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GENETIC VARIABILITY, HERITABILITY AND YIELD PERFORMANCE OF CHICKPEA GENOTYPES UNDER SEMI-ARID CONDITIONS

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ABSTRACT

Chickpea production is still meager in semi-arid conditions due to environmental stresses coupled with a lack of genetic variation. Twenty-five chickpea genotypes including five check cultivars were evaluated for genetic heritability, variability and yield performance, using randomized complete design in semi-arid environments. Morphological, phenological, and yield traits were recorded and analyzed using ANOVA, genetic parameters, PCA, and correlation analysis. To quantify the magnitude of genetic and environmental impacts on the expression of the traits, genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated. The values of PCV consistently outperformed GCV, indicating pronounced environmental modulation of the performance of the trait in semi-arid settings. Significant genetic variation ($p < 0.01$) was recorded for all tested characteristics. Significant heritability coupled with high genetic advance was recorded for pods per plant ($h^2 = 0.81$; GA = 46.3%), seeds per pod ($h^2 = 0.59$; GA = 41.9%), and seed yield ($h^2 = 0.77$; GA = 41.6%), thus indicating the predominance of additive gene action and supporting the effectiveness of direct selection. Principal component analysis revealed that pods per plant, seeds per pod, secondary branching, and 100-seed weight contributed to genetic divergence. Similarly, correlation analysis indicated that early phenology resulted in yielding advantage in moisture stress and that seed yield correlated positively with pods per plant, biological yield, and secondary branches. The continuous excellence performance of D-3113, D-1113, and D-1211 implies that they are suitable as elite breeding materials to enhance chickpea productivity in semi-arid conditions.

Keywords: Chickpea; Genetic variability; Heritability; Yield components; Semi-arid conditions

ANOVA: Analysis of variance; **PCA:** Principal component analysis; **GA:** Genetic advance

1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a significant grain legume often referred to as gram, garbanzo, or channa that belongs to the family Leguminosae and subfamily Papilionaceae (Koul et al., 20220). It is a self-pollinating, diploid with a 2n = 16 genome and a size of 732 Mb (Coyne et al., 2020). Because of its high nutritional content, viz. 23% protein, 64% carbohydrates, essential minerals, and dietary fiber, chickpeas rank among the most important pulse crops of the world with maximum digestibility (Begum et al., 2023). It is called "poor man's meat" and contributes much to the output of pulses throughout the world (David et al., 2024).

The only domesticated species of the genus Cicer, containing about 40 species, is the cultivated chickpea, C. arietinum (Mehmetoğlu et al., 2023). Originating in the Southern Caucasus and Northern Persia, it is now grown in tropical, and temperate climates (Dixit et al., 2022). The annual world production of chickpeas stands at 16.50 mmt on an area of 13.20 mha. Pakistan, Australia, Turkey, and India remain the leading producers of the crop (FAO, 2023). Chickpea assumes great importance in Pakistan's pulse economy with an area of 0.79 mha, which is mainly concentrated in Punjab and Khyber Pakhtunkhwa (Pakistan Economic Survey, 2023–24).

Chickpea productivity is still poor and erratic in Pakistan and other semi-arid areas, despite its importance. Unpredictable rainfall, protracted dry spells, high temperatures, and poor soil quality negatively affect the growth, flowering, pod setting, and seed filling of this region. Almost 75% of the province's chickpeas are grown in semi-arid regions, especially Karak, D.I. Khan, Lakki Marwat, and Bannu, but yields are still well below potential (Abdullah et al., 2023).

Their narrow genetic base constrains the development of high-yielding and climate-resilient cultivars (Singh et al., 2022; Shahnaz et al., 2025). To achieve this, however, it is pertinent for breeders to have genetically diversified germplasm with desirable features that include early blooming, effective biomass partitioning, enhanced pod and seed properties, and tolerance to moisture stress. This pertains to recent findings by (Gaur et al., 2021). Successful selection for all those characters then depends upon the accurate understanding of genetic diversity, heritability, and the contribution of important yield components.

In this context, the selection of promising lines and determination of the relative importance of yield-related traits are based on the evaluation of chickpea genotypes under natural semi-arid field conditions. However, there seems to have been little focus on the identification of trait arrangements that can ascertain the efficiency of selection in semi-arid conditions although there has been an evaluation of the chickpea germplasm. The quantitative basis for distinguishing the variability caused by factors controlled by genetics from those caused by the environment can be obtained through the calculation of GCV and PCV, heritability, and genetic progress. In regions with rainfall and water stress where the expressions are often overshadowed by the varying values brought on by the environmental factors, the information provided can be very beneficial for breeders. Therefore, the current study places emphasis on the need for genetic explanation based on traits to provide informed selection methods in chickpea improvement programs.

