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# GENETIC VARIABILITY AND PHENOTYPIC TRAIT ASSOCIATIONS IN CHICKPEA(*CICER ARIETINUM L.*)GENOTYPES AT SEEDLING STAGE

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***Abstract*** *This study evaluated Genetic variability, heritability and genetic advance in the early development of chickpea. Twenty-five chickpea genotype were utilized in a Completely Randomized Design (CRD) with three replications at The University of the Punjab, Lahore. Morphological data were collected for seven traits length of seedling(SL), Length of root(RL), Root-and-Shoot-ratio(RTSR), Biomass of seedling(SB), Length of leaf(LL), width of Leaf(LW) and Area of leaf(LA) at early stage and analyzed. The Combined analysis of variance (ANOVA) revealed a significant difference is high highly ($P \leq 0.01$) in all genotypes for all examined traits, underscoring substantial genetic variability within the current chickpea genotypes. Notably, traits such as Leaf-Area, Root-length, Leaf-length, and Leaf-width exhibited elevated heritability and GA, indicating feasibility based on phenotype selection to enhance these traits. This insight provides valuable information for the targeted improvement of chickpea varieties through selective breeding based on these specific phenotypical characteristics.*

**Keywords:** *Genetic Variance; Chickpea; Heritability; Genetic advance; genotypic*

## Introduction

Around the world, chickpeas (*Cicer arietinum L.*) are a significant pulse crop that are cultivated and eaten, particularly in Afro-Asian nations (Jukanti et al., 2012). The most significant grain legume crop in Pakistan is the chickpea, a significant source of vegetable protein for daily consumption(Ali and Malik, 2021; Ali et al., 2010b; Atta et al., 2008). It notably enhances nutrition by complementing cereal-based diets. Chickpeas are renowned for restoring soil fertility by fixing nitrogen, thereby contributing to productive and sustainable agricultural systems (Ahmed et al., 2017). In Pakistan, chickpea output is poor and unstable, which may be linked to the evolution of cultivars with a narrow genetic base. As a highly self-pollinated crop, it had limited variation. This use of limited and closely related germplasm lines in crop improvement initiatives has led to the evolution of cultivars with narrow genetic bases, making them susceptible to biotic stresses (Aaliya et al., 2016; Ahmad et al., 2012; Ahmad et al., 2021; Chauhan et al., 2023; Malik et al., 2010). Any breeding program aimed at increasing agricultural yields must include the presence of genetic variance (Ali et al., 2017; Ali et al., 2015; Qureshi et al., 2004). Therefore, a study of genetic variation using appropriate criteria such as genetic coefficient of variation, heritability estimates, and genetic progress is critically important to begin efficient chickpea breeding (Ali et al., 2013; Ali et al., 2016; Ali et al., 2010a; Gul et al., 2013). Correlation research gives information on the correlated response of major plant features, resulting in a directional model for yield response (Ali et al., 2011; Ali et al., 2014; Usman Saeed et al., 2012). The sole objective of this study is to investigate the association between different quantitative parameters in chickpea genetic resources through genotypic variability, correlations, and path coefficient, aiming to develop effective selection criteria for high-yielding chickpea varieties and lines.

