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Estimation of Phenotypic and Genotypic Correlation Analysis in F₃ Populations of Bread Wheat Genotypes

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A R T I C L E   I N F O

A B S T R A C T

Wheat is one of the most important crops all over the world in terms of yield, production, consumption, cultivation, and adoptability. Wheat genotypes exhibiting different yield associated traits which influence each other in many ways. Therefor genotypic and phenotypic correlations are the breeder's utmost priority to know about the inter-relationship between two or more traits which may be either directly influencing each other in a positive direction or indirectly swaying each other in a negative direction in breeding programs. To find out phenotypic and genotypic correlations among different productive traits, this study was designed at the research area of The Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, during 2022-23. The experiment was carried out by using 27 wheat genotypes comprising of nine parents and 18 F₃ populations evaluated in RCB design with three replications. Overall the study exhibited that kernel yield plant⁻¹, which is one of the most yield contributing trait, was significantly correlated with thousand-kernel weights, tillers plant⁻¹ and biomass yield, along some other yield contributing traits. The parental genotype, Janbaz, and cross combinations Watan × AUP-5008, Pirsabak-2005 × AUP-5008, Saleem-2000 × Janbaz and Watan × Tatara were the most promising genotypes for most of quantitative traits and; hence are recommended to be evaluated in further breeding schemes. Both phenotypic and genotypic correlation study exhibited that kernel yield spike⁻¹ was significant and positively associated with plant height, tillers plant⁻¹, thousand-kernel weight and biomass yield. Based on correlations, yield, and production the parental genotype, Janbaz, and F₃ combinations Watan × AUP-5008, Pirsabak-2005 × AUP-5008, Saleem-2000 × Janbaz and Watan × Tatara were the most promising genotypes for most of the quantitative traits, which can be incorporated in further breeding program.

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Introduction

Wheat (*Triticum aestivum* L.) is the most necessary part of daily consumptive food globally. It belongs to the family Poaceae (Gramineae), with chromosome numbers 2n=6x=42, hence, basic chromosome numbers x=7 and genomic formula is AABBDD. The genetic makeup of a particular genotype which influence yield is the most crucial tool for wheat breeders (Endashaw et al., 2021), so it is necessary for breeders to know about the yield contributing factors of particular specie while crossing wheat genotypes.

Wheat holds an important position not only as a key crop for food security but also as a valuable cash crop on global scale. The importance of wheat is reflected in the significant global trade volume. The results claimed by

Food and Agriculture Organization (FAO), globally the production of wheat according to year 2020 was about 776.5 Mt with increase of 778.3 Metric ton in 2021 and then suddenly declined to 770.3 Mt in 2022. The total area 9,178 thousand hectares was under cultivation in the year 2020-21, with an increased by 4.2% over the last cropping season of about 8,805 thousand hectares. The consecutive findings of (Bilal et al., 2021) revealed that year 2020-21 showed an unexceptional high production 27.293 M tons by uplift of 8.1% from the previous year. To obtain adequate amount of production, it is very important to develop potential crops to reach its goal, and to meet the population need worldwide.

Plant breeders are trying to alter the basic genes either by modification like in genetic engineering or crossing it with other genotypes to reach heritable characters. Based on the crucial importance for enlightening low heritable parameters, correlation is used for desirable and undesirable traits association, when the purpose is indirect selection (Waitt and Levin, 1998) for particular traits during research. Therefor correlation analysis is the most important parameter after heritability, and genetic advance.

Correlation is showing us the degree and dimensions about genotypic and phenotypic linkage about a particular trait so it is an important factor (Meherbabu et al., 2023).

Phenotypic correlation is the best option for breeders to find the association between two important yields associated traits in rice (Saleh et al., 2020). Correlation coefficient analysis could be used as an important tool to bring information about appropriate relationship between yield and some yield components (Gerema et al., 2020). Based on the assumptions of (Meherbabu et al., 2023), that selecting a particular trait with positive correlation is the shortest way to achieve increase in yield. Association of yield related traits in wheat had been testified by different workers by the presence of genetic inconsistency for yield and associated traits. Various researchers observed the genotypic correlation for various yield contributing traits like kernel yield and yield related traits. Phenotypic variance is small as compared to genetic variation therefor selection will be more helpful for further breeding program. The genotypic association signifies the genetic segment of the phenotypic correlation in progeny propagation scheme (Kadam et al., 2022).

