

CORRELATION, HERITABILITY AND PATH ANALYSIS OF MORPHOLOGICAL AND YIELD-ASSOCIATED TRAITS IN *TRITICUM AESTIVUM* L.

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ABSTRACT

In agriculture, the demand for any breeding initiative is the versatility and co-relationship of genetic traits; these traits have a remarkable impact on grain yield. This research aims to analyze the genetic diversity and to examine both, the direct and alternate impacts of the key yield components on grain yield in ten genotypes of bread wheat. By using the Randomized Complete Block Design (RCBD) with three replications, significant variations between wheat cultivars were noted in every aspect of growth and yield component. AS-9 and AS-8 were identified as the highest-yielding varieties, based on the average performance. The principal results highlighted strong relationships between number of tillers plant⁻¹ and grain yield plant⁻¹. Spike length showed positive interrelation with the number of grains spike⁻¹, seed index and grain yield plant⁻¹. Both traits, the numbers of grains spike⁻¹ and seed index have a strong positive correlation, which positively influences grain yield plant⁻¹. The research findings showed the capabilities to enhance overall seed yield in wheat through selective breeding by focusing on the interaction of positive correlation on the traits like number of tillers plant⁻¹, spike length, spikelets spike⁻¹, number of grains spike⁻¹, seed index and grain yield plant⁻¹, due to interrelated positive correlations. High levels of heritability values were found in almost all of the traits which indicate their genetic consistency. Path analysis showed a negative straight impact on the grain yield plant⁻¹, while spike length and number of grains spike⁻¹ had significant positive indirect effects. Overall, the study provides valuable insight into potential selection criteria and breeding strategies for creating high-yielding wheat varieties.

Keywords: Bread wheat; Correlation; Genetic diversity; Heritability; Path analysis; Grain yield

INTRODUCTION

Wheat is a well-known self-pollinated grain crop and is also termed “king of cereals” in terms of productivity and overall food trade. It serves as a primary food grain crop in various countries including Pakistan (Kumar *et al.*, 2023a; Kumar *et al.*, 2023b; Khyber *et al.*, 2019). It is a member of Triticeae, which is a tribe of the Poaceae family, classified by Linnaeus in 1753. The importance of wheat is not only limited to being a primary necessary food source but it is also a valuable source of essential vitamins and minerals (Kumar *et al.*, 2023b). Additionally, it provides essential vitamins i-e., thiamin (0.30mg/100g), riboflavin (0.07 mg/100g), and niacin (1.7 mg/100g). Because of these nutritive elements, wheat isn't just a great source of carbohydrates but it also acts as an overall nutritional quality diet, particularly in regions where food scarcity exists (Abro *et al.*, 2019a).

Worldwide, Wheat is the most widely grown crop, covering 222.11 million hectares with a mass production of approximately 779.76 million tons and a productivity of 2.94 tons per hectare. Pakistan is the seventh largest producer of wheat in the world. Globally, wheat is one of the most important commodities in terms of area of growth, trade value, and family diets (Arain *et al.*, 2024). The staple wheat crop ensures food security for the people of Pakistan. Over 22 million acres are used for the cultivation of wheat, which contributes 1.8% of GDP and 7.8% of the value contributed to agriculture (Abro *et al.*, 2019b).

Investigation on interrelations highlighted the association of various characters with grain yield. Breeders find it valuable to acknowledge the link between a large number of targeted traits during the selection of varieties that exhibit a high number of specified qualities (Abo-Elwafa *et al.*, 2023). Furthermore, grain yield is a multiplex character which highly influenced by the interaction with different environmental phenomena which are impacting on grain yield reduction directly and consequently. The suitable option to improve wheat production is the development of productive varieties which help in adapting to the harsh environment and in resisting biotic and abiotic stress. Further, it could also be improved if required genetic differences are present within germplasm (Kumar *et al.*, 2023b). It is essential to understand the relationships between plant traits which are obtained via correlation coefficient and path coefficient analysis. In plant breeding, correlation proves to be an important

component as it was introduced in the late 19th century. The main purpose of correlation is to evaluate one or more morphological traits and serve as a basis for selection concerning other desirable plant characteristics. Correlation measures variation between two variables either in a positive or negative direction. In Positive correlation, the characters are directly proportional to each other; if a character increases the other related characters will also increase. Similarly, in negative correlation the characters are inversely proportional to each other; if a character increases the other characters will decrease simultaneously (Vavilov *et al.*, 1951).

The primary goal of a plant breeder is to develop a superior genotype; character correlation is used as the tool for an effective selection, which is important to evolve for better varieties. Therefore, evaluating the correlation between yield and the units that contribute to it, may impart a useful indicator for selection to improve bread wheat yield. Genetic correlation plays a significant role in studying genetic modification in two traits under selection pressure. The environmental correlation helps study the related changes in two traits that are influenced by environmental factors (Sahar *et al.*, 2024). Path analysis could be used to compute the yield of the direct and subsequent impacts resulting from one or more of the components (Ahmad and Gupta, 2023). Path coefficient analysis makes it possible for independent variables to have a direct or indirect impact on dependent variables, which ultimately helps plant breeders consider the yield components and comprehend the source of the relationship between two variables (Dewey and Lu, 1959)

High heritability estimate becomes a part of the genetic relationship between ancestors and their offspring. The amount of a trait that is passed down from generation to generation completely depends on its heritability. For a successful breeding program, it is important to understand heritability parameters and evolve the association between the vital complex traits (Siyal *et al.*, 2024). It is realized that multiplex traits, which are governed by additive gene action are affected by environmental variation. Moreover, the amounts of heritability of the above characters are negatively correlated with the environment. If the heritability is low, it indicates that there is a higher impact of environmental factors on the genotype of the characters. Additionally, research has shown that studies like heritability estimations are useful for assessing the performance of parents in hybrids (Kashif and Khaliq, 2004). The present studies were carried out by using numerous statistical procedures such as correlation coefficient, path analysis, and heritability to determine the relationship between various economic traits that affect grain production.

MATERIALS AND METHODS

Experimental material and design

This research work was carried out during the Rabi season of 2023-24 at the Agriculture Research Center located in Tandojam, Sindh, Pakistan. The objectives were to investigate correlation, heritability, and path analysis within different genotypes of bread wheat (*Triticum aestivum* L.). Regarding this purpose, ten advanced lines such as; AS-1, AS-2, AS-3, AS-4, AS-5, AS-6, AS-7, AS-8, AS-9, and AS-10 were examined for yield and their contributing traits cultivated in three replications using Randomized Complete Block Design as experimental design. Every line was grown comprised of two rows, each measuring 4m in length and 30cm in width, per replication. Sowing was performed by using dibbling method placed at intervals of 20cm between plants and 30cm between the rows.

Crop management

The field was prepared using two plows prior surface leveling. Weeds and cultural management were used to protect the crop from adverse effects. During 6 irrigations, DAP (Di Ammonium Phosphate), Urea, macro and micronutrients was applied to fulfill their nutrient requirements at different growth stages of the crop. The crop was harvested in March 2024.

Data collection

In each replication, ten plants were selected randomly and also flagged for collection of data to assess characters like number of tillers plant⁻¹, spikelets spike⁻¹, spike length (cm), peduncle length (cm), plant height (cm), number of grains spike⁻¹, seed index (g), harvest index (%), Grain yield plant⁻¹ (g) and total biomass plant⁻¹ (g).

Statistical analysis

Analysis of variance was calculated which is suggested by Gomez and Gomez, (1984) through software Statistix 8.1. The Least Significant difference was elucidated to differentiate between the mean performances and to check the level of significance among the advanced lines developed by Steel and Toorie (1980).

