Original Research Article



CHICKPEA SEEDLING TRAIT GENETIC VARIATION AND HERITABILITY ESTIMATES: CONSEQUENCES FOR BREEDING PROGRAMS

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Abstract Among other names, Bengal gram, Channa, or garbanzo bean is a pulse crop essential for providing healthful food to the world's expanding population. With a growing global population, chickpeas are a valuable crop that will only grow in importance due to climate change. They also provide wholesome nourishment. Kabuli and desi are the two primary types. According to a study at the University of Punjab Lahore, chickpea seedlings have substantial genetic variants with high genetic components and broad-sense heritability of 95.97%. Root length demonstrated a substantial genotypic influence with a PCV of 6.62% and a higher GCV than SL. A considerable genotypic diversity was observed in the Root-to-Seedling Length Ratio, with a heritability value of 89.47% and genetic advance of 10.389%. There was no discernible genotypic variance in seedling biomass, Substantial genotypic differences were observed in leaf features, suggesting a high degree of genetic variability. The correlation matrix showed Numerous connections between the seven attributes in chickpea seedlings, indicating a possible physiological and genetic basis for the relationships. Breeding initiatives, breeding programs, and new kinds with enhanced traits can all benefit from these discoveries.

Keywords: *chickpea; pulse; genotypic variation; physiological; breeding programs*

Introduction

Sometimes referred to as the poor man's meat, grain legumes are an essential nutritional component of the diets of millions living in impoverished nations. Given that other foods they eat are low in protein, legumes play a major role in vegetarians' diets as they are essential sources of protein, calcium, iron, phosphorus, and other minerals (Merga & Haji, 2019). A versatile crop, legumes can be used in many agricultural systems as feed or directly consumed as food in various processed forms. The first pulse to be domesticated in the ancient world was the chickpea (Khamassi et al., 2012). It is primarily called garbanzo beans, channa, and Bengal gram (Parwada et al., 2022). Because of their function in fixing nitrogen, legume crops are frequently cultivated in rotation alongside cereals. Nevertheless, in emerging nations, the yields and production of legume crops have stagnated during the last few decades. Many of these countries have focused their agricultural research and development efforts on reducing crop losses and raising grain yields and production to achieve food security (Merga & Haji, 2019). Chickpeas are the most available and reasonably priced source of lipids (11.4%), ash (4.8%), sugars (57-60%), protein (19.5%), and moisture (4.9–15.59%) (Huisman & Van der Poel, 1994). Because it may be used for so many different purposes, chickpeas are preferred over

edible beans in some areas (Siddique et al., 2000). It is believed that the areas in present-day southeast Turkey and the neighboring Syrian lands are the origins of the cultivated chickpea (Ali, Ahsan, et al., 2010; Ali et al., 2011; Ali & Malik, 2021; Ali, Muhammad, et al., 2010; Keneni et al., 2013). The two most widely recognized types of chickpeas are Kabuli and Desi. Typically, the Desi cultivar features brightly colored seed coatings, geometric seed forms, and superior nutrients (Moreno & Cubero, 1978). The Kabuli cultivar is distinguished by its large seeds, beige or white hue, and "rams-head" shaped seed covers (Keneni et al., 2013). A good supplement to diets based on cereals, chickpea seed has a protein level of 21% (range: 17-26%). This is especially crucial in developing countries where people might not have access to animal protein or prefer a vegetarian diet (Aaliya et al., 2016; Ahmad et al., 2012; Ahmad et al., 2021; Flowers et al., 2010).

Method and Material

The current study was conducted in an experimental setting at the Department of Plant Breeding and Genetics, University of the Punjab Lahore. Five genotypes of chickpeas made up the main experimental material: line 161, line 1118, line 220, line 2009 and line 108. Each of these samples was gathered from the University of Agriculture in Faisalabad. In RCBD, three replications of each

genotype were used for this experiment. A variety of parameters are estimated, including the following: seedling length (SL), root length (RL), biomass of seedlings (SB), root-to-seedling length ratio (RSLR), leaf length (LL), leaf width (LW), and leaf area (LA). Table 1 displays the calculated and observed values. In PBG Lab-II at the Department of Plant Breeding and Genetics, biomass is assessed using a weighing scale. The necessary parameters for RSLR and LA are calculated: RL divided by SL, LL multiplied by LW, and factor 0.69 for both values.

