J.Hortic.Agric.Sci.Vol.3(1), 149-155,2026
www.jahps.org

https://doi.org/10.63459/jhas.2026.1.29

Research article *Available on: https://jahps.org* OPEN ACCESS

Journal of Horticulture and Agricultural Sciences

Estimation of correlation and heritability in wheat genotypes for various yield traits

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Submitted on: 10-01-2026 ***Revised on: 15-02-2026*** ***Accepted on: 10-03-2026***

ABSTRACT

The present study was conducted at the Barley and Wheat Research Institute, ARI, Tandojam, during the Rabi season 2019-2020. A randomized complete block design with three replications was used to study the yield-related traits in eight locally growing wheat genotypes. The current experiment was conducted to estimate the association between yield traits and heritability in wheat genotypes. The positive correlation for major yield traits and high heritability was found among wheat genotypes. The results are highly significant at $P < 0.01$ for plant height, spike length, spikelets/spike, grains/spike, and seed index, and at $P < 0.05$ for tillers/plant and grain yield/plant; biological yield/plant and harvest index were not significant. The average performance revealed that Moomal 2002 had the highest number of grains per spike (58.13). In the instance of NIA Sarang, the grain yield plant^{-1} was the highest (11.26 g), and the lowest grain yield plant^{-1} was registered in Imdad 2005 (10.12 g). Relationship between many characteristics, such as plant height, spikelets/spike^{-1} was positive and highly significant (0.82**), grains spike^{-1} (0.49**), and grain yield/plant (0.39*). The high broad sense heritability values for plant height (h^2=87.44%), tillers plant^{-1} (h^2=58.00%), spike length (h^2=95.16%), spikelets spike^{-1} (h^2=95.10%), grains/spike (h^2=97.14%), seed index (h^2=99.47%), grain yield/plant (h^2=63.64%), and harvest index (h^2=88.849%) were recorded while biological yield plant^{-1} (h^2=23.39%) showed low heritability indicating significant environmental variance. The result of the current study would be highly valuable in selecting the stable wheat cultivars in terms of yield attributes for future breeding programs.

Keywords: Correlation, heritability, grain yield, wheat, significant, variance

INTRODUCTION

Wheat (*Triticum aestivum* L.) is a hexaploid (2n = 6x = 42) and one of the main cultivated species. It is self-pollinated annual plant of the true grass family Poaceae, widely cultivated as a staple food source worldwide. Human attempts to control their food supply and prevent starvation are intimately related to the history of wheat domestication and utilization. Wheat is now the most significant food source and is grown all over the world. In the West, durum wheat (*Triticum durum*) and bread wheat (*Triticum aestivum*) have been growing for generations to offer energy and vital nutrients to human being. Breeders have been working to improve wheat for almost a century, concentrating on characteristics that affect grain production and, more recently, quality characteristics. Since the 1960s, extensive studies on storage proteins, which make up gluten, have significantly improved the qualities of wheat that make it suitable for processing into various food products (Igrejas & Branlard, 2020).These are mainly cereal crops in the world that occupy 17% of the world's cultivated area, provide food for approximately 40% of the world's population, and supply 20% of the whole calories and protein in the human diet. Pakistan is one of the world's principal wheat-producing countries and is ranked among the top 10 wheat-producing countries in the world. (Mollasadeghi et al., 2011). Wheat contributes 8.9% to the agricultural value added and 1.6% to Pakistan’s GDP. Production saw a slight increase of 0.5%, rising from 25.076 million tons the previous year to 25.195 million tons, though it fell significantly short of the 4.9% growth target. The sown area declined by 0.6%, dropping to 8,740 thousand hectares from 8,797 thousand hectares the prior year. This reduction in acreage was attributed to a shift in land allocation toward oilseeds and other competing crops. Despite the smaller cultivation area, higher yields and optimal grain development during the 2018-19 growing season (as reported by the GOP, 2019) led to a marginal rise in output. To increase the effects of any plant through selection, genetic parameters must first be evaluated. Many techniques can be used to calculate the level of genetic parameters and the spread of traits. Inheritance plays a predictive role in improving the desired traits. A high genetic value implies a simple selection process (Khan et al., 2008). Genetic estimates and information on the genetic development of different traits are important for effective breeding programs. (Eid, 2009; Kahrizi et al., 2010). Progress requires the development of a suitable plant biotype. Even more exact knowledge of the interrelationships between the characteristics is necessary to produce an association rather than differences between them, as evidenced by the current high level of GDP due to long-term breeding (Flohr et al., 2018; Quintero et al., 2018). Before starting any program, the relationship between yield and other yield-related traits is necessary to be understood. Comprehensive research is useful for improving performance by selecting indirect characteristics related to performance. This research evaluates the heritage and estimates the progress to find the correlation between the performance of the heritage and its components to find appropriate standards for the goals and performance improvement. Genetic research provides breeders with valuable genetic information to predict the genetic interactions of different generations. Degewione & Sharif(2013).Correlation studies serve as invaluable tools for breeders, aiming to enhance physiological or performance characteristics, particularly those with high heritability. According to Gupta & Verma (2000), correlation quantifies the strength and direction of association between two variables, providing critical insights for targeted trait improvement. The current study aimed to estimate the correlation and heritability in maize genotypes for yield-related traits.