Simple Correlations

Simple correlation coefficients (r) which was suggested by Snedecor and Cochran (1980) were calculated using the following formula:

$$\text{Coefficient of Correlation (r)} = \frac{\text{Covariance}}{\text{Geometric mean of covariance}}$$

$$r = \frac{\sum xy}{\sqrt{(\sum x)^2 - (\sum y)^2}}$$

$$\sum xy = \frac{\sum xy - (\sum x)(\sum y)}{N}$$

$$\sum x^2 = \frac{\sum X^2 - (\sum X)^2}{N}$$

$$\sum y^2 = \frac{\sum Y^2 - (\sum Y)^2}{N}$$

Where:

- X = Independent attributes
 Y = Dependent attributes
 N = Recorded observation numbers

Estimation of heritability

Heritability estimates were determined by Falconer and Mackey, (1996).

Variance

$$\text{Variance} = \frac{\sum x^2 - \frac{[\sum(x^2)]}{N}}{N-1}$$

Phenotypic variance $\sigma^2 p = VF_2$

Environmental variance $\sigma^2 e = \frac{VP1 + VP2}{2}$

Genotypic variance $\sigma^2 g = VF_2 - V_e$ or $V_p - V_e$

Heritability $h^2 = \frac{V_g}{VF_2} \times 100$ or $\frac{V_g}{V_p} \times 100$

Path coefficient analysis

Yield-attributing characters and their direct and indirect impact on grain yield were analyzed via the method used by Dewey and Lu, (1959) as follows:

$$r_{ij} = P_{ij} + \sum r_{ik} p_{kj}$$

The residual impact was calculated by utilizing the below formula, which assesses how well the casual elements explain the variability of the dependent element yield.

$$I = p^2 R + \sum p_{ij} r_{ij}$$

Thus, $p_{ij} r_{ij}$ = product of every variable's impact directly and its correlation coefficient to yield; $p^2 R$ = residual impact.

RESULTS AND DISCUSSION

The analysis of variance was executed to examine the genetic variability of agro-morphological traits in ten wheat genotypes (Table 1). These results indicated a high substantial variation at a 1% significance level within all bread wheat varieties in overall experimental materials, revealing the existence of considerable genetic variation in studied parameters. The effective genetic variability within the traits is necessary which helps the breeder to develop the superior varieties in future breeding programs. Similar researches were previously documented by various researchers; including (Kumar *et al.*, 2023a; Kumar *et al.*, 2023b; Kumar *et al.*, 2023c; Rana *et al.*, 2023; Khyber *et al.*, 2019; Kumar *et al.*, 2019) also noted that all of the treatments had a significant impact on the various characteristics which are examined. Significant results indicate the increased genetic variability between all the traits which were similarly demonstrated by (Ahamed *et al.*, 2021; Khan *et al.*, 2017). These results are in agreement with Kumar *et al.*, (2023a) who also investigated greater variations among the 100 tested genotypes, about all the traits.

Table 1. Mean squares for grain yield and its components of various traits in wheat genotypes.

Source of variance	Replication	Genotypes	Error
D.F	2	9	18
Number of tillers plant ⁻¹	0.98	20.20**	1.16
No. of Spikelets spike ⁻¹	3.20	10.42**	0.43
Spike length	0.00	8.52**	0.46
Peduncle Length	15.08	56.90**	2.06
Plant height	109.40	142.52**	3.59
Number of grains spike ⁻¹	2.27	263.43**	2.69
Seed index	0.40	84.61**	0.96
Harvest index	3.35	19.28**	4.60
Grain yield plant ⁻¹	0.69	57.41**	2.68
Total biomass plant ⁻¹	4.83	150.08**	3.56

Evaluation of genotypes through morphological characters

Number of tillers plant⁻¹

Tillers plant⁻¹ ranged from 5.33 to 12.76. The highest number of tillers plant⁻¹ was observed by AS-5 (12.76) followed by AS-8 (11.70), independently; whereas the lowest number of tillers plant⁻¹ was produced by AS-6 genotype (5.33). The mean tillers plant⁻¹ were 8.63 whereas five genotypes exceeded from average mean (Fig. 1).

Spikelets spike⁻¹

Spikelets spike⁻¹ ranged from 17.1 to 22.53. The maximum number of spikelets spike⁻¹ was produced by AS-1 (22.53) followed by AS-6 (21.53), respectively; although the least number of spikelets spike⁻¹ was resulted by AS-3 genotype (17.1). The mean spikelets spike⁻¹ was 19.41 whereas four genotypes exceeded from average mean (Fig. 2).

Spike length

The spike length ranged from 10.25 to 15.41 cm. The spike length was observed maximum for both genotypes AS-6 (15.41 cm) and AS-1 (15.11 cm), whereas minimum spike length (10.25 cm) was produced by the AS-8 genotype respectively. The overall mean for this trait was 12.45 cm and four cultivars were greater than the general mean (Fig.3).

Peduncle length

The peduncle length ranged from 28 to 40.28 cm. Maximum peduncle length was produced by AS-3 (40.28 cm) followed by AS-8 (39.38), whereas minimum peduncle length was produced by AS-4 (28.00 cm). The mean peduncle length was 34.11 cm and four genotypes were greater than the general mean (Fig. 4).

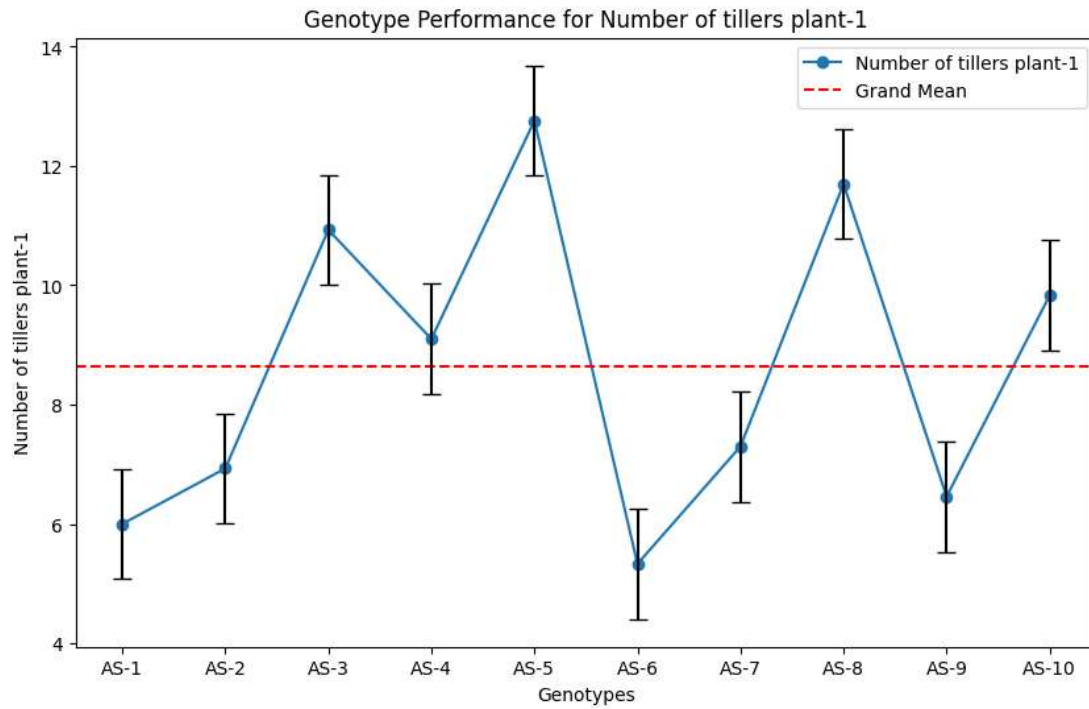


Fig.1. Mean performance of tillers plant⁻¹ of bread wheat genotypes.

