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PHENOTYPIC PROFILING OF CHICKPEA (CICER ARIETINUM L.) VARIETIES FOR MORPHOLOGICAL TRAITS

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**Abstract** Chickpeas are legume crops cultivated and eaten, particularly in Asian nations. This is an excellent source of protein and carbs, with the protein quality considered superior to that of other pulses. The current study aimed to examine the genetic progress of different parameters at the seedling stage by analyzing their phenotypic attributes. During the 2022–2023 growing season, a Randomized complete block design (RCBD) experiment was set up in the University of the Punjab's agricultural area. Five different genotypes were used in the experiment. At the seedling stage, data on seven morphological criteria were collected. A combined variance (ANOVA) and correlation analysis was carried out using statistical tools. The PCV and GCV for leaf-width, root length, root-shoot ratio have shown little variation, indicating that these parameters were because of genetic factors with less influence of outer-factors (environment). Root-shoot ratio has shown a significant correlation for root length. Similarly leaf area has shown a strong correlation with leaf width. The parameters, Root length, leaf width and root-shoot ratio have shown high heritability, which signifies the ease of selection based on phenotypic appearance.

**Keywords:** chickpea; heritability; genetic advance; phenotypic variation

### Introduction

Chickpea is the second most widely grown crop worldwide (Varshney et al., 2013). Chickpea is grown large and has significant value as a food-feed-fodder (Soltani et al., 1999). It is inexpensive source of protein-meals. Several factors, including climate, soil conditions, and agronomic practices, influence chickpeas productivity. These hardy legumes are a rich source of protein and contain essential nutrients such as fiber, vitamins, and minerals. Chickpeas play a crucial role in sustainable agriculture because they can fix nitrogen in the soil, enhancing soil fertility and reducing the need for synthetic fertilizers. Additionally, efforts target improving nutritional content, meeting market preferences, and incorporating traits for efficient crop management practices. Thus, Chickpea breeding plays a pivotal role in creating resilient, high-performing varieties that contribute to food security and worldwide agricultural sustainability. Two distinguishable varieties of cultivated chickpeas exist Desi and Kabuli. Desi types, characterized by pink flowers, anthocyanin coloration on stems, and seeds with a colored and thick coat, belong to the macrosperma category. In contrast, Kabuli types, classified as macrosperma, exhibit white flowers, the absence of anthocyanin coloration on stems, and have white seeds possess a ram's head shape, a thin seed coat, and

a smooth seed surface (Jukanti et al., 2012). Chickpea originated from the Old World and is primarily cultivated in Central and West Asia, South Europe, Ethiopia, and North Africa (Ali, Ahsan, et al., 2010; Ladizinsky & Adler, 1976). To date, studies primarily focus on enhancing production through improving cultivar genetic potential and mitigating the impact of diseases, insects, drought, and cold. Methods for selecting resistance to pests and desirable agronomic traits have been devised to achieve these goals (Singh 1997). The primary obstacles to achieving higher chickpea yields include limited genetic diversity in cultivated varieties, biotic challenges like pod borer, Fusarium wilt, and Ascochyta blight, along with abiotic factors such as drought, heat, cold, and salinity (Ali et al., 2011; Ali et al., 2014; Ali & Malik, 2021; Aswathi et al., 2019). To improve various traits and generate high-yielding varieties, it is essential to understand the genetics of the yield and related traits (Ali, Ahsan, et al., 2010; Ali, Muhammad, et al., 2010). Genetic variability is crucial for improvement, allowing plant breeders to select high-yielding genotypes. The current study aimed to gather insights into the genetic variability of seedling characteristics in chickpea to establish seedling selection criteria for future breeding programs.

### Materials and Methods

This trail was laid out in the research area of the Faculty of Agriculture Sciences of Punjab University, Lahore, using a Randomized-Complete-Block-Design (RCBD) to check phenotypic variation in chickpea genotypes. Three replications of each of the five genotypes were conducted, arranged in different blocks, to reduce variability and take potential spatial effects into account. Five chickpea genotypes, Tamman, Thal 2020, C44, Paidaar-91 and TG Striker, were utilized in the Ayub Agricultural Research Institute, Faisalabad experiment. Each block's planting was done randomly, and the experiment included careful data collecting at prearranged intervals along with routine fertilization and irrigation. After 10 days of 100 percent germination, the data was noted for 7 morphological traits viz. Seedling length (cm), Root-Length (cm), Root and Shoot ratio, Leaf-length (cm), Leaf-width, Leaf-Area (cm<sup>2</sup>) and seedling biomass at an early stage. Data of given parameters was analyzed through Statistics analysis software. Data on phenotypic traits was observed using Fisher's analysis of variance (Steels, 1997). The correlation and pathway analysis were evaluated to check how diverse parameters are effecting each other (Kashiani et al., 2012). Phenotypic variances ( $\sigma^2p$ ) And genotypic variance ( $\sigma^2g$ ) were evaluated through a combined ANOVA table (Comstock & Robinson, 1952). The GCV, PCV and ECV were taken through mean values, as described by (Singh et al., 1985).

