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GENETIC VARIATION AND HERITABILITY ESTIMATES IN CHICKPEA SEEDLING TRAITS: IMPLICATIONS FOR BREEDING PROGRAMS

RASHEED MU*, MALIK A, ALI MS

Department of Plant Breeding and Genetics, Faculty of Agricultural Sciences, University of the Punjab, P.O BOX. 54590, Lahore, Pakistan
**Correspondence author email address: ur36402@gmail.com*

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Abstract *Chickpea, also known as Bengal gram, Channa, or garbanzo bean, is a vital pulse crop that offers wholesome food to the growing population. Originating from modern-day southeast Turkey and Syria, chickpea germplasm is abundant in Ethiopia, serving as a secondary centre of genetic diversity for various dietary legumes. Two main varieties are desi and Kabuli. A study at the University of Punjab Lahore found significant genetic variations in chickpea seedlings, with high genetic components and a broad-sense heritability of 87.04%. Root length showed a significant genotypic effect, with a PCV of 16.39% and a larger GCV than SL. The root-to-seedling length ratio showed a significant genotypic variance, with a heritability estimate of 69.98% and a genetic advance of 5.740%. Seedling biomass did not show significant genotypic variation. Leaf characteristics showed substantial genotypic differences, indicating extensive genetic heterogeneity. The correlation matrix showed substantial correlations between seven qualities in chickpea seedlings, suggesting genetic and physiological links between the qualities. These findings can inform breeding efforts, improve breeding programs, and generate new varieties with improved features.*

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Keywords: *Chickpea; root length, heritability; genetic advance; breeding program*

Introduction

Chickpea, (*Cicer arientum* L.) is the second most important pulse crop next to beans and other field pulses, which has great significance (Singh et al., 2021). It is mainly known as Bengal gram, Channa, and garbanzo bean in different areas of the world (Jukanti et al., 2012). Pulses are rich in sources of carbohydrates, proteins, sulfur-containing amino acids, dietary fibers, vitamins, minerals, and unsaturated fatty acids. Chick pea was the first pulse domesticated in the Old World (Khamassi et al., 2011). Being a valuable crop that feeds the world's dramatically increasing population with wholesome food, chickpeas will only grow in importance because of climate change and global warming. Recently, nutritionists working in the food and health sectors in several nations have emphasized the importance of chickpeas for both physical health and nutrition (Merga and Haji, 2019). The most affordable and accessible source of protein (19.5%), lipids (11.4%), sugars (57–60%), ash (4.8%), and moisture (4.9–15.59%) is chickpeas (Huisman and Van der Poel, 1994).

The centre of origin for the cultivated chickpea has been hypothesized to be the regions in modern-day southeast Turkey and the adjacent territories of Syria (Keneni et al., 2012). Ethiopia has a vast number of chickpea germplasm collections from various geographical locations, serving as the secondary centre of genetic diversity for numerous dietary legumes worldwide (Hagedorn, 1984; Mekibeb et al., 1991) and chickpeas in specific (Moreno and Cubero, 1978).

Two main varieties of chickpeas are known: desi and Kabuli. The desi variety typically has geometric seed shapes, colorful seed coatings, and nutrition (less than 200 mg of each seed) (Moreno and Cubero, 1978). The Kabuli variety is characterized by large seeds (more than 350 mg per seed), "rams-head" shaped seed coverings, and beige or white tints (Keneni et al., 2012). Although the two varieties can be combined, desi and Kabuli chickpea have significant consumer and culinary preferences. Chickpea seed, with a protein content of 21% (range: 17–26%), is a valuable addition to diets based on cereals. This is particularly important in developing nations where individuals may not have access to animal protein or may want to follow a vegetarian diet. (Flowers et al., 2010).

Material and Methods

The present research was conducted in the experimental field of the Department of Plant Breeding and Genetics, University of the Punjab Lahore. The main experimental material comprised 5 chickpea genotypes: line 117, variety AUG-27, line 820, line 114, and line Pb2000. These all samples were collected from the University of Agriculture, Faisalabad. This experiment was conducted in RCBD with 3 replications of each genotype. Estimation of different traits are Seedling Length (SL), Root Length (RL), Root-to-Seedling length ratio (RSLR), Seedling biomass (SB), Leaf Length (LL), Leaf width (LW), Leaf Area (LA). Observed and calculated values are shown in Table 1.

All measurements are precisely estimated after the germination of chickpea. SL, RL, LL, LW are measured by length measuring scale. Biomass is plant weight above and below the ground surface (Hendrix et al., 1991). Biomass is measured by weighing scale in PBG Lab-II at the Department of Plant Breeding and Genetics. Calculations of their required parameters measure RSLR and LA, the division of RL by SL and the multiplication of LL with LW and factor 0.69, respectively, for both values.

