

Exploring Genetic Variability Of Kabuli Chickpea (*Cicer Arietinum* L.) Elite Lines Based On Yield Contributing Traits

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ABSTRACT

Chickpea (*Cicer arietinum* L.) is a valuable leguminous crop that is cultivated globally, with a high level of protein content, good nutritional value and biological fixation of nitrogen to help in enhancing soil fertility. However, in Pakistan, the production of chickpea is low considering the biotic and abiotic stresses, socioeconomic conditions like uncertified seeds and modern farming methods. In this experiment, the genetic

variability of 26 genotypes of Kabuli chickpea and a check, that were gathered at the Pakistan Agricultural Research Council (PARC), was checked in a randomized complete block design (RCBD) field experiment conducted at the University of Agriculture, Faisalabad. Morphological and yield characteristics such as the plant height, the number of pods and seeds per plant, hundred seed weight, biological yield and harvest index-were measured. The examination of the genotypes (ANOVA) showed the presence of significant differences between genotypes in most of the traits, which implies a high level of genetic diversity. The seed yield and the characteristics like the number of seeds per plant and plant height have positive relationships implying they may be used as selection criteria in breeding programs. Data demonstrated by principal component analysis (PCA) indicated that PC1 was correlated with percent germination, plant height, number of leaflets, leaf weight, seed yield, and seeds per plant, whereas PC2 was positively correlated with biological yield, seed yield, and seeds per pod. PC3 made its contribution in flowering time, weight of leaves, number of pods and harvest index. The coefficient of variation of the majority of traits was low, which proved the extent of reliability of the experimental data. Cluster analysis found that genetic difference among them is significant with Clusters 8 and 10 having the most ideal parents to breed as they are complementary. According to these analyses, five high-performing genotypes G9, G15, G16, G20 and G26 were picked due to their high yield potential.

Keywords: Chickpea, Genotypes, Yield, Morphology, Variability, Breeding, Clustering, PCA, Selection, Agronomy.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an annual, self-pollinating, diploid grain legume ($2n = 2x = 16$), which has significant value in the production of food and food security worldwide as well as in human nutrition. It is ranked as the third highest pulse crop in the world, after faba bean and field pea (Asati et al., 2022). The species *C. arietinum* belongs to the genus *Cicer* that is a domesticated and widespread domesticated species as it is a genus containing 46 species. Chickpea is primarily cultivated in arid/semi-arid areas in over 50 countries, and it constantly faces abiotic stressors, especially drought and heat, which cause the instability of yields (Arriagada et al., 2022). It has a relatively small genome size of about 739 Mb and this has facilitated genetic and genomic studies (Varshney et al., 2013).

Chickpea has been greatly appreciated due to its nutritional value whereby carbohydrates and protein make up almost 80 percent of the seed dry weight. It is the poor man meat due to its cheap prices and good protein content (17.22%). Seeds of Chickpea have amino acids (18 in number), as well as other nutritionally beneficial unsaturated fatty acids like linoleic and oleic acids, among others. Phytosterols, essential minerals (Ca, Mg, P, and K), and vitamins such as riboflavin, niacin, thiamin, folate, and β -carotene are found in large amounts in them (Jukanti et al., 2012; Zhang et al., 2024).

The origin of the chickpea has been a greatly contested one. Even though in earlier works areas including Greece, Himalayas, Mediterranean, and Ethiopia have been suggested as areas of origin or diversity, recent data is leaning towards south-eastern

Turkey and north-eastern Syria as the main area of origin. It was in this region that the wild progenitor (*C. reticulatum*) and closely related species are found and this proves that they contributed to the domestication of chickpea (Gaur et al., 2012).

The chickpea that has been cultivated is broadly categorized into Desi and Kabuli. The seeds of desi chickpea are small, angular, wrinkled and have thick seed coat whereas the seeds of Kabuli chickpea are only large, smooth, and creamy in color with a thin seed coat. The nutritional composition of the two types has been found to be significantly different with Desi chickpea tending to be higher in protein content (29.2%) than Kabuli chickpea (20.55%) (Begum et al., 2023). Kabuli chickpea, nevertheless, is less high in fiber (NDF and ADF) and more in starch and crude fat (Bampidis and Christodoulou, 2011).

Chickpea is a leguminous crop that adds to sustainable agricultural technologies by means of the biological nitrogen fixation (BNF) (Ahmad et al., 2019). Chickpea has the capability to fix 140 kg N ha⁻¹ through symbiosis with the *Rhizobium* species, eliminating the need to use synthetic fertilizers and enhancing soil fertility (Biabani et al., 2011; Singh et al., 2018). Chickpea germplasm characterization is also necessary to determine the genetic variability of yield, nutritional behavior and resistance to stress. These are important studies especially to Pakistani agriculture where agroclimatic conditions differ and thus, high yield, nutrient-rich and stress-tolerant chickpea cults are to be developed to improve food security and minimize malnutrition.

MATERIALS AND METHOD

Collection of Germplasm

The twenty-six high performing Kabuli chickpea genotypes of which one is a commercial variety as check provided by Chickpea Biotechnology Lab, CAS, UAF and which were dispatched by Agriculture Research Council (PARC), Pakistan to undergo NUYT trial

The experiment was conducted using a total of 25 chickpea genotypes, labeled G1 to G25, along with a check variety named Taman. These genotypes were evaluated to assess their growth, yield, and other agronomic traits. The selection included diverse genetic material to capture variability for comparative analysis. This setup allowed for the identification of superior genotypes under the given experimental conditions.

Field Analysis

The current study was conducted at the research area of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. The experiment was conducted in Randomized Complete Block Design (RCBD). There were twenty-six genotypes, each genotype has three replications. The plant × plant, row × row, and block × block spacing will be kept 6 inches, 12 inches and 36 inches, respectively. Each genotype has 4 rows, each 4 meters long. The plot size per genotype will require an area of 52 ft². The sowing will be done by using a handheld dibbler. Standard agronomic, especially irrigation at regular interval and plant protection practices will be followed throughout the growing session.

Data Collection

The data were collected based on different chickpea morphological and yield related traits. In this respect, we will select randomly 8 plants from each genotype. The following traits were recorded.

Germination percentage

For the calculation of germination percentage (GP), the number of plants growing in each of the four rows for one genotype were counted. The total number of seeds were already noted at the time of sowing. The germination percentage was calculated by the following formula:

$$GP (\%) = (\text{number of germinated plants} / \text{total number of sown seeds}) \times 100$$

Plant height at flowering

Plant height (PH1) was measured at flowering using a meter rod, in centimeters. The meter rod was placed at the base of the plant and extended to the top of the plant. After recording the height of all plants, the average was calculated to ensure accuracy.

Number of leaflets per leaf

When the plant was at the flowering stage, data for the number of leaflets (NLL) was recorded. For this purpose, a branch with fully developed leaves was selected from the top of the plant. The leaf was detached, and the number of leaflets was counted. Then, the average was calculated to ensure accuracy.

Fresh leaf weight

Fresh leaf weight (FLW) was measured by collecting fully developed leaves. It was done by using digital weighing balance in grams. Then, the average was calculated to ensure accuracy.

Dry leaf weight

Dry leaf weight (DLW) was measured by collecting fully developed leaves which were dried at fifty degrees centigrade for twenty-four hours. It was done by using digital weighing balance in grams. Then, the average was calculated to ensure accuracy.

Days to 50% flowering

Days to 50% flowering (DFF) were recorded by counting the number of days from sowing to the date when approximately 50% of the plants in a plot exhibited at least one open flower.

Plant height at harvesting

Plant height (PH2) was measured at harvesting using a meter rod, in centimeters. It was done by placing plants on the ground. The meter rod was placed at the base of the plant (excluding roots) and extended to the top of the plant. After recording the height of all plants, the average was calculated to ensure accuracy.

Number of pods per plant

The number of pods per plant (NOS) were calculated after the harvesting of plants. For this purpose, eight representative's plants in field were selected and then harvested. We calculated pods per plant manually and then took averages for ensuring accuracy.

2.3.9 Number of seeds per pod

Number of seeds per pod (NSP) were calculated by following formula:

$$\text{NSP} = \frac{\text{number of seeds per plant}}{\text{number of pods per plant}}$$

Number of seeds per plant

The number of seeds per plant (NOP) were calculated after the threshing of plants. For this purpose, eight representative plants in field were selected and threshed after harvesting. We calculated seeds per plant manually and then took averages for ensuring accuracy.

Seed yield per plant

After the manual threshing of representative's plants, we calculate seed yield per plant (SY) in grams by using digital weighing balance. Then, the average was calculated to ensure accuracy.

Hundred seed weight (HSW) was calculated by the following formula

$$\text{HSW} = \frac{\text{Total weight of seeds}}{\text{Number of seeds weighed}} \times 100$$

Biological yield

The biological yield (BY) was calculated after the harvesting of representative's plants. It was done by directly placing harvested plant on digital weighing balance in grams. Then, the average was calculated to ensure accuracy.