2. MATERIALS AND METHODS

2.1 Experimental Site and Climatic Conditions

The field study was conducted in the semi-arid region of Khyber Pakhtunkhwa, Pakistan, at Agriculture Research Station (ARS), Ahmad Wala, Karak (32°93′ N, 71°23′ E). In the (2021–2022) chickpea growing seasons, the study was conducted.

Meteorological data for both cropping seasons were provided by the agrometeorological observatory nearest to the Karak region, and it included meteorological data such as monthly mean maximum and minimum temperatures (°C), total monthly rainfall (mm), and average relative humidity (%). During the agricultural season, these environmental factors reflect typical semi-arid climatic conditions with considerable temperature variations and irregular, low rainfall (Fig. 1).

2.2 Plant Materials and Experimental Design

Twenty advanced lines and five standard check cultivars among the 25 genotypes of chickpea were evaluated. The genotypes and check varieties used in the experiment are presented in (Tab. 1). A randomized complete block design was used with three replications in setting of this experiment. Each genotype was sown in two rows, each measuring three meters. Plant-to-plant spacing was 15 cm, while the spacing between the rows was 30 cm. From seeding to harvest, all replications used the same agronomic techniques, such as fertilizing, weeding, hoeing, and plant protection measures. Five plants were selected randomly from each replication of each genotype. Throughout the crop cycle, normal crop management techniques were used to reduce environmental fluctuations.

2.3 Data collection

Data on all the phenological, morphological, and yield-related attributes were recorded for five randomly selected plants from each replication by following standard protocols. Days to 50% emergence and days to 50% flowering were worked out as the number of days from sowing to 50% seedling emergence and flowering, respectively, while days to 90% maturity was recorded at 90% physiological maturity of plants, following the technique outlined by Ali et al. (2020). The plant height was measured from base to apex using a measuring scale, following the recommendations of Singh et al. (2020). The counting of primary and secondary branches per plant was done for each selected plant manually, following the methodology of Khan et al. (2021). Pods per plant and seeds per pod were estimated by counting every pod in tagged plants and averaging the number of seeds per pod, following Khan et al. (2019). For the measurement of 100-seed weight, 100 air-dried seeds were weighed on an electronic balance, following Kumar et al. (2018). Whole plants were harvested to calculate biological yield and seed yield; after that, biomass and grain weights were measured, and data were translated into kg ha^{-1} by following the technique described by Gul et al. (2023). Harvest index was calculated as the ratio of seed yield to biological yield and presented in percent form, as described by Anjum et al. (2022). These consistent measurements thus allowed for the correct assessment of genetic diversity in yield performance among the tested chickpea genotypes.

Table 1: List of chickpea genotypes

S. No	Genotype	S. No	Genotype
1	D-1215	**14**	D-2709
2	D-1915	**15**	D-1113
3	D-0810	**16**	D-1515
4	D-8697	**17**	D-0514
5	D-1414	**18**	D-0515
6	D-3011	**19**	D-3910
7	D-3613	**20**	D-2793
8	D-2508	**21**	D-KARAK-1 (check)
9	D-2015	**22**	D-KARAK-2 (check)
10	D-3113	**23**	D-NIFA-2005 (check)
11	D-1213	**24**	NKC-5-5-20 (check)
12	D-1211	**25**	NKC-10-99 (check)
13	D-1112		