To find out inter-dependency of traits, it is utmost priority to know about correlation between two desired traits for selection of the particular genotype(s) in the breeding program (Lichthardt et al., 2020; Passioura, et al., 2020). The association of various parameters is generally determined by the presence of linkage and pleiotropic effect of different genes. In the present study, a simple correlation is calculated for each pair of the response variable and an explanatory variable to identify the correlation of kernel yield with other yield traits in wheat. Keeping in view the importance of this, the current study will be conducted to know about correlation of yield attributing traits, analyse phenotypic and genotypic correlation by environmental influence, and to evaluate high yielding genotypes to incorporate in future breeding program.

Materials and Methods

To evaluate genetic diversity in F_3 populations to 27 genotypes of bread wheat including 9 parents and 18 crosses in the present study were carried out at The University of Agriculture Peshawar in November 2022-23. The genotypes which were used in the experiment have wide range of adoptability in terms of yield, production and cultivation by growers. The experimental block located at longitude 34.026°N, latitude, 71.4814°E with altitude 359 m /1178 feet above sea level, soil class was loam (32.6 % sand, 42.56% silt, and 20% clay). According to 30-years climatic data Peshawar is warm to hot, semi-arid and subtropical climate with mean annual temperature of 22.7°C (72.9°F) and with annual rainfall of 445 mm. The experimental materials were provided by Agricultural University Peshawar (UAP), The Cereal Crops Research Institute (CCRI), Pirsabak, Nowshera at Khyber Pakhtunkhwa, Nuclear Institute of Food and Agriculture Peshawar (NIFA), and Pakistan Agriculture Research Centre Islamabad (PARC) Table 1. To minimize environmental influence, the wheat genotypes were allocating in RCB design with 3 replications having plant to plant distance 15 cm and row to row distance was 30 cm in 4 rows of 3 m length. Data were taken from ten randomly selected plants from each entry. All agronomic cultural practices i-e seed bed preparation, sowing, irrigation, fertilizer application, harvesting, threshing and storing etc. were applied uniformly to control environmental error. For proper computation data were taken on days to heading (when the awns emerged from leaf sheath), days to maturity (when the plant stopped physiological growth), plant height (when plant stopped further cell division), tillers plant^{-1}(the numbers of plumule branching per seed), flag leaf area, spikelet's spike^{-1}, spike length, grains spike^{-1}, thousand-kernel weight, grain yield spike^{-1}, biological yield and harvest Index at their proper time.

Statistical Analysis
Correlation
The genetic correlation (r_g) and phenotypic correlation (r_p) between two characters, X_1 and X_2, was estimated according to (Kwon and Torrie 1964).

Genetic correlation

$$r_g = \frac{Cov\ G(x_1.x_2)}{\sqrt{\sigma G(x_1).\sigma G(x_2)}}$$

Where:
CovG(X_1X_2) = Genetic covariance among trait X_1 and X_2.
VG(X_1) and VG(X_2) = Genetic variance for trait X_1 and X_2, respectively.

Phenotypic correlation

$$r_p = \frac{CovP\ (x_1.x_2)}{\sqrt{\sigma P(x_1).\sigma P(x_2)}}$$

Where:
COVP (X_1X_2) = Phenotypic covariance among traits X_1 and X_2
VP(X_1) and VP(X_2) = Phenotypic variance for traits X_1 and X_2, respectively.

Observations
For proper computation data was taken on the following traits at their proper time. For each parameter randomly ten plants were selected from each entry and data were taken on those selected plants.

Results and Discussion

Days to Heading
Days to heading is also an essential character for breeder to count it because it provides life cycle for a particular specie, so the growers have much time to ready for next crop cultivation.

Table 1. List of wheat lines including 9 parents and 18 F₃ populations used in the research during 2021-22.

