gupta *et al.*, 2021) because of their high content of vitamins, minerals and important amino acids, including lysine, methionine, threonine, valine, and leucine, as well as ß-carotene, calcium, magnesium, phosphorus, and potassium (Jukanti *et al.*, 2012; Thudi *et al.*,2014). Chickpea productivity reduced by abiotic factors *viz.*, drought; heat, excessive salt and cold (Asati *et al.*, 2022) and biotic factors including Ascochyta blight, Fusarium wilt and Helicoverpa (Yadav *et al.*, 2023).

The basic information on the existence of genetic variability in a population and the relationship between different traits is essential for any successful plant breeding programme (Yadav *et al.*, 2005; Tripathi *et al.*, 2015; Tiwari *et al.*, 2018; Mishra *et al.*, 2020; Makwana *et al.*, 2021; Mishra *et al.*, 2021a; Mishra *et al.*, 2021b; Shyam *et al.*, 2021; Tripathi *et al.*, 2022; Jain *et al.*, 2022). The genotypic coefficient of variation estimates the heritable variability, while phenotypic co-efficient measures the role of environment on the genotype. Hence, Selection depends on heritability, selection intensity, and the genetic advance of traits (Barfa *et al.*, 2017; Asati and Yadav 2020; Rajpoot *et al*., 2020; Choudhary *et al.*, 2021; Yadav *et al.*,2021; Yadav *et al.*, 2022a; Yadav *et al.*, 2022b; Ningwal *et al.*, 2023a; Ningwal *et al.*, 2023b; Rajput *et al.*, 2023; Shrivastava *et al.*, 2023). The efficiency of selection with higher yield is depends upon the existing variability and other genetic factors (Singh, 2006). The assessment of major characteristics and their interrelatedness is important in developing selection criteria for improving existing genotypes (Paliwal *et al.*, 2022). Path coefficient analysis helps to determine the direct effect of traits and their indirect effects on other traits. A directional model based on seed yield and its components that provides the chance for selection is used in correlation analysis to evaluate the mutual relationship between two parameters (Khan and Qureshi, 2001). Mahalanobis's D^2 statistics is a powerful tool in quantifying the degree of variability at the genotype level.

Formatted: Indent: First line: 0"

The purpose of this investigation was to estimate the total genotypic variability, correlations, path analysis and diversity through Mahalanobis's D^2 statistics for important traits to select superior chickpea cultivar(s) for accelerating breeding programme in upcoming days.

Materials and method

Split this section into;

Description of study area

Research design

Data collection

Data analysis

The investigation was carried out to know the genetic variability, correlation and path analysis of 83 chickpea (63 desi and 20 kabuli type) genotypes (Table 1). The experiment was carried out at Agriculture Research Farm, Department of Plant Breeding & Genetics College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya (RVSKVV), Gwalior, Madhya Pradesh. India. All the 83 genotypes were sown in randomized block design (RBD) with two replications. The genotypes were planted during November, 2021 and harvested during the March 2022. Each entry was planted in 4 rows of 3m length, keeping row to row and plant to plant distance of 30 x 15, respectively. All the recommended package of practices was followed. Data were recorded on 10 different characters including days to 50 % flowering, days to maturity, plant height, numbers of branches per plant, numbers of pods per plant, total numbers of seeds per pod, 100-seed weight, harvest index, biological yield per plant and seed yield per plant. Five plants from each replication were randomly selected from each genotype for recording observations for all the traits.

Genotypic (GCV) and phenotypic coefficient of variation (PCV) was calculated as per formulae suggested by Burton Burton (1952), heritability in the broad sense (h^2) as proposed by Burton and De (Burton and De, 1953) and genetic advance as per the method described by Johnson *et al.* (1955). The correlation coefficients were determined the degree of a character's relationship with yield as well as among the variables that contribute to yield. The Weber and Moorthy (1952) and Miller *et al.* (1958) formulae was employed to calculate the correlations between genotype and phenotype. The method initially given by Wright (1921) and later developed by Dewey and Lu

Formatted: Indent: First line: 0"

(1959) was used to perform path coefficient analysis in order to figure out the direct and indirect impacts of the various characters on yield. The genetic divergence was estimated by using D^2 analysis given by Mahalanobis (1928) and the genotypes were grouped into different clusters according to Tocher's method as described by Rao (1952). Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1979).

Results and Discussion

Separate discussions from results

Variability Studies

The ANOVA implies that the mean sums of squares due to genotypes were significant for all the traits under study *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, numbers of pods per plant, 100-seed weight, biological yield per plant, harvest index and seed yield per plant except total numbers of seeds per pod (Table 2). This substantial variability provides a good prospect for improving traits of interest in chickpea breeding programmes as suggested by Dehal *et al.* (2016), Katkani *et al.* (2022), Sharma *et al.* (2023a) and Sharma *et al.* (2023b).

Results revealed that PCV% was higher than GCV% for all the traits under investigation (Table 3). High genotypic and phenotypic coefficient of variance were recorded for numbers of pods per plant, biological yield, seed yield per plant, harvest index, 100- seed weight and plant height. Similar findings were also reported by Hailu *et al.* (2020) and Ningwal *et al.* (2023a). This suggests that substantial phenotypic variation is present among the genotypes in respect to investigated traits indicating the scope of exploiting variability for further improvement of these traits. High heritability coupled with higher genetic advance as percentage of mean was documented for seed yield per plant, hundred seed weight, plant height, numbers of branches per plant, biological yield per plant, harvest index, numbers of pods per plant. It means these characters are governed by additive gene action. These results are in accordance with the finding of Thakur *et al.* (2018) and Ningwal *et al.* (2023a).