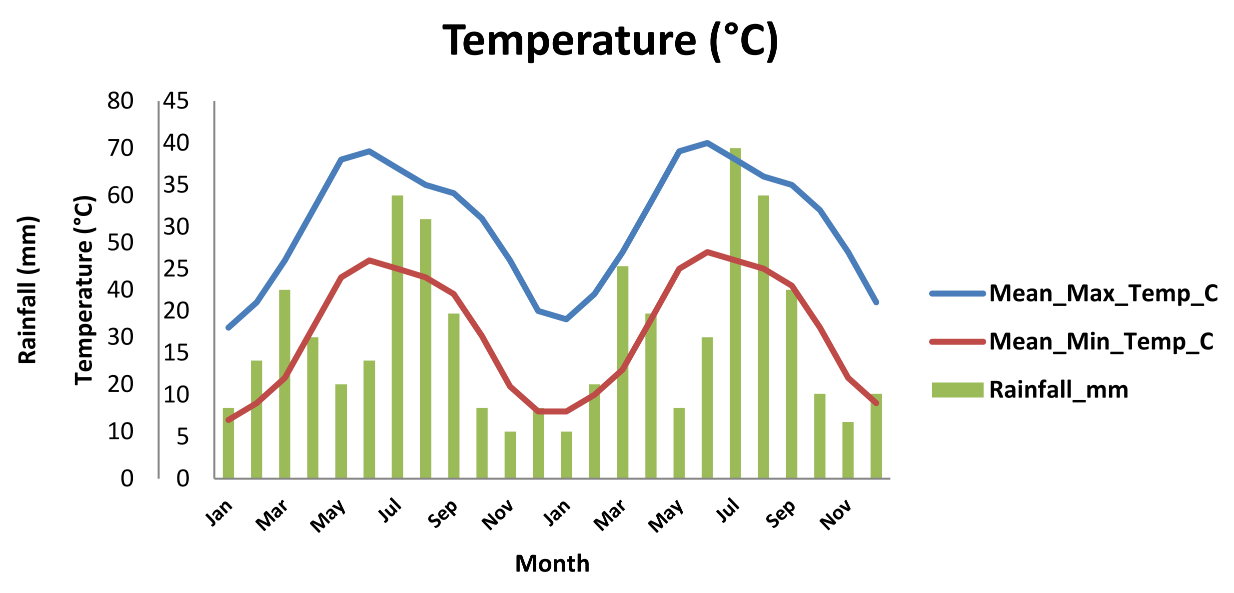

Fig. 1: Monthly mean maximum and minimum temperatures (°C) and total monthly rainfall (mm) recorded at Ahmad Wala, Karak (Khyber Pakhtunkhwa) during the 2021 and 2022 cropping seasons

2.4 Statistical Analysis

The analysis was carried out using the R software and Statistics 8.1 program for the ANOVA of all the recorded data. Mean separation was performed using the LSD test at a five percent significance level. PCA and correlation analysis using the heatmap were carried out to establish genetic classification and associations. Cluster analysis using the Ward.D2 method was employed to establish the genetic diversity between the genotypes.

3. RESULTS

Variance analysis proved the existence of genetic variability in the studied materials by the large differences that were highly significant ($p < 0.01$) in all studied phenological, morphological, and productivity traits among the chickpea genotypes (Tab. 2). This variability is required in selection and proves the lack of masking of genetic differences by environmental influences. The presence of significant heterogeneity in the days to emergence, flowering, and maturity times proves that different genotypes have uptake and growth periods different from each other. In agricultural terms, the advantage of early types lies in the fact that early-emerging and early-flowering lines always tend to avoid terminal water stress, which can be a serious limiting factor in semi-arid areas (Gaur et al., 2021).

There are considerable variations in branch characteristics, pods per plant, seeds per pod, and seed weights, which indicate the genetic diversity in reproductive ability and assimilate partitioning. Additive genetic activity, which promotes positive selection, can be estimated from the variations in yield contributing traits (Khan et al. 2021). There were also variations in plant heights and seed weights. There are variations in plant heights, contributing to variations in plant architecture and biomass production methods. It appears that some genotypes own a better ability in utilizing the same. This could be due to favorable canopy structure, branching index, or sink-source ratio. Similar results have been reported in studies on the improvement of chickpea by Singh et al. (2020) and Ali et al. (2022).

3.1 Genetic Variability, Heritability and Genetic Advance

Differences were observed for the traits using the estimation of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (Table 3). The difference between PCV and GCV for pods per plant, seeds per pod, seed weight per 100 seeds, biological yield, and seed yield was small, indicating the tighter genetic control of the characters. For every character, PCV exceeded the values of GCV slightly, suggesting the presence of environmental influences. The presence of great exploitable genetic variability for the studied traits within the testing germplasm was revealed by the high values of GCV and PCV for the number of pods per plant, seeds per pod, and seed yield, which were 24.99 and 27.75%, and seeds per pod, which were 26.51 and 34.49%, and seed yield, which were 23.05 and 26.22%, respectively.

The predominance of additive effects is confirmed by the interaction of high heritability and high genetic progress for these traits, implying that phenotypic selection would have a good possibility of success even in earlier generations. In contrast, for semi-arid environments, traits such as plant height and harvest index had lower heritability and greater differences for PCV and GCV, implying a greater sensitivity for these traits and less reliability for selection.