Parents	Sources	F₃ Populations	
Janbaz	(AUP)	AUP-4008 × Janbaz	Saleem-2000 × Janbaz
Pirsabaq-2005	(CCRI)	Fakhr-e-Sarhad × Tatara	Watan × AUP-5008
Saleem -2000	(NIFA)	AUP-4008 × AUP-5008	Saleem-2000 × AUP-5008
Fakhr-e-Sarhad	(NIFA)	Pirsabak-2005 × Janbaz	Watan × Janbaz
Barsat	(NIFA)	Pirsabak-2005 × Tatara	Pirsabak-2005 × AUP-5008
AUP-5008	(AUP)	Fakhr-e-Sarhad × AUP-5008	Barsat × AUP-5008
AUP-4008	(AUP)	Fakhr-e-Sarhad × Janbaz	Barsat × Janbaz
Tatara	(NIFA)	AUP-4008 × Tatara	Watan × Tatara
Watan	(PARC)	Barsat × Tatara	Saleem-2000 × Tatara

Table 2. Phenotypic correlation (above diagonal) and genotypic correlation (below diagonal) among 12 different traits for 18 F₃ populations of wheat evaluated at The University of Agriculture, Peshawar, during 2021-22.

Traits	PH	SL	SLPS	FLA	TPP	GPS	DH	DM	TGW	BY	HI	GYPS
PH	-	0.27*	0.29*	0.45**	0.31**	0.07	0.24*	0.05	0.28*	0.40**	-0.38**	0.24*
SL	0.40**	-	0.56**	0.75**	-0.48**	0.27*	0.51**	0.31**	-0.46**	-0.44**	-0.07	-0.46**
SLPS	0.33**	0.66**	-	0.32**	-0.16	0.14	0.69**	0.50**	-0.25*	-0.20	-0.21*	-0.26*
FLA	0.57**	0.66**	0.34**	-	-0.37**	0.19	0.49**	0.22*	-0.33**	-0.09	-0.31**	-0.23*
TPP	0.29*	-0.74**	-0.18	-0.39**	-	-0.15	-0.13	-0.49**	0.65**	0.79**	-0.27*	0.67**
GPS	0.12	0.39**	0.14	0.25*	-0.14	-	-0.14	0.08	-0.15	-0.20	0.08	-0.12
DH	0.46**	0.86**	0.89**	0.66**	-0.11	-0.2	-	0.53**	-0.31**	-0.16	-0.22*	-0.26*
DM	0.30**	0.57**	0.82**	0.49**	-0.67**	0.08	0.53**	-	-0.39**	-0.48**	0	-0.49**
TGW	0.30**	-0.78**	-0.32**	-0.43**	0.73**	-0.18	-0.32**	-0.59**	-	0.59**	-0.25*	0.48**
BY	0.39**	-0.66**	-0.23*	-0.12	0.89**	-0.21*	-0.08	-0.59**	0.63**	-	-0.35**	0.86**
HI	-0.44**	-0.32**	-0.38**	-0.40**	-0.39**	0.06	-0.67**	-0.32**	-0.26*	-0.27*	-	0.16
GYPS	0.23*	-0.76**	-0.33**	-0.26*	0.73**	-0.14	-0.31**	-0.69**	0.51**	0.91**	0.16	-

*Significant at 5%, **Significant at 1%, level respectively; Abbreviations: PH - plant height, SL - spike length, SLPS - spike lets spike⁻¹, FLA - flag leaf area, TPP - tillers plant⁻¹, GPS - grains Spike⁻¹, DH - days to heading, DM - days to maturity, TGW -thousand -grains weight, BY – biomass yield, HI - harvest index and GYPS - kernel yield spike⁻¹

Days to spike emergence exhibited significant positive phenotypic linkage with spikelets spike⁻¹ (r_p=0.69), number of days to reach physiological maturity (r_p =0.53), longer spike (r_p=0.51), broader flag leaf (r_p =0.49) and plant height, however, significant negative relationship was observed with harvest index and kernel yield (Table 2).

Genotypic relationship of days to spike emergence was highly significant with tall plants (r_g=0.46), expanded flag leaf (r_g= 0.66) spikelets spike⁻¹ (r_g=0.89), longer spike (r_g= 0.86) and days to maturity (r_g= 0.53), while the genotypic correlation was negative with thousand-kernel weight and harvest index (Table 2). Our results were contrary with the findings of (Meherbabu et al., 2023) who found negative association of days to heading with spike lets spike⁻¹ and spike length. The recent findings of (Šućur et al., 2023) supporting our results where they stated that days to heading have significant positive correlation with plant height (r = 0.65). Hence days to reach physiological maturity leads to primary growth and maximum number of cell divisions take place.