2.3.14 Harvest index (%)

The harvest index (HI) was calculated by using the following formula:

$$\text{Harvest index} = \frac{\text{Grain yield}}{\text{Biological yield}} \times 100$$

Statistical Analysis

Analysis of variance will be performed to check the variation among all genotypes by using above mentioned parameters (Steel et al., 1997). Principal Component Analysis will be conducted to analyze the morphological traits (Gabriel, 1971). Correlation analysis will be used to study the relationship among yield related traits (Yule, 1897). Cluster analysis was performed to group genotypes based on similarity in yield-contributing traits (Edwards and Cavalli-Sforza, 1965).

RESULTS AND DISCUSSION

Chickpea is an important pulse crop exhibiting substantial genetic variation among genotypes, which provides opportunities for genetic improvement. Evaluating this variability is essential for effective breeding programs. In the present study, Analysis of Variance (ANOVA) was used to assess the significance of genetic differences among

twenty-six chickpea genotypes for various agronomic traits.

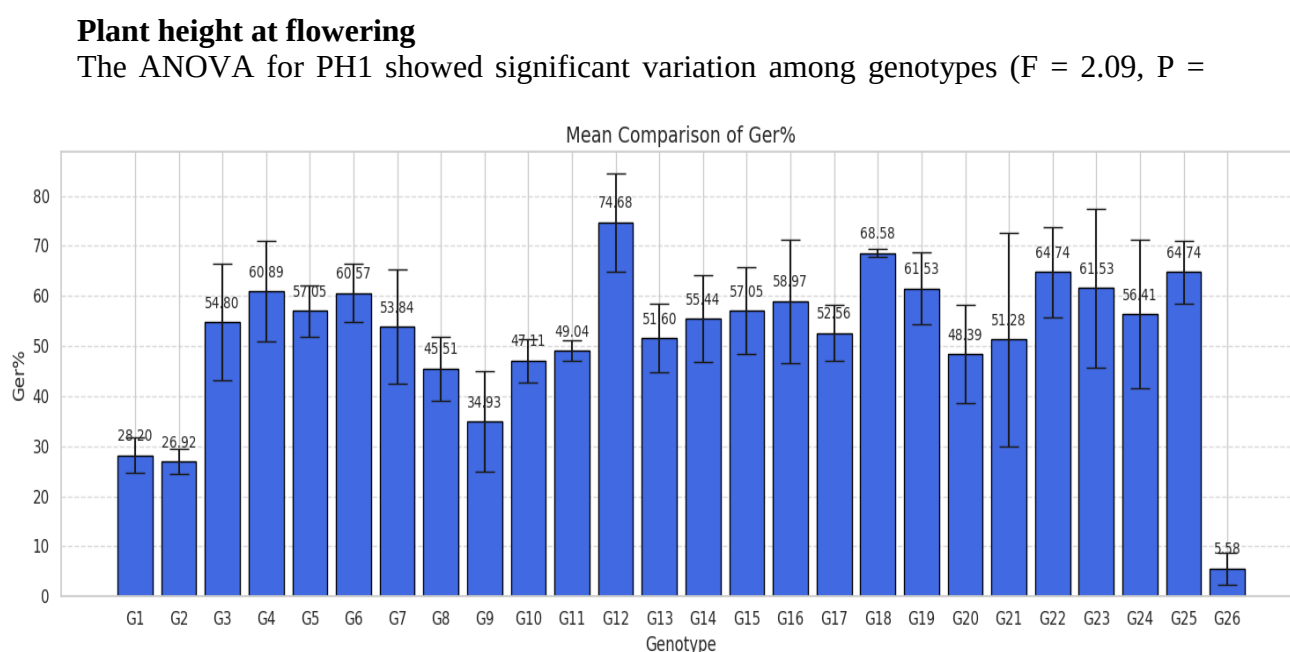
Analysis of Variance (ANOVA)

ANOVA is a widely used statistical method for testing hypotheses and comparing treatment effects across multiple genotypes and experimental designs (Steel and Torrie, 1989). In this study, ANOVA revealed significant differences among chickpea genotypes, indicating the presence of substantial genetic variability suitable for selection and improvement.

Germination Percentage

The analysis of variance showed highly significant differences among chickpea genotypes for germination percentage (GP), confirming a strong genetic influence on this trait. The genotypic mean square (625.90) was considerably higher than the error mean square (160.29), supporting the existence of genetic variability. Similar results were reported by Soltani et al. (2006). Mean comparison further revealed wide variation in GP among genotypes (Figure 3.1). Genotype G12 recorded the highest germination percentage (74.68%), indicating superior seed vigor, whereas G26 showed the lowest GP (5.58%), reflecting poor germination ability. The remaining genotypes exhibited intermediate values, demonstrating diverse germination responses. Genetic parameter analysis indicated moderate heritability (49.19%) for germination percentage, along with high phenotypic (34.13%) and genotypic (23.94%) coefficients of variation. The high genetic advance as a percentage of the mean (34.59%) suggests that substantial improvement in germination percentage can be achieved through selection. However, the relatively high coefficient of variation (24.33%) indicates notable environmental influence, suggesting that selection should be performed under controlled conditions to achieve reliable improvement.

Figure 3.1 Mean comparison of genotypes for GP



0.013). The genotypic mean square (124.21) was more than double the error mean square (59.47), indicating that the variation is primarily due to genetic differences rather than random error. The replication mean square (924.60) was comparatively high but not statistically significant. These findings suggest that plant height at flowering is influenced by genotype, making it a promising selection criterion, similar finding also reported by Mallikarjuna et al (2019). The mean comparison for PH1 highlights significant differences in plant height among the genotypes (Figure 3.2). Genotype G23 exhibits the tallest plants at first flowering at 65.66, indicating rapid initial vertical growth. Conversely, G1 shows the shortest plants at 32.77, suggesting slower early growth or a more compact growth habit. The range of heights, from 32.77 to 65.66, highlights significant genotypic variation in early plant development and stature. The analysis of PH1 across varieties showed significant genetic variation (F-ratio = 2.088) but with low heritability (26.63%). The phenotypic (16.55%) and genotypic (8.54%) coefficients of variation indicate a considerable influence of the environment. A genetic advance of 4.9381 units (9.08% of the mean) demonstrates low potential for meaningful improvement through selection. The moderate coefficient of variation (14.17%) confirms the presence of environmental effects. These results indicate that early plant height is a trait with low heritability, making it a poor candidate for effective selection in this breeding program.