Table 1 Mean performance of genotypes for various characters

Genotype	SL	RL	RSLR	SB	LL	LW	LA
line 117	18.207	10.273	0.564	1.267	0.657	0.420	0.190
variety AUG-27	18.007	10.410	0.578	1.170	0.643	0.453	0.201
line 820	17.360	10.603	0.611	1.213	0.607	0.413	0.173
line 114	17.860	10.090	0.565	1.133	0.600	0.410	0.170
line Pb2000	18.293	11.233	0.614	1.140	0.663	0.460	0.211

Results and Discussions

The experimental inquiry on chickpea seedlings involved the assessment of numerous morphological parameters, including 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 and Ilhan Cagirgan, 2004). The statistical analysis indicated substantial variances among these features, as evidenced by the calculated p-values in Table 2.

Seedling Length (SL) demonstrated a highly significant variation across the investigated chickpea genotypes (p = 0.0003**). The phenotypic coefficient of variation (PCV) was 2.84%, whereas the genotypic coefficient of variation (GCV) and environmental coefficient of variance (ECV) were 2.00% and 0.77%, respectively. SL's broad-sense heritability (h^2) was strikingly high at 87.04%, indicating a substantial genetic component. The genetic advance (GA) was 3.281%, underlining the potential for genetic improvement in Seedling Length, as shown in (Arshad et al., 2002).

Root Length (RL) also revealed a significant genotypic effect (p = 0.0067**), with a PCV of 16.39% and a larger GCV (3.91%) compared to SL. The heritability estimate for RL was 69.98%, showing a high genetic contribution. The genetic advance for RL was substantially larger at 5.740%, suggesting the possibility of successful selection for enhanced root length.

The Root-to-Seedling Length Ratio (RSLR) revealed a significant genotypic variance (p = 0.0043**), with a considerably lower PCV of 0.91%. The heritability for RSLR was 70.59%, and the genetic advance was 5.749%, demonstrating the possibility for genetic improvement in the root-to-shoot length ratio. Seedling Biomass (SB) did not reveal significant genotypic variation (p = 0.2924), with PCV, GCV, and ECV values of 2.84%, 2.69%, and 6.67%, respectively. The heritability for SB was moderate at 14.00%, and the genetic advance was 1.768%. Leaf characteristics, including Leaf Length (LL), Leaf Width (LW), and Leaf Area (LA), displayed substantial genotypic differences with p-values of 0.0139*, 0.0033**, and 0.0040**, respectively. LL, LW, and LA revealed moderate to high PCV (1.11%, 0.86%, 0.64%) and GCV (4.19%, 5.18%,8.90%), indicating extensive genetic heterogeneity. The heritability estimates for LL, LW, and LA were 63.66%, 75.13%, and 77.25%, respectively, demonstrating a high genetic influence on these leaf attributes. The genetic improvements for LL, LW, and LA were 5.871%, 7.873%, and 13.725%, showing the possibility for genetic enhancement in leaf morphology.

Table 2 Genetic parameters for various seedling traits in chickpea

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)	0.0003**	2.84%	2.00%	0.77%	87.04%	3.281%

Root Length (RL)	0.0067**	16.39%	3.91%	2.56%	69.98%	5.740%
Root to shoot length ratio (RSLR)	0.0043**	0.91%	3.90%	2.52%	70.59%	5.749%
Seedling biomass (SB)	0.2924	2.84%	2.69%	6.67%	14.00%	1.768%
Leaf Length (LL)	0.0139*	1.11%	4.19%	3.17%	63.66%	5.871%
Leaf Width (LW)	0.0033**	0.86%	5.18%	2.98%	75.13%	7.873%
Leaf Area (LA)	0.0040**	0.64%	8.90%	4.83%	77.25%	13.725%

The correlation matrix illustrates the pairwise correlations between the seven qualities. A positive correlation means the two attributes tend to rise or diminish together (Ali et al., 2017; Ali et al., 2015; Ali et al., 2013; Ali et al., 2016). A negative correlation shows that the two features move in opposite directions. The strength of the link is indicated by the size of the correlation coefficient, which runs from -1 to 1. A correlation coefficient 0 implies no association between the two attributes shown in Table 3.

The correlation matrix demonstrates that there are multiple substantial correlations between the qualities. For example, seedling length (SL) and leaf area (LA) are positively connected (r = 0.6898), indicating that seedlings with longer stems tend to have larger leaves. Seedling biomass (SB) and leaf width (LW) are likewise strongly associated (r = 0.8020), indicating that seedlings with more biomass are likely to have wider leaves (Ali et al., 2014; Ali and Malik, 2021; Asif et al., 2020). Root length (RL) and root-to-shoot length ratio (RSLR) are inversely associated (r = -0.1833), indicating that seedlings with longer roots are likely to have lower RSLR values.