MATERIALS AND METHODS

Experimental Location: The experiment was conducted during Rabi Season 2019–2020, at Barley and Wheat Research Institute at Sindh Agriculture University, Tandojam (25.42 °N, 68.54 ^{o}E).

Experimental Design: Eight wheat genotypes: Sindhu, Hamal, Imdad-2005, Moomal-2002, NIA-Sunder, Bhatti, NIA-Sarang, and Khirman were evaluated using a Randomized Complete Block Design (RCBD) with three replications. Each genotype was grown in three rows, each having a length of 15 feet. The row-to-row and plant-to-plant spaces were maintained at 25 cm and 15 cm, respectively.

Traits studied: The following yield-related traits were recorded in this experiment in maize genotypes; all the traits were measured for five plants per replication.

Plant height (PH) (cm): The height of the plant was measured from the soil surface to the top of the plant using measuring tape in centimeters when the plant reached physiological maturity.

Tillers per plant (TPP): The total tillers were counted in a plant at the maturity level.

Spike length (SL) (cm): The length of a spike was measured during the fully matured condition using a measuring tape in centimeters.

Spikelets per spike (SPS): The spikelets were counted from the mature spike of the maize genotypes.

Grains per spike (GPS): The number of grains was counted in a spike after harvesting the fully matured spike.

Grain yield per plant (GYPP) (g): The harvested plants were threshed, and their grains were measured in grams using a digital weight balance.

Seed index (1000-grain weight, g) (SI): The seed index was measured for 1000 seeds from each plant using a digital weight balance in grams.

Biological yield per plant (BYPP) (g): The biological yield of the plant was measured by weighing the whole mature plant, along with grains, using a digital weight balance in grams.

Harvest index (HI) (%): The harvest index in percentage was measured using the following formula:

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

The analysis focused on elucidating genetic relationships and inheritance patterns among these traits to widen wheat breeding strategies.

STATISTICAL ANALYSIS

The statistical analyses were performed for analysis of variance (ANOVA). Statistix 8.1 software was used following the methodology of Gomez & Gomez (1984). Phenotypic correlation coefficients were calculated using the approach suggested by Snedecor & Cochran (1980), and broad-sense heritability estimates were derived according to the principles described by Allard (1960).

RESULTS AND DISCUSSION

Mean squares from the analysis of variance

Analysis of variance (ANOVA) for yield and yield-related traits, as summarized in Table-1, indicated significant genotypic variation. Genotypes exhibited highly significant differences ($P<0.01$) for plant height, spike length, spikelets per spike, grains per spike, and seed index. Differences were significant at $P<0.05$ for tillers per plant and grain yield per plant, while biological yield per plant and harvest index showed non-significant variation among genotypes. Sohail et al. (2018) also found significant differences for the traits studied in wheat genotypes. Elbashier et al. (2019) revealed significant differences in ANOVA for grains per spike, harvest index, 1000-seed weight, and plant height. Kumar et al. (2019) also found significant differences in analysis of variance for plant height, tillers per plant, spikelets per spike, spike length, 1000-grain weight, harvest index, and grain yield per plant in wheat genotypes.

Table 1.Mean square from analysis of variance for several quantitative characters of wheat genotypes

Characters	Replication (D.F=2)	Genotype (D.F=7)	Error (D.F=14)
Plant height	5.14	14.58**	1.42
Tillers plant^{-1}	0.85	0.45*	0.16
Spike length	0.26	2.66**	0.10
Spikelets spike^{-1}	0.20	3.64**	0.14
Grains spike^{-1}	18.32	52.22**	1.13
Seed index	6.08	76.52**	0.17
Grain yield plant^{-1}	1.17	0.50*	0.15
Biological yieldplant^{-1}	9.83	2.81^{NS}	3.76
Harvest index (%)	40.17	26.08^{NS}	79.73

***= Significant at 0.05%, **= Significant at 0.01% level of probability, NS = non-significant, D.F= Degrees of freedom**