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Genotype	SL	RL	RSLR	SB	LL	LW	LA
line 161	17.89a	10.38b	0.56b	1.02a	0.57a	0.4a	1.15a
line 1118	17.50ab	10.54ab	0.57b	1.02a	0.42c	0.31c	1.17a
line 220	17.12b	9.47c	0.61a	1.05a	0.57a	0.36b	1.05b
line 2009	16.47c	9.40c	0.56b	0.75c	0.46b	0.32c	1.08b
line 108	16.57c	10.83a	0.61a	0.96b	0.45b	0.33c	0.8c

Table 1 Average	genotype	performance	of studiedtraits
Table I Average	genotype	performance	or studicult and

SL stands for seedling length, LA for leaf area, LW for leaf width, RSLR for root-shoot length ratio, SB for seedling biomass, RL for root length, and LL for leaf length

Results and Discussion

In the chickpea seedling experiment, several morphological characteristics were measured, such as Seedling Length (SL), Root Length (RL), Root-to-Seedling Length Ratio (RSLR), Seedling Biomass (SB), Leaf Length (LL), Leaf Width (LW), and Leaf Area (LA) (Toker & Ilhan Cagirgan, 2004). As seen by the computed p-values in Table 2, the statistical analysis revealed significant variations across these features. Among the chickpea genotypes under investigation, Seedling Length (SL) showed a highly significant variance ($p=0.0040^{**}$). In contrast to the genotypic and environmental coefficients of variation, which were 3.53% and 0.72% respectively, the phenotypic coefficient of variation (PCV) was 3.60%. At 95.97%, SL's broad-sense heritability (H²) was remarkably high, suggesting a significant genetic component. There is room for genetic improvement in Seedling Length, as demonstrated by the genetic advance (GA) of 6.062% (Ali et al., 2017; Ali et al., 2015; Ali et al., 2013; Ali et al., 2016; Arshad et al., 2003). In comparison to SL, Root Length (RL) had a greater GCV (6.26%) and a PCV of 6.62%, indicating a significant genotypic effect (p $= 0.0067^{**}$). The heritability estimate of 89.47% for RL showed a substantial genetic contribution. It

appears that selection for longer roots may be successful because the genetic progress for RL was significantly greater, at 10.389%.There was a substantial analysis of variance ($p = 0.0043^{**}$) in the Root-to-Seedling Length Ratio (RSLR), with a significantly lower PCV of 4.64%. The root-to-shoot length ratio may benefit from genetic improvement, as evidenced by the heritability of 70.59% and the genetic advance of 5.749% for RSLR.With PCV, GCV, and ECV values of 4.64%, 3.90%, and 2.52%, respectively, Seedling Biomass (SB) did not show significant genotypic variation (p = 0.2924). SB had a moderate heritability of 70.59% and a 5.749% genetic progress.

With p-values of 0.0139*, 0.0033**, and 0.0040**, respectively, leaf parameters such as leaf length (LL), leaf width (LW), and leaf area (LA) showed significant genotypic differences. Moderate to high PCV (15.37%, 10.95% and 14.76%) and GCV (14.03%, 9.77%, and 13.80%) were found in LL, LW, and LA, demonstrating significant genetic variability. The genetic improvements demonstrate the potential for genetic improvement in leaf morphology for LL, LW, and LA, which were 22.467%, 15.319%, and 22.659%, respectively.

Traits	Analysis of Variation (P) value	Phenotypic Coefficient of variation (%)	Genotypic Coefficient of variation (%)	Environmental Coefficient of variance (%)	Broad Sense Heritability (%)	Genetic Advance (%)
Seedling Length (SL)	0.0040**	3.60%	3.53%	0.72%	95.97%	6.062%
Root Length (RL)	0.0067**	6.62%	6.26%	2.15%	89.47%	10.389%
Roottoshootlengthratio(RSLR)	0.0043**	4.64%	3.90%	2.52%	70.59%	5.749%
Seedling biomass (SB)	0.2924	12.69%	12.54%	1.97%	97.58%	21.741%
Leaf Length (LL)	0.0139*	15.37%	14.03%	6.28%	83.30%	22.467%
Leaf Width (LW)	0.0033**	10.95%	9.77%	4.93%	79.74%	15.319%
Leaf Area (LA)	0.0040**	14.76%	13.80%	5.22%	87.47%	22.659%

Table 2 Geneti	c factors of	different	chickpea	seedling features	5

The seven attributes' pairwise correlations are displayed in the correlation matrix. When two characteristics increase or decrease together, they have a positive correlation. A negative correlation indicates a tendency for the two qualities to move against each other. The size of the correlation coefficient, which ranges from -1 to 1, indicates the strength of the relationship (Ali et al., 2014; Asif et al., 2020; Balqees et al., 2020). Table 3 displays a correlation coefficient 0, which denotes no link between the two attributes.

