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UNVEILING GENETIC POTENTIAL FOR CHICKPEA IMPROVEMENT THROUGH HERITABILITY AND TRAIT CORRELATIONS

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Abstract *Pulses, a staple crop in underdeveloped countries, provide protein, dietary fibre, and minerals. Chickpea, a drought-resistant crop, is a significant vegetarian diet in South Asia, providing high-quality protein, carbohydrates, minerals, and trace elements. The University of Punjab Lahore's Department of Plant Breeding and Genetics studied genetic differences in chickpea traits. The research involved five genotypes and found significant genetic differences in leaf area, root length, root shoot length ratio, seedling biomass, leaf width, root length, and leaf area. The study suggests that selective breeding can enhance chickpea types through genetic selection. Five out of seven traits showed high broad-sense heritability estimates, suggesting a significant fraction of phenotypic variation attributed to genetic causes. The study also found that genotypes with longer leaves tend to have wider leaves, potentially influencing total leaf area and photosynthetic capability. Longer leaves may contribute to higher seedling biomass production due to increased light interception and resource acquisition. Longer roots also have higher RSLR values, suggesting effective resource allocation between aboveground and belowground plant components. The minimal association between LA and RL supports independent management of these traits, stressing the need for breeding programs to include both aspects for increasing photosynthetic capacity and root system efficiency.*

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Keywords: *chickpea; heritability; genetic advance; biomass; photosynthetic capacity*

Introduction

Pulses have been widely farmed crops around the world since ancient times. They are a great protein, dietary fiber, and mineral source and have various health advantages. Pulses are described as "Nutritional seeds for a sustainable future" and the year 2016 was recognized as "The International Year of Pulses", jointly by the United Nations and the Food and Agriculture Organization (FAO, 2016). The vegetarian population is mostly dependent on pulses for their protein requirement (Huisman & Van der Poel, 1994). Pulses and grains are commonly consumed as staple meals in underdeveloped countries (Mekibeb et al., 1991). This combination maintains the essential amino acid balance(Boye et al., 2010; Upali et al., 2014; Young & Pellett, 1994). Chickpea is a drought-resistant crop; thus, it does not require intense irrigation and may be cultivated in places deprived of rainfall (Kaur & Prasad, 2021). Chickpea is considered a nutritious vegetarian diet and one of South Asia's most significant human and domestic animal foods (Moreno & Cubero, 1978). It is an inexpensive source of high-quality protein in the diets of millions in underdeveloped countries who cannot afford animal protein for balanced nutrition. In addition to proteins, it provides a good source of carbohydrates, minerals and trace elements (Zia-Ul-Haq et al., 2007)). Like other legumes, Chickpea contributes to the cereal staple with a variety of tastes and textures and adds nutrients (carbohydrates, minerals) to the staple dish, ensuring a balanced diet, covering all nutrient requirements (Duhan et al., 1999). Its flour, called Besan, is used in many ways for cooking, e.g. blended with wheat flour to produce roti or chapatti. Young plants and green pods are eaten like spinach. Turkey and Latin America also utilize a limited fraction of canned chickpea (Jukanti et al., 2012).

On the therapeutic side, chickpea seed is utilized as a tonic, stimulant and aphrodisiac (Pandey, 1993). The seed is eaten as an appetizer and also possesses anthelmintic effects. It also alleviates thirst and burning sensation. Seeds usually treat bronchitis, leprosy, skin problems, blood disorders and biliousness (ZIA-UL-HAQ et al., 2008). Seeds are also used to treat liver and spleen disorders; seeds enrich the blood and cure skin ailments and inflammation of the ear (Yili et al., 2015). Its significant protein content is abundant in zinc, nutritious dietary fiber, calcium, magnesium, phosphorus, potassium, iron and vitamins (Kayan & Adak, 2012).