Performance of the wheat genotypes for key traits

Table-2 summarizes the agronomic performance of wheat genotypes across key traits. The variety Hamal exhibited the tallest plants (103.10 cm), followed by Khirman (101.57 cm) and Sindhu (101.40 cm), while NIA Sunder recorded the shortest plant height (95.97 cm). Sindhu had the most tillers per plant (6.73), closely followed by NIA Sarang (6.70), while Imdad-2005 had the fewest tillers (5.70). Significant differences existed in the spike morphology: Bhittai had the smallest spikes (7.63 cm), whereas Hamal had the tallest spikes (10.47 cm), topping Moomal-2002 (10.17 cm). The spikelet count per spike was highest in Hamal (19.43) and Sindhu (18.33), but lowest in Bhittai (16.07). Grain number per spike peaked in Moomal-2002 (58.13) and was the lowest in NIA Sarang (45.57). Seed index (1000-seed weight) was greatest in Sindhu (41.46 g) and minimal in Hamal (27.50 g). For grain yield per plant, NIA Sarang outperformed others (11.26 g), trailed by Khirman (11.08 g), while Imdad-2005 yielded the least (10.12 g). The biological yield plant^{-1} was the highest (22.25 g) in the case of variety Hamal, which produced the maximum biological yield plant^{-1}, followed by NIA Sarang (21.29 g), and the minimum BYPP was produced by Khirman (18.99 g). The greater harvest index (63.47 g) was observed in Khirman and Moomal 2002, whereas the minimum harvest index was recorded in Hamal (49.17 g). Earlier researchers like Fikri & Sartika (2018) reported significant variation in all the traits except biological yield per plant. Previous studies have highlighted key factors influencing grain yield improvement in wheat. BYPP and HI were found to be crucial selection measures for improving GYPP by Fellahi et al. (2013). The possibility of selective breeding was further highlighted by Ayer et al. (2017), who noted notable genotypic heterogeneity in their experimental populations. Ghallab et al. (2016) suggested that increasing total biomass accumulation and vegetative growth could directly increase grain production. Iqbal et al. (2017), on the other hand, highlighted the possibility of trade-offs between yield-related traits; for example, genotypes that perform well in early maturity frequently yield less grain per plant, indicating the necessity of balanced trait selection strategies.

Table 2. Mean performance of several characters in bread wheat genotypes

Genotypes	PH (cm)	TPP	SL (cm)	SPS	GPS	SI (g)	GYPP (g)	BYPP (g)	HI (%)
Sindhu	101.40	6.73	9.97	18.33	54.27	41.46	10.88	20.52	50.22
Hamal	103.10	6.07	10.47	19.43	51.67	27.50	10.96	22.25	49.17
Imdad 2005	99.80	5.70	8.73	16.87	51.07	29.23	10.12	19.95	50.18
Moomal 2002	100.40	5.83	10.17	17.93	58.13	28.86	10.47	20.33	63.47
NIA Sunder	95.97	6.50	9.00	16.53	49.00	36.38	10.50	19.97	52.97
Bhittai	98.33	6.40	7.63	16.07	46.43	29.60	10.27	20.46	50.22
NIA Sarang	99.13	6.70	8.60	17.73	45.57	32.24	11.26	21.29	52.76
Khirman	101.57	6.43	9.07	18.27	53.40	26.68	11.08	18.99	63.47
LSD at (5%)	2.08	0.71	0.54	0.66	1.86	0.72	0.69	3.3964	7.64

Note: PH= Plant height, TPP= Tillers per plant, SL= Spike length, SPS= Spikelets per spike, GPS= Grains per spike, SI= Seed index, GYPP= Grain yield per plant, BYPP= Biological yield per plant, HI= Harvest index, cm= centimeter, g= gram

CORRELATION COEFFICIENT

Correlation analysis aims to identify key morphological traits that can serve as proxies for indirect selection of desirable plant characteristics. In this study, plant height exhibited a highly significant positive correlation ($P<0.01$) with SPS (r=0.82**) and GPS (r=0.49**), and significant positive associations ($P<0.05$) with GYPP (r=0.39*) and SI (r=0.58*). However, correlations with TPP ($r=0.11^{NS}$), SL ($r=0.24^{NS}$), BYPP ($r=0.27^{NS}$), and HI ($r=0.02^{NS}$) were non-significant. Spikelets per spike showed a highly significant positive correlation with SI (r=0.79**) and a significant association with GPS (r=0.44*) and GYPP (r=0.46*), but no significant links to BYPP and HI. GPS correlated strongly with SI (r=0.67**) but displayed non-significant relationships with other traits. There were non-significant correlations between the yield of grain per plant, BYPP ($r=0.22^{NS}$), and SI ($r=0.22^{NS}$). These results are consistent with Saleh et al. (2018), who highlighted the enhancement of biological yield through morphological trait relationships. On the other hand, they differ from Abdurrehman et al. (2013), who found that correlations for spike length varied. The usefulness of these features for selection was further supported by earlier research Fellahi et al. (2013) and Dabi et al. (2016), which showed strong positive correlations between spikelets per spike, grains per spike, and grain production. Khan & Hassan (2017) also emphasized the need to give breeding programs priority to parameters that have a good association with grain yields. Interestingly, there was a direct positive correlation between the seed index and GYPP, indicating that improving both traits could maximize yield results. According to Ghallab et al. (2016), these trait benefits might be amplified through repetitive selection across generations. .Haydar et al. (2020) estimated a significant association between plant height and grain yield per plant. Sohail et al. (2018) also estimated a positive and non-significant association of grain yield per plant with spike length and seed index. Kumar et al. (2019) also found a non-significant but positive association of plant height with spike length and harvest index. Grain yield was also non-significantly associated with spike length, seed index, biological yield, and harvest index