Days to Maturity

Least days to maturity in wheat crop is the best indication for a desirable variety, because it contracts crop duration. Phenotypic correlation for days to reach physiological maturity was highly significant positive correlated with longer spike (r_p=0.31), numbers of spikelets spike⁻¹ (r_p=0.50), as well as days to heading (r_p=0.53), while it was highly significant negatively correlated with tillers plant⁻¹ (r_p=-0.49), thousand-kernel weight (r_p=-0.39), kernel yield (r_p=-0.49) and total biomass yield (r_p=-0.48) mentioned in Table 2.

Genotypic correlation for days to maturity was highly significant positively linked with spikelets spike⁻¹ (r_g=0.82), longer spike (r_g=0.57), numbers of days to heading (r_g=0.53), expanded flag leaf (r_g=0.49) and tall plants (r_g= 0.30), whereas, it was highly significant negative linked with kernel yield (r_g=-0.69), tillers plant⁻¹ (r_g= -0.67),1000- kernel weight (r_g= -0.59), biomass yield (r_g=-0.59) and harvest index Table 2. Highly significant phenotypic correlations for plant maturity with longer spikes and days to heading have also been observed by (Kalhoro et al., 2023). Tallness of plant and spike length both traits are time consuming, so it increases life cycle.

Plant Height (cm)

Plant height is one of the main components in any breeding program as it influences plant vigour and stature by both genetic and environmental factor. Highly visualized positive phenotypic correlation for plant height was recorded with broader flag leaf (r_p=0.45), biomass yield (r_p=0.40), tillers plant⁻¹, longer spike, spikelets spike⁻¹, days to heading, kernel yield plant⁻¹, and thousand -kernel weight. However, plant height was significantly negative correlated with harvest index mentioned in Table 2.

Genotypically, plant height exhibited positive significant correlation with spike length (r_g=0.40), spike lets spike⁻¹ (r_g=0.33) flag leaf area (r_g= 0.57), days to headings (r_g= 0.46), days to maturity (r_g=0.30) and biomass yield (r_g= 0.39). The trait thousand-kernel weight (r_g= 0.30) was significantly correlated with kernel yield (r_g=0.23) and tillers plant⁻¹ (r_g= 0.29) mentioned in Table 2. Our findings are parallel with (Kumar et al., 2018), (Baye et al., 2020) found highly significant negative correlation (r_p= -0.7847)

with spikelets plant[-1] On the other hand the results of (Meherbabu et al., 2023) and (Zare et al., 2017) revealed highly significant but negative correlation of plant height with spike length (r_g= -0.8613), these results were not with the conformity of our findings, it may be due to the crossing over of chromosomes in meiosis in the inter-Phase-I of cell cycle.

Tillers Plant[-1]

Tiller plant[-1] influencing crop yield and especially biological yield in terms of straw production. Phenotypic association for tillers plant[-1] was highly significant and positive correlated with plant height (r_p=0.31), thousand kernel weight (r_p=0.65), kernel yield (r_p=0.67) and biomass yield (r_p =0.79), while it was highly significant negative correlated with longer spike (r_p=-0.48), days to reach physiological maturity (r_p =- 0.49) and flag leaf area, however, it exhibited significant negative co-relation with harvest index (Table 2).

Genotypically tillers plant[-1] showed significant positive correlations with biomass yield (r_g=0.89), thousand kernel weight (r_g= 0.73), and plant height, however, significantly negative correlation was found with days to physiological maturity (r_g= -0.67), spike length (r_g=-0.74), harvest index (r_g=-0.39), and flag leaf area (r_g=-0.39). Subhani, (2000) reported highly significant correlation of tillers plant[-1] with kernel yield plant[-1] (Table 2). Similar results was showed by (Meherbabu et al., 2023) who discovered that negative and significant correlation for number of tiller per plant (r_p= -0.7068) with spike length, and number of spikelets per plant (r_p= -0.7847) with spike length at phenotypic level only. He also described that number of tillers per plant revealed positive and highly significant correlation with number of spikes per plant (rp= 0.9409, rg= 0.9958) and grain yield (r_p= 0.8387, r_g= 0.8709) while positive and significant correlation with biological yield (rp= 0.7789, rg= 0.7683) at both phenotypic and genotypic level respectively.