Material and method

The current research project was conducted in the experimental field of the Department of Plant Breeding and Genetics, University of the Punjab Lahore. The major experimental material comprised 5 chickpea genotypes viz line 5006, variety CM-98, line 698, line 620, line 810. All these measurement samples were gathered from Arid Agriculture University. This experiment was conducted in RCBD with 3 replications of each genotype. Determine the many traits are Root-to-Seedling length ratio (RSLR), Seedling Length (SL), Leaf Length (LL), Seedling biomass (SB), Leaf width (LW), Root Length (RL), Leaf Area (LA). Observed and computed values are reported in Table 1. All measurements are properly measured following the germination of chickpea. SL, RL, LL, LW are measured by length measurement scale. Biomass is stated as the weight of a plant above and below the ground surface (Summers & Hendrix, 1991), Biomass is measured by the weight of organisms in a given volume in PBG Lab-I at the department of Plant Breeding and Genetics. Computations of their needed parameters measure RSLR and LA, the division of RL by SL and multiplication of LL with LW and factor 0.69 correspondingly for both values (Toker & Ilhan Cagirgan, 2004).

Results and discussion

Leaf Traits

Leaf Area (LA): ANOVA demonstrated significant genotypic variations, demonstrating variable genetic capacity for leaf size development across the investigated genotypes (Table 1). This offers possibilities for breeding efforts to select lines with larger leaves, perhaps leading to enhanced light collection and photosynthetic efficiency (Aaliya et al., 2016; Ahmad et al., 2021; Keneni et al., 2012).

Leaf Length (LL): Like LA, considerable genotypic variation was identified, showing genetic control over leaf length. Breeding strategies targeting better photosynthetic capacity should select genotypes with longer leaves, assuming wider leaves are not linked with decreasing light interception efficiency (Ali et al., 2017; Ali et al., 2015; Ali et al., 2013).

Leaf Width (LW): Genotypic differences were also significant for LW, showing the genetic influence on this feature. Selection for wider leaves could be useful in specific breeding aims but should be balanced with considerations of maintaining appropriate leaf angle and light utilization (Ali et al., 2016; Ali et al., 2014; Ali & Malik, 2021).

Root Traits:

Root Length (RL): A highly significant F-value implies substantial genetic control on RL. This is positive for breeding projects that generate cultivars with deeper root systems, perhaps leading to increased drought tolerance and nitrogen scavenging capability (Asif et al., 2020; Azhar et al., 2021; Balqees et al., 2020).

Root Shoot Length Ratio (RSLR): Significant genotypic effects were observed for RSLR, demonstrating the genetic influence on balancing resource allocation between aboveground and belowground plant components. Selecting genotypes with appropriate RSLR values could be critical for efficient resource utilization and adaptation to varied environmental situations.

Seedling Biomass and Shoot Length:

Seedling Biomass (SB): While the F-value implies a genetic effect on SB, the comparatively high P-value compared to other variables indicates other factors, including environmental or non-additive genetic interactions, might play a more significant role. Further research might be needed to understand the determinants of SB variance completely (Ghafoor et al., 2020; Iqbal et al., 2021).

Shoot Length (SL): The highly significant F-value and low P-value demonstrate substantial genetic control over SL. This implies good potential for breeding efforts to select strong seedlings with taller shoots, possibly contributing to early establishment and potentially higher output.

Table 1 Mean Performance of genotypes

Genotype	Shoot Length (SL)	Root length (RL)	Root-to-shoot ratio (RSLR)	Seedling biomass (SB)	Leaf Length (LL)	leaf width (LW)	Leaf Area (LA)
line 5006	18.667b	11.007b	0.590b	1.107b	0.643a	0.440b	0.210a
variety CM-98	18.760a	11.027b	0.588bc	1.160a	0.650a	0.443b	0.195c
line 698	18.433c	10.660c	0.578c	1.090c	0.610ab	0.403c	0.170d
line 620	17.993d	11.387a	0.633a	1.113ab	0.607b	0.430b	0.180d
line 810	17.893d	10.383c	0.580c	1.160a	0.640a	0.460a	0.203b

Overall, the AOVA demonstrates significant genetic differences for most chickpea attributes. This holds tremendous promise for enhancing chickpea types through selective breeding (Table 2). Breeding programs can leverage these discoveries to target specific traits, such as root depth, leaf size, or seedling vigour, based on their breeding goals and adaptation needs. Further research should look into the individual genes behind these features and their interaction with environmental factors to optimize breeding tactics further and speed the production of superior chickpea genotypes (Laraib Iqra et al., 2020; L. Iqra et al., 2020; Mazhar et al., 2020).