**Results and discussions**

Combined analysis of variance (ANOVA) of seedling-length, root-length, root and shoot ratio, seedling-biomass, leaf-length, leaf-width and leaf-area was performed (Table 1). ANOVA shows that the seedling length, seedling biomass, root-shoot ratio and leaf length have significant results for genotypes. It shows that high variation was found in genotypes for these parameters. As genetic variability presence secured, the breeders have to isolate the heritable portion for non-heritable to improve specific traits containing high heritability (Ali et al., 2013; Ali et al., 2016; Ali, Ahsan, et al., 2010; Workie & Debella, 2018). Parameters like leaf area and leaf width have shown non-significant results. It shows that no variation was found in these parameters. Genotypic and phenotypic variance of all parameters were calculated. The root length parameter (0.1575) showed the highest genotypic variance. Meanwhile,

the root length also showed the highest phenotypic variance (0.1624). The parameter leaf area showed the lowest genotypic value and the phenotypic value. The highest value for the genotypic coefficient of variance (GCV) was observed in seedling Biomass (7.606), and the highest value of the phenotypic coefficient of variance (PCV) was observed in the leaf area. PCV and GCV are classified into three categories:>20 as high, 10-20% as moderate and 0-10% as low (Deshmukh et al., 1986). The values of the genotypic coefficient of variance ranged from 0.8118 (seedling length) to 7.606 (seedling biomass). The phenotypic coefficient of variance ranged from 1.04596 (seedling length) to 11.28203 (leaf area). GCV value indicates the true genetic potential of genotypes. The current experiment showed higher values of PCV than that of GCV, proving the existence of environmental variation.

Broad sense heritability and genetic advance were estimated for all seven parameters. Estimation of heritability is categorized into three levels: high (30-60%), medium (10-30%) and low (5-10%) (Dabholkar, 1994). The traits seedling length, leaf length, leaf width, root length, root shoot ratio and seedling biomass have shown a high heritability. The parameter leaf area has shown medium heritability (Asif et al., 2020; Balgees et al., 2020; Farooq et al., 2021; Ghaffoor et al., 2020; Iqbal et al., 2021; Kumar et al., 2013) and has already reported high heritability and genetic advance for the parameters including seedling biomass, root and seedling length. The heritability estimate of characters' leaf width, root length, and root shoot ratio was above 85%. The results indicated that parameters seedling length, leaf area, leaf length, root shoot ratio and seedling biomass have low Genetic advance percentage. The parameters leaf width and seedling biomass have a moderate genetic advance percentage. Genetic advance as a percentage of the mean (GA) has been classified into 0-10% as low, 10-20% as moderate, and >20 as high. The high value of genetic advance and heritability indicates that genetic gain would be high for selection in these traits if utilized for further breeding. The traits with high genetic advance and heritability could result in better selection variation in these traits because of additive gene action (Laraib Iqra et al., 2020; L. Iqra et al., 2020; Johnson et al., 1955; Mazhar et al., 2020)

**Table 1. Genetic components for various traits of chickpea**

| Traits | MS      | GM    | CV     | GV     | GCV%   | PV     | PCV%    | EV      | ECV%   | h <sup>2</sup> <sub>bs</sub> % | GA      |
|--------|---------|-------|--------|--------|--------|--------|---------|---------|--------|--------------------------------|---------|
| SL     | 0.0806* | 17.5  | 0.807  | 0.0202 | 0.8118 | 0.0335 | 1.04596 | 0.0199  | 0.8077 | 60.2426                        | 1.1185  |
| LA     | 0.0006* | 0.159 | 11.374 | 0.0001 | 6.4031 | 0.0003 | 11.2803 | 0.00033 | 11.374 | 32.2211                        | 6.4515  |
| LL     | 0.0017* | 0.588 | 3.0423 | 0.0005 | 3.621  | 0.0007 | 4.39114 | 0.00032 | 3.0423 | 68                             | 5.3001  |
| LW     | 0.0015* | 0.39  | 1.1694 | 0.0005 | 5.732  | 0.0005 | 5.81096 | 0.00002 | 1.1694 | 97.3001                        | 10.036  |
| RL     | 0.4799* | 10.3  | 0.8287 | 0.1575 | 3.8524 | 0.1624 | 3.91137 | 0.0073  | 0.8287 | 97.0074                        | 6.735   |
| RSR    | 0.0019* | 0.589 | 1.4212 | 0.0006 | 4.1724 | 0.0007 | 4.33075 | 0.0001  | 1.4212 | 92.8205                        | 7.1352  |
| SB     | 0.0197* | 0.934 | 7.2458 | 0.005  | 7.606  | 0.0081 | 9.63597 | 0.0046  | 7.2458 | 62.3045                        | 10.6565 |