Formatted: Indent: First line: 0"

Correlation Coefficient Analysis

Correlation provides the magnitude of linear association between pairs of characters and form the basis of selection index, thereby aiding the breeder in crop improvement programme through simultaneous manipulation of the paired traits. Genotypic and phenotypic correlations, for various yield-attributing traits were estimated considering seed yield per plant as a dependent variable (Table 4; Table 5). It was revealed from the results that the genotypic correlation coefficients for most of the characters were higher than the phenotypic correlation coefficients. This indicated that there was a strong inherent association between various characters investigated and was less influenced by environmental effects. Highly significant and positive genotypic correlation for seed yield per plant was recorded with numbers of pods per plant followed by biological yield per plant, total numbers of seeds per plant, plant height, harvest index and days to 50% flowering. These results are in accordance with the findings of Bhanu *et al.* (2017), Jain *et al.* (2022), Ningwal *et al.* (2023a) and Rajput *et al.* (2023).

Path-coefficient analysis

The direct and indirect effects of different independent characteristics on the dependent character are measured via path coefficient analysis. It demonstrates the relationship between these independent characters and seed yield results from their direct influence on yield or from their indirect impact through other accrediting characters. In the present investigations, path coefficient analysis has been performed at genotypic and phenotypic levels taking yield as a dependent variable (Table 6; Table 7; Fig.1; Fig.2). In general, genotypic direct and indirect effects were somewhat higher in magnitude when equated to the phenotypic effects.

Genotypic path coefficient analysis revealed that biological yield per plant had the highest positive direct effect on seed yield per plant tracked by harvest index, plant height, numbers of pods per plant, days to 50% flowering and days to maturity. Whilst phenotypic path coefficient analysis exposed that biological yield had the highest positive direct effect on seed yield per plant trailed by harvest index, plant height, numbers of pods per plant, numbers of branches per plant and days to 50% flowering. These findings are closely similar with earlier results of Shrivastava *et al.* (2012) and Jain *et al.* (2022) for days to 50% flowering, plant height, numbers of pods per plant and days to maturity. Moreover, Kumawat *et al.* (2021) reported comparable findings for biological yield per plant and harvest index.

Genetic divergence (D^2 analysis)

Mahalanobis (D^2) statistics is a compelling tool widely used by plant breeders to measure the degree of divergence at genotypic level.

Composition of clusters

Grouping of the genotypes (Table 8) was carried-out by Tocher's method as per suggested by Rao (1952). Eighty-three chickpea genotypes which were evaluated for nature and magnitude of genetic divergence were grouped into 12 clusters. Cluster IV, VI, VII, VIII, IX, X, XI and XII were mono genotypic, whereas cluster I, II, III and V were poly genotypic. This confirmed the diversity present in the experimented material. Cluster I was the largest comprising of 35 genotypes followed by cluster II which had 28 genotypes, cluster III had 8 genotypes while cluster V had 4 genotypes. Cluster IV, VI, VII, VIII, IX, X, XI and XII had only one genotype in each. Therefore, it can be concluded that the selection of parents for hybridization should not be based on geographical diversity only, but it should have a base of both geographical origin as well as genetic divergence.

Intra and inter cluster distances

The intra and inter cluster distances D^2 between all possible pairs of 12 clusters were computed and presented in Table 9 and depicted in Fig.3. Cluster V showed maximum intra cluster D^2 value (D^2 = 12.00), while cluster III had 11.09 intra cluster value, cluster II showed 10.80. The highest inter cluster distance (D=33.82) was observed between genotypes of cluster V and cluster XII, tracked by cluster XI and cluster XII (D=29.07). These clusters are quite divergent from each other and the genotypes belonging to them can be used for hybridization programme as crosses between genotypes belonging to the clusters with maximum inter cluster distance, may give higher heterotic response resulting in better recombinants.

Cluster means for various characters

The results clearly indicated appreciable difference among cluster means for most of the characters (Table 10). Highest cluster mean for days to maturity, plant height and seed yield per plant was evident in cluster IX, whereas cluster IX had high values of mean for biological yield per plant which indicated that genotypes having high seed yield and tall plants were concentrated in these clusters. Therefore, it is suggested that parent selected for hybridization among the genotypes of above said clusters would produce higher heterosis and segregants for more than one economic character. The potential lines are identified from different clusters and used as parents in a hybridization programme. These findings are in accordance of earlier studies of Janghel *et al.* (2020) and Katkani *et al.* (2022).

Contribution of various characters towards genetic divergence

The utility of D^2 analysis is enhanced by its application to estimates the relative contribution of various characters to genetic divergence. The contribution of each character towards total genetic diversity is presented in Table 11 and Fig.4. The percentage contribution of 10 quantitative characters towards genetic divergence exposed that biological yield per plant had maximum share towards genetic divergence followed by harvest index, numbers of pods per plant, 100 - seed weight, days to maturity, plant height and seed yield per plant. These characters were liable for expressing maximum diversity among the clusters. These findings are similar to the results of Tiwari and Babbar (2017), Nimbalkar *et al.* (2017), Tiwari *et al.* (2018) and Biswal and Babbar (2022).

Conclusion

based on Analysis of variance it is concluded that significant difference was exist for the entire seed yield and its contributing traits indicating presence of considerable amount of variability among the genotypes. High phenotypic and genotypic coefficient of variation recorded for numbers of pods per plant followed by biological yield per plant indicating the pre-dominance of additive gene action and selection based on these traits may be rewarding. Seed yield per plant shared highly significant and positive association with biological yield per plant and total numbers of seeds per plant. The path analysis revealed that biological yield per plant showed a highest direct effect on seed yield per plant tracked by harvest index and plant height. Cluster I was the largest comprising of thirty-five genotypes trailed by cluster II having twenty-eight genotypes. Genotypes belongs to these clusters may be used as parents to produce transgressive segregants. Make conclusions in independent paragraphs..not a one continuous parapgraph

Missing;

Recommendations

Declaration of conflict of interest

References

Asati, R, Yadav, RK. (2020). Genetic Variability Studies in F2 Generation of Rice (Oryza sativa L.). International Journal of Current Microbiology and Applied Sciences. Special Issue. 2548-2554.