## Materials & methods

The pot experiment was laid out during Rabi-2023 at glass house, Faculty of Agriculture, Punjab University Lahore, utilizing a Complete Randomized Design (CRD) to limit possible variability. A Total of twenty-Five genotypes of Chickpea (including some advanced lines+ old + new cultivars), namely 18FCK46, 18FCK47, 18FCK48, 18FCK49, 18FCK50, 18FCK51, 18FCK52, 18FCK53, 18FCK54, 18FCK55, 18FCK56, C44, Paidar-91, Punjab-91, bittal-98, Balkassar-2000, CM-2008, Tamman, Thal 2020, Bittal-2021, Bittal-2022, Pb-Noor-2009, Noor-2013, Noor2019, Noor2022) were selected for the plant material based on their diverse genetic origins collected from different research institutes of the Punjab province. Standards pots filled with sand were used in each experimental unit, and seeds were sown at various spaces and a constant depth. For every genotype, almost 100% germination rate were recorded. The pots had the same growth circumstances throughout the experiment, including regular fertilizer delivery, watering, and ambient variables. Important characteristics like seedling length, root-length, root/shoot ratio, leaf length, seedling biomass, leaf breadth, and leaf area were calculated during the seedling stage of data collection. Statistical approaches were applied to evaluate genotype variations. The outcomes were then analyzed to make interpretations of genetic variability and trait associations between genotypes. CRD has been employed to compute the analysis of variance (ANOVA) for each variable. The study used Fisher's analysis of variance and a Tukey test at a 1% significance level to compare treatment means (Steel and Torrie, 1980). Heritability is calculated as suggested by(Burton and Devane, 1953). The genetic advance was evaluated according to the formula given by (Johnson et al., 1955). Path analysis was carried out according to the method given by (Dewey and Lu, 1959).

## Results and discussions

### Analysis of variance

Descriptive statistics were used to examine the phenotypic characteristics of the chickpea varieties. The following parameters were assessed: shoot length, root length, seedling biomass, RS ratio, leaf length, leaf breadth, and leaf area**.** The analysis of variance shows that each parameter showed significant results($p<0.01$) concerning genotypes, suggesting that genotypes had higher genetic variance for all these parameters. Several scholars that employed germplasm for their investigations have already identified genetic diversity in chickpea for several features(Ali et al., 2010a; Asif et al., 2020; Atta et al., 2008; Bhanu et al., 2017; Choudhary et al., 2023; Gul et al., 2013; Karthikeyan et al., 2022; Saki et al., 2009; Zali et al., 2011) Such High genetic variation is crucial for plant breeding programs, providing potential traits for targeted selection (Talekar et al., 2017). Glasshouse-controlled environment coupled with a Completely Randomized Design ensures reliability of findings.

### Phenotypic and genotypic coefficient of variation

The PCV and GCV values have been classified as high (>20%), medium (10-20%), or low (10%) (Burton and Devane, 1953**)**. In this study, the character Leaf-Area (19.095, 19.368) showed high GCV & PCV values, respectively, among all traits, followed by Root-length(11.400, 11.838), leaf-width(10.783, 11.597) and Leaf length(10.328, 10.629). All these characters were in the moderate range(less than 20). Furthermore, Low GCV and PCV were noted for Seedling-length(4.997, 5.037), Seedling-Biomass (7.179, 7.515), and R-S-ratio(8.994, 9.826), respectively. The phenotypic coefficient of variation is slightly higher than the genotypic- coefficient of variation across all characteristics. This suggests that the parameters were partly influenced by environmental factors rather than genetic diversity among individuals (Karthikeyan et al., 2022). This suggests a degree of trait plasticity, where traits can be influenced more than genetic diversity. Also, the minimal differences between GCV and PCV values for all characters inferred limited environmental impact. However, significant variability was observed, indicating that genetic factors influenced the observed traits more than environmental factors (Balqees et al., 2020; Chauhan et al., 2023; Ghafoor et al., 2020; Iqbal et al., 2021). The findings demonstrate that a phenotypic-based selection approach may effectively improve chickpea. However, the low Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation values suggest that this approach may not be strongly influenced by observable characteristics or have restricted genetic diversity and, therefore the forward selection process is ineffective for improving characteristics related to Seedling-length, Seedling—biomass & RS-ratio. This insight into GCV and PCV is crucial for breeders and researchers, guiding effective breeding strategies and crop management practices.