Where \* is p value < 0.05, \*\* is p value < 0.01, SL = seedling length, RL = root length, RS ratio = root shoot ratio, SB = seedling biomass, LL = leaf length, LW is leaf width

Correlation is an important term plant breeders use to check whether two morphological or physiological parameters have positive or negative effects on each other. Correlation analysis can be utilized to check the significance level of two traits. Correlation was performed for each parameter (Table 2). Root length and leaf width have shown a strong and highly significant correlation with RS ratio and leaf area, respectively. RS ratio increases with an increase in

root length, and leaf area will increase with an increase in leaf width. Leaf area has a significant positive correlation with leaf length. The area will increase with an increase in leaf length. Seedling Biomass has shown a negative significant correlation with seedling length. Seedling length will be negatively affected by seedling biomass (Iqbal et al., 2021; L. Iqra et al., 2020; Naveed et al., 2012; Qurban & Muhammad, 2011; Waseem et al., 2014).

**Table 2. Correlation among different traits of chickpea**

| Traits | SL       | RL       | RSR     | SB      | LL      | LW       |
|--------|----------|----------|---------|---------|---------|----------|
| RL     | -0.0697  |          |         |         |         |          |
| RSR    | -0.327   | 0.9625** |         |         |         |          |
| SB     | -0.6378* | 0.2329   | 0.3914  |         |         |          |
| LL     | -0.0573  | -0.2008  | -0.1825 | -0.1781 |         |          |
| LW     | 0.1424   | 0.1339   | 0.0726  | 0.1288  | 0.2884  |          |
| LA     | 0.0954   | 0.0227   | -0.0197 | 0.0275  | 0.6355* | 0.9223** |

Where \* is p value < 0.05, \*\* is p value < 0.01, SL = seedling length, RL = root length, RS ratio = root shoot ratio, SB = seedling biomass, LL = leaf length, LW = leaf width

Path analysis shows how different traits/parameters are correlated with the yield. Correlation and regression analysis were performed in path analysis to check the direct and indirect effects of different traits. Pathway analysis for all seven parameters was performed (Table 3). Results showed that RL, LL, and LW directly affect seedling length. The RS ratio, seedling biomass, and leaf area have a highly negative

direct effect on seedling length. RS ratio has a positive indirect effect on seedling length through root length. Leaf area has a positive indirect effect on seedling length through leaf width. Leaf length and Leaf width have a negative indirect effect on Seedling Length through Leaf Area (Laraib Iqra et al., 2020; Mazhar et al., 2020; Mustafa et al., 2018; Naseem et al., 2020; Naveed et al., 2012).

**Table 3. Path analysis for different traits of chickpea**

| Traits           | root length | S-R ratio | Seedling biomass | leaf length | leaf width | leaf area |
|------------------|-------------|-----------|------------------|-------------|------------|-----------|
| root length      | 1.663       | -2.03     | -0.007           | -0.308      | 0.302      | -0.131    |
| S-R ratio        | 1.597       | -2.113    | -0.012           | -0.268      | 0.186      | 0.053     |
| seedling biomass | 0.387       | 0.656     | -0.031           | -0.273      | 0.29       | -0.158    |
| leaf length      | -0.334      | 0.369     | 0.005            | 1.532       | 0.65       | -3.653    |
| leaf width       | 0.223       | -0.174    | -0.004           | 0.442       | 2.254      | -5.301    |
| leaf area        | 0.038       | 0.019     | -0.001           | 0.974       | 2.079      | -5.748    |

**Conclusion**

This trail depicted high values of heritability for all parameters. As the parameters show higher heritability, hybrid genotypes may be evaluated through selection, and genetic advance can lead toward the development of synthetic variety. A highly significant correlation of root length with RS ratio and leaf width with leaf area, and a higher direct effect of leaf width toward seedling length in the pathway can be effective for selecting yield-attributing traits.

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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.

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Not applicable

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