Flag Leaf Area

Flag leaf area have direct influence on chlorophyll content and serve as the glucose factory in the presence of sunlight, so its correlation study cannot be under estimated in any breeding program. Phenotypic correlation of flag leaf area showed highly prominent positive association with spikelets spike[-1], plant height (r_p=0.45), spike length (r_p=0.75), whereas, flag leaf showed highly prominent negative correlation with thousand kernel weight, and harvest index (Table 2).

Genotypically flag leaf area was highly and significantly positive correlated with spike length (r_g=0.66), days to heading (r_g=0.66), days to maturity (r_g=0.49), plant height (r_g=0.57), spikelets spike[-1] (r_g= 0.34) couple with this; low significant positive correlation was found with grains spike[-1]. On the other hand, highly significant negative association was found with harvest index (r_g=-0.40), tillers plant[-1] (r_g=-0.39), thousand kernel weight (r_g= - 0.43) and biomass yield. The phenological association describe us the extent of various traits which have been showed by the genes and ecological forces. Same results were mentioned by (Kadam et al., 2022), who have recorded the phenotypic relationship of flag leaf area with taller plants.

Spikelet's Spike[-1]

Number of spike lets spike[-1] is also a grain yield contributing parameter, so this trait cannot be neglected in any crop breeding program. Spikelets spike[-1] exhibited prominent positive phenotypic co-relationship with days to heading (r_p =0.69), days to maturity, (r_p =0.50) plant height, spike length (r_p=0.56) and flag leaf area, whereas, significant negative linkage was exhibited with kernel yield, thousand-kernel weight, grains spike[-1] and harvest index (Table 2).

Genotypically spikelets spike[-1] showed high significant linkage with tall plants, longer spike (r_g=0.66), days to reach physiological maturity (r_g=0.82), days to reach heading (r_g=0.89) and with broader flag leaf, while highly visual and contrast correlation was found with harvest index (r_g=-0.38), and numbers of spikelets spike[-1]. Negative genotypic correlation was found with thousand-kernel weight, kernel yield and biomass yield, mentioned in (Table 2). Spike lets spike[-1] showed significant and positive correlation with length of spike, plant height, biomass yield plant[-1], yield spike[-1] and number of grains spike[-1] at genotypic and phenotypic level which was with the same channel of earlier findings of (Kalholo et al., 2023).The results of (Meherbabu et al., 2023) was not with the conformity of our results who stated that spike lets per spike is highly significant correlated with tillers per plant (r_p= 0.9409, r_g= 0.9958) at phenotypic and genotypic level. Our results were same in quantity (r_p= -0.7068) with (Ullah et al., 2021) but contrast in quality who revealed that spikelets per spike was negatively correlated with spike length at phenotypic level only.

Spike Length (cm)

Spike length exhibited direct effect on grain yield, so, this trait cannot be overlooked in any breeding scheme. This parameter showed significant positive phenotypic association with broader flag leaf (r_p =0.75), spikelets spike[-1] (r_p =0.56), days to spike emergence (r_p =0.51), and days to physiological maturity, whereas high visualize negative correlation was observed with tillers plant[-1], thousand-kernel weight, kernel yield biological-yield and harvest index (Table 2).

Genotypically spike length exhibited highly significant association with days to heading (r_g= 0.86), spikelets spike[-1](r_g= 0.66), flag leaf area (r_g = 0.66), grains spike[-1](r_g = 0.39), and days to maturity (r_g= 0.57), whereas, highly prominent negative correlation was found with thousand kernel weight r_g= - 0.78), tillers plant[-1], organic yield, kernel yield and harvest index (Table 2). A significant and positive correlation of spike length was with plant height, yield spike[-1] and number of grains spike[-1] at genotypic and phenotypic level, these findings is nearer with the findings of (Kumar et al., 2018; Sharma et al., 2018). Spike length expressed direct and significant effects on kernel yield, however, (Ljubičić et al., 2021) founded that spike length exhibited direct influence on spikelets spike[-1] and grains spikes[-1] which were contrary to our findings. The findings of (Meherbabu et al., 2023) showed that spike length had highly significant positive correlation with spike lets per spike (r_g=0.9883), whereas negative and significant correlation was found for spike length (r_p= -0.7847) with spike lets per spike at phenotypic level only.