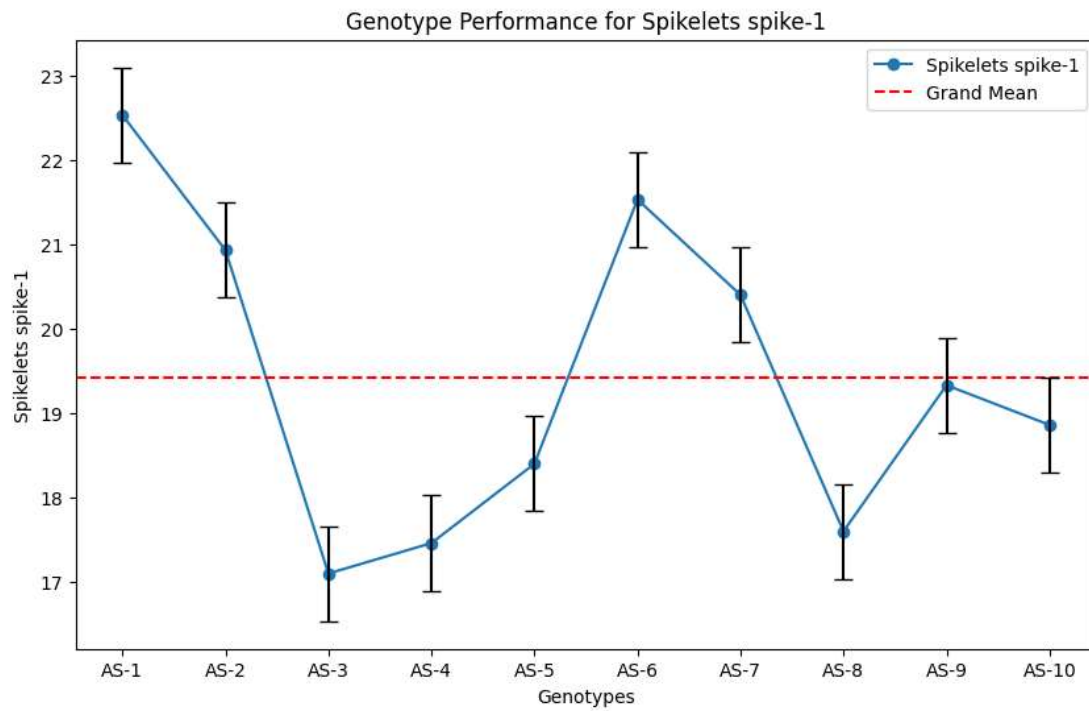


Fig.2. Mean performance of spikelets spike⁻¹ of bread wheat genotypes.

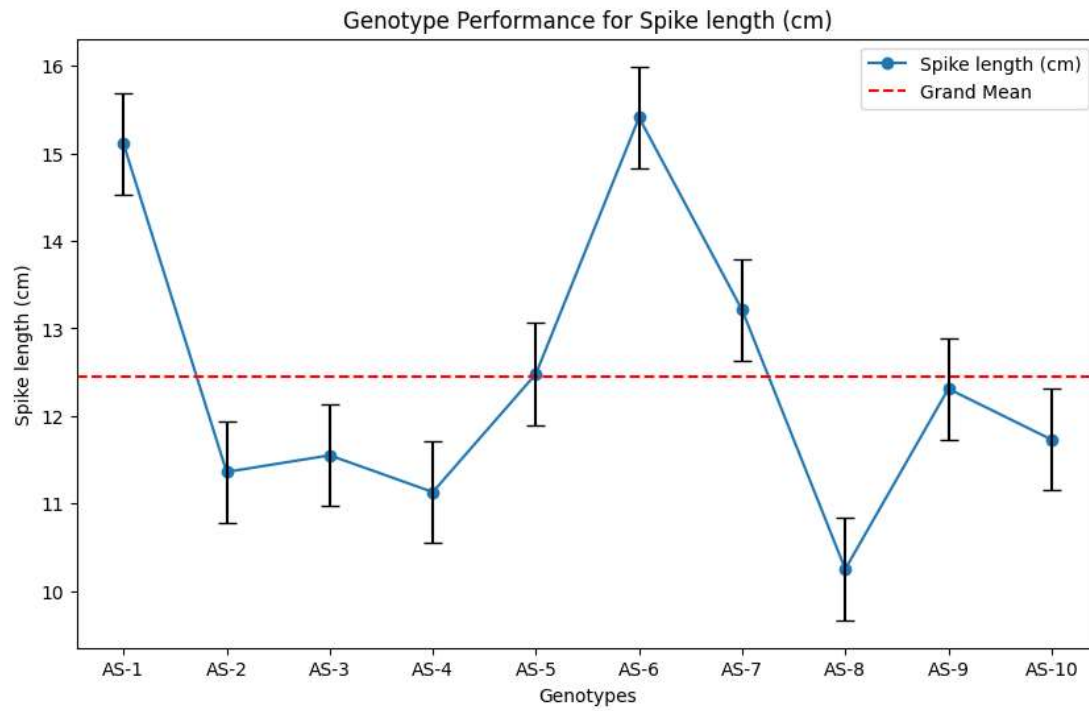


Fig. 3. Mean performance of spike length (cm) of bread wheat genotypes.

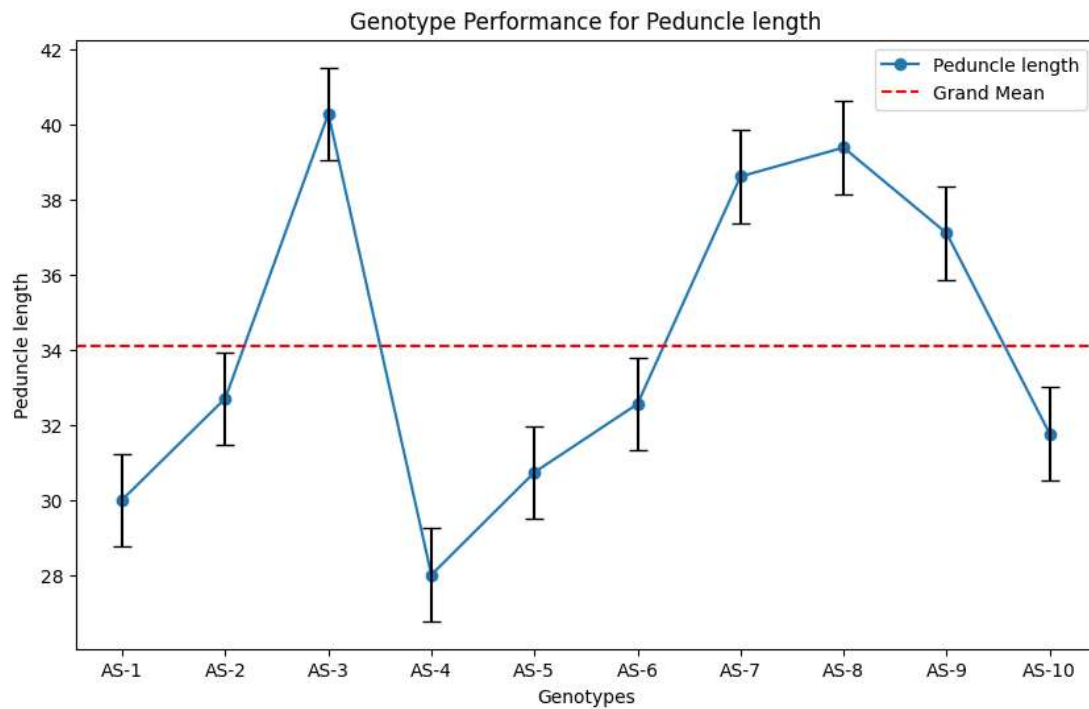


Fig. 4. Mean performance of peduncle length (cm) of bread wheat genotypes.