Traits	LA	LL	LW	RL	RSLR	SB
LL	0.8583**					
LW	0.9025*	0.5930*				
RL	0.6211*	0.4036*	0.6091**			
RSLR	0.3315	0.1139	0.3755	0.8661**		
SB	-0.0291	0.0167	-0.1427	-0.1217	-0.0679	
SL	0.5656*	0.6176*	0.4259	0.2307	-0.2736	-0.1013

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Table 3	Pearson	correlation	hetween	distinct	features	over	many genotypes	
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SL stands for seedling length, LA for leaf area, LW for leaf width, RSLR for root-shoot length ratio, SB for seedling biomass, RL for root length, and LL for leaf length. * = > p value < 0.05, **=> is p value < 0.01)

Table 4 Regression analysis for shoot length of chickpea							
Variables	Coefficient	Std Error	Т	Р	VIF		
LA	-4.80312	9.97934	-0.48	0.6432	58.1		
LL	3.14581	3.06539	1.03	0.3348	15.0		
LW	1.11416	4.46759	0.25	0.8093	20.9		
RL	1.38261	0.15471	8.94	0.0000	8.6		
RSLR	-23.7697	2.16752	-10.97	0.0000	5.8		
SB	-0.02823	0.31737	-0.09	0.9313	1.2		

SL stands for seedling length, LA for leaf area, LW for leaf width, RSLR for root-shoot length ratio, SB for seedling biomass, RL for root length, and LL for leaf length

These associations demonstrate that the attributes underlying physiological genetic have and connections. For instance, the fact that cell division and expansion control both characteristics could account for the positive correlation between SL and LA. The possible explanation for the positive correlation between SB and LW is that both attributes are impacted by photosynthate accumulation (Faroog et al., 2021; Ghafoor et al., 2020; Iqbal et al., 2021). There can be a trade-off between root and shoot growth, which explains the negative correlation between RL and RSLR. The correlation data can inform chickpea breeding attempts. Breeders can choose seedlings with long stems and large leaves, for instance, by taking advantage of the favorable relationship between SL and LA. Additionally, breeders might choose seedlings with wide leaves and high biomass by exploiting the positive correlation between SB and LW. Breeders choosing desirable chickpea traits should carefully balance root and shoot growth, considering the negative correlation between RL and RSLR.

Regression Analysis

These associations demonstrate that the attributes underlying physiological and genetic have connections; for instance, for every unit change in the independent variable LA, the coefficient shows the estimated change in the dependent variable (Laraib Igra et al., 2020; L. Igra et al., 2020; Mustafa et al., 2018; Naseem et al., 2020; Naveed et al., 2012; Qurban & Muhammad, 2011; Waseem et al., 2014). The negative coefficient, in this instance, points to a bad association. The link is not statistically significant

at standard significance levels (e.g., 0.05), as indicated by the high p-value (0.6432). There may be problems with multicollinearity with other variables, as indicated by the high VIF (58.1). The positive coefficient indicates a positive correlation between LL and the dependent variable. This association is not statistically significant at conventional levels, as indicated by the p-value (0.3348). The relatively high (15.0) points to the possibility VIF of multicollinearity. The positive coefficient indicates a positive correlation between LW and the dependent variable. However, the p-value (0.8093) suggests no statistical significance in this link. VIF (20.9) indicates the possibility of crossovers. The positive coefficient indicates a positive correlation between RL and the dependent variable. The statistical significance of this link is indicated by the extremely low p-value (0.0000). In comparison, the VIF (8.6) is medium. The negative coefficient indicates a negative correlation between RSLR and the dependent variable. The statistical significance of this link is indicated by the extremely low p-value (0.0000). The VIF of 5.8 is deemed to be fair. The negative coefficient indicates a negative correlation between SB and the dependent variable. It is clear from the high p-value (0.9313) that there is no statistical significance in this association. Given the low VIF (1.2), there may not be much of the phenomenon.

Conclusion

In short, the dependent variable is statistically significantly predicted by RL and RSLR, but not by the other variables in this regression model (LA, LL, LW, and SB). Furthermore, as shown by the high VIF values of LA, LL, and LW, multicollinearity might be problematic. All variables showed significant genotypic variation but seedling biomass, indicating the possibility of future genetic advancement. Substantial heritability was shown for seedling length, root length, root-to-shoot length ratio, leaf length, leaf breadth, and leaf area, indicating strong genetic influence over these traits; there are notable relationships among a multitude of traits, highlighting potential trade-offs and synergistic relationships.

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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

Not applicable

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