Table 3.Correlation coefficient (r) between several traits in wheat cultivars

Traits	PH	TPP	SL	SPS	GPS	GYPP	SI
TPP	0.11^{NS}						
SL	0.24^{NS}	0.40*					
SPS	0.82**	0.13^{NS}	0.11^{NS}				
GPS	0.49**	-0.23^{NS}	0.00^{NS}	0.44*			
GYPP	0.39*	0.46*	0.06^{NS}	0.46*	0.10^{NS}		
SI	0.58*	-0.00^{NS}	0.09^{NS}	0.79**	0.67**	0.22^{NS}	
BYPP	0.27^{NS}	0.16^{NS}	0.04^{NS}	0.24^{NS}	0.04^{NS}	0.22^{NS}	0.22^{NS}
HI	0.02^{NS}	0.35^{NS}	0.05^{NS}	0.25^{NS}	0.01^{NS}	0.41*	0.11^{NS}

****, *= Significant at 1% and 5% probability level respectively, NS= Non-significant**

Table4. Heritability estimates in broad sense (h^2b.s %) for several characters in bread wheat genotypes

Traits	Phenotypic variance (δ^2 p)	Genotypic variance (δ^2 g)	Heritability % (Broad sense)
Plant height	15.05	13.16	87.44
Tillers plant^{-1}	0.50	0.29	58.00
Spike length	2.69	2.56	95.16
Spikelets spike^{-1}	3.69	3.5	95.10
Grains spike^{-1}	52.60	51.09	97.14
Seed index	76.58	76.35	99.47
Grain yield plant^{-1}	0.55	0.35	63.64
Biological yield plant^{-1}	4.06	0.95	23.39
Harvest index (%)	50.66	46.35	88.84

HERITABILITY ESTIMATES (B.S)

Breeders can predict gene activity and inheritance patterns in segregating populations by using heritability analysis, which provide crucial insights into the genetic architecture of characteristics (Degewione & Sharif, 2013). By calculating the percentage of phenotypic variance that may be attributed to genetic causes, these estimations help pick the best breeding practices. High heritability was observed in the seed index (99.47%), grains per spike (97.14%), spike length (95.16%), spikelets per spike (95.10%), plant height (87.44%), and harvest index (88.84%), based on the broad-sense heritability (H^2) estimations for key parameters. GYPP (63.64%) and TPP (58.00%) have moderate heritability. On the other hand, biological yield per plant had low heritability (23.39%). Strong genetic control, little environmental influence, and a great deal of potential for successful phenotypic selection are indicated by the elevated H^2 values for most characteristics. These results support the usefulness of PH, TPP, and SL as priority traits in breeding programs, as reported by Farshadfar et al. (2013), who also found significant heritability for these traits. Haydar et al. (2020) found high heritability for grain yield per plant and seed index. Kumar et al. (2019) found low heritability (b.s) for biological yield per plant, which strongly supports our results that an environmental variance had a greater influence on the said trait.

CONCLUSIONS

The study concluded that all the yield-related traits in eight wheat genotypes were significant, showing great variation, which is important for plant breeders for selection. However, biological yield and harvest index expressed no variation. Plant height, tillers per plant, harvest index, and spikelets per spike were significantly associated with grain yield per plant. All the traits were highly heritable except biological yield per plant.

RECOMMENDATIONS

Based on the current study, it is recommended that two genotypes, NIA Sarang and Khirman, be cultivated to maximize grain yield. These genotypes show the maximum grain yield per plant.

ACKNOWLEDGMENT

The authors are highly thankful to the staff of Barley and Wheat Research Institute, Agriculture Research Institute, Tandojam for offering field for performing experiment and other technical support during the whole period of study

CONFLICTS OF INTEREST

The authors have declared no conflict of interest

AUTHOR'S CONTRIBUTION

MIP conducted study, **NAB** designed the study, **IAP** helped in data collection and analysis, **SNSJ**, **JAP** and **Naila** notably assisted in writing the initial draft of the manuscript, **HAJ**, **MYB** and **SS** revised the draft and polished the language

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