Plant height

The plant height is categorized from 71.19 to 84.56 cm. The genotype AS-9 revealed highest plant height (84.56 cm) within all cultivars subsequently by AS-2 (83.66 cm), AS-7 (83.33 cm), AS-5 (83.16 cm) and AS-3 (83.06 cm), although least plant height was revealed by AS-4 genotype (64.46 cm). The mean height was 78.37 cm and six genotypes were greater than the general mean (Fig. 5).

Number of grains spike⁻¹

The number of grains spike⁻¹ ranged from 66.83 to 95.75. Number of number of grains spike⁻¹ was highest (95.75) in case of genotype AS-8 followed by AS-9 (91.29), and minimum number of grains spike⁻¹ was produced by genotype AS-1 (66.83). The average number of grains spike⁻¹ was 79.81 and five genotypes exceeded the general mean (Fig. 6).

Seed index

The seed index ranged from 39.68 to 56.01 g. Maximum seed index was recorded by genotype AS-9 (56.01 g), followed by AS-7 (53.8 g) and minimum seed index was produced by AS-1 (39.68 g). The average seed index was 48.91 g and four genotypes exceeded the general mean (Fig. 7).

Harvest index

The harvest index ranged from 39.26 to 46.95 %. However, AS-3 showed maximum harvest index (46.95 %) among all genotypes followed by AS-2 (46.35 %) and AS-4 (46.11 %), and minimum harvest index was observed by AS-6 (39.26 %). The average harvest index was 43.76 % and five genotypes exceeded the general mean (Fig. 8).

Grain yield plant⁻¹

The grain yield plant⁻¹ was categorized from 31.72 to 43.98 g. The extreme grain yield plant⁻¹ was produced by AS-9 (43.98 g) followed by AS-8 (43.19 g), and minimal grain yield plant⁻¹ was found in the genotype AS-6 (31.72 g) respectively. The average grain yield plant⁻¹ was 37.12 g and five genotypes exceeded the general mean (Fig. 9).

Total biomass plant⁻¹

The total biomass plant⁻¹ ranged from 73.31 to 95.72 g. Maximum total biomass plant⁻¹ was produced by genotype AS-9 (95.72 g) followed by AS-8 (95.37 g) and minimum was observed by AS-7 (73.31 g). The average total biomass plant⁻¹ was 83.41 g and three genotypes exceeded the general mean (Fig. 10).

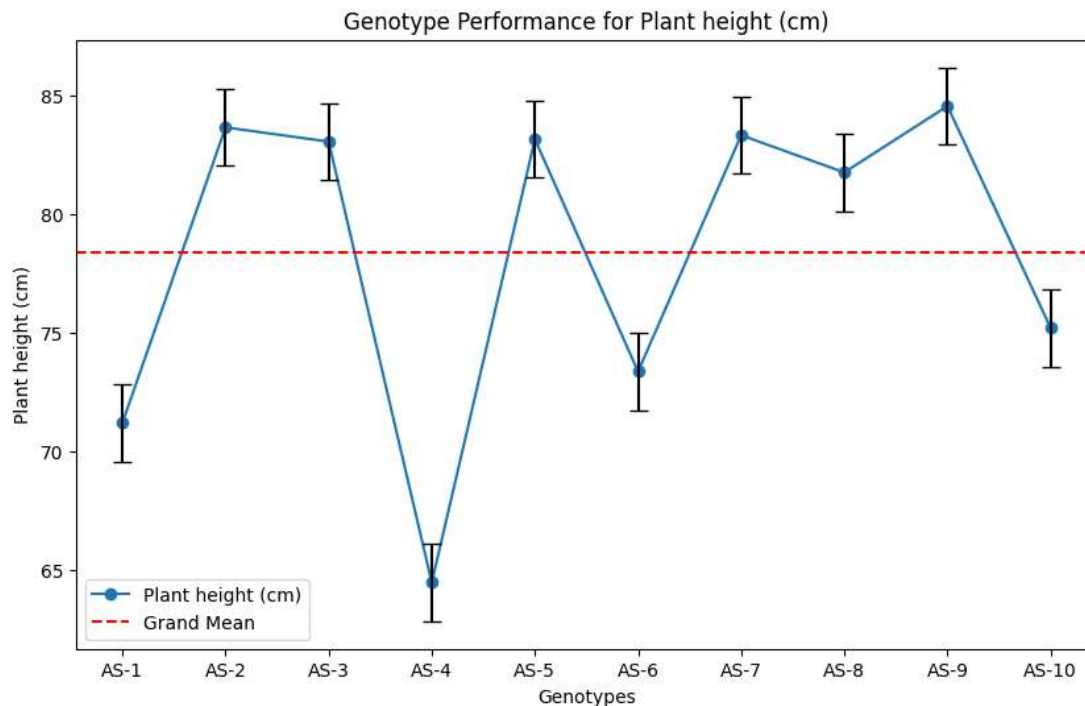


Fig.5. Mean performance of plant height (cm) of bread wheat genotypes.

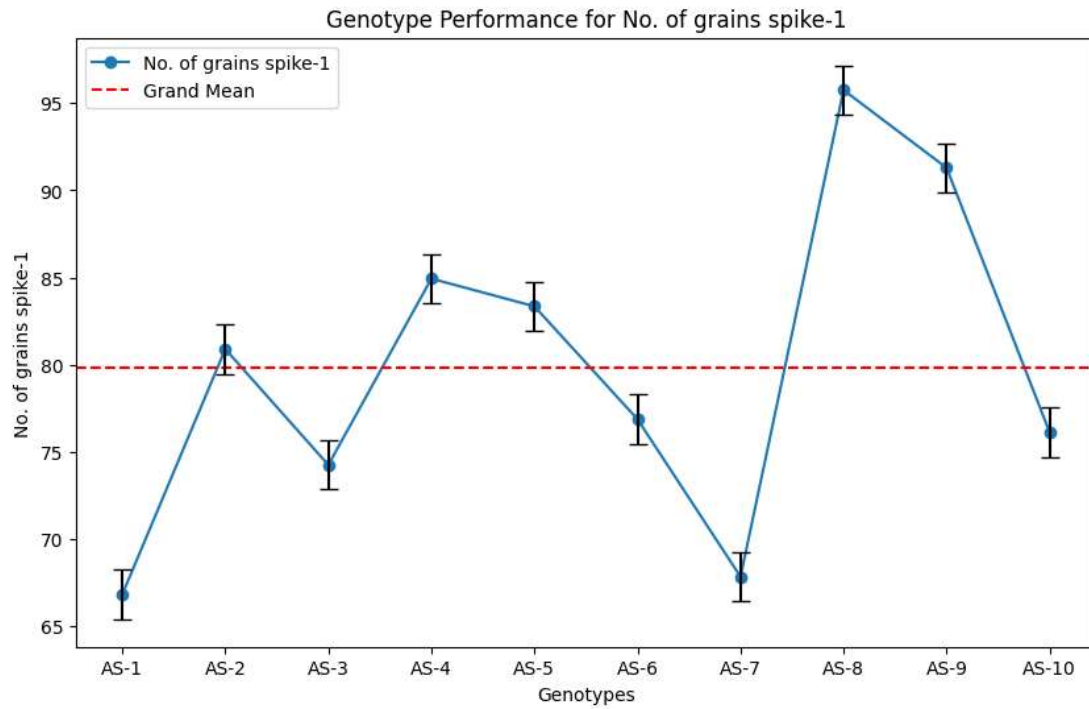


Fig.6. Mean performance of grain spike⁻¹ of bread wheat genotypes.