Table 3 Pearson Correlation among different traits in various genotype

Traits/P<0/05	SB	SL	LA	LL	LW	RL
SL **P<0.05**	-0.1013 0.7196					
LA **P<0.05**	-0.0291 0.9181	0.5656* 0.0280				
LL **P<0.05**	0.0167 0.9529	0.6176* 0.0142	0.8583** 0.0000			
LW **P<0.05**	-0.1427 0.6119	0.4259* 0.1134	0.9025** 0.0000	0.5930* 0.0198		
RL **P<0.05**	-0.1217 0.6657	0.2307 0.4082	0.6211* 0.0135	0.4036* 0.1358	0.6091* 0.0159	
RSLR **P<0.05**	-0.0679 0.8100	-0.2736 0.3238	0.3315* 0.2275	0.1139 0.6861	0.3755* 0.1678	0.8661** 0.0000

* = > p value < 0.05, **=> is p value < 0.01, SL=Seedling Length, LA=Leaf Area, LW= Leaf Width, RSLR=Root-shoot length ratio, SB=seedling biomass, RL=Root Length, LL=Leaf Length

Table 4 Regression Analysis

Variables	Coefficient	Std Error	T	P	VIF
LA	-66.9615	7.78676	-8.60	0.0000	687.0
LL	21.9389	2.68664	8.17	0.0000	910.8
LW	27.6599	4.61749	5.99	0.0002	1246.4
RL	1.68234	0.35346	4.76	0.0010	4340.4
RSLR	-24.1180	5.17960	-4.66	0.0012	2891.5
SB	1.02433	0.65554	1.56	0.1526	189.8

These correlations show underlying genetic and physiological links between the qualities. For example, the positive link between SL and LA may be because both features are regulated by cell division and expansion. The positive link between SB and LW may be because the buildup of photosynthates influences both qualities. The negative association between RL and RSLR may be due to a trade-off between root growth and shoot growth. The correlation results can be used to inform breeding efforts for chickpeas. For example, breeders can use the positive association between SL and LA to select seedlings with both long stems and large leaves (Ahmad et al., 2021; Sarwar et al., 2022; Sarwar et al., 2021). Breeders can also exploit the positive association between SB and LW to select high biomass and wide-leaf seedlings. Breeders should be mindful of the negative association between RL and RSLR and carefully balance root growth and shoot growth while selecting desired chickpea features (Ali et al., 2016; Balqees et al., 2020; Ghafoor et al., 2020; Iqbal et al., 2021).

Regression Analysis

Although the coefficient for Leaf Area (LA) is negative (-4.80312), the p-value of 0.6432 indicates that it does not significantly impact SL prediction. The individual significance of the variable may be affected by multicollinearity with other variables, as indicated by the high variance inflation factor (VIF) of 58.1. A positive correlation between SL and leaf length (LL) is evident, with a coefficient of 3.14581 and a p-value of 0.3348, but this association is not statistically significant. Leaf Width (LW): Like LL, LW shows a positive correlation with SL, although it's not statistically significant (p = 0.8093). The positive coefficient (1.38261) and statistically significant p-value (0.0000) of root length (RL) show that RL is strongly positively related to short-term learning (SL). This indicates that seedlings with longer roots tend to grow to be taller (Iqra et al., 2020a; Iqra et al., 2020b; Mazhar et al., 2020; Naseem et al., 2020).

RSLR, or Root-to-Shoot Length Ratio, demonstrates a negative correlation with SL, as seen by its negative coefficient (-23.7697) and statistically significant p-value of 0.0000. This suggests that longer seedlings are linked with lower RSLR values, which imply higher shoot growth relative to root growth. Seedling Biomass (SB) appears to have minimal to no effect on SL in this model, as indicated by the negative coefficient (-0.02823) and non-significant p-value of 0.9313.

Conclusion

All variables other than seedling biomass demonstrated considerable genotypic variation, showing the prospect of genetic improvement. Seedling length, root length, root-to-shoot length ratio, leaf length, leaf breadth, and leaf area displayed substantial heritability, showing significant genetic influence over these characteristics. All characteristics except seedling biomass showed encouraging genetic progress, showing potential for successful selection and improvement. Significant connections exist between numerous attributes, emphasizing possible trade-offs and synergistic linkages. For example, longer seedlings tend to have bigger leaves and lower root-to-shoot ratios. Root length and root-to-shoot length ratio have the largest impact on seedling length. Leaf features and seedling biomass indicate lesser but possibly substantial impacts.

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MUR wrote the initial draft of manuscript. AA, MSA edit the manuscript in original. All authors have read and approved the final manuscript.

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The authors declare that they have no competing interests.