Asati R, Tripathi MK, Tiwari S, Yadav RK, Tripathi N. Molecular Breeding and drought tolerance in chickpea. Life. 2022;12:1846. https://doi.org/10.3390/life12111846

Barfa D, Tripathi MK, Kandalkar VS, Gupta J C and Kumar G. Heterosis and combining ability analysis for seed yield in Indian mustard [*Brassica Juncea* (L.) Czern & Coss.]. Ecology, Environment and Conservation. 2017;23(Suppl):75-83

Bhanu AN, Singh MN, Tharu R and Saroj SK. Genetic variability, correlation and path coefficient analysis for quantitative traits in chickpea genotypes. *Indian Journal of Agricultural Research.* 2017; 51(5): 425-430.

Biswal M and Babbar A. Cataloguing for Diverse Advance Breeding Lines of Desi Chickpea (Cicer arietinum L.) for Phenological and Yield Attributing Traits. *Biological Forum – An International Journal.* 2022; 14(1): 303-307.

Burton GW. Quantitative inheritance in grasses. Proced. 6th Int. Grassland Cong., 1952;1:127-183.

Burton GW, De V. Estimating heritability in tall Fescue from replicated clonal material. Agron. J. 1953;45:475-481.

Choudhary ML, Tripathi MK, Tiwari S, Pandya RK, Gupta N, Tripathi N, *et al*. Screening of pearl millet [*Pennisetum glaucum* (L.) R. Br.] Germplasm lines for drought tolerance based on morpho-physiological traits and SSR markers. Current Journal of Applied Science and Technology. 2021;40(5):46-63.

Cobos MJ, Rubio J, Fernández-Romero MD, Garza R, Moreno MT, Millán T, Gil J. Genetic analysis of seed size, yield and days to flowering in a chickpea, recombinant inbred line population derived from a Kabuli × Desi cross. Ann Appl Biol. 2007; 151:33–42.

Dehal IB, Kalia R and Kumar B. Genetic estimates and path coefficient analysis in chickpea under normal and late sown environments. Legume research. 2016; 39(4): 510-516.

Dewey DR, Lu KHA. Correlation and path coefficient analysis of component in crested wheat grass seed production. Agron. J. 1959; 51:515-518.

Gupta, N., Tiwari, S., Tripathi, M.K. and Bhagyawant, S.S. (2021). Antinutritional and protein-based profiling of diverse desi and wild chickpea accessions. Current Journal of Applied Science and Technology40(6):7-18

Hailu F. Genetic Variability, Heritability and Genetic Advance of Kabuli Chickpea (*Cicer arietinum* L.) for Agronomic Traits at Central Ethiopia. *International Journal of Plant Breeding and Crop Science*. 2020; 7(1): 710-714.

Jain N, Babbar A, Kumawat, Sarla Yadav RK, Asati. R. Correlation and path coefficient analysis in the promising advance chickpea lines. Pharma Innovation. 2022; 11(5):2124-2128.

Janghel DK, Kumar K, Sunil R, Chhabra AK. Genetic diversity analysis, characterization and evaluation of elite chickpea (*Cicerarietinum* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences. 2020;* 9(1): 199-209.

Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in wheat. Agron. J. 1955;47: 314-318.

Jukanti AK, Gaur PM, Gowda CLL, Chibbar RN. Chickpea: nutritional properties and its benefits. Br J Nutr. 2012; 108:S11–S26

Katkani D, Babbar A, Upadhyay S and Goyal V. Computation of Genetic Variability and Divergence Analysis in Advance Breeding Lines of Chickpea. Biological Forum – *An International Journal*. 2022; 14(2): 611-617.

Khan M, and Qureshi S. Path coefficient and correlation analysis studies on variation induced by gamma irradiation in M_1 generation of chickpea (*Cicer arietinum* L.). *Online J. of Biol. Sci.* 2001*;* **3:** 108-110.

Kumawat S, Babbar A, Tiwari A, Singh S and Solanki RS. Genetic studies on yield traits of late sown elite *Kabuli* chickpea lines. *Indian Journal of Agricultural Sciences. 2021;* 91 (4): 634–8.

Mahalanobis, P. C. Study on the generalized distance in statistics. Proc. Nat. Ins. Sci. India. 1936; 2: 49-55

Makwana K, Tiwari S, Tripathi MK, Sharma AK, Pandya RK, Singh AK. Morphological characterization and DNA finger printing of pearl millet [*Pennisetum glaucum* (L.)] germplasms. Range Mgmt. & Agroforestry. 2021;42(2):205-211

Mishra N, Tripathi MK, Tiwari S, Tripathi N, Trivedi HK. Morphological and molecular screening of soybean genotypes against yellow mosaic virus disease. Legume Research. c2020. DOI: 10.18805/LR-4240.

Mishra N, Tripathi MK, Tiwari S, Tripathi N, Gupta N, Sharma A, *et al*. Evaluation of diversity among soybean genotypes *via* yield attributing traits and SSR molecular markers. Curr.. J Appl. Sci. Technol. 2021a; 40(21):9-24.

Mishra N, Tripathi MK, Tiwari S, Tripathi N, Gupta N, Sharma A. Morphological and physiological performance of Indian soybean [*Glycine max* (L.) Merrill] genotypes in respect to drought. Legume Research. 2021b. DOI:10.18805/LR-4550

Miller PA, Williams JE, Robinson HF, Comstock R E. Estimates of variance and co-variance in upland cotton and their implications in selection. Agron. J. 1958; 50:126-131.

Ningwal R, Tripathi MK, Tiwari S, Yadav RK, Tripathi N, Solanki RS, Asati R, Yasin M. Assessment of genetic variability, correlation and path coefficient analysis for yield and its attributing traits in chickpea (*Cicer arietinum* L.). Pharma Innovation. 2023a;12(3):4851-4859

Ningwal R, Tripathi MK, Tiwari S, Asati R. Yadav RK, Tripathi N, and Yasin Identification of Polymorphic SSR Marken and Diversity Analysis in a Set of Desi Chickpea Genotypes, Biological Forum-An International Journal. 2023b; 15(3): 45-51.