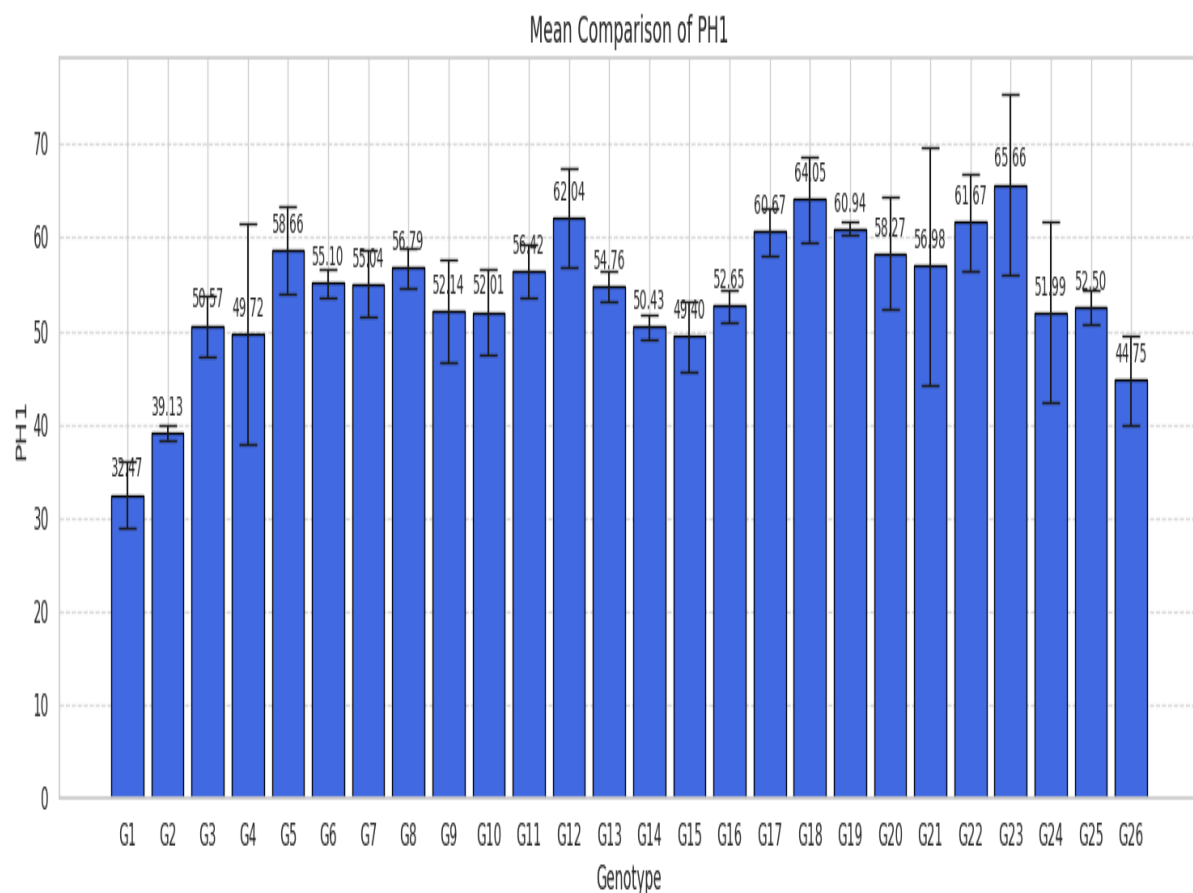


Figure 3.2 Mean comparison of genotypes for PH1

Number of leaflets per leaf

The ANOVA revealed highly significant genotypic differences for NLL ($F = 12.15$, $P = 0$). The mean square for genotypes (2.542) was markedly higher than the error (0.209), confirming substantial genetic variability. The replication effect was minimal. These results point to a strong genetic basis for leaflet number, which can aid selection for improved foliage traits in chickpea. Similar findings were reported by Soltani et al. (2006). The mean comparison for NLL reflects the vegetative vigor and leaf production capacity of each genotype (Figure 3.3). Genotype G24 exhibits the highest NLL at 15.56, suggesting a robust canopy development and photosynthetic potential. Most other genotypes show a narrower range of NLL, typically between 11.23 and 13.78, indicating a general consistency in leaf production. The variation observed highlights differences in plant architecture and growth habits. The analysis of the NLL revealed highly significant genetic variation ($F\text{-ratio} = 12.147$) with high heritability (78.79%). The phenotypic (7.97%) and genotypic (7.07%) coefficients of variation are close, indicating a low environmental influence and that most of the observed variation is genetic. A genetic advance of 1.6124 units (12.93% of the mean) demonstrates moderate potential for improvement through selection. The very low coefficient of variation (3.67%) and small standard error (0.2641) confirm high experimental reliability. These results indicate that the number of leaves is a highly heritable trait with strong potential for effective selection in breeding programs.

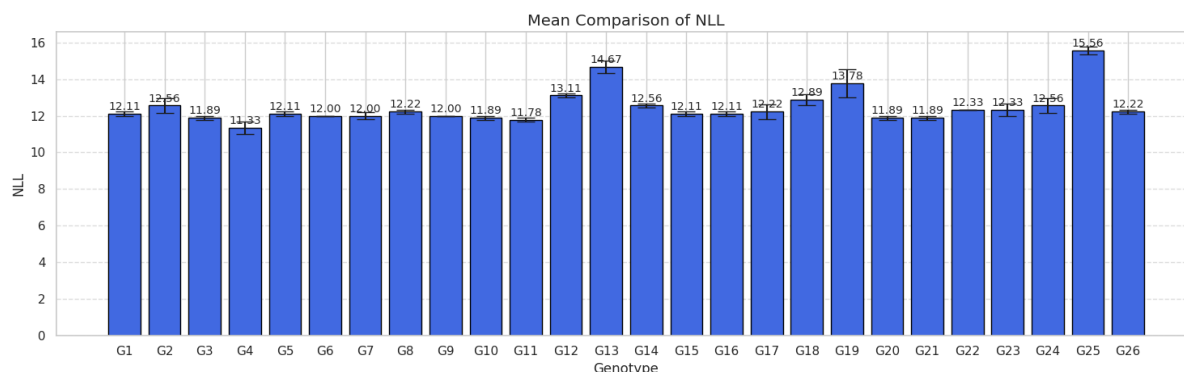


Figure 3.3 Mean comparison of genotypes for NLL

Fresh leaf weight The analysis of variance revealed highly significant differences among the chickpea genotypes for FLW ($F = 3.34$, $P = 0$). The genotypic mean square (10576.9) was significantly greater than the error mean square (3169.7), confirming genetic variability. The replication effect (0.001) was small and non-significant. These results match those reported by Irshad et al. (2022) and indicate fresh leaf weight is largely governed by genetic factors, making it useful for varietal selection, similar findings were reported by Eker et al (2022). The mean comparison for FLW of each genotype, illustrating variations in the water content and fresh biomass of the leaves (Figure 3.4). Genotype G19 exhibits the highest FLW at 0.48, implying larger or more turgid leaves. In contrast, several genotypes, including G1, G2, G3, G4, G5, G10, G15, G16, G20, G21, G22, and G26, show lower FLW, ranging from 0.29 to 0.35, which could be attributed to differences in leaf size, thickness, or water retention capacity.

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The analysis of FLW across varieties revealed significant genetic variation (F-ratio = 3.3358) with moderate heritability (43.78%). The phenotypic (20.93%) and genotypic (13.85%) coefficients of variation indicate substantial variability, suggesting good potential for selection. This is supported by a Genetic Advance as a Percentage of Mean (GAM) of 18.88%, which demonstrates meaningful improvement potential through breeding. The moderate coefficient of variation (15.70%) and small standard error (0.0325) confirm acceptable experimental reliability. These results indicate that fresh leaf weight is a moderately heritable trait with sufficient genetic variability for effective selection in breeding programs.

Dry leaf weight

The ANOVA for DLW showed a non-significant genotypic effect ($F = 1.35$, $P = 0.182$), indicating limited genetic variation for this trait among the genotypes (Table 4.9). The genotypic mean square (4060.40) was only slightly higher than the error mean

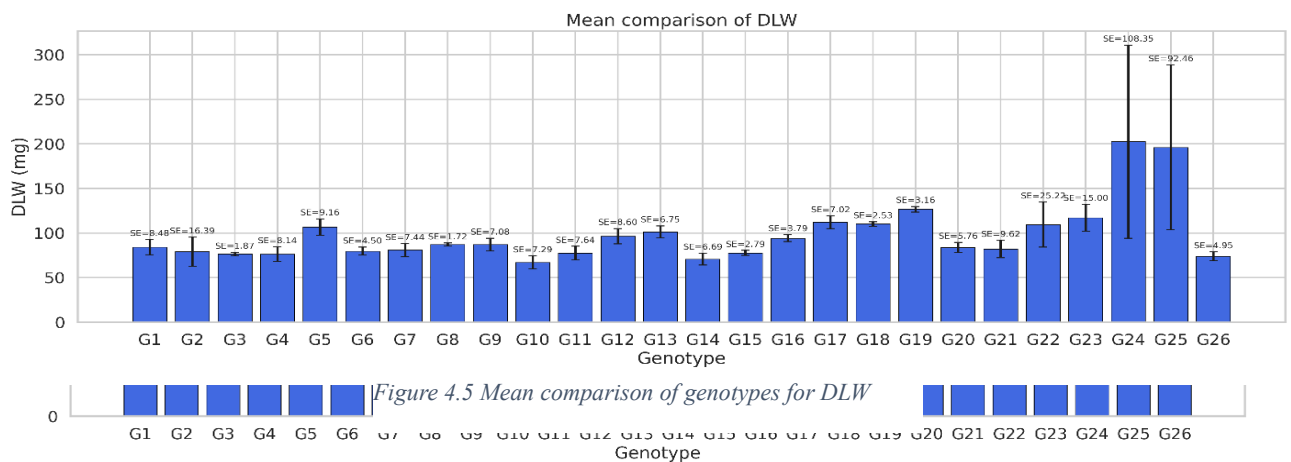


Figure 3.4 Mean comparison of genotypes for FLW

square (3384.87), suggesting that environmental factors may have played a greater role. The low replication mean square further supports this. Hence, dry leaf weight may not be a reliable trait for selection in this population. This mean comparison for DLW of each genotype, revealing considerable variation in biomass accumulation among them (Figure 3.5). Genotype G24 displays a notably higher dry leaf weight of 0.20, indicating superior dry matter production in its leaves compared to most other genotypes. In contrast, genotypes like G1, G2, G3, G4, G10, G11, G14, G15, G21, and G26 show lower dry leaf weights, typically ranging from 0.07 to 0.09, suggesting differential resource allocation or growth patterns.