There were significant differences between genotypic and phenotypic variation among the various traits, but environmental contribution resulted in the former always being greater than the latter. The following characters: pods per plant, seeds per pod, secondary branches per plant, 100-seed weight, biological yield, and seed yield showed good heritability coupled with high genetic gain (Tab. 3). This combination indicates that additive gene action predominates, so direct selection can be effective to improve these qualities.

Strong genetic control is suggested by the high heritability of pods per plant (0.81) and seeds per pod (0.59), which explains why genotypes with higher pod-setting capacity performed consistently across replications. The significant impact of branching and reproductive vigor on production is shown in the high genetic progress for pods per plant (46.30%). Strong genetic control was also demonstrated by seed yield ($h^2 = 0.77$; GA = 41.60%), indicating that genotypes with strong yield components convert their genetic potential into increased output. Itana et al. (2024); Verma et al. (2023) observed similar results in chickpeas.

At the same time, the traits that are more sensitive to the environment, like plant height, principal branches, and harvest index, have shown lower heritability. It could be hypothesized that the plant height will be less heritable in semi-arid conditions due to the fact that soil moisture and temperature stress are believed to influence plant height to a greater degree. In general, selection based on seed size, branching ability, and pod characteristics is more reliable compared to selection for plant height or harvest index.

3.2 Descriptive Statistics and Trait Variation

Descriptive statistics for branching traits (PBPP and SBPP), pods per plant, seeds per pod, seed weight, biological yield, and seed yield showed significant genotype variation for all the above-mentioned traits (Tab. 4). The range of values is wide, which demonstrated the strong population variety. Greater variability in the branching features and yield components was exhibited; however, characteristics like days to emergence and maturity showed a tight range and low CV value, reflecting their intrinsic stability.

There is biological significance to this variance. Since branching increases the number of reproductive sites, thereby improving pod set and ultimately seed yield, the genotypes with more secondary branches usually produce more pods (Singh et al., 2021). Since larger seeds have often arisen from better assimilate partitioning throughout the seed-filling period, a feature highly susceptible to moisture availability and genotype-specific adaptation, the wide variation in seed weight is of equal significance (Kumar et al., 2018).

The large variation in biological production and seed yield indicated that there is significant variation among the tested genotypes in their light absorption capacity, biomass storage, and efficiency of transformation into grains. Variability is an important component of selection under semi-arid conditions, where small physiological differences may cause large differences in yield.

Table 2: Mean square values (ANOVA) for various studied traits in chickpea genotypes

Traits	Replications (2)	Genotypes (24)	Error (48)	CV (%)
Days to 50% emergence	1.1	4.0*	0.52	13.97
Days to 50% flowering	4.0	173.0**	10.5	7.56
Days to 90% maturity	5.9	22.5**	2.7	1.73
Primary branches plant^{-1}	0.4	0.7**	0.2	17.49
Secondary branches plant^{-1}	1.7	11.3**	2.1	28.17
Pods plant^{-1}	146.3	722.6**	52.2	27.61
Seeds pod^{-1} (g)	0.1	0.5**	0.1	29.29
Plant height (cm)	31.5	69**	24.7	8.59
100-Seed weight (g)	1.3	18.0**	1.2	13.04
Biological yield (kg ha^{-1})	8254189	4873053*	1005712	29.23
Seed yield (kg ha^{-1})	20329	265594**	23720	25.94
Harvest index (%)	82.2	67.8**	34.3	28.46

* *Significant*, ***Highly significant*

Table 3: Variance components, heritability, genotypic and phenotypic coefficient of variance and genetic advance of studied traits

Trait	V_g	V_e	V_p	GCV (%)	PCV (%)	H²	GA	GA (%)
DTE	1.14	0.52	1.66	11.59	13.99	0.68	1.80	19.60
DTF	54.61	10.45	64.63	7.04	7.66	0.84	13.91	13.26
DTM	6.60	2.65	9.26	1.47	1.74	0.71	4.45	2.55
PBPP	0.16	0.19	0.35	12.16	17.98	0.45	0.55	16.67
SBPP	3.07	2.11	5.18	21.82	28.34	0.59	2.77	34.45
PP	223.48	52.18	275.66	24.99	27.75	0.81	27.70	46.30
SP	0.13	0.08	0.22	26.51	34.49	0.59	0.57	41.92
PH	14.74	24.65	39.40	5.27	8.62	0.37	4.78	6.57
HSW	5.57	1.22	6.78	11.93	13.16	0.82	4.40	22.24
BY	1289113.6	1005712	2294825.6	21.18	28.26	0.56	1747.55	32.60
SY	80624.66	23720	104344.66	23.05	26.22	0.77	512.38	41.60
HI	11.17	34.27	45.44	13.96	28.16	0.24	3.33	13.92