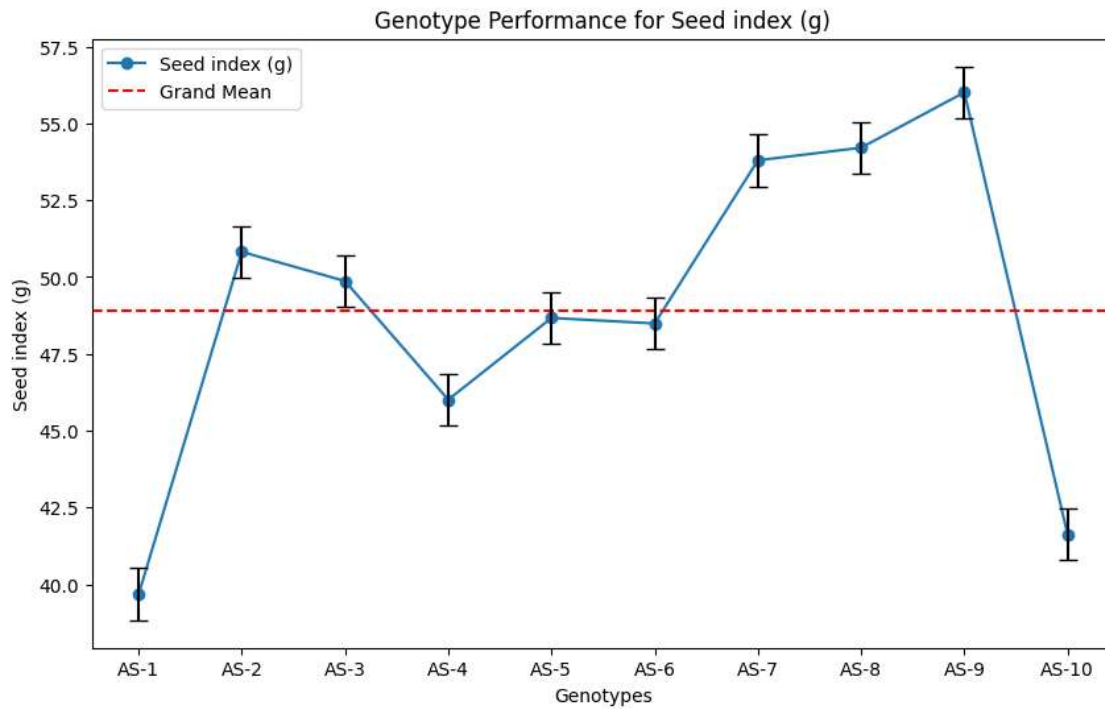


Fig.7. Mean performance of seed index (g) of bread wheat genotypes.

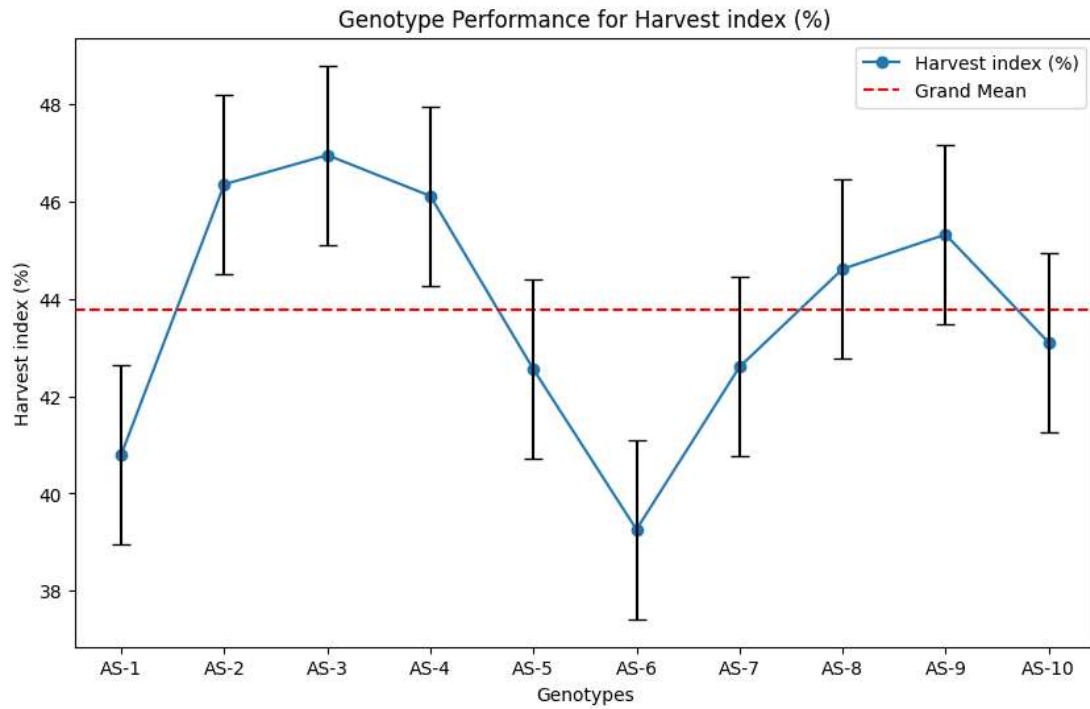


Fig.8. Mean performance of harvest index (%) of bread wheat genotypes.

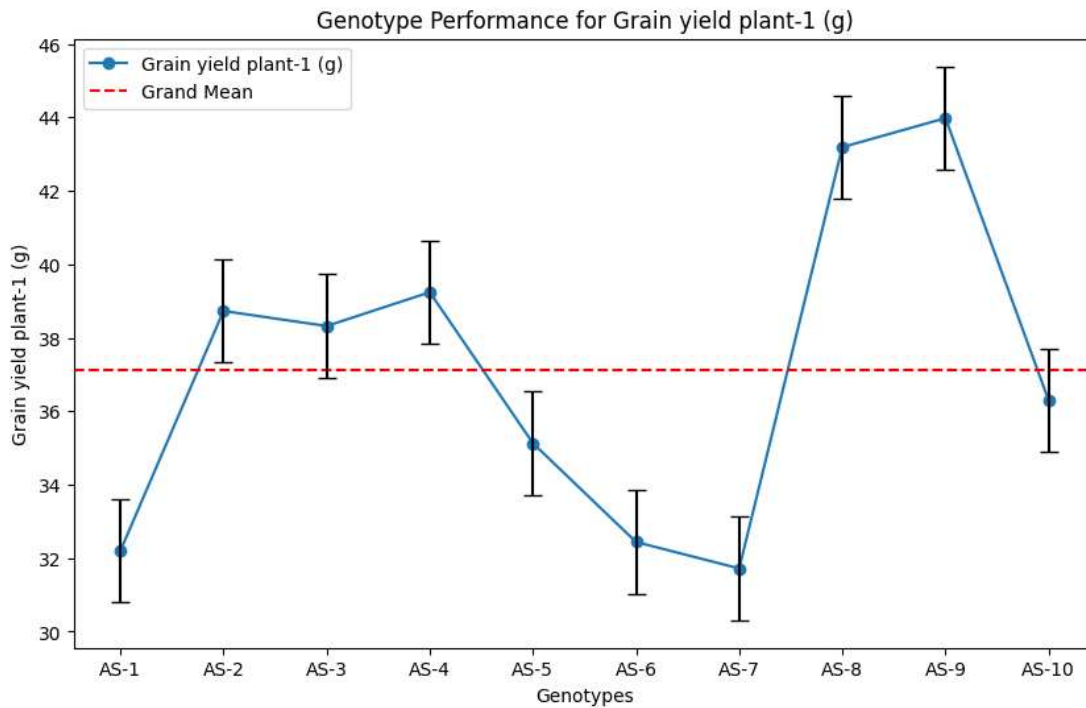


Fig.9. Mean performance of grain yield plant⁻¹ (g) of bread wheat genotypes.