Grains Spike[-1]

Grains spike-[1] provides positive impact on grain yield. Phenotypic association of grains spike-[1] exhibited significant and positive link with spike length. Genotypically grains spike-[1] showed significant co-relationship with long spike (r_g=0.39), and flag leaf area, while it was significant and negatively correlated with biomass yield (Table 2). The contrary results of (Meherbabu et al., 2023) revealed that grains per ear is highly significant negatively correlated with harvest index (r_g= -0.7091) and number of spikelets per ear (r_g= -0.8024) with harvest index at genotypic level only while, biological yield (r_p= -0.7519) for phenotypic level only. These results are not with the conformity of (Crespo-Herrera et al., 2018) who have observed prominent association for grains spike-[1] with flag leaf area which may be due to crossing over in the inter phase level of meiosis-II.

Thousand Kernel Weight (g)

Thousand grain weights is the best selection criteria in breeder's hand as it directly exhibiting best genotype by weighing thousand grains. Phenotypically thousand kernel weight was highly significant positive correlated with tiller plant -[1](r_p=0.65), organic yield (r_p=0.59), and kernel yield spike-[1] (r_p=-0.48), while highly contrast correlation was found with longer spike (r_p=-0.46), broader flag leaf, numbers of days to heading, and days to physiological maturity (r_p=-0.39) mentioned in Table 2.

Genotypically thousand kernel weight was highly significant positive correlated with number of tillers plant-[1](r_g=0.73), grain yield (r_g=0.63) and kernel yield (r_g=0.51), while it was significantly negative associated with tall plants, longer spike (r_g=-0.78), spikelets spike -[1], flag leaf area (r_g=-0.43), number of days to spike emergence (r_g=-0.32), and days to physiological maturity (r_g=-0.59) (Table 2). Our findings were parallel with (Kadam et al., 2022), but were contrary with the results of (Tarkeshwar et al., 2020) who founded positive and non-significant genotypic correlation with spike length.

Grain Yield Spike[-1] (g)

Phenotypically grain yield spike-[1] was highly significant positive correlation was found with tillers plant-[1] (r_p = 0.67), thousand-grain weight (r_p = 0.48) and total yield (r_p = 0.86), while highly significant negative inter-relationship was found with plant maturity (r_p=-0.49). Grain yield spike-[1] showed highly significant positive genotypic correlation with 1000-grain weight (r_g = 0.51), tillers plant-[1] (r_g = 0.73) and biological yield (r_g = 0.91), highly significant negative correlation with spike length (r_g = -0.76), spikelets spike-[1] (r_g = -0.33), plant heading (r_g = -0.31), plant maturity (r_g = -0.69), whereas significant opposite correlation was found with flag leaf area (Table 2). Significant positive correlation of grain yield with spike length, 1000-grain weight and spike length have also been observed by (Mohamed et al., 2014). Number of spikelets per ear revealed positive and highly significant correlation with Number of Grains per ear (r_p= 0.8573) at phenotypic level only while negative and significant correlation was found for harvest index (r_g= -0.8024) at genotypic level only (Meherbabu et al., 2023). (Kumar et al., 2020) also found similar results.

Biomass Yield (kg)

Phenotypically biomass yield was highly prominent and positive associated with numbers of tillers plant-[1] (r_p=0.79), tallness of plant (r_p=0.40), and thousand kernel weight (r_p=0.59), while it was prominent negative correlated with longer spike, (r_p = -0.44), spike lets spike-[1], broader flag leaf, grains spike-[1], days to spike emergence, and highly and negatively significant associated with days to maturity, (r_p=-0.48). Genotypically it was significantly negative correlated with, taller plants (r_g=0.39), tillers plant-[1](r_g=0.89), and thousand kernel yield (r_g=0.63), though it was significantly negative correlated with spike length (r_g=-0.66) and days to maturity (r_g=-0.59) (Table 2). Our results were also in with the conformity of (Kadam et al., 2022). The results of (Meherbabu et al., 2023) stated that biological yield revealed positive and highly significant correlation with grain yield (r_p= 0.9671, r_g= 0.9965) while positive and significant correlation with number of tillers per plant (r_p= 0.7789, r_g= 0.7683) at both phenotypic and genotypic level.