Days to 50% flowering

The ANOVA was highly significant genotypic variation for DFF ($F = 3.52$, $P = 0$). The genotypic mean square (7.688) was more than three times the error mean square (2.186), confirming substantial genetic control. The replication effect (18.666) was also minimal in influence. These results indicate that flowering time is a genetically controlled trait, beneficial for selecting early or late-maturing lines, similar findings were reported by Alemu et al. (2017). This mean comparison for number of days

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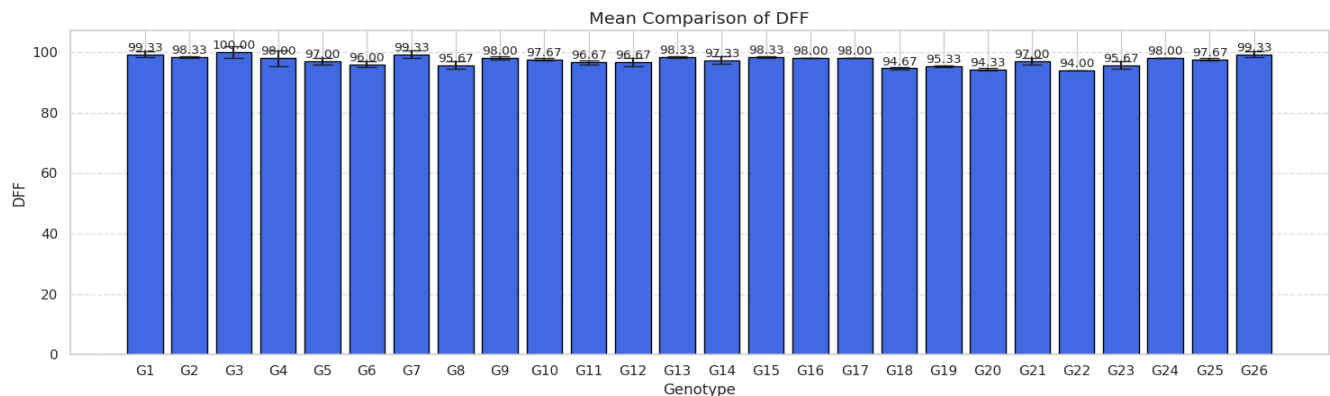
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required for 26 different genotypes (G1 to G26) to complete DFF (Figure 3.6). The values largely cluster between 94 and 100 days, indicating a relatively consistent



flowering onset across most genotypes. Genotypes such as G4, G5, G6, G15, G16, G17, G24, G25, and G26 exhibit similar DFF values, ranging from 97 to 99 days, suggesting comparable phenological development in terms of flowering time. The analysis of DFF across chickpea varieties revealed significant genetic variation (F-ratio = 3.5159) with moderate heritability (45.61%). The low phenotypic (2.06%) and genotypic (1.39%) coefficients of variation indicate that while genetic differences exist, the overall variability for this trait is limited in the studied population. A genetic advance of 1.884 units (1.94% of the mean) suggests a small potential for improvement through selection. The very low coefficient of variation (1.52%) and standard error (0.853) confirm high experimental reliability. These results indicate that days to 50% flowering is a moderately heritable trait, but successful selection would be challenging due to the low genetic variability.

Plant height at harvesting

The results from revealed highly significant genetic variability for plant height at harvest PH2 (F = 3.03, P = 0). The genotypic mean square (153.862) was much higher than the error mean square (50.76). The replication mean square (162.726) was again relatively high but not significant. These findings indicate meaningful genetic diversity in final plant height, making it a viable trait for selection in breeding, similar finding were reported by Mallikarjuna et al, (2019). The mean comparison for PH2 of each genotype, reflecting their final stature (Figure 3.7). Genotype G9 exhibits the tallest plants at maturity at 97.50, indicating strong vertical growth throughout its life cycle. Most other genotypes show mature heights ranging from 80 to 96, demonstrating a general consistency in final plant height. The variation observed, from 68.42 (G1) to 97.50, is important for understanding growth habits and potential for lodging. The analysis of PH2 revealed significant genetic variation (F-ratio = 3.0312) with moderate heritability (40.37%). The close values for the phenotypic (10.34%) and genotypic (6.57%) coefficients of variation suggest that genetic factors play a key role, although environmental influence is present. A genetic advance of 7.6732 units (8.60% of the mean) demonstrates low-to-moderate potential for improvement through selection. The low coefficient of variation (7.98%) and standard error (4.1134) confirm

high experimental reliability. These results indicate that later-stage plant height is moderately heritable with enough genetic variability for selection to be somewhat effective.

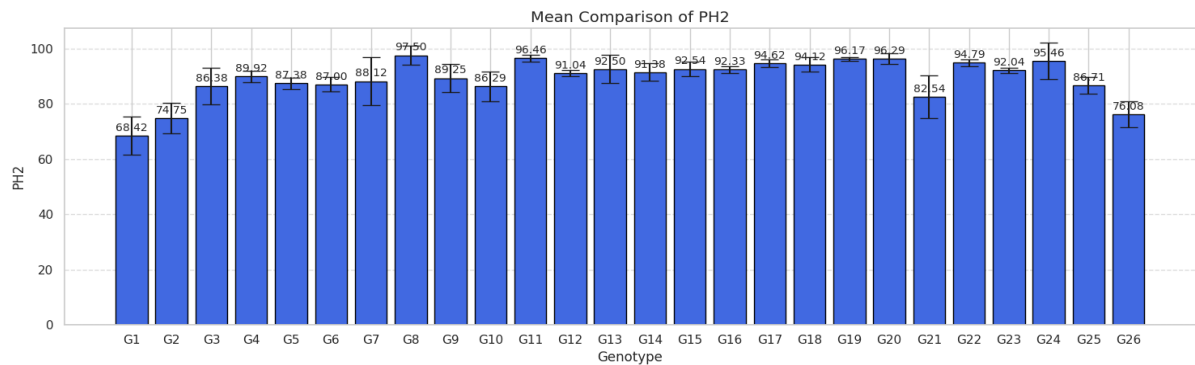


Figure 3.7 Mean comparison of genotypes for PH2.

Number of pods/ plants

The ANOVA for nu NOP showed a non-significant genotypic effect ($F = 0.53$, $P = 0.95$), with the genotypic mean square (133) being much lower than the error mean square (252). This suggests little to no genetic variation for this trait under the studied conditions. Therefore, selection for pod number may not be effective in this set of genotypes. This mean comparison for NOP revealing considerable variation (Figure 3.8). Genotype G9 demonstrates the highest number of pods per plant at 60.79, indicating superior pod-setting capacity. Other genotypes show ranging from 34.86 (G22) to 55.58 (G26), suggesting diverse genetic potentials for pod development. The observed differences are critical for identifying genotypes with high reproductive efficiency.

Number of seeds/ pod

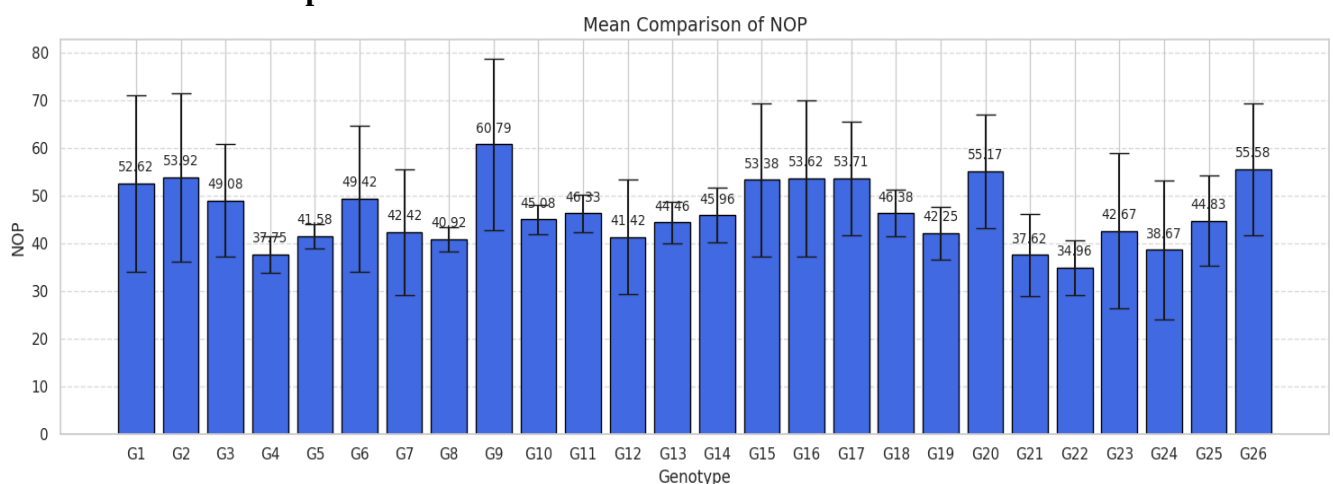


Figure 3.8 Mean comparison of genotypes for NOP

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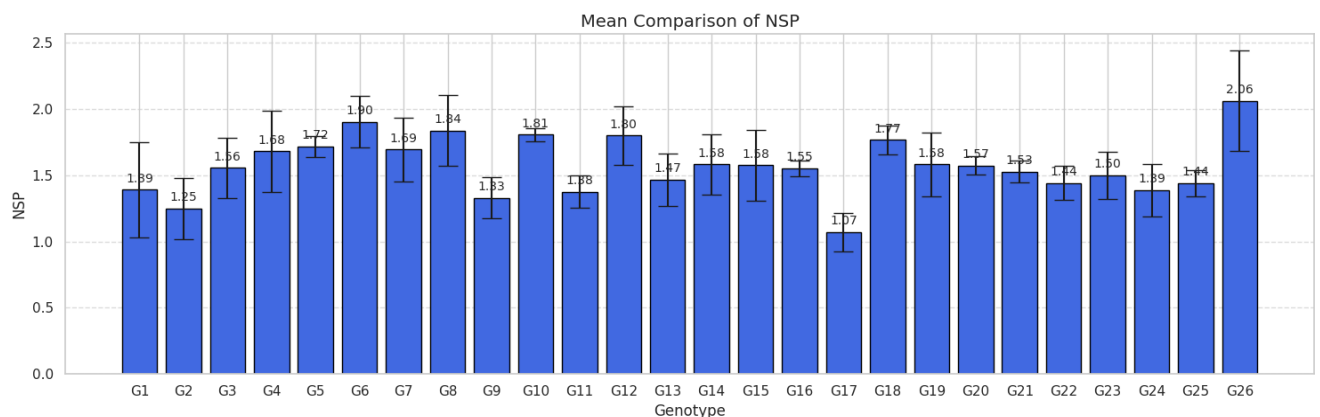
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The ANOVA revealed a significant genotypic difference ($F = 1.95$, $P = 0.022$) for NSP. The genotypic mean square (0.142) was nearly twice the error mean square (0.072), indicating moderate genetic variability. This trait could be utilized in breeding programs to improve seed productivity per pod, similar findings were reported by Hasan and Deb (2017). The mean comparison for NSP reflecting the efficiency of pod filling and seed development within each pod (Figure 3.9). Genotype G26 again exhibits the highest NSP at 2.06, suggesting optimal seed development and packing within its pods. In contrast, Genotype G17 shows the lowest number of seeds per pod at 1.17. The relatively narrow range of variation, typically between 1.50 and 2.00 for most genotypes, indicates a certain level of consistency in this trait across the population. The analysis of the NSP showed significant genetic variation (F -ratio = 1.9547) but with low heritability (24.14%). The high phenotypic (19.71%) and lower genotypic (9.69%) coefficients of variation indicate a substantial environmental influence on this trait. A genetic advance of 0.1541 units (9.80% of the mean) demonstrates a low potential for improvement through direct selection. The moderate coefficient of variation (17.17%) supports the observation of environmental effects. These results indicate that while genetic differences exist, the number of seeds per plant is a trait with low heritability, making it difficult to achieve progress through selection in this material.