Nimbalkar, R. D., Katre, Y. Y. and Phad, D. S. Genetic diversity in Chickpea (*Cicer arietinum* L.). BIOINFOLET. 2017; 14(1): 60-63.

Paliwal S, Sharma S and Pathak N. Principal component analysis in mungbean [*Vigna radiata* L. Wilczek] genotypes under two seasons. The Pharma Innovation Journal. 2022; 11(3):1500-1505

Rajput S., Jain S., Tiwari S., Sikarwar R. S., Tripathi, N., Barela A. and Tripathi, M. K. (2023). Evaluation of gene-based markers against Fusarium wilt disease in chickpea (*Cicer arietinum* L.). Current Journal of Applied Science and Technology, 42(6): 26-32.

Rajpoot NS, Tripathi MK, Tiwari S, Tomar RS, Kandalkar VS. Characterization of Indian mustard germplasm on the basis of morphological traits and SSR markers. Current Journal of Applied Science & Technology. 2020; 39(48):300-311.

Rao, C. R. Advanced Statistical methods in Biometric Research. John Wiley and Sons, Inc., New York. Pp. 1952; 357-363.

Sahu VK, Tiwari S, Tripathi MK, Gupta N, Tomar RS, Yasin M. Morpho-physiological and biochemical traits analysis for Fusarium wilt disease using gene-based markers in desi and Kabuli genotypes of chickpea (*Cicer arietinum* L.). Indian J Genet. 2020a;80:16.

Sahu VK, Tiwari S, Gupta N, Tripathi MK, Yasin M. Evaluation of physiological and biochemical contents in desi and Kabuli chickpea. Legume Research. 2020b. DOI:10.18805/LR-4265

Sharma S., Tripathi M. K., Tiwari S., Solanki R. S., Chauhan S., Tripathi N., Dwivedi N.and Kandalkar, V. S. 2023a. The Exploitation of genetic variability and trait association analysis for diverse quantitative traits in bread wheat (*Triticum aestivum* L.). urrent Journal of Applied Science and Technology, 42(8) 19-33.

Sharma S., Tripathi M. K., Tiwari S., Solanki R. S., Chauhan S., Tripathi N., Dwivedi N.and Tiwari, P.N. 2023b.Discriminant function analysis for yield improvement in bread wheat (*Triticum aestivum* L.). The Pharma Innovation Journal, 12(5): 224-232.

Solanki, R.S., Babbar, A. andTripathi, N.(2022) Genetic diversity analysis in *kabuli* chickpea (*Cicer arietinum* L.) genotypes based on quantitative traits and molecular markers. Bangladesh Journal of Botany 51(3): 581-587.

Shrivastava A, Babbar A, Shrivastava SP and Shukla SS. Variability studies in some genotypes of chickpea (*Cicer arietinum* L.) under rice fallow. Journal of Food Legumes. 2012; 25(1):70-72

Shrivastava A, Tripathi MK, Solanki RS, Tiwari S, Tripathi N, Singh J, & Yadav RK. Genetic correlation and path coefficient analysis of yield attributing parameters in Indian mustard.

Current Journal of Applied Science and Technology, 2023; 42(7), 42–58. https://doi.org/10.9734/cjast/2023/v42i74079

Shyam C, Tripathi MK, Tiwari S, Tripathi N. Genetic components and diversity analysis in Indian mustard [*Brassica juncea* (Linn.) Czern & Coss] based on different morpho-physiological traits. Current Journal of Applied Science and Technology. 2021; 40(20):34-57. DOI:10.9734/CJAST/2021/v40i2031462

Singh RK. and Chaudhari BD. 1979. Biometrical methods in Quantitative Genetic analysis. Kalyani Publishers, New Delhi. pp 204-214, 229-252.

Singh SP (2006). Genetic variability and response to selection in chickpea. (*Cicer arietinum* L.). Int. J. Plant Sci. 1(2): 232-233.

Thakur NR, Toprope, V.N. and Phanindra. K.S. Estimation of genetic variability, correlation and path analysis for yield and yield contributing traits in chickpea (*Cicer arietinum* L.). *International Journal of Current Microbiology and Applied Sciences*. 2018; 7(2): 2298-2304

Thudi M, Gaur PM, Krishnamurthy L, Mir RR et al. Genomics-assisted breeding fordrought tolerance in chickpea. Funct Plant Biol. 2014; 41(11):1178–1190

Tiwari N, Tiwari S and Tripathi N. 2018. Genetic characterization of Indian little millet (*Panicum sumatrense*) genotypes using random amplified polymorphic DNA markers. Agriculture and Natural Resources, 52:347-353.

Tiwari A and Babbar A. 2017.Genetic divergence in chickpea (*Cicer arietinum* L.) genotypes under normal and late planting. Environment and Ecology. 2017; 35(2C): 1357-1363.

Tripathi MK, Tomar SS, Tiwari VK, Awasthi D, Gupta JC. Heterosis in Indian mustard [*Brassica juncea* (L) Czern and Coss]. Prog. Res. 2015;10(Special-VI):3376-3379.

Tripathi N, Tripathi MK, Tiwari S, Payasi DK. Molecular breeding to overcome biotic stresses in soybean: update. Plants (Basel). 2022;11(15):1967.

Varshney RK, Song C, Saxena RK, Azam S, Yu S et al. Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. Nat Biotechnol. 2013; 31:240–246

Webber CR, Moorthy BR. Heritable and non-heritable relationship and variability of oil content and agronomic characteristics in the F generation of soybean crosses. J. Agron. 1952;44:202-209.

Wright S. Correlation and causation. J. Agril. Res. 1921;20:557-587.