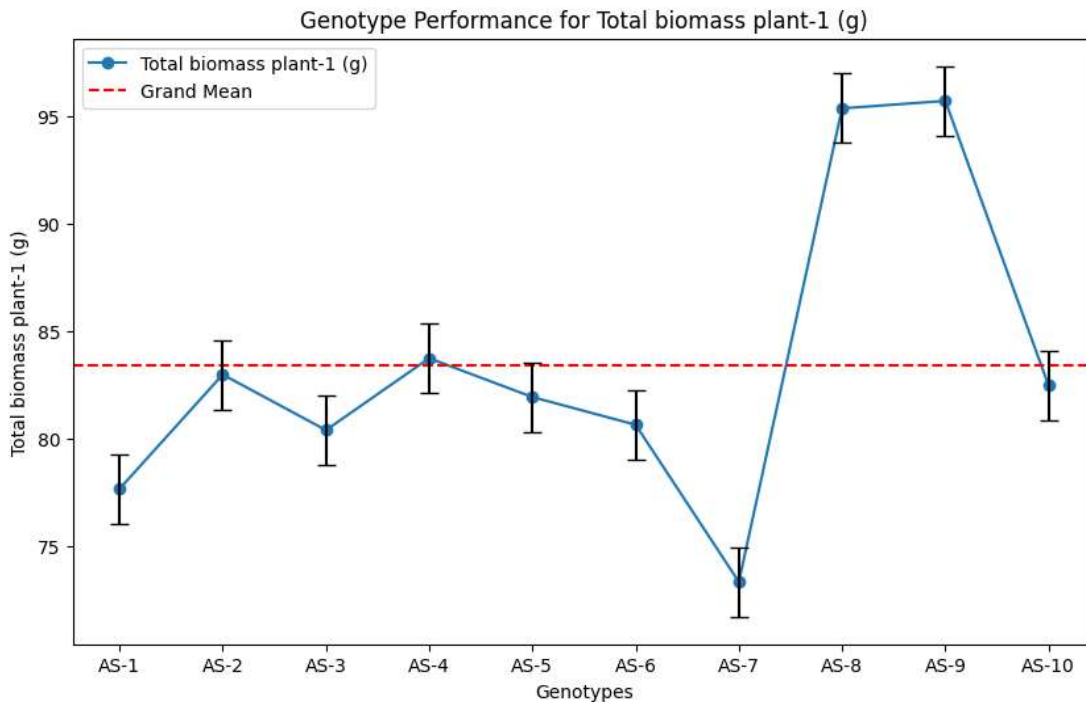


Fig.10. Mean performance of total biomass plant⁻¹ (g) of bread wheat genotypes.

Simple correlation among grain yield and its attributing features

Correlation coefficients are investigated between yield and its contributing factors. The data exhibited that number of tillers plant⁻¹ (0.732**), seed index (0.520**), harvest index (0.727**), and total biomass plant⁻¹ (0.838**) showed a positive significant interrelation with grain yield plant⁻¹ at 1% degree of significance (Fig. 11). In context, spike length (0.432*) and number of grains spike⁻¹ (0.416*) revealed a positively significant relationship with grain yield plant⁻¹ at a 5% degree of significance. Positive and non-significant relation was observed for spikelets spike⁻¹ (0.317), peduncle length (0.325), and plant height (0.232). Kumar *et al.*, (2023a) and Singh *et al.*, (2023) demonstrated that harvest index, test weight, and tillers plant⁻¹ revealed highly significant and positively interrelated with grain yield plant⁻¹, these results are in line with our results. On the other hand, results are contradictory to the results of Kumar *et al.*, (2023a), Kumar *et al.*, (2023b) and Kumar *et al.*, (2023c) who indicated that the character plant height was highly significant but negatively correlated with grain yield plant⁻¹. Likewise, Ozukum *et al.*, (2019) reported that both characteristics such as spikelets spike⁻¹ and plant height are positive and non-significantly correlated with grain yield plant⁻¹, these research results are in line with our results. Khadka *et al.*, (2020) and Abo-Elwafa *et al.*, (2023) illustrated that plant height was positively and non-significantly associated with grain yield plants which is in support of our results. Ahamed *et al.*, (2021) examined that peduncle length was non-significantly but positively associated with grain yield plant⁻¹.

Correlation among characters

The tillers plant⁻¹ was non-significantly positive interrelated with spike length (0.193), peduncle length (0.157), number of grains spike⁻¹ (0.346), seed index (0.084), harvest index (0.289) and total biomass plant⁻¹ (0.195). However, it showed a negative and significant relationship to plant height (-0.432*) at a 5% level of significance. Similarly, a negative but non-significant association was revealed with spikelets spike⁻¹ (-0.069) (Fig. 11). Our results are in favor of the research of Ullah *et al.*, (2021) described that several number of tillers plant⁻¹ was negative but significantly interrelated to plant height (-0.304*). Kumar *et al.*, (2023b) and Rana *et al.*, (2023) reported similar results of harvest index and seed index having positively and non-significantly associated with tillers plant⁻¹.

The trait spikelets spike⁻¹ exhibited high and positive significance associated with spike length (0.665**), number of grains spike⁻¹ (0.599**) and total biomass plant⁻¹ (0.673**) at 1% to the level of significance and harvest index (0.414*) at 5% level of significance, whereas the data indicated a positive and non-significant relationship to

remaining traits (Fig. 11). In this context, Singh *et al.*, (2023) reported that similar results of ear length (0.717**) and number of grains spike⁻¹ (0.449**) positively correlated with spikelets spike⁻¹. Singh *et al.*, (2020) reported that the harvest index (0.141**) showed a positive and highly significant relation with spikelets spike⁻¹. It demonstrated a positive correlation to peduncle length (0.063), these findings are slightly similar to our results.

The spike length was positively significant to several grains spike⁻¹ (0.599**), harvest index (0.688**) and total biomass plant⁻¹ (0.712**) at a 1% level of significance. In the context, it showed a positive correlation to peduncle length (0.408*) and seed index (0.477*) at a 5% level of significance. Plant height (0.297) showed positive and non-significant interrelation with spike length (Fig. 11). Singh *et al.*, (2023) found similar results of spike length having a positive and significant association with total biomass plant⁻¹ (0.720**) and seed index (0.294**).

The peduncle length revealed a significant positive interrelation with plant height (0.690**) and seed index (0.666**) at 1% degree of significance, whereas it revealed a positive and non-significant positive to the rest of the characters (Fig. 11). Rana *et al.*, (2023) illustrated a similar result of peduncle length having a positive significant association with plant height (0.674**) and seed index (0.288**) at a 1% level.

The plant height demonstrated a positive significant interrelation to seed index (0.652**) and the rest of the traits expressed positive and non-significant correlation (Fig. 11). Singh *et al.*, (2023) analyzed a highly significant and positive correlation with the seed index (0.313**). Rana *et al.*, (2023) also indicated the positive and significant relation between plant height and seed index (0.476**) this research work is in support of our results. The number of grains spike⁻¹ displayed positive significance with seed index (0.518**) and total biomass plant⁻¹ (0.894**) at a 1% level of significance. Additionally, the harvest index (0.331) resulted in a positive non-significant correlation with several grains spike⁻¹. The Seed index was positively correlated with total biomass plant⁻¹ (0.454*) at a 5% level of significance. Similarly, the harvest index (0.306) expressed a positive non-significant correlation with the seed index. The harvest index (0.252) indicated positive and non-significant interrelationship with total biomass plant⁻¹ (Fig. 11). Similar outcomes were also examined by (Khan and Naqvi *et al.*, 2012; Ayer *et al.*, 2017; Abro *et al.*, 2019b).