### Heritability and genetic advance percentage

Heritability is a crucial metric for assessing the transmission of traits from parents to offspring. It quantifies the contribution of genotypes to overall variation and establishes the relationship between genotypic and phenotypic variance. High heritability estimates indicate strong genetic influence, making selection based on observable traits effective. Lower heritability suggests environmental factors, necessitating progeny testing. Heritability values fall into three categories: low (less than 10%), moderate (30–60%), &high (>60%) according to (Robinson et al., 1949). In the present research, heritability values ranged from 83.784% to 98.426%. All the studied traits showed high heritability(>60), indicating that high heritability in phenotypic traits indicates significant genetic factors contributing to observed variation within a population. A close heritability value indicates substantial genetic differences among individuals. However, it doesn't negate environmental influences but emphasizes the role of genetics in shaping observed phenotype differences. Genetic advance percentage measures expected improvement in a trait through selective breeding. Higher percentages indicate greater potential for improvement. Heritability is preferred as traits with higher heritability are more likely to be passed on to future generations. Focusing on traits with substantial genetic advance and high heritability is strategic for indirectly enhancing and sustaining the targeted trait through selective breeding practices. genetic advance is categorized into Low (< 10), Med.(10-20) and High (>20) according to (Iqra et al., 2020a; Iqra et al., 2020b; Johnson et al., 1955; Naseem et al., 2020; Naveed et al., 2012). In this investigation, genetic advance ranged 10.213% to 38.783%. The highest genetic advance was noted for Leaf-Area(38.783), followed by root length (22.616), leaf length (20.672) and Leaf Width (20.653), while the trait Root-shoot ratio (16.959), Seedling-biomass (14.127) and Seedling length(10.213) exhibit lower Genetic advance percentage. Traits like Leaf Area (97.205, 38.783), Root length (92.743, 22.616), Leaf length (94.415, 20.672), And leaf width (86.452, 20.653)had higher heritability and genetic advance, which indicates that genetics significantly influence trait variation, making selection of superior individuals efficient. Thus, based on genetic makeup, Phonological selection can improve traits with minimal effort.

**Table 1: Genetic parameters for 7 phenotypic traits in 25 chickpea genotypes**

| Traits | M.S | G.M | C.V | G.V | P.V | E.V | G.C.V | P.C.V | E.C.V | $h^2_{bs}$% | G.A |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **SL** | 2.311 | 17.494 | 0.770 | 0.764 | 0.777 | 0.018 | 4.997 | 5.037 | 0.774 | 98.426 | 10.213 |
| **RL** | 3.913 | 9.827 | 3.910 | 1.255 | 1.353 | 0.147 | 11.400 | 11.838 | 3.906 | 92.743 | 22.616 |
| **RTSR** | 0.005 | 0.423 | 4.850 | 0.001 | 0.002 | 0.000 | 8.994 | 9.826 | 4.846 | 83.784 | 16.959 |
| **SB** | 0.019 | 1.078 | 2.720 | 0.006 | 0.007 | 0.001 | 7.179 | 7.515 | 2.722 | 91.256 | 14.127 |
| **LL** | 0.011 | 0.582 | 3.080 | 0.004 | 0.004 | 0.000 | 10.328 | 10.629 | 3.076 | 94.415 | 20.672 |
| **LW** | 0.006 | 0.392 | 5.250 | 0.002 | 0.002 | 0.000 | 10.783 | 11.597 | 5.228 | 86.452 | 20.653 |
| **LA** | 0.123 | 1.055 | 3.960 | 0.041 | 0.042 | 0.002 | 19.095 | 19.368 | 3.966 | 97.205 | 38.783 |

M.S= mean square, G.M =Grand mean, C.V = Coefficient of variation, G.V = Genotypic variance, P.V = Phenotypic variance, E.V = Environmental variance, G.C.V: Genotypic-Coefficient of Variation, P.C.V: Phenotypic-Coefficient of Variation, $h^2$: broad sense heritability, G.A = Genetic Advance%