Yadav RK, Tripathi MK, Tiwari S, Tripathi N, Asati R, Patel V, Sikarwar RS, Payasi DK. Breeding and Genomic Approaches towards Development of Fusarium Wilt Resistance in Chickpea. Life 2023, 13, 988. https://doi.org/10.3390/life13040988

Yadav PK, Tiwari S, Kushwah A, Tripathi MK, Gupta N, Tomar RS, *et al*. Morpho-physiological characterization of bread wheat genotypes and their molecular validation for rust resistance genes Sr2, Sr31 and Lr24. Proc. Indian Natl. Sci. Acad. 2021;87:534-545.

Yadav PK, Singh AK, Tripathi MK, Tiwari S, Rathore J. Morpho-physiological characterization of maize (*Zea mays* L.) genotypes against drought. Biological Forum: An International Journal. 2022a;14(2):0975-1130.

Yadav PK, Singh AK, Tripathi MK, Tiwari S, Yadav SK, Tripathi N. Morpho-Physiological and molecular characterization of maize (*Zea Mays* L.) genotypes for drought tolerance. European Journal of Applied Sciences. 2022b;10(6):65-87

Yadav LN, Tripathi MK, Sikarwar RS, Mishra AK. Heterosis in sesame. Sesame & Safflower Newsl. 2005;20:6-10

Table 1 List of chickpea genotypes used in the present study

S.No.	**Name of genotype**	**S.No.**	**Name of genotype**	**S.No.**	**Name of genotype**	**S.No.**	**Name of genotype**	**S.No.**	**Name of genotype**
1	SAGL 162380	**18**	BGD 112	**35**	SAGL 152216	**52**	NBeG 47	**69**	RVSSG 77
2	SAGL 162379	**19**	RVG 205	**36**	SAGL 152218	**53**	JG 322	**70**	BG 362
3	SAGL 152320	**20**	RVSSG 71	**37**	SAGL 152405	**54**	GJG 3	**71**	ICCV 2
4	SAGL 152348	**21**	ICC 4958	**38**	SAGL 171015	**55**	JG 218	**72**	RVKG 111
5	JGG 1	**22**	ICCV 10	**39**	SAGL 161015	**56**	JSC 35	**73**	RVKG 151
6	RVSSG 44	**23**	RVSSG 72	**40**	SAGL 190028	**57**	RVSSG 54	**74**	RVSSG 78
7	RVSSG 42	**24**	RVSSG 74	**41**	JG 14	**58**	HC 5	**75**	RVSSG 89
8	JAKI 9218	**25**	JG 33	**42**	JG 315	**59**	GG 2	**76**	RVSSG 36
9	RVG 202	**26**	ICC 4812	**43**	RVG 201	**60**	GCP 101	**77**	SAGL 190004
10	SAGL 190001	**27**	JG 130	**44**	JG 74	**61**	GG 1	**78**	SAGL 190006
11	SAGL 190002	**28**	SAGL 190007	**45**	JG 12	**62**	GBM 2	**79**	SAGL 162304
12	JG 11	**29**	SAGL 190008	**46**	SAGL 190029	**63**	VIJAY	**80**	SAGL 152228
13	JG 16	**30**	RVSSG 70	**47**	JSC 37	**64**	RVSSG 30	**81**	SAGL 171017
14	SAGL 190003	**31**	SAGL 190009	**48**	JG 63	**65**	RVSSG 31	**82**	SAGL 171005
15	RVSSG 88	**32**	RVSSG 86	**49**	RVG 203	**66**	JGK 3	**83**	MNK 1
16	SAGL 190005	**33**	SAGL 190011	**50**	JG 36	**67**	JGK 5		
17	RVSSG 68	**34**	SAGL 190012	**51**	ANNAGIRI	**68**	JGK 2		

Table 2 Analysis of variance for 10 characters of 83 chickpea genotypes

Source of variation	**df**	**Mean sum of squares**									
		DT50%F	**DTM**	**PH**	**NBPP**	**NPPP**	**TNSPP**	**100S-W**	**BY**	**HI%**	**SYPP**
Replication	1	0.4879**	32.9879**	1081.4049**	36.1355**	571.4328**	1.6780**	4.0566**	2.4396**	1.1522**	2.9987**
Treatments	82	44.1564**	169.8630**	196.9068**	2.5969**	936.8304**	0.1834	58.6552**	214.7388**	261.3937**	31.5860**
Error	82	25.7318	33.0855	28.7998	4.9471	23.8805	0.1079	10.1639	6.5720	3.9516	8.3553

*** Significant at 5% and ** Significant at 1%**

DT50%F=Days to 50% flowering, **DTM**=Days to maturity, **PH**=Plant height, **NBPP**=Numbers of branches per plant, **NPPP**=Numbers of pods per plant, **TNSPP**=Total numbers of seeds per pod, **100-SW**=Hundred seed weight, **BY**=Biological yield per plant, **HI%**=Harvest Index, **SYPP**=Seed yield per plant

Table 3 Genetic parameters of variability for yield and its contributing traits for chickpea genotypes

S.No.	Traits	Range		Grand Mean	Coefficient of variance		h^2 (b)%	Genetic advance as % mean
		Min	**Max**		**GCV%**	**PCV %**		
1.	**DT50%F**	44	70	56.3	5.39	8.34	41.7	7.173
2.	**DTM**	83	128	107.4	7.69	8.57	80.5	14.229
3.	**PH**	26	77	43.8	20.92	22.64	85.4	39.826
4.	**NBPP**	2.8	7.6	5.53	19.59	20.59	90.5	38.390
5.	**NPPP**	7.67	91	39.9	53.41	54.1	97.5	18.620
6.	**TNSPP**	1.0	2.0	1.34	14.5	22.6	41.2	19.161
7.	**100-SW**	8.9	37	20	24.58	27.04	82.7	46.055
8.	**BY**	6.5	52	20.6	49.40	50.18	96.9	37.210
9.	**HI%**	11	67	45	25.18	25.37	98.5	35.488
10.	**SYPP**	1.25	23	8.3	41.03	47.84	73.5	56.490

Table 4 Phenotypic correlation coefficient for yield and its attributing traits in chickpea genotypes