Harvest Index

Phenotypically harvest index exhibited highly significant negative correlation with tall plants (r_p=-0.38), broader flag leaf and with biomass yield (r_p=-0.35). Non-significant positive phenotypic correlation was found with kernel yield spike-[1], significant negative correlation was found with spikelets spike-[1], tillers plant-[1], days to spike emergence, thousand kernel weights, along this harvest index showed non-significant negative correlation with longer spike (Table 2).

Genotypically harvest index was highly significant negative correlated with plant height (r_g=-0.44), larger spike, spikelets spike-[1] (r_g=-0.38), broader flag leaf (r_g=-0.40), tillers plant-[1] (r_g=-0.39), days to heading (r_g=-0.67) and days to maturity. Significant negative correlation was found with thousand kernel weight, and biomass yield (Table 2). Our findings are in same channel with that of (Tarkeshwar et al., 2020, but contrary with (Meherbabu et al., 2023) who revealed that harvest index was negative and significantly correlated for grain yield (r_g= -0.9970), number of grains per ear (r_g= -0.7091) and number of spikelets per ear (r_g= -0.8024) at genotypic level only while, biological yield (r_p= -0.7519) for phenotypic level only. (Dhunde et al., 2021) who observed significant positive correlation with biomass yield.

Conclusion

Phenotypic correlation revealed that kernel yield spike-[1] was prominent and positively associated with plant height, tillers plant-[1], thousand kernel weight and biomass yield while it was significantly negative associated with spike length, spikelets spike-[1], flag leaf area and numbers of days to heading and maturity. Similarly, genotypic correlation of kernel yield spike-[1] was significant and positively linked with plant height, tillers plant-[1], thousand kernel weight and grain yield, whereas, it showed significant negative correlation with longer spike, spikelets spike, broader flag leaf, days to heading and days to maturity. Therefor kernel yield can be incorporated in further breeding program. Based on performance like correlation, yield and production the parental genotype Janbaz, and F[3]

combination Watan × AUP-5008, Pirsabak-2005 × AUP-5008, Saleem-2000 × Janbaz and Watan × Tatara were the most promising genotypes for most of the quantitative traits, which can be incorporated in further breeding program.

References

Baye, A., Berihun, B., Bantayehu, M., & Derebe, B. (2020). Genotypic and Phenotypic Correlation and Path Coefficient analysis for yield and yield-related traits in advanced bread wheat (Triticum aestivum L.) lines. *Cogent Food & Agric., 6:1752603.*

Bilal, M., Zakria, S.M. (2021). Improving water productivity by adoption of high efficiency irrigation systems among vegetable growers in district Rawalpindi, *Punjab Pakistan. Pakistan Journal of Agriculture Science.* 58(3). https://doi.org/10.38211/joarps.2023.04.01.56

Crespo-Herrera, I.A., Crossa, J., Huerta- Espino, J., Vargas, M., Mondal, S., Velu, G., Payne, T.S., Braun, H., Singh, R.P. (2018). Genetic gains for kernel yield in CIMMYT's semi-arid wheat yield trials grown in suboptimal environments. *Crop Sci*, 5:1890-98.

Dhunde, B.B., Devmore, J.P., Mahadik, S.G., Palshetkar, M.G., Vanve, P.B., Bhave, S.G., Thorat, B.S. (2021). Correlation and path analysis studies on yield and its components in green gram [Vigna radiata L. Wilczek]. *The Pharma Innovation Journal.* 10 (1):727-30.

Endashaw, G.S., & Alemnesh, S. (2021). Estimation of Genetic Variability, Heritability and Genetic Advance in Bread Wheat (Triticum aestivum L.). Int. J. of Res. Stu. Agric. Sci., (IJRSAS) 9:17-26. DOI: http://dx.doi.org/ 10.20431/2454-6224.0709004.

FAO. Crop Prospects and Food Situation – Quarterly Global Report No. 2, July. (2022). Rome. Available: *https://doi.org/10.4060/cc0868en*.

Gerema, G. (2020). Evaluation of durum wheat (Triticum turgidum) genotypes for genetic variability, heritability, genetic advance and correlation studies. *J. Agric. Natural Resource.*, 2:150–159.