Number of seeds per plant

The ANOVA demonstrated non-significant differences among genotypes for NOS ($F = 0.8$, $P = 0.722$). The genotypic mean square (671.95) was lower than the error mean



square (838.76), indicating that most variation observed is due to environmental factors. Thus, this trait may not be a reliable target for selection. This mean comparison for NOS for each genotype revealing considerable variation (Figure 3.10). Genotype G26 shows a remarkably higher NOS at 120.75, indicating a strong genetic potential for seed production. This is significantly higher than most other genotypes, which range from 49.00 to 88.83. The substantial variation underscores the genetic diversity in seed-setting ability, a key trait for yield improvement.

Figure 3.10 Mean comparison of genotypes for NOS

Seed yield

According to the genotypic effect on SY was non-significant ($F = 0.54$, $P = 0.953$), suggesting a lack of genetic variability among genotypes for this trait. The genotypic mean square (30.418) was substantially lower than the error mean square (56.809). This result implies that seed yield may be strongly influenced by environmental conditions rather than genetics, similar findings were reported by Hasan and Deb (2017). This mean comparison for SY for each genotype revealing considerable variation (Figure 3.11). Genotype G9 demonstrates the highest SY at 27.12, followed closely by G26 at 27.00, identifying these as potentially superior yielding genotypes. In contrast, genotypes like G21 show a considerably lower seed yield at 13.52. The substantial variation in seed yield, ranging from 13.52 to 27.12, highlights the genetic potential for improving yield through selection and breeding.

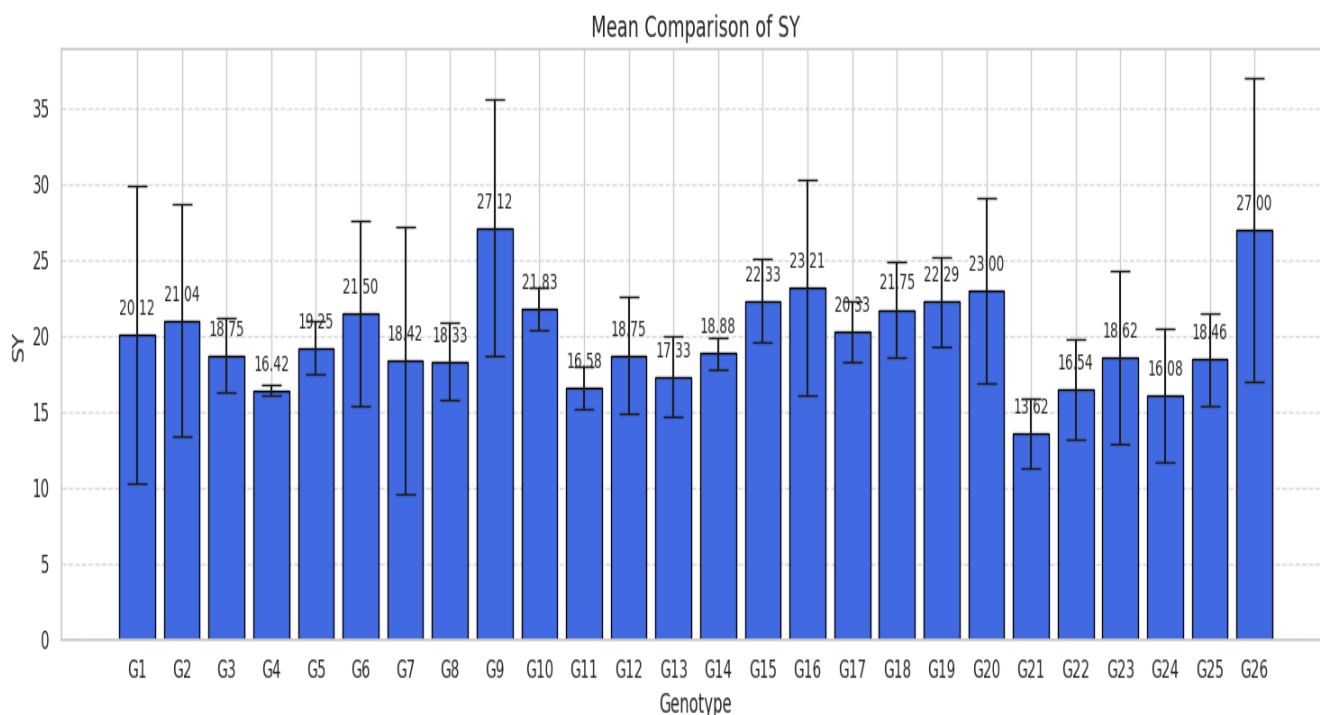


Figure 3.11 Frequency distribution of SY.

Hundred Seed weight

The ANOVA revealed highly significant genotypic differences for HSW ($F = 4.86$, $P = 0$). The genotypic mean square (46.520) was significantly higher than the error (9.570), confirming strong genetic control over this trait. Since seed weight directly affects market value and yield, this trait holds promise for selection and improvement, similar findings were reported by Hasan and Deb (2017). The mean comparison for HSW of each genotype revealing considerable variation (Figure 3.12). Genotype G17 stands out with a significantly higher HSW of 37.46, suggesting the production of larger or heavier seeds compared to other genotypes. Conversely, G1 and G7 show lower hundred seed weights at 22.83 and 23.21 respectively, indicating smaller or less dense seeds. The variation across genotypes, ranging from 22.38 to 37.46, points to genetic

diversity in seed characteristics. The analysis of HSW revealed highly significant genetic variation (F-ratio = 4.8611) with moderate-to-high heritability (56.28%). The phenotypic (16.70%) and genotypic (12.53%) coefficients of variation indicate substantial genetic variability with a lower environmental influence. This is further supported by a high genetic advance as a percentage of the mean (19.36%), which demonstrates strong potential for improvement through breeding. The moderate coefficient of variation (11.04%) and low standard error (1.7861) confirm good experimental reliability. These results indicate that seed weight is a highly heritable trait with excellent genetic variability, making it a prime target for effective selection.