Character	**DT50%F**	**DTM**	**PH**	**NBPP**	**NPPP**	**TNSPP**	**100-SW**	**BY**	**HI%**	**SYPP**
DT50%F	**1.000**	0.1070	0.0697	0.2164	0.3060**	0.1704	-0.2370*	0.0034	0.2111	0.2598*
DTM		**1.000**	-0.1600	-0.1770	-0.2577**	0.0442	-0.2220*	0.0805	-0.1620	-0.1370
PH			**1.000**	0.1922	0.1597	0.1157	-0.0020	0.0051	0.0555	0.3077**
NBPP				**1.000**	0.3804**	0.2254*	0.0071	-0.3020**	0.2894**	0.1417
NPPP					**1.000**	0.2060	-0.212	0.0382	0.3878**	0.5068**
TNSPP						**1.000**	-0.035	-0.01	0.2059	0.1873
100-SW							**1.000**	-0.014	0.1576	-0.0830
BY								**1.000**	-0.4289**	0.4244**
HI%									**1.000**	0.2857**
SYPP										**1.000**

*** Significant at 5% and ** Highly Significant at 1%**

Table 5 Genotypic correlation coefficient for yield and its attributing traits in chickpea genotypes

Character	**DT50%F**	**DTM**	**PH**	**NBPP**	**NPPP**	**TNSPP**	**100-SW**	**BY**	**HI%**	**SYPP**
DT50%F	**1.0000**	-0.2444*	-0.0451*	-0.2306*	0.3673**	0.8173**	-0.6235**	0.1475	0.2807*	0.2500*
DTM		**1.0000**	-0.2508*	0.1932	-0.3292**	0.1636	-0.3168**	0.1358	-0.1968	-0.2586*
PH			**1.0000**	-0.2103*	0.1467	0.2404*	-0.0553	0.0319	0.0401	0.3174**
NBPP				**1.0000**	-0.3739**	-0.8634**	0.1536	0.3052**	-0.2843**	-0.1062
NPPP					**1.0000**	0.3681**	-0.2578*	0.0559	0.3853**	0.5464**
TNSPP						**1.0000**	0.0184	-0.0607	0.3383**	0.3701**
100-SW							**1.0000**	0.0066	0.1659	-0.1566
BY								**1.0000**	-0.4295**	0.5184**
HI%									**1.0000**	0.3127**
SYPP										**1.0000**

*** Significant at 5% and ** Highly Significant at 1%**

Table 6 Phenotypic path coefficient analysis for yield and its component traits in chickpea genotypes

Character	**DT50%F**	**DTM**	**PH**	**NBPP**	**NPPP**	**TNSPP**	**100-SW**	**BY**	**HI%**	**SYPP**
DT50%F	**0.0539**	0.0058	0.0038	0.0117	0.0165	0.0092	-0.0128	0.0002	0.0114	0.2598
DTM	-0.0048	**-0.0451**	0.0072	0.008	0.0116	-0.002	0.0100	-0.0036	0.0073	-0.1368
PH	0.0156	-0.0358	**0.2235**	0.043	0.0357	0.0259	-0.0005	0.0011	0.0124	0.3077
NBPP	0.0134	-0.011	0.0119	**0.062**	0.0236	0.014	0.0004	-0.0187	0.0179	0.1417
NPPP	0.0619	-0.0521	0.0323	0.0769	**0.2022**	0.0417	-0.0429	0.0077	0.0784	0.5068
TNSPP	0.0018	0.0005	0.0012	0.0024	0.0022	**0.0107**	-0.0004	-0.0001	0.0022	0.1873
100-SW	0.0231	0.0216	0.0002	-0.0007	0.0207	0.0034	**-0.0975**	0.0014	-0.0154	-0.0832
BY	0.0021	0.0503	0.0032	-0.1887	0.0238	-0.0059	-0.0088	**0.625**	-0.2681	0.4244
HI%	0.0928	-0.0711	0.0244	0.1272	0.1704	0.0905	0.0693	-0.1885	**0.4396**	0.2857

Table 7 Genotypic path coefficient analysis for yield and its component characters in chickpea genotypes

Character	**DT50%F**	**DTM**	**PH**	**NBPP**	**NPPP**	**TNSPP**	**100-SW**	**BY**	**HI%**	**SYPP**
DT50%F	**0.1866**	-0.0456	-0.0084	-0.043	0.0686	0.1525	-0.1163	0.0275	0.0524	0.2500
DTM	-0.0184	**0.0753**	-0.0189	0.0145	-0.0248	0.0123	-0.0239	0.0102	-0.0148	-0.2586
PH	-0.0129	-0.0715	**0.2852**	-0.06	0.0419	0.0685	-0.0158	0.0091	0.0114	0.3174
NBPP	0.0824	-0.069	0.0752	**-0.3574**	0.1337	0.3086	-0.0549	-0.1091	0.1016	-0.1062
NPPP	0.0841	-0.0754	0.0336	-0.0856	**0.2289**	0.0843	-0.059	0.0128	0.0882	0.5464
TNSPP	-0.319	-0.0638	-0.0938	0.3369	-0.1437	**-0.3902**	-0.0072	0.0237	-0.132	0.3701
100-SW	-0.0167	-0.0085	-0.0015	0.0041	-0.0069	0.0005	**0.0268**	0.0002	0.0044	-0.1566
BY	0.1141	0.105	0.0246	0.2359	0.0432	-0.0469	0.0051	**0.7732**	-0.3321	0.5184
HI%	0.1498	-0.105	0.0214	-0.1517	0.2056	0.1805	0.0885	-0.2292	**0.5336**	0.3127