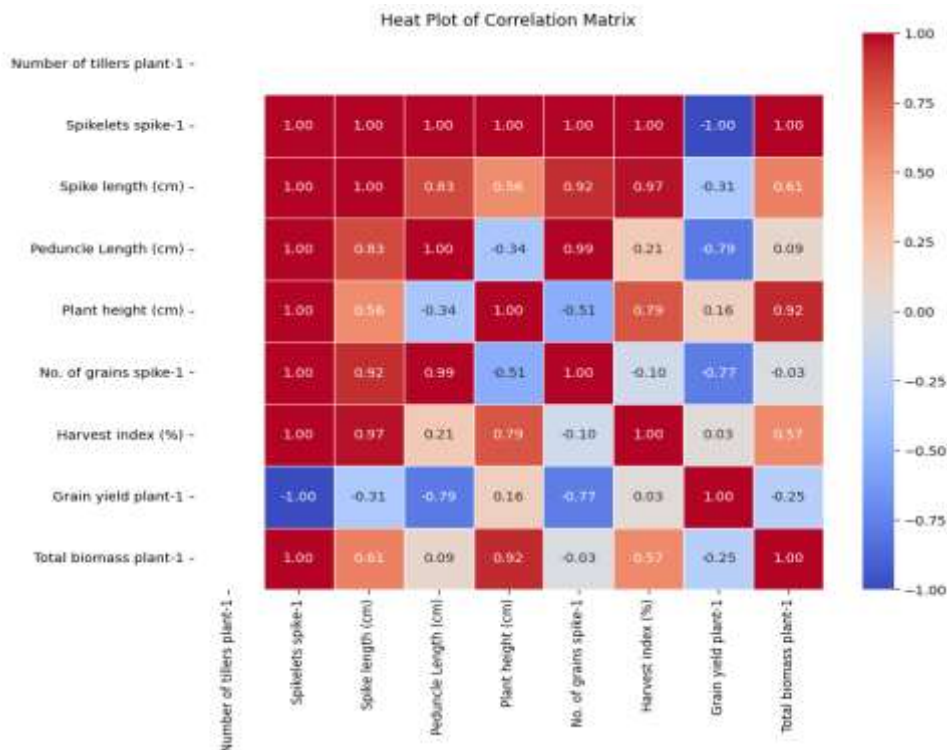


Fig.11. Correlation among ten studies characters in the studied wheat genotypes.

Heritability estimates

Environmental stress factors can influence the phenotypic expression of quantitative traits, often leading to reduced heritability values. Traits governed by strong genetic control may still exhibit variation under such

conditions, whereas those with lower heritability are more prone to environmental influence. Hence, considering genotype \times environment interaction is crucial in selecting stable and high-yielding genotypes in wheat breeding programs. Heritability estimates play a vital role in making decisions about the selection of characters but selection depends on only this factor and may be moderately effective as it fluctuates along with the environment. The broad sense heritability estimates were ranked from 37.03 to 97.49% (Fig. 12). Regarding Johnson *et al.*, (1955) heritability estimates ranged from low ($P < 30\%$) moderate (30-60%), and high ($>60\%$) values. In the present experiment, the highest heritability was exhibited by the seed index (98.49%). The present results are in favor of the seed index reported by Zewdu *et al.*, (2024), Olumekun *et al.*, (2022) and Ozukum *et al.*, (2019) concluded with high heritability. Heritability of 96.86% and 96.67% was recorded for total biomass plant⁻¹ and plant height, independently. These outcomes are supported by the results of Zewdu *et al.*, (2024) and Ozukum *et al.*, (2019) who stated that biological yield and plant height showed higher heritability. These outcomes contradicted with results of Olumekun *et al.*, (2022) and Lamara *et al.*, (2022) demonstrated low heritability values for plant height. In the context, the characters peduncle length, spikelets spike⁻¹, grain yield plant⁻¹, spike length, number of tillers plant⁻¹, and harvest index exhibited high heritability estimates of (95.24%), (94.60%), (93.87%), (92.96%), (92.51%) and (70.54%), respectively. Zewdu *et al.*, (2024) also reported high heritability estimates for said characters except tillers per plant⁻¹. Lone *et al.*, (2017) and Rana *et al.*, (2023) reported high heritability estimates of the studied traits. These results are consonance with our findings and Dragov *et al.*, (2022a) and Dragov *et al.*, (2022b) illustrated similar results for spikelets spike⁻¹. Furthermore, Kumar *et al.*, (2023b) and Rana *et al.*, (2023) also revealed similar findings for several tillers plant⁻¹ and peduncle length. The same outcomes were highlighted by Kadar and Moldovan *et al.*, (2003) while studying exotic and indigenous wheat cultivars and found high heritability estimates for plant height, number of tillers plant⁻¹, and grain yield plant⁻¹. Likewise, moderate heritability was exhibited for spike length followed by thousand kernel weight number of kernels spike⁻¹ and grain yield plot⁻¹ among all the locations indicating a good situation for efficient choice in said characters. In recent observation, heritability estimates were illustrated as low for several grains spike⁻¹ describing that the broad-sense heritability value for several grains spike⁻¹ was 37.04 percent. These outcomes were supported by Somro *et al.*, (2019), Mohsin *et al.*, (2009) and Ozukum *et al.*, (2019) who reported low heritability value for tillers plant⁻¹. According to our result, high heritability recommends that characters expressed were less affected by environmental circumstances. Thus, direct phenotypic selection in early segregating populations on these characters would be fruitful and lead to better results. As in our case, the moderate heritability value resulted in the trait number of grains spike advocating that the environment has a huge impact on the expression. Heritability solely does not come up with sufficient genetic information in regards to upgrading genotypes via selections.

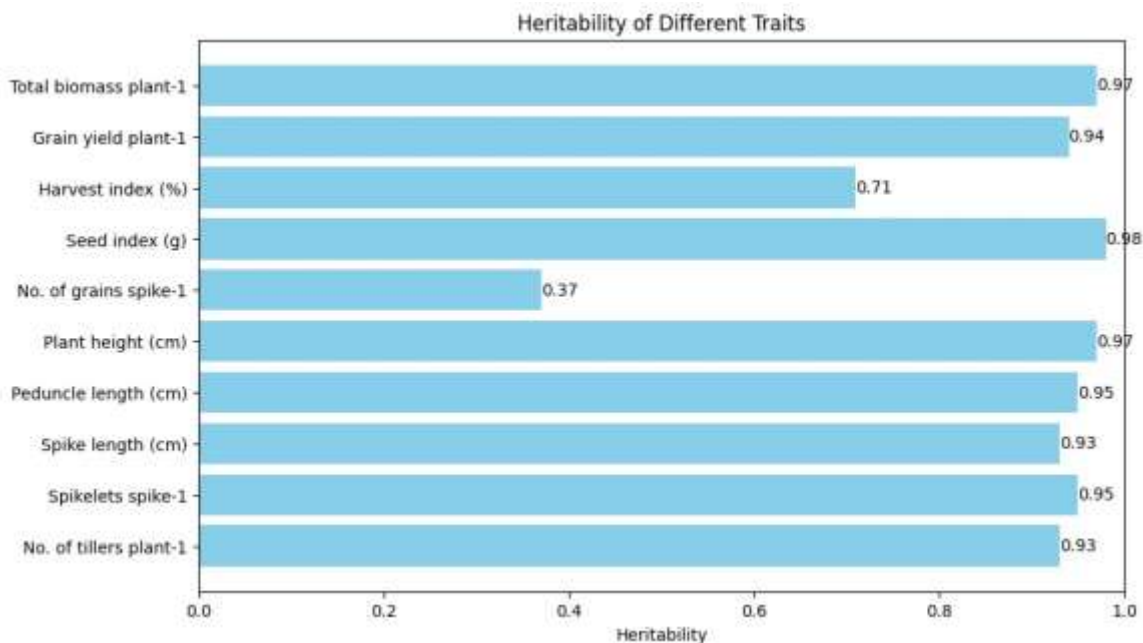


Fig.12. Heritability among ten studies characters in the studied wheat genotypes.