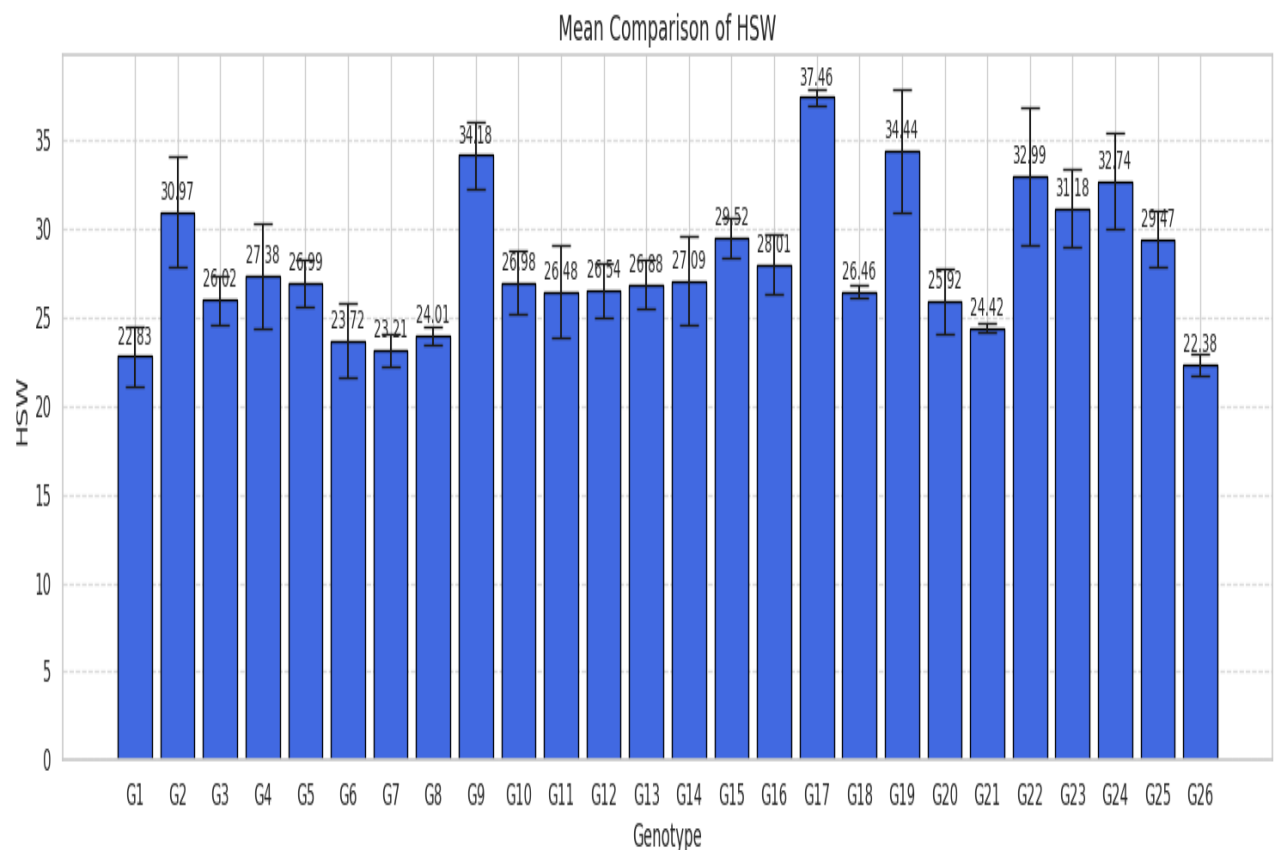


Figure 3.12 Mean comparison of genotypes for HSW

Biological yield

The ANOVA showed a non-significant genotypic effect on BY (F = 0.93, P = 0.568). The genotypic mean square (315.47) was nearly equal to the error mean square (339.64), indicating a weak genetic influence. Consequently, biological yield appears to be environmentally driven in the studied population. This mean comparison for BY show significant range among the genotypes, indicating varying levels of overall growth and biomass accumulation (Figure 3.13). Genotype G9 exhibits the highest biological yield at 79.96, suggesting its superior capacity for producing total plant biomass. In contrast, G11 shows a considerably lower BY at 41.29, highlighting a marked difference in growth potential.

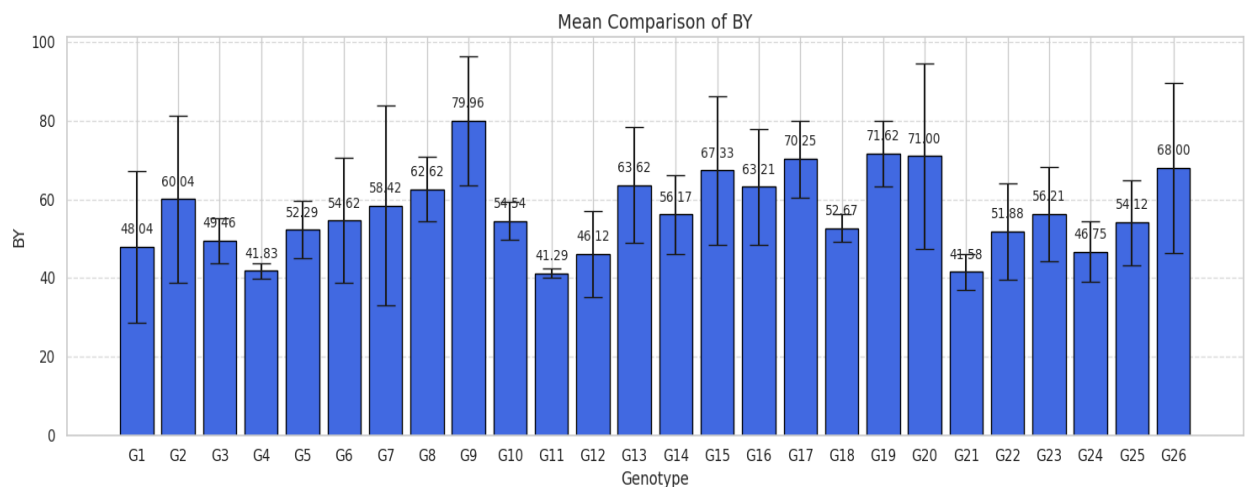


Figure 3.13 Mean comparison of genotypes for BY

Harvest index

The ANOVA showed non-significant variation among genotypes ($F = 0.86$, $P = 0.646$) for HI. The mean square for genotypes (44.434) was lower than the error mean square (51.402). This suggests that harvest index is not strongly governed by genetic factors under the current conditions, limiting its value for direct selection. This mean comparison for HI of each genotype revealing considerable variation (Figure 3.14). Genotype G18 shows the highest HI at 42.39, suggesting a superior partitioning of dry matter to the economic yield. This indicates that G18 is more efficient in converting total biomass into marketable produce. Conversely, genotypes like G8, G9, G10, G14, G17, G19, and G20 exhibit lower harvest index values ranging from 29.03 to 34.00, implying a relatively higher proportion of biomass remaining in vegetative parts.

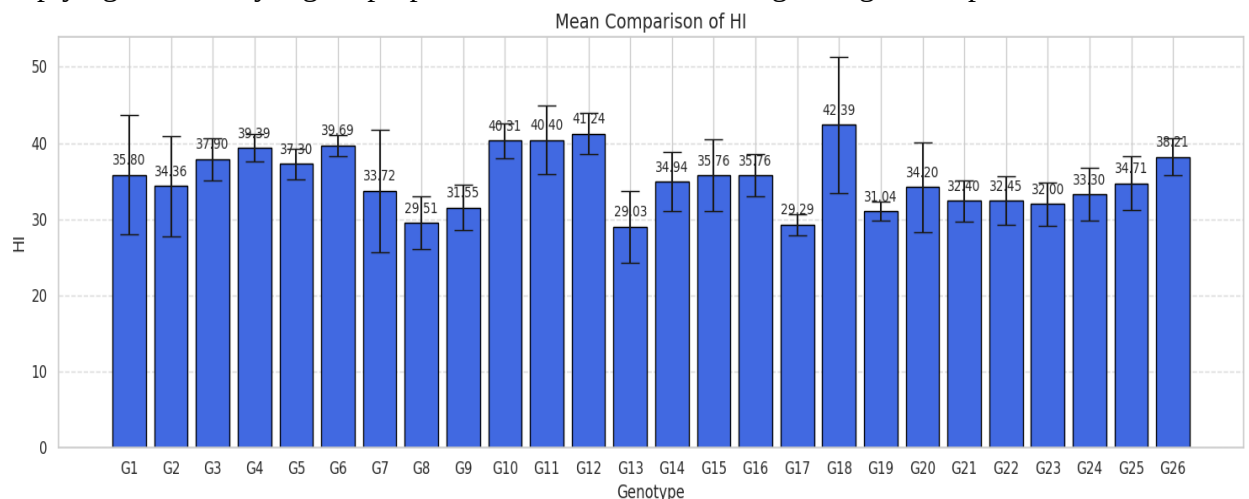


Figure 3.14 Mean comparison of genotypes for HI%

Coefficient of Variation

The coefficient of variation (CV) is a valuable statistical tool that helps in comparing the degree of variation between different datasets, regardless of their units or scales. We

calculated coefficients of variation value of different parameters for assessing reliability of the results. CV value for the characters no. of seed/plant, seed weight, biological yield, dry leaf weight, no. of pods/plant and germination % are 40.22, 37.86, 32.3, 34.11 and 24.33 respectively are high. CV value for the characters like days to 50% flowering, fresh leaf weight, no. of leaflets/leaf, plant height at flowering, plant height at harvesting, no. of pods per plant, harvest index and hundred seed weight are 1.52, 15.69, 3.67, 14.17, 7.98, 18.17, 20.34 and 11.04 are low. Generally, CV values are considered as benchmark for reliability of data. Conversely parameters having greater than 20% CV value are considered less reliable and means greater variability in dataset. Therefore, characters like days to 50% flowering, fresh leaf weight, no. of leaflets per leaf, plant height at flowering, plant height at harvesting, no. of pods per plant, no. of seeds per pod, harvest index and hundred seed weight have less or equal to 20 % CV value which shows that less variability in data and consider as reliable. Characters like no. of seeds per plant, seed yield, biological yield, dry leaf weight and germination % have higher CV value, which shows that higher variability and less reliability in dataset.

Principal Component Analysis

Principal Component Analysis (PCA) is an effective statistical method for reducing data dimensionality. It converts a broad set of variables into a smaller subset while preserving the majority of the original dataset's informational content. PCA helps in simplifying complex datasets, making data visualization and interpretation easier. By identifying the principal components, it reveals the directions of maximum variance in the data. PCA reduces noise and redundancy, improving the efficiency of machine learning models. Overall, PCA enhances data analysis by making large datasets more manageable and insightful.