Table 8 Distribution of chickpea genotypes into different clusters

Cluster No.	**No. of genotypes**	**Name of the genotypes**
Cluster I	35	ICCV 2, RVSSG 89, JG16, SAGL 152228, JG 130, RVG 202, SAGL 190028, RVG 201, JGG 1, JG 33, SAGL 17005, SAGL 161015, SAGL 190004, RVSSG 78, SAGL 152348, SAGL 152320, ICC 4958, RVSSG 42, SAGL 190001, SAGL 162379, RVSSG 44, SAGL 162380, SAGL 190003, RVSSG 71, RVG 205, RVSSG 88, SAGL 190011, JG 74, JG 12, SAGL 171015, SAGL 152216, RVSSG 30, JGK 2, RVSSG 72
Cluster II	28	SAGL 190008, RVSSG 54, SAGL 190012, JG 14, ICCV 10, GBM 2, RVSSG 70, HC 5, GG 1, SAGL 190009, SAGL 171017, RVSSG 68, ICC 4812, SAGL 152405, JG 218, RVSSG 74, GCP 101, GJG 3, SAGL 190007, JG 315, NBeG 47, JG 11, JG 36, ANNAGIRI, SAGL 190029, RVG 203, JSC 35, GG 2
Cluster III	8	SAGL 190006, MNK 1, BG 362, SAGL 162304, VIJAY, JGK 3, RVSSG 77, RVSSG 36
Cluster IV	1	JG 322
Cluster V	4	JGK 5, RVKG 151, RVSSG 31, SAGL 190005
Cluster VI	1	JG 63
Cluster VII	1	SAGL 152218
ClusterVIII	1	JSC 37
Cluster IX	1	RVKG 111
Cluster X	1	SAGL 190001
Cluster XI	1	JAKI 9218
Cluster XII	1	BGD 112

Table 9 Inter and intra cluster D^2values for different clusters

Cluster No.	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**	**Cluster IX**	**Cluster X**	**Cluster XI**	**Cluster XII**
Cluster I	**10.21**	15.92	20.48	17.19	17.23	21.36	22.99	21.53	21.71	18.53	17.73	28.78
Cluster II		**10.8**	19.29	15.07	21.28	14.42	14.93	14.03	16.87	18.74	22.3	19.1
Cluster III			**11.09**	27.48	17.98	16.93	17.07	21.33	16.84	17.59	25.69	24.18
Cluster IV				**0**	28.75	23.14	20.85	16.07	19.74	20.19	16.39	22.41
Cluster V					**12**	21.89	26.41	28.32	27.32	24.41	28.66	33.82
Cluster VI						**0**	10.13	13.27	17.77	19.39	27.3	17.99
Cluster VII							**0**	9.86	10.37	16.29	24.05	11.41
Cluster VIII								**0**	13.11	15.84	21.33	12.82
Cluster IX									**0**	12.66	19.55	13.39
Cluster X										**0**	15.35	23.26
Cluster XI											**0**	29.07
Cluster XII												**0**

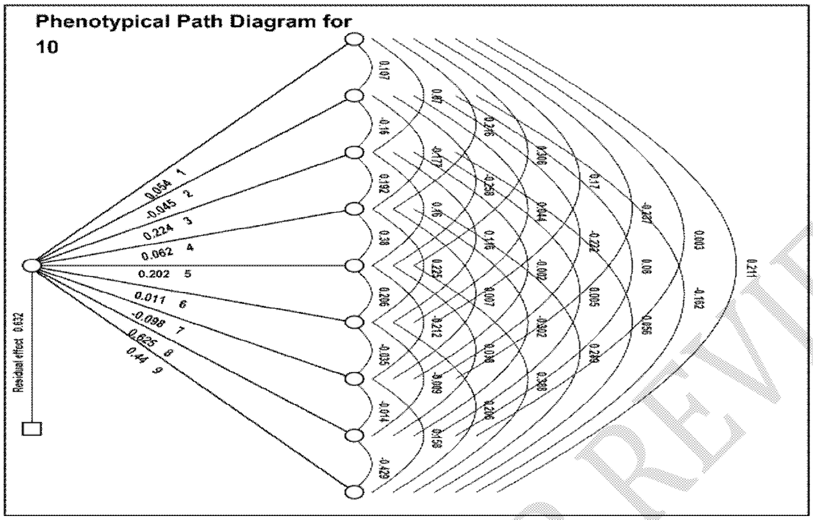
Table 10 Cluster mean for yield and its component traits of chickpea genotypes employing Tocher's Method

Cluster	**DT50%F**	**DTM**	**PH**	**NBPP**	**NPPP**	**TNSPP**	**100-SW**	**BY**	**HI%**	**SYPP**
Cluster I	55.53	109.34	43.37	5.53	26.51	1.32	21.67	**15.19**	47.83	7.12
Cluster II	57.91	104.30	43.60	5.90	61.12	1.41	18.88	18.72	48.26	9.05
Cluster III	52.88	112.69	41.29	4.12	22.29	1.25	19.02	40.10	**24.68**	7.22
Cluster IV	57.50	100.00	32.83	6.84	58.00	1.30	17.00	15.25	**67.77**	**3.41**
Cluster V	52.63	108.50	46.38	4.79	**12.83**	**1.13**	15.32	16.76	24.81	3.72
Cluster VI	57.50	98.50	**77.83**	5.67	72.50	1.30	**12.32**	27.35	42.10	**23.50**
Cluster VII	**70.00**	114.50	62.00	6.66	73.00	1.25	17.95	34.46	46.40	15.90
Cluster VIII	**51.50**	**83.00**	58.83	6.50	70.50	1.25	**26.91**	34.44	55.24	17.25
Cluster IX	61.00	**120.50**	**29.00**	**3.33**	48.00	**2.00**	20.85	**44.44**	45.19	14.00
Cluster X	63.50	92.50	33.67	**7.34**	22.50	1.34	23.78	41.81	45.42	17.50
Cluster XI	60.50	113.50	52.17	5.66	15.00	1.34	26.00	31.00	63.85	4.47
Cluster XII	53.50	111.50	36.00	6.34	**91.50**	1.25	16.75	41.39	50.77	18.00