Table 4: mean, standard deviation, range and LSD values of studied traits in chickpea genotypes

Traits	Mean	SD	Min	Max	CV (%)	LSD
DTE	9.21	1.29	7	12	13.97	1.18
DTF	104.92	8.04	96	118	7.56	33.62
DTM	174.67	3.04	169	181	1.73	2.73
PBPP	3.29	0.59	2	4	17.49	1.57
SBPP	8	2.28	4	12	28.17	15.03
PP	59.83	16.60	26	94	27.61	12.57
SP	1.36	0.47	1	2	29.29	0.56
PH	72.85	6.28	64	82	8.59	8.16
HSW	19.78	2.60	15.6	24.2	13.04	2.06
BY	5360.86	1514.87	2433.33	9782.14	29.23	3523.12
SY	1231.77	323.02	183.88	1698.20	25.94	246.55
HI	23.94	6.74	6.13	44.91	28.46	9.42

3.3 Principal component analysis (PCA)

With a wide distribution of genetic diversity among the genotypes, PCA showed that the first two principal components explained 40.9% of total variability, as revealed by (Fig. 2). The vectors for pods per plant, seeds per pod, 100-seed weight, and features concerning branching were all the longest, indicating their significance in genotype differentiation.

Secondary branches, seeds per pod, and pods per plant cluster along the same axis, indicating that these characteristics are highly inter-related and serve as coordinated drivers of yield. In contrast, days to emergence and days to flowering clustered independently, indicating that earliness is a separate influence on variability. Whereas genotypes distributed across opposite quadrants reflect divergent genetic backgrounds, genotypes within the same quadrant share similar characteristic profiles.

The two discussed strategies above, which include emphasizing pod number, seed size, and branching, are supported as ways of increasing yield in semi-arid conditions by the great influence of yield components on PC1. Similar PCA-based differentiation patterns were reported by Babbar et al. (2018) and Vyshnavi et al. (2021).

3.4 Correlation Analysis

Several important factors explaining yield formation were found through correlation analysis (Fig. 3). Strong positive correlations were found between seed yield and biological yield (r = 0.57***), pods per plant (r = 0.44***), and secondary branches per plant (r = 0.25*). These connections arise because more branching increases the number of reproductive nodes, in turn producing more pods and a higher biomass, which in turn raises seed yield.

The advantage of being early in the semi-arid conditions was revealed through the negative association between seed production and days to blooming (r = –0.43***) and days to emergence (r = –0.25*). Although early-blooming lines escape terminal drought and produce higher seed yields, early-emerging lines develop advanced root growth that helps in better water abstraction. These results support those presented by authors Gaur et al. (2021) and Ali et al. (2020). The earlier results shown by authors Khan et al. (2019) and Sharma et al. (2022) could be verified through the negative association between pod number and late blooming and late maturity, implying that late growth impairs the ability to reproduce in the drought-stress condition during the critical growth stage. Pods per plant and seeds per pod showed a strong positive association, suggesting that those lines having the highest ability to reproduce always had the highest values in several seed-related parameters.

3.5 Cluster Analysis

There were four groups of genotypes established through hierarchical clustering, showing a significant level of genetic variation (Fig. 4). Those belonging to the same group had a comparable pattern of characteristics, while the genotypes belonging to different groups had different performance characteristics. Wide inter-cluster distances indicate the opportunity to choose genetically divergent parents for hybridization, thereby improving heterosis and widening the genetic base. The importance of cluster-based selection in the process of breeding chickpea was further addressed in studies by Ahmad et al. (2019) and Singh et al. (2021).

Taken together, the results indicate that early phenology, vigorous branching, high podding, and efficient biomass partitioning are the major contributors to chickpea productivity under semi-arid conditions. In fact, due to the combined presence of these traits, the performance of these genotypes, D-3113, D-1113, and D-1211, has been outstanding. The enhanced abilities of drought escape, sink potential, and optimal source-sink relationships under drought stress due to enhanced drought tolerance can all be attributed to the gains achieved by these genotypes. The semiarid environments, where the variety of drought stress faces intense selective pressure due to unpredicted rainfall and hot climates, would particularly benefit from the above-mentioned gains. Hence, the major genetic gains in improving chickpeas can be achieved through enhancing early flowering, tree vigor, contribution of the tree, and seed size.