Path coefficient analysis

The data demonstrated in Fig. 13 indicates the most important yield components and their phenotypic correlations were estimated. The direct influence on grain yield by spike length was -0.2255 producing 52.12 percent of whole phenotypic association negatively. Conversely, Kashif and Khaliq, (2004) documented a significant positive direct impact of spike length on the grain yield plant⁻¹. However, the variation observed might be attributed to distinct environmental factors and spike length followed by thousand kernel weight number of kernels spike⁻¹ and grain yield plot⁻¹ diversity in breeding materials utilized. Whereas, the alternate effect through spikelets spike⁻¹ 0.2594 gave a positive pathway which produced 59.96 percent, those via several grains spike⁻¹ and seed index also revealed positive impacts i.e. 0.2322 and 0.1665 which made 53.67 and 38.48 percent contribution towards seed yield plant⁻¹. Matching outcomes were found by Mohsin *et al.*, (2009) revealed the positive indirect effect of several grains spike⁻¹ and spikelets spike⁻¹ to grain yield plant⁻¹. In this case, choosing spike length directly might lead to a yield reduction, opting for indirect selection methods such as spikelets spike⁻¹, number of grains spike⁻¹, and seed index could prove advantageous.

The direct impact of spikelets spike⁻¹ towards grain yield plant⁻¹ was estimated as -0.2707, which demonstrates 85.17 percent through spikelets spike⁻¹ to grain yield plant⁻¹ in the negative pathway. The same outcomes were found by Kashif and Khaliq, (2004). However, an indirect impact through spike length was in positive pathway 0.2082 which makes 65.51 percent, those via several grains spike⁻¹ and seed index also revealed positive effects i.e. 0.2219 and 0.1584 which made 69.82 and 49.84 percent contribution towards the grain yield plant⁻¹. The results are depicted by Veesar *et al.*, (2019) who demonstrated a negative indirect effect of the number of grains spike⁻¹ and seed index to seed yield plant⁻¹. These outcomes distinctly showed that while the direct impact of spikelets spike⁻¹ was negative, it contributed positively through other characteristics likewise, spike length, grains count spike⁻¹, and seed index, ultimately enhancing the yield.

The direct effect of several grains spike⁻¹ on grain yield plant⁻¹ was -0.2924 in the negative pathway which produced about 70.20 percent phenotypic correlation. Moreover, its alternate effect via spike length was 0.2741 in positive direction which formed 65.81 percent of grain yield plant⁻¹. Its indirect effect via spikelets spike⁻¹ was 0.2826 in a positive direction, which formed 67.85 percent through the seed index, it was 0.1522 in the positive pathway with a 36.54 percent indirect effect on the grain yield plant⁻¹. The outcomes of our study are depicted by Ayer *et al.*, (2017) demonstrated the positive direct effect of several grains spike⁻¹ (0.010) on grain yield. Additionally, there was a relative indirect and positive impact (0.238) on grain yield through biological yield and a low positive indirect effect (0.133) through harvest index. Elevated indirect effects via spike length, seed index, and spikelets spike⁻¹ implied that opting for indirect selection based on these traits for several grains spike⁻¹ could potentially lead to an enhancement in grain yield.

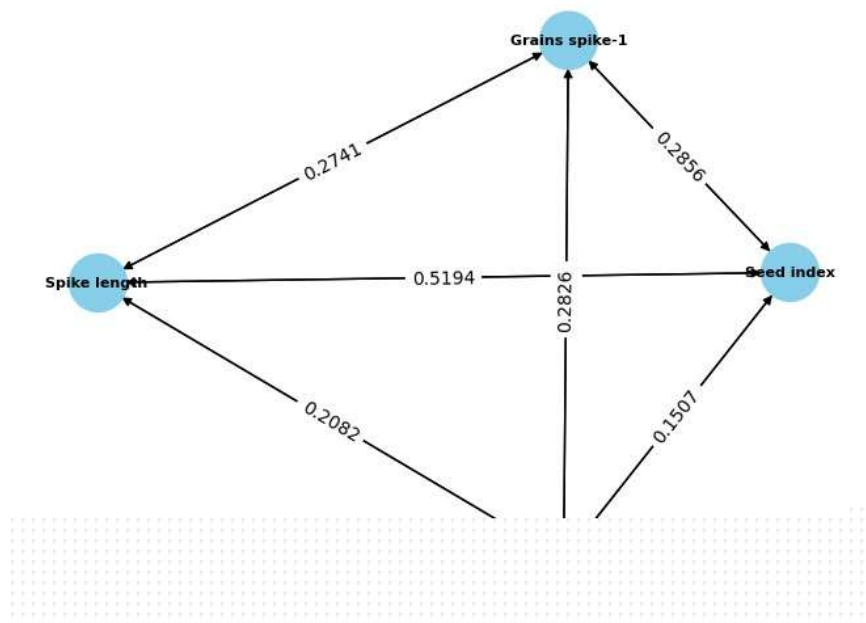


Fig.13. Direct and alternate pathways of spike length, spikelets spike⁻¹, grains spike⁻¹ and seed index on grain yield plant⁻¹ in wheat.

The results showed that the direct effect of seed index on grain yield plant⁻¹ had been -0.4348 in the negative direction with 83.47 percent to grain yield plant⁻¹. Our outcomes are supported by Kashif and Khaliq, (2004) who also found a negative direct effect of 1000-grain weight with grain yield plant⁻¹. Whereas it's indirect effect via spike length 0.5194 was in a positive pathway with 99.71 percent contribution, while the other characters such as spikelets spike⁻¹ 0.1507 were in a positive pathway and produced 28.93 percent indirect impact on grain yield. The alternate effect was a positive direction through grains spike⁻¹ 0.2856 and formed a 54.82 percent contribution towards the grain yield plant⁻¹. These outcomes are in line with (Abo-Elwafa *et al.*, 2023). Although many traits showed negative direct effects on grain yield, their indirect contributions, particularly via spike length, number of grains per spike, and seed index, were significantly positive. These findings underscore the effectiveness of indirect selection for these traits, which can enhance grain yield more reliably than direct selection under certain conditions.

Conclusion

The present study confirmed substantial genetic variability among wheat genotypes for all evaluated traits. Genotypes AS-9 and AS-8 demonstrated superior grain yield, highlighting their potential for yield improvement. Positive and significant associations were observed between grain yield and traits such as tillers plant⁻¹, spike length, number of grains spike⁻¹, seed index, harvest index, and total biomass plant⁻¹, indicating their additive contribution to yield enhancement. High heritability estimates for most traits suggest genetic stability and promise for effective selection. Although path analysis revealed negative direct effects on grain yield, traits like spike length and number of grains spike⁻¹ exerted strong positive indirect effects, supporting their use in indirect selection strategies. These findings provide a useful basis for designing breeding programs aimed at developing high-yielding wheat cultivars.

Author's contributions

Conceived and designed the experiments: WD Sipio, Performed the experiments: WD Sipio & JM Keerio, Nadia Sipio, Analyzed the data MA Rajput, M Memon & AA Goraya, Contributed reagents/materials/analysis tools: C Kumar, R Sajid & NJ Baloch, Wrote the paper: WD Sipio & JM Keerio.

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