Table 11 Contribution of various traits towards clustering in chickpea genotypes

S. No.	**Source**	**Contribution %**
1	Days To 50% Flowering	0.06
2	Days To Maturity	3.56
3	Plant height	1.88
4	Numbers of primary branches per plant	0.03
5	Numbers of pods per plant	28.83
6	Total numbers of seeds per pod	0.18
7	100 -seed weight	3.67
8	Biological yield per plant	30.97
9	Harvesting index	30.56
10	Seed yield per plant	0.26
	Total	**100.00**

Fig. 1. Phenotypic path diagram for 10 characters in chickpea genotypes



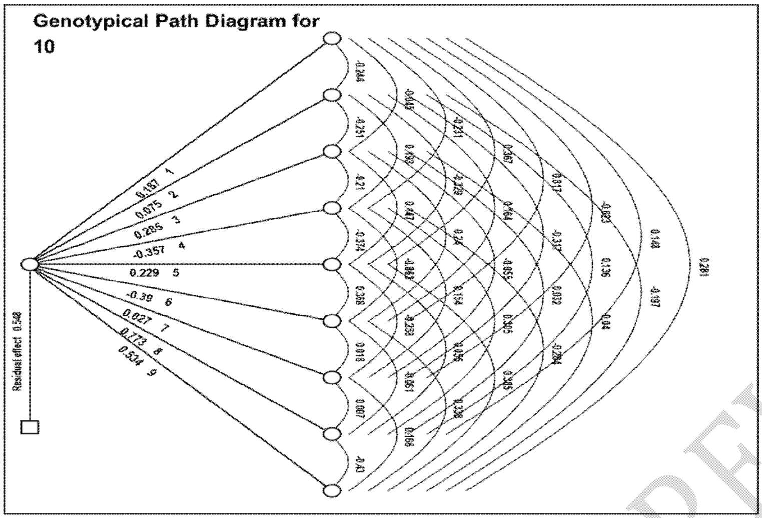


Fig. 2. Genotypic path diagram for 10 characters in chickpea genotypes

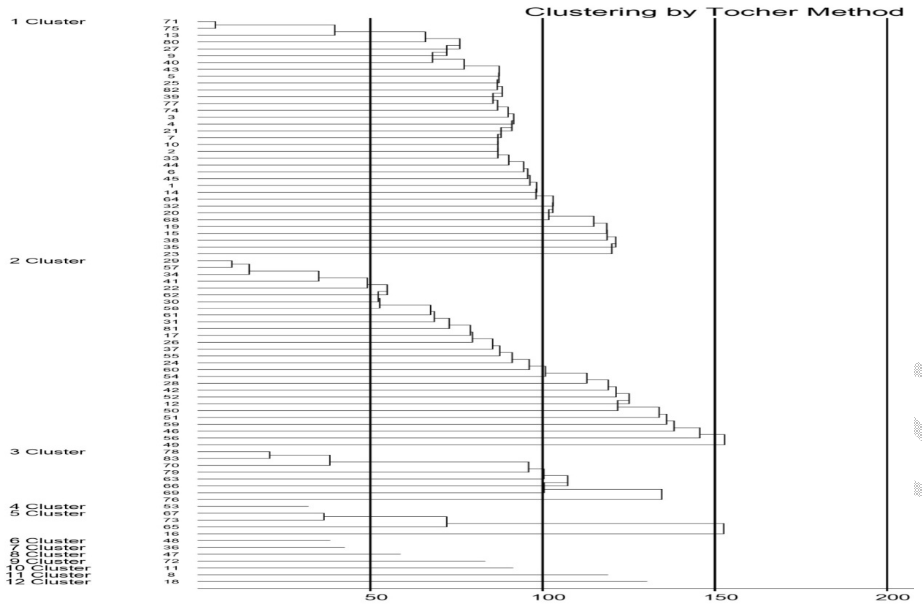


Fig. 3 Cluster diagram of diverse chickpea genotypes based on D^2 analysis

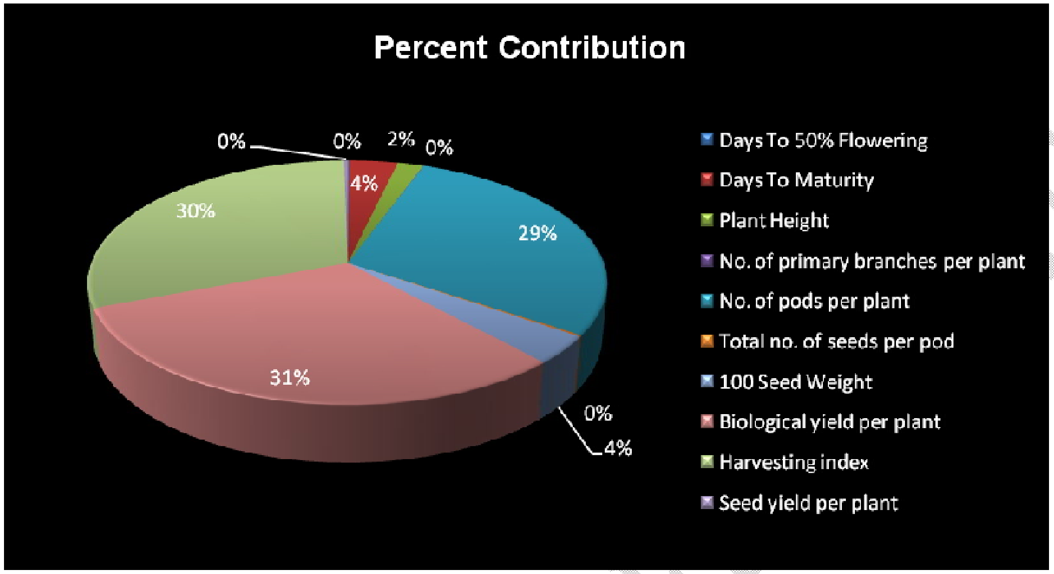


Fig. 4 Percent contribution of traits in cluster