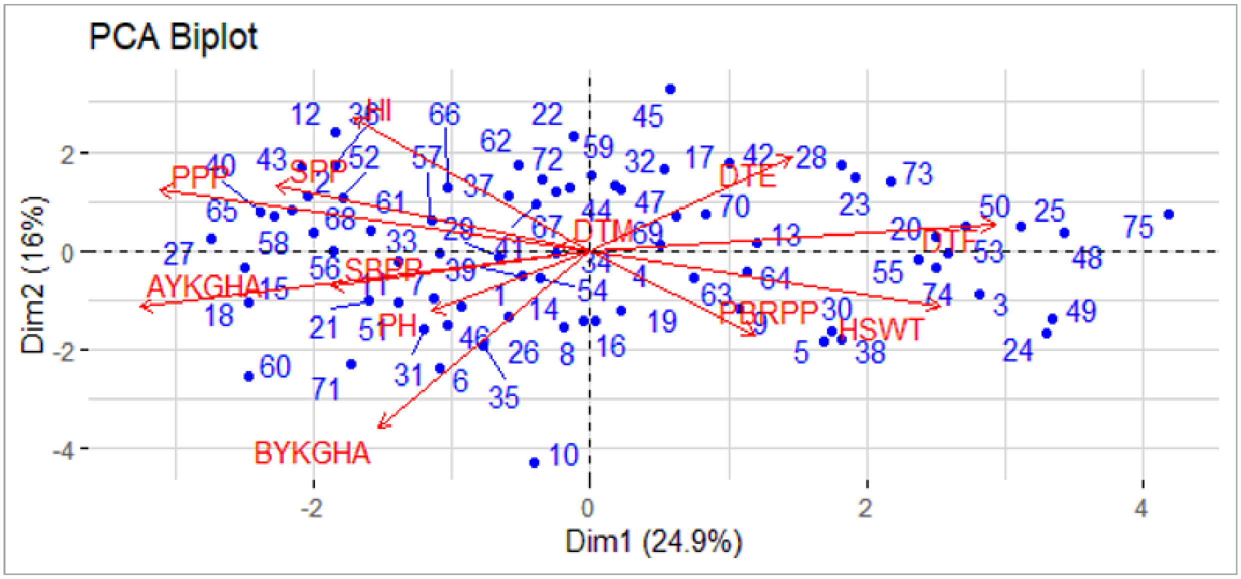

Fig. 2: Principal component analysis (PCA) biplot showing traits contribution and genotype grouping in chickpea