Computational steps of Principal Component Analysis

All the three principal components (PCs) PC1, PC2 and PC3 had Eigen values >1 and contributed 61.10% of total cumulative variability among various genotypes. PC-1 was the component that generated the most variability (25.4%), followed by PC-2 and PC-3 which accounted for 21% and 14.7% respectively. The PC 1 revealed positive factors loadings for germination percentage, plant height at flowering, no. of leaflets per leaf, dry leaf weight, fresh leaf weight, seed yield and number of seed per plant. PC-2 showed that biological yield, Seed yield and number of seed per pod were the positive factors loading. The parameters which contributed to positive factors loading towards PC-3 were the plant height at germination %, days to 50 % flowering, fresh leaf weight, no. of pods per plant, plant height at flowering, no. seeds per pod, seed yield, biological yield and harvest index %. The results demonstrated that for germination percentage, plant height at flowering, no. of leaflets per leaf, dry leaf weight, fresh leaf weight, seed yield and number of seed per plant made the highest contributions toward PC-1 with values of 0.317, 0.162, 0.233, 0.233, 0.237, 0.393 and 0.112 respectively. The parameters hundred seed weight and biological yield were the highest contributors to PC-2 with values of 0.287 and 0.082 respectively. The parameters germination %, biological yield and harvest index % were the highest contributors to PC-3 with the values of 0.409, 0.24 and 0.497 respectively.

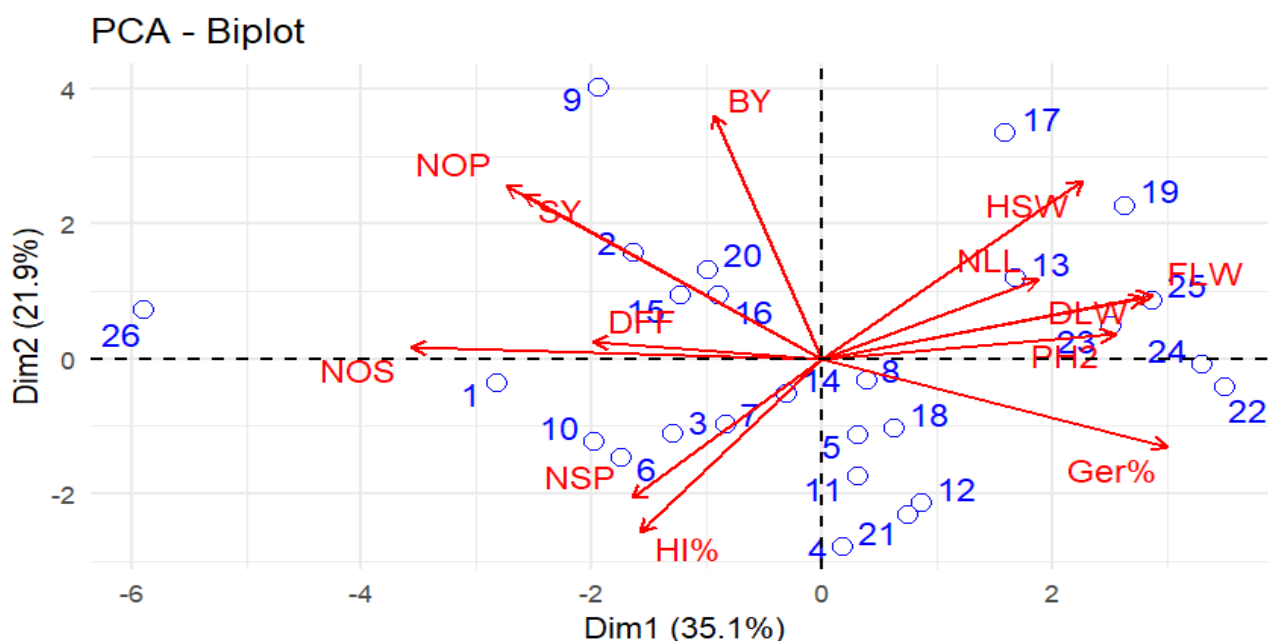
Biplot

A principal component biplot is a graphical tool used to represent the performance of parameters as vectors on a plot. The length of each vector reflects the amount of variance explained by that specific parameter. Biplots also help visualize relationships between different traits if the angle between two parameter vectors is less than 90° , it indicates a positive correlation; if the angle is greater than 90° , the correlation is negative (Gabriel 1971). The PCA biplot explains the variability among the 26 chickpea genotypes using the first two principal components. The red vectors represent the traits, and their length indicates the extent of their contribution to the variability. Traits such as HSW, PH2, SY, BY, NSP, NOP, and PH1 are represented by longer vectors, suggesting that these traits play a major role in differentiating the chickpea genotypes. In contrast, DFF and Ger% have relatively shorter vectors, indicating a smaller contribution to overall variation. The blue points indicate the genotypes, and their placement relative to the vectors highlights their trait associations. For instance, genotypes such as 17, 19, 24, and 25 are positioned in the direction of yield-related traits, showing their potential as high-performing lines, whereas genotypes like 26 and 9 are positioned away from these vectors, reflecting divergent performance.

Figure 3.15 Biplot graph for PCA

Correlation Analysis

Correlation was done to establish the level and direction of associations between



various agronomic traits. The correlation coefficient (r) has a value of -1 to +1 with the positive value representing a direct relationship and the negative value representing an inverse relationship between traits. The value that is near zero indicates weak or no linear relation. There was testing of significance of correlations at probability levels of 5% and 1% (α). These relationships are the key to understanding major traits that can be

successfully used in the process of selection and crop improvement programs.

Percent germination was correlated with other traits

The percent germination was found to be associated with the traits of study variably. Very strong positive relationships were found with the height of plants at harvesting (0.645) and flowering (0.690), which shows that improved germination also leads to improved vegetative performance which agrees with Singh et al. (2021). The percentage of germination also had positive but nonsignificant correlations with dry leaf weight, number of leaflets per leaf, number of seeds per pod, 100-seed weight, and harvest index which reflect a generally positive but weak relationship. On the other hand, there were also high levels of negative correlation with the days to 50 percent flowering (-0.464) and with the volume of pods per plant (-0.563), seeds per plant (-0.562), and seed yield (-0.461) indicative of the fact that a higher percentage germination may not always lead to better reproductive performance under the current circumstances. It was found to have a negative association with biological yield although not significant.

Correlation of height of plant at flowering with other traits.

The number of days to 50% flowering (0.690**), fresh leaf weight (0.624**), germination percentage (0.690**), and height of the plant at harvesting (0.774) had highly significant positive correlation with plant height at flowering, which was in line with the findings by Banik et al. (2017). The existence of these relations means the coordinated vegetative development. There were non-significant positive relationships with dry weight of leaves, number of leaflets per leaf, number of seeds per pod, 100 seed weight, and biological yield. Nonetheless, one of the most important negative correlations was noted with the number of pods per plant (-0.430) and indicates that over growth of plants at flowering can inhibit the aftermath of pods. Negative but insignificant associations with harvest index, number of seeds per plant, and seed yield.

Correlation of Number of Leaflets per Leaf and other Traits.

Dry and fresh leaf weight had a positive positive relationship with the number of leaflets per leaf (0.616** and 0.584** respectively), which shows that it greatly contributes to the leaf biomass as reported by Ton and Anlarsal (2017). The positive, yet non-significant correlations were found with the biological yield, percentage of germination, the height of the plant at flowering and harvesting, and the weight of 100 seeds. Negative but non-significant relationships were observed with days to 50% flowering, harvest index, the number of pods per plant, the number of seeds per plant, the number of seeds per pod, and seed yield indicating that this trait did not have a great impact on yield.

Association of Fresh Leaf Weight with Other Traits

The weight of fresh leaf had very strong, significant positive relationships with the dry leaf weight (0.564**), the number of leaflets per leaf (0.584**), and the height at flowering (0.624**), which corroborates the findings of Singh et al. (2021). There were also significant positive relationships with the percentage of germination and the height of the plant at harvesting. On the other hand, the correlation was significantly negative

with days to 50% flowering (-0.549) and this means that fresh leaf biomass in plants was greater which resulted into the plants flowering earlier. There were negative relationships (though not significant) between relationship with harvest index, number of pods per plant, number of seeds per plant, number of seeds per pod, and seed yield.

Association of Dry Leaf Weight with Other Traits

The dry leaf weight also had very significant positive correlation with fresh leaf weight (0.564**), leaflets per leaf (0.616**), and 100-seed weight (0.462**), and this confirms previous stipulations made by Ton and Anlarsal (2017). There was a non-significant and positive correlation with germination percentage and plant height characteristics. Nevertheless, the number of seeds per plant (-0.474**) and days to 50% flowering (-0.136) had a highly significant negative correlation with dry leaf weight and a significant negative correlation with days to 50% flowering, respectively. Its relation with biological yield, harvest index, the number of pods per plant, the number of seeds per pod and yield of seeds was negative but not significant.

Relationship between Days to 50% Flowering and Other Traits.