### Correlation

The correlation among traits is crucial for successful breeding programs in plant breeding and genetics. It involves the association between traits like yield, disease resistance, and nutritional content. Understanding these relationships helps breeders make informed decisions during the selection process. Positive correlations enable the co-occurrence of desirable traits, while negative correlations guide trade-offs. This knowledge aids in designing efficient breeding strategies for high-yielding, resilient, and nutritionally rich plant varieties. In the current study, Seedling length had shown a positive and strong correlation (P less than 0.01) With LL (0.6333), SB (0.5972), LW (0.5525) and LA (0.4348), indicating that an increase in SL will also increase LL, SB, LW and LA respectively. Similarly, Root length also had a positive and highly significant association with SB (0.6971), LL(0.6798) and LW(0.5312), LL is also positively and strongly correlated with LW(0.8159). SB(0.2078) and LL(0.3301) showed positive and weak correlations with RTSR, which indicates that with an increase in RTSR, the corresponding traits will also increase. Still, in terms of association, there will be a weak association between them.

**Table 2. Correlation coefficient analysis**

| Traits | SL | RL | RTSR | SB | LL | LW |
|---|---|---|---|---|---|---|
| **RL** | 0.7382* | | | | | |
| **RTSR** | 0.3782* | 0.1796 | | | | |
| **SB** | 0.5972** | 0.6971** | 0.2078 | | | |
| **LL** | 0.6333** | 0.6798** | 0.3301 | 0.5365** | | |
| **LW** | 0.5525** | 0.5312** | 0.422** | 0.4603** | 0.8159** | |
| **LA** | 0.4348** | 0.4954* | 0.1944 | 0.3172* | 0.8502** | 0.7779* |

*=Significant( P< 0.05), **= highly significant (P < 0.01)

### Path coefficient analysis

Path analysis measures the direct influence of variables, separating correlation coefficients into direct and indirect effects and providing information on character contribution for plant population yield improvement(Kumar et al., 2018; Naveed et al., 2012; Qurban and Muhammad, 2011; Waseem et al., 2014). The result of Path analysis (Table 3) showed that high positive direct effect was observed on seedling length by R-S ratio(3.729) and leaf-length (3.244). On the other hand, leaf-area(-0.648) shows slightly negative direct effect. While root length (2.206), leaf width (2.647) and leaf area(2.758) show indirect positive effects through leaf length. Similarly, all the traits show slightest indirect negative effect through leaf area.

**Table:3 Path Analysis**

| Traits | root length | S-R ratio | seedling biomass | leaf length | leaf width | leaf area |
|---|---|---|---|---|---|---|
| **root length** | **0.388** | 0.670 | 0.587 | 2.206 | 0.926 | -0.321 |
| **S-R ratio** | 0.070 | **3.729** | 0.175 | 1.071 | 0.736 | -0.126 |
| **seedling biomass** | 0.270 | 0.081 | **0.842** | 1.741 | 0.802 | -0.206 |
| **leaf length** | 0.263 | 1.231 | 0.452 | **3.244** | 1.422 | -0.551 |
| **leaf width** | 0.206 | 1.574 | 0.388 | 2.647 | **1.743** | -0.504 |

| | | | | | | |
|---|---|---|---|---|---|---|
| **leaf area** | 0.192 | 0.725 | 0.267 | 2.758 | 1.356 | **-0.648** |

## Conclusion

Based on Experimental results, it is concluded that Direct selection is feasible for most yield-attributing traits due to wide range of genetic variation. Traits like; Root-length, Leaf- length, and Seedling-biomass strongly correlated with seedling-length. Leaf length and Root-shoot-ratio had a high positive direct effect on SL. Leaf-Area, Root-length, Leaf-length and leaf width showed high heritability coupled with high genetic advance. These traits may be influenced by additive-gene action.

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## Declaration

**Conflict of interest**

There is no conflict of interest among the authors.

**Data Availability statement**

All authenticated data have been included in the manuscript.

**Ethics approval and consent to participate**

These aspects are not applicable in this paper.

**Consent for publication**

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