Table 2 Genetic Parameters of different genotypes

Traits	Analysis of Variation (P) value	Phenotypic Coefficient of variation (%)	Genotypic Coefficient of variation (%)	Environmental Coefficient of variance (%)	Broad Sence Heritability (%)	Genetic Advance (%)
Seedling Length (SL)	0.0000**	2.17%	2.11%	0.49%	94.83%	3.608%
Root Length (RL)	0.0089**	3.98%	3.27%	2.26%	67.72%	4.724%
Root to shoot length ratio (RSLR)	0.0055**	4.22%	3.52%	2.32%	69.66%	5.155%
Seedling biomass (SB)	0.0160*	3.30%	2.61%	2.03%	62.29%	3.611%
Leaf Length (LL)	0.0242*	4.21%	2.54%	3.35%	36.49%	2.696%
Leaf Width (LW)	0.0121*	7.08%	5.70%	4.19%	64.98%	8.070%
Leaf Area (LA)	0.0074**	9.50%	8.20%	4.78%	74.61%	12.436%

High Heritability: Five out of seven traits (SL, RL, RSLR, SB, and LW) demonstrated high broad-sense heritability estimates (>60%), indicating a considerable fraction of phenotypic variation ascribed to genetic causes (Table 2). This shows effective selection for these qualities can be done through breeding programs (Arshad et al., 2002).

Moderate Heritability: Leaf length (LL) demonstrated moderate heritability (36.49%), showing both genetic and environmental factors contribute to variance in this characteristic. Breeding programs may need to incorporate environmental management measures alongside selecting strategies for LL.

Low Heritability: Leaf area (LA) displayed the lowest heritability (74.61%), suggesting a stronger influence of environmental influences on this characteristic. Breeding initiatives seeking LA improvement might need to focus on environmental optimization, stress tolerance and genetic selection. Seedling Length (SL): With the highest heritability estimate (94.83%) and genetic progress (3.608%), SL emerges as a very promising attribute for quick improvement through breeding. Selection for longer seedling-length genotypes could lead to rapid establishment and higher early output. Root Length (RL): High heritability (67.72%) and moderate genetic progress (4.724%) emphasize the possibility of breeding operations to generate cultivars with deeper root systems. This could considerably improve drought tolerance and nutrient absorption in chickpea plants. Root Shoot Length Ratio (RSLR): Like RL, RSLR demonstrated high heritability (69.66%) and moderate genetic progress (5.155%). Selecting genotypes with appropriate RSLR values could be crucial for the effective utilization of resources and adaptation to varied settings. Leaf Width (LW): Despite significant heritability (64.98%), LW demonstrated the largest genetic advance (8.070%). This shows rapid improvement in leaf width can be attainable through breeding, potentially altering photosynthetic capacity and biomass production (Mazhar et al., 2020; Naseem et al., 2020; Qurban & Muhammad, 2011; Sarwar et al., 2022).

Correlation analysis

Moderate to strong positive correlations: Several pairings of traits demonstrated moderate to strong positive correlations (r > 0.5), indicating that gains in one trait correspond with increases in the other (Table 3). These include:

LL and LW: A high positive connection (r = 0.8124) shows that genotypes with longer leaves also tend to have wider leaves, potentially influencing total leaf area and photosynthetic capability.

LW and SB: A moderate positive association (r = 0.5972) shows that broader leaves might contribute to higher seedling biomass production, presumably due to increased light interception and resource acquisition.

RL and RSLR: A strong positive association (r = 0.8464) reveals that genotypes with longer roots also tend to have higher RSLR values, suggesting effective allocation of resources between aboveground and belowground plant components (Ali, Ahsan, et al., 2010; Naveed et al., 2012; Qurban & Muhammad, 2011).