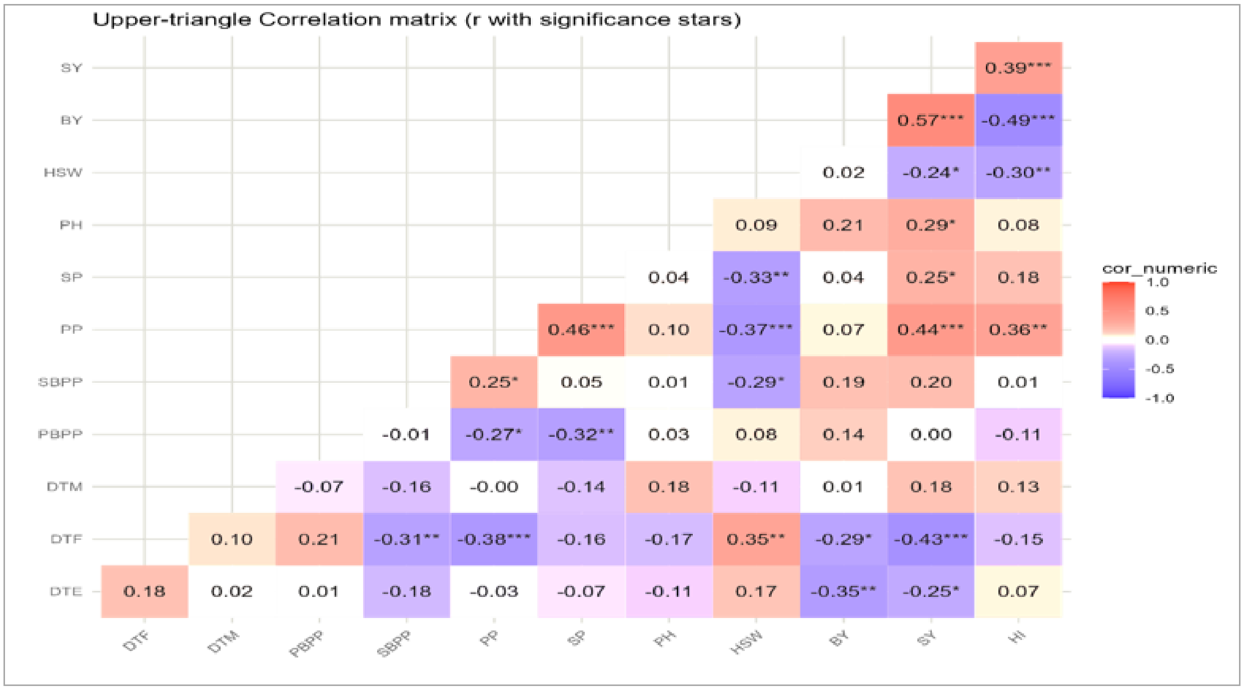

Fig. 3: Pearson's correlation heatmap showing interrelationships among morphological, yield and yield-related traits in chickpea genotypes

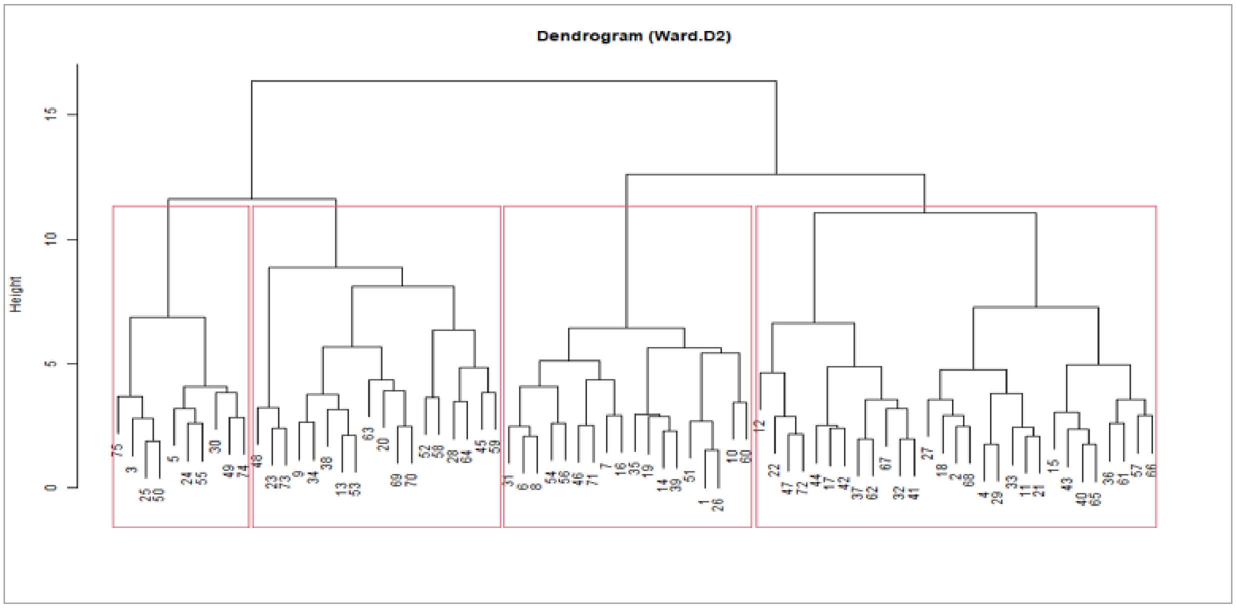

Fig. 4: Dendrogram showing genetic diversity among chickpea genotypes based on Ward's method (Ward.2)

4. DISCUSSION

In a semi-arid ecosystem, significant genetic variability was found to exist among chickpea genotypes regarding phenological, morphological, as well as yield parameters. This type of variability is necessary in the advancement of breeding, especially under water-deficit regions where variation in the manifestation of key traits related to yield can be extensive. A great amount of variability was recorded for all the parameters tested. This denotes that the diversity of these genetically varying factors among the tested material was adequate to undergo successful development. Confirmation from other researchers conducted on chickpeas was provided by reports from Ali et al. (2020), Singh et al. (2020), and Akhtar et al. (2022) about such variability.

The genetic nature of chickpea species in a semi-arid condition is revealed by the extent of GCV and PCV expressed for yield and the contributing factors. The existence of environmental effect is ascertained by the magnitude of PCV being greater than GCV for all the factors; however, the high correlation coefficient among the factors for pods per plant, seeds per pod, and yield of seeds indicates the genetic potential is well determined by the quasi-susceptibility and, in drought areas, the genetic differences can often be clouded by the variability of the environment.