Kadam , D.J., Karwar, S.H., Jadhav, P.S.(2022). Correlation analysis for different characteristics in wheat. *The Pharm. Inno J.*, 11: 98- 100.

Kalhoro, A.A., Ali, S., Basharat, A., Waseem, H., Arshad, M., Muhammad, A., Nadia, M., Sadia, N.Z., Irum, H., Munawar,A., Mahreen, K., Sabeen, A., Hafsa, N., Khuram, S.(2023). Screening of Seven Bread Wheat Genotypes for Agro- Morphological Diversity in Sindh. *J. Positive School Psych.,* http://journalppw.com.7:175-187.

Kumar, A., Singh, L., Lal, K., Yadav, K. (2018). Studies on Genetic Variability, Correlation and Path Coefficient for Yield and Its Component Traits in Wheat (Triticum aestivum L. em. Thell.). *Int. J. Env. & Climate Change.*, 8:1057-1067.

Kumar, P., Solanki, Y.P., Singh, V. (2020). Genetic Variability and Association of Morpho-physiological Traits in Bread Wheat (Triticum aestivum L.). *Current Journal of Applied Science and Technology., 35:95-105. 23.*

Kwon, S.H., & Torrie, J.H. (1964). Heritability and inter-relationship among traits of two Soybean Populations. *Crop Sci.*, 2:196- 198.

Lichthardt, C., Chen, T.W.S., Stützel, H. (2020). Co-evoluation of sink and source in the recent breeding history of winter wheat in Germany. *Frontiers in Plant Science.*, 10, 1771.https:// doi.org/10.3389/fpls.2019.01771.

Meherbabu, A., Kumar, V.S.V., Janeja, H.S., Talekar, N. & Sandal, S.S. (2023). Analysis of Genetic Variability, Correlation and Path for Yield and Its Attributing Traits in Wheat (*Triticum aestivum* L.) Inter. J. Env. & Climate Change., 8:1057-1067.

Mohamed, A., & El-Shafi, A. (2014). Estimates of genetic variability and efficiency of selection for grain yield and its components in two wheat crosses (Triticum aestivum L.) *Inter. J. Agric. Crop Sci.*, 2: 83-90.

Passioura, J.B. (2020). Translational research in agriculture. Can we do it better? Farrer Review. *Crop & Pasture Science.,* 71: 517–528, https://doi.org/10.1071/CP20066

Saleh, M.M., Fariza, A.A. (2020). Evaluation of yield traits in some primitive wheat genotypes to ensure sustainability of wheat production. *Innovations in Agric.,* 10: 1-4.

Sharma, P., Kamboj, M.C., Singh, N., Chand, M., Yadava, R.K. (2018). Path Coefficient and Correlation Studies of Yield and Yield Associated Traits in Advanced Homozygous Lines of Bread Wheat Germplasm. International. *J. of Current Microb. & Appl. Sci.*, 2:51-63.

Subhani, G.M. (2000). Correlation and path coefficient analysis in bread wheat under drought stress and normal conditions. *Pakistan J. Biological Sci.*, 1: 72-77. DOI:10.4081/ija.2023.2194.

Tarkeshwar, K.K., Yadav, M., Gaur, S.C., Chaudhary, R.P., Mishra, G., (2020). Correlation and Path Coefficient for Yield and its Component Traits in Bread Wheat (Triticum aestivum L.). *International Journal of Current. Microb. & appl. Sci.* Special Issue., 11: 688-696.

Ullah, M.I., Mahpara, S., Bibi, R., Shah, R.U., Ullah, R., Abbas, S., Ullah, M.I., Hassan, A.M., El-Shehawi, A.M., Brestic, M., Zivcak, M., (2021). Grain yield and correlated traits of bread wheat lines: Implications for yield improvement. *Saudi Journal of Biological Sciences.*, 10:5714-9.

Waitt, D.E., Levin, D.A., (1998). Genetic and phenotypic correlations in plants: A botanical test of Cheverud's conjecture. *Heredity.*, 3:310–31.

Zare, M., Shokrpour, M., Nejad, S.E.H., (2017). Correlation and Path coefficient analysis in wheat (Triticum aestivum L.) under various drought conditions. *Bangladesh J. Bot.*, 4:1309-1315.