The positive correlation between days to 50 percent flowering and flowering plant height (0.690 2 star) was found as expected by Saki et al. (2009). It was observed that harvest index, number of pods per plant, number of seeds per plant, and seed yield showed positive but non-significant correlation. Conversely, significant negative correlations were observed to be of high significance with fresh leaf weight, germination percent and vegetative height at harvesting meaning that delayed flowering is related to low vegetative vigor. There was also a strong negative correlation with the dry weight of leaf.

Relationship between Plant Height at Harvesting and other Traits.

The height of plants at harvest was strongly and positively related to the percentage of germination (0.645**) and height of plants at the time of flowering (0.774**), similar to Banik et al. (2017). The fresh leaf weight and 100-seed weight also had significant positive correlations. On the other hand, a very high negative correlation was observed with days to 50% flowering, and number of seeds per plant was significantly negatively correlated. Other relationships such as the relationship with harvest index, number of pods per plant, number of seeds per pod, and seed yield were not significant.

Relationship between Number of Pods per Plant and other Traits.

The positive relationships with biological yield (0.638**), the number of seeds per plant (0.589**), and seed yield (0.808**) were of great significance, which validates the significant contribution of the number of pods per plant to the formation of the yield, as shown by Ton and (Anlarsal, 2017). Those with non-significant positive correlations were days to 50 percent flowering, harvest index, and weight of 100 seeds. There were very important negative relationships with germination percentage and plant height on flowering.

Relationship of Number of Seeds per Pod with other Traits.

There were very strong positive correlations between number of seeds per pod and harvest index (0.508**) and number of seeds per plant (0.638**), in line with Saki et al. (2009). A very important negative relationship was also found with 100-seed weight (-0.673) and one can observe a trade-off between seed size and seed number. Most other associations were not significant.

Positive correlation between the number of seeds per plant and other characteristics

Seed numbers per plant were, also, significantly and positively correlated with number of pods per plant (0.589), number of seeds per pod (0.638), and seed yield (0.736), as found by Singh et al. (2021). It was found that there were significant negative correlations with the dry leaf weight, germination percentage, height of the plant at the time of harvesting, and 100-seed weight that were suggestive of compensatory interaction among yield components.

Correlation of Seed Yield and other Traits.

The seed yield showed very significant positive correlation with biological yield (0.758**), number of pods per plant (0.808**), number of seeds per plant (0.736**), and 100-seed weight (0.798**), which is similar to the results of Saki et al. (2009). Negative correlation was very significant with the percentage of germination, and other correlations were not very significant.

Weight of Hundred-Seed was related to other traits

The weight of a hundred seeds revealed very significant positive correlations with the weight of the dry leaves and with the seed yield. There was also a significant positive correlation with height of the plants at harvesting. Nevertheless, it had very important negative correlations with harvest index, seeds per plant and seeds per pod, which were a trade-off between seed size and seed numbers.

Association of Biological Yield with Other Traits

Biological yield exhibited highly significant positive correlations with number of pods per plant and seed yield, supporting Saki et al. (2009). A highly significant negative correlation was observed with harvest index, while other relationships were mostly non-significant.

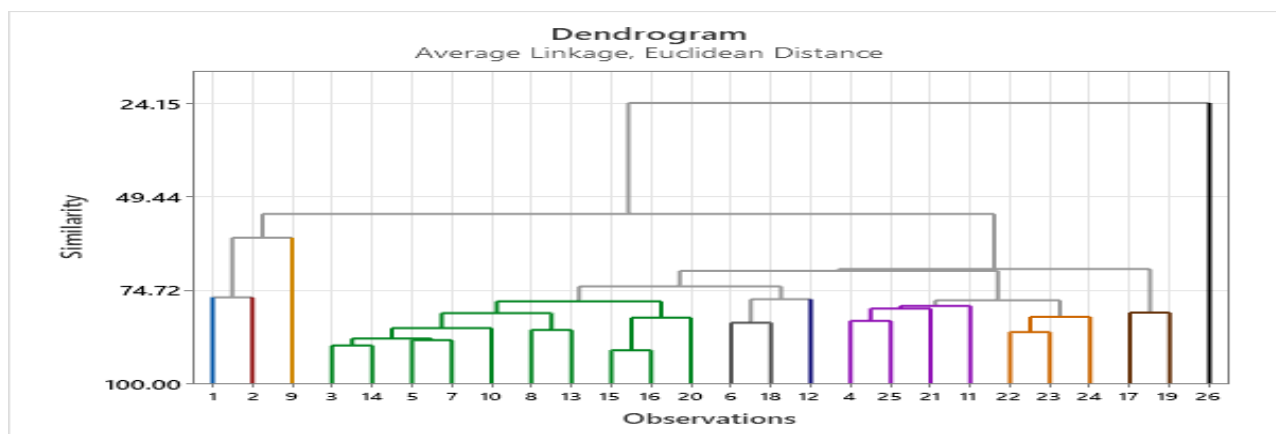
Association of Harvest Index with Other Traits

Harvest index showed a highly significant positive correlation with number of seeds per pod and a significant positive correlation with number of seeds per plant, similar to Banik et al. (2017). Conversely, it exhibited highly significant negative correlations with biological yield and 100-seed weight. Associations with other traits were non-significant.

Cluster Analysis

The cluster analysis identified 10 distinct clusters of 26 chickpea genotypes in terms of morphological characteristics, indicating that there was a lot of genetic variation.

Clustering pattern did not depend on geographical origin, and it confirms previous results on genetic divergence not always being geography-dependent (Gediya et al., 2019). Cluster 6 had the best combination with the highest level of biological yield and high number of seeds, and had higher 100-seed weight, and number of pods thus it has good prospects of yield increase. Cluster 10 also had excellent seed yield whose main reasons were that the highest number of seeds per plant and the highest number of seeds per pod but the percentage of germination is low which restricts its application to a wider range. Conversely, Clusters 4 and 9 had the lowest yield attributes indicating little value of yield selection. Cluster 7 had the highest germination percentage and harvest index and is, therefore, appropriate in enhancing crop establishment and crop efficiency. Cluster 8 was found to be superior in seed size and height of the plants whereas Cluster 5 exhibited a combination of early flowering, good germination, high harvest index and seeds per pod which is useful in coming up with early and efficient chickpea varieties. The inter-cluster distance analysis (figure 3.17) indicated that Cluster 8 and Cluster 10 have the highest level of genetic divergence, then Cluster 1 and Cluster 8 showing that these groups have a wide genetic variation. The fact that these clusters are so large implies that inter-cluster crosses are bound to generate high heterosis and transgressive segregants. On the contrary, Cluster 4 and Cluster 9 are closely genetically similar since their minimum genetic distance does not allow creating



genetic variability, as Mallikarjuna et al. (2020) state. To achieve successful breeding, preference should be given to genotypes of clusters that have high inter-cluster distance and high performance of traits. Accordingly, crossing genotypes from Cluster 8 (high 100-seed weight) with those from Cluster 10 (high number of seeds per plant) is recommended to combine complementary traits and enhance yield potential in future chickpea breeding programs.

Range and Mean Performance of Morphological and Yield Traits in Chickpea

The evaluation of chickpea genotypes revealed substantial genetic variability in morphological and yield-related traits. Germination percentage ranged from 5.58% to 74.68% (mean 52%), highlighting differences in seed vigor, while days to 50% flowering varied from 94 to 100 days. Vegetative traits such as fresh leaf weight (285.51–486.78 mg) and dry leaf weight (66.98–202.39 mg) reflected diversity in biomass accumulation. Plant height ranged from 32.47–65.66 cm at flowering and 68.42–97.50 cm at harvest. Yield components were highly variable, with pods per plant

(34.96–60.79), seeds per plant (48.54–120+), and 100-seed weight (22.38–37.46 g). Biological yield varied from 41.29–79.95 g, seed yield from 13.63–27.13 g, and harvest index from 29.03%–42.38%. This wide variation highlights strong genetic potential for chickpea improvement.

SUMMARY

Chickpea (*Cicer arietinum* L.) is an important pulse crop; it is the third-largest pulse crop in the entire world following faba bean and field pea as well as it is the crop that has large areas of cultivation in arid and semi-arid areas. Being a source of protein (1722 percent protein) and a legume, it is beneficial to human nutrition and enhances the soil fertility due to nitrogen fixation. The 26 Kabuli chickpea genotypes tested by this study comprised of a commercial check and that was tested at the University of Agriculture, Faisalabad on the field using a randomized complete block trial with three replications. Morphological and yield-related characteristics were found to be recorded in the form of plant height, pods per plant, seed yield, biological yield, harvest index, germination, flowering time, weights of leaves, and 100-seed weight. The statistical tests (ANOVA, correlation, and PCA) showed the level of genetic variability was significant. Characteristics such as pods per plant, a seed yield, 100-weight of a seed and biological yield were of high heritability suggesting that the same can be enhanced. The positive correlations between seed yield and other characteristics indicate proper selection criterion. Cluster analysis was used to classify the genotypes into 10 clusters, Cluster 6 and 10 having the best yield properties and Cluster 8 having the highest 100-seed weight and plant height. Clusters 8 and 10 showed the most disparity capturing the possible parental combinations in which to breed. Significant in the study is the importance of genetic diversity in producing high yielding and stress resistant chick's pea varieties with the role of ensuring food security, improved nutrition and sustainable agriculture in Pakistan and related countries.

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