Their suitability for use as criteria for selection can also be argued by the high heritability associated with high genetic progress for the traits. In breeding, the traits are suitable for selection by providing high yields and stress tolerance when used to develop chickpea cultivars. The results' clarity can also be supported by the fact that there have been similar explanations regarding the association of GCV-PCV regarding stress in chickpeas and other grain legumes. Most importantly, rather than basing decisions solely on genotype rank, there is now a comprehensive framework for selection based on GCV, PCV, Correlation, and PCA. The elimination of a major drawback that might often be associated with testing in single environments enhances the application of this character interpretation outside the experimental environment.

The early emergence, blooming, and maturity of the genotypes showed continuous and uniform patterns, indicating that these traits have been genetically controlled and are very important for adaptation to xeric environment conditions. Due to the fact that the semi-arid environment characterizes Karak, early phenology is especially advantageous for avoiding terminal dryness, mitigating heat stress during flowering, and utilizing residual soil moisture more effectively. In this regard, the negative relationships that seed yield manifested with days to bloom and emergence offer further corroboration of the adaptive significance of early maturity. Early-flowering genotypes probably initiate reproductive phases under better moisture conditions, which could be responsible for better pod set and grain filling.

Among the studied features, branching features, pods per plant, and seeds per pod showed the highest genetic advancement and variability, indicating their prime role in yield production. Pods per plant and secondary branches per plant were highly heritable features, showing additive gene action, and thus proving to be reliable indices of selection. High positive association of branching with number of pods per plant agreed with the fact that branch number increases the number of reproductive sites. This relation is supported by previous literature where branching is often correlated with a higher yield potential and reproductive capacity by Khan et al., 2021 and Singh et al., 2021.

The high heritability and genetic advance displayed by seed yield and biological yield indicate that the traits are genetically controlled and not as affected by environmental alterations as might have been expected. Genotypes with higher biomass production most likely maintained stronger source-sink dynamics, allowing more assimilates to be concentrated on pod and seed development. It is known that under drought-stressed conditions, this type of efficient partitioning increases seed production (Varshney et al., 2021). The positive correlation between seed yield and biological yield further supports the idea that those genotypes capable of accumulating more biomass are better positioned to convert environmental resources into grain, especially under moisture limitations.

PCA and cluster analysis validated the genetic difference between genotypes and demonstrated the importance of branching, seed size, and pod-related traits while describing variability. Similarly, the wide dispersion of genotypes across PCA quadrants supports a variety of adaption processes, considering that some of the genotypes possess unique trait combinations that are advantageous in semi-arid zones. Cluster analysis revealed opportunities to exploit heterosis by selecting parent genotypes from divergent clusters and provided further detail on genetic relationships. In fact, similar strategies have been presented in order to increase production increases and widen the genetic base in chickpea breeding studies.

The fact that genotypes D-3113, D-1113, and D-1211 outperformed others for most of the large variability of the characteristics measured indicates that these genotypes possess an optimum combination of earliness, vigor of branches, density of pods, weight of seeds, and biomass partitioning that meets the requirements of adaptability for growth in arid conditions and plant improvement programs on a high degree of inherent adaptability. Such genotypes are highly useful in water-scarce environments where productivity is contingent on drought escape, effective partitioning, and reproductive resilience.

Overall, the present study provides evidence that early phenology, robust branching ability, high pod number and large seed weight are the most effective choices to improve the yield of chickpea under semi-arid conditions. Those traits are heritable, genotypically sound, and strongly related to drought adaption tactics. Along with making some conceptual advances in knowledge of trait interactions within stressful situations, results provide verified targets for breeders aiming at developing superior yielding and climate-resilient chickpea cultivars.

5. CONCLUSION

The traits having maximum significance for seed production under semi-arid conditions were early phenology, high branching, more pods, and heavier seeds. High genetic variability was observed among the tested chickpea genotypes for all traits. The effectiveness of GCV and PCV, as well as their utility as better markers for selection of chickpea genotypes for adaptation under water limitations, was established by traits such as secondary branches per plant, pods per plant, seeds per pod, and seed yield, which had high genotypic CoV, heritability, and gain. The utility of genotypes D-3113, D-1113, and D-1211 as superior breeding material was emphasized because of their continuous performance of desirable trait combination, as well as their constancy. In semi-arid conditions, efficiency of selection can be enhanced, and gain from selection can be ushered in by adopting joint selection based on GCV & PCV, along with phenology and yield. Further research work can emphasize selection of genotypes across different environments, adopting molecular markers, which can add more strength to selection & adaptation practices.

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