Weak to negligible correlations: Other pairs of attributes revealed weak or negligible correlations (r < 0.3), suggesting little to no association between them. These include:

LA and RL: A negligible connection (r = -0.0798) shows that leaf area is not considerably impacted by root length, presumably due to different genetic and environmental variables affecting both features.

RSLR and SB: A weak negative association (r = -0.1098) shows that genotypes with higher RSLR might have somewhat lower seedling biomass; however, this link is not statistically significant.

SL and RL, SL and RSLR: Weak positive correlations were identified between shoot length (SL) and root length and RSLR, indicating potential co-regulation of these features but not a substantial reliance.

Table 3 Correlation Analysis of different traits

	LA	LL	LW	RL	RSLR	SB
LL	0.749					
LW	0.8124	0.7178				
RL	-0.0798	0.2	-0.0837			
RSLR	-0.1933	-0.0346	-0.2168	0.8464		
SB	0.3045	0.4498	0.5972	-0.1098	-0.1669	
SL	0.1956	0.3251	0.2485	0.2055	-0.3339	0.0037

The provided P-values indicate the statistical significance of each correlation coefficient. Lower P-values (e.g., < 0.05) show a larger possibility that the observed link is unrelated and significant. The signs of the correlation coefficients (+ or -) show the direction of the link. Positive correlations signify that both attributes increase or decline together, while negative correlations suggest an inverse link where one trait increases as the other lowers. Selecting genotypes with wider leaves (LW) can indirectly encourage increased seedling biomass (SB) and potentially higher yield. The minimal association between LA and RL supports independent management of these traits, stressing the need for breeding programs to include both aspects for increasing photosynthetic capacity and root system efficiency (Ahmad et al., 2012; Waseem et al., 2014).

Regression Analysis

Root Length (RL): The significant positive coefficient (1.63) and P-value of 0 suggest that RL is the strongest predictor of the dependent variable (Table 4). This indicates that cultivars or breeding lines with larger root systems will likely perform better.

Table 4 Regress analysis for shoot length of chickpea

Variables	**Coefficient**	**Std Error**	**T**	**P**	**VIF**
LA	-1.14881	1.88155	-0.61	0.5584	4.9
LL	-3.09376	1.37162	-2.26	0.0541	3.7
LW	3.30775	1.09359	3.02	0.0164	5
RL	1.62979	0.08201	19.87	0	4.9
RSLR	-29.5306	1.35349	-21.82	0	4.3
SB	-1.62756	0.5465	-2.98	0.0177	2.1

R-Squared: 98.67%

Adjusted R-Squared: 97.67%

Regression Equation

Y = 20.682 – 1.149 (LA) – 3.093(LL) + 3.308 (LW) + 1.630 (RL) – 29.530 (RSLR) – 1.628 (SB)

Root Shoot Length Ratio (RSLR): Despite a high T-value (-21.82), the P-value is 0, indicating probable multicollinearity with other factors. However, if multicollinearity is eliminated and RSLR remains considerable, it proposes favoring genotypes with optimal RSLR values for effective resource allocation. Leaf Area (LA), Leaf Length (LL), Leaf Width (LW), Seedling Biomass (SB): These qualities have non-significant P-values (>0.05), suggesting they may not be directly influencing the dependent variable in your model. Focusing on other qualities like RL and RSLR can be more successful for your specific breeding aims (Ali et al., 2011; Ali, Muhammad, et al., 2010; Waseem et al., 2014).

Conclusion

This research demonstrates tremendous genetic variation and new pathways for enhancing chickpea cultivars through selective breeding. By focusing on high-heritability features like root length and improving resource allocation through RSLR, breeding programs can generate chickpea varieties with better yield, stress tolerance, and adaptation to varied environments.

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Declarations

Data Availability statement

All data generated or analyzed during the study are included in the manuscript.

Ethics approval and consent to participate

Not applicable

Consent for publication

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Conflict of Interest

Regarding conflicts of interest, the authors state that their research was carried out independently without any affiliations or financial ties that could raise concerns about biases.