Assessment of Genetic variability, Correlation and Path coefficient Analysis for Yield Associated Traits in Wheat (*Triticum aestivum* L.)

Abstract

Comment [Ma1]: Rewrite abstract according to the objectives and results/outcome please

The present study was carried out during the two successive seasons 2020-21 and 2021-22 at the Crop Research Farm, R.A.K. College of Agriculture, RVSKVV, Sehore (MP), . The present study evaluated genetic variability, heritability, correlation, and path analysis among diverse wheat genotypes for key agronomic traits. Significant differences (P<0.01) were observed among genotypes for all studied traits, indicating substantial genetic variability that can be utilized for selection and hybridization. Phenotypic coefficient of variance (PCV) was higher than genotypic coefficient of variance (GCV) for all traits, highlighting environmental influence. High heritability estimates were recorded for most traits, suggesting strong genetic control, whereas genetic advance as a percentage of the mean was high for traits like the number of effective tillers per plant and 1000-seed weight. Correlation analysis revealed significant positive associations of seed yield per plant with biological yield, 1000-seed weight, and the number of grains per spike at both genotypic and phenotypic levels, emphasizing their importance in yield improvement. Path analysis identified biological yield, 1000-seed weight, and harvest index as key contributors to seed yield, suggesting their prioritization in breeding programs. These findings provide valuable insights for wheat breeders aiming to enhance genetic gains and develop high-yielding wheat varieties.

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Key words-ANOVA, GCV, PCV, Heritability, Genetic Advance, Correlation, Path

Comment [Ma4]: **Variability, Correlation, heritability, Traits, Wheat**

INTRODUCTION

Wheat (*Triticum aestivum* L.) havingchromosome number 2n=6x=42, [AABBDD] (hexaploid) is widely cultivated, self-pollinating annual plant belongs to the (Gramineae) family. According to Wani *et. al.*,(2018*)* wheat holds great significance as it is one of the primary cerealcrop used as a staple food source worldwide. In terms of global food crops, wheat ranks second after rice (Bhanu et. al., 2018). Wheat plays a crucial role in providing approximately 20% of the calories and protein consumed by people worldwide, contributing to the sustenance of around 40% of the global population.

Comment [Ma5]: Wheat (*Triticum aestivum* L.), with a chromosome number of 2n = 6x = 42 [AABBDD] (hexaploid), is a widely cultivated, self-pollinating annual plant that belongs to the *Gramineae* family.

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According to the Food and Agriculture Organization FAO, 2023, global wheat production reached approximately 776.5 mt in 2021. The productionwasestimatedtoslightlyincreaseto778.3 mt in 2022 and then decrease to 770.3 mt in 2023. Wheat holds a crucial position not only as a key crop for food security but also as a valuable cash crop on a global scale (Crespo-Herrera et. al., 2018). The importance of wheat is reflected in the significant global trade volume.In the 2023-24 season, world wheattradereachedarecordhighof186.6 mt, surpassing the previous season by 1.2 percent or 2.3 mt (FAO, 2023. This highlights the significant role of wheat in meeting global food demands and economic activities.

Comment [Ma7]: According to the Food and Agriculture Organization (FAO), global wheat production reached approximately 776.5 million tons (mt) in 2021. The production was estimated to slightly increase to 778.3 mt in 2022, before decreasing to 770.3 mt in 2023.

Comment [Ma8]: The importance of wheat is evident in the significant volume of global trade

Comment [Ma9]: In the 2023-24 cropping season, globle wheat trade reached a record high of 186.6 mt, surpassing the previous season by 1.2 percent, or 2.3 mt (FAO, 2023)

Comment [Ma10]: and supporting economic activities.

In order to establish a successful breeding program, the presence of genetic diversity within the population is crucial. Verma *et. al.,* 2013 confirm that plants with higher genetic variability aremore likely to benefit from favorable hybrid crosses and generate productive recombinants, thus leading to a broader heritability within the populationduringtheprocessofgenetic improvement. Estimation of heritability in combination with genetic advance are usually more useful than heritability alone for forecasting genetic gain under selection. However, a traitwith a high heritability does not always have a high genetic advance (Johnson *et. al.,* 1955). Correlation revealsthedegreeanddirectionofassociationat phenotypic and genotypic levels btw the yieldand its contributing traits. However, it should be noted that the correlation could sometimes fail to give accurate insights into the individual impactof each character on the dependent character. It is understandable that a path analysis would be necessarytodeterminewhichcharactersactually affect seed yield.So path analysis is used to measure the indirect and direct effects of traits (Dhunde *et al.*, 2021). It is impossible to begin an effective breeding programme without first establishing genetic variability using appropriate metrics including GCV and PCV, Genetic advance (GA) and heritability (h^2b) (Salman *et al.,* 2021).

Comment [Ma11]: Plants with higher genetic variability are more likely to benefit from favorable hybrid crosses and produce productive recombinants, thereby increasing the heritability within the population during the process of genetic improvement."

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MATERIALS AND METHODS

The present study was carried out during the two successive seasons 2020-21 and 2021-22 at the Crop Research Farm, R.A.K. College of Agriculture, RVSKVV, Sehore (MP). The experiment involved six genetically diverse parent plants that exhibited a wide range of variation. Total of 15 crosses derived from these parents were selected for further investigation. In the Rabi season of 2021-2022, the final experimental material, consisting of the selected crosses, was evaluated using a randomized block design with three replications. Each plot consisted of four rows for parents and F1. Each row was 3m long and 30 cm apart, and the seeds within row were spaced 3.5 cm apart. The sowing was made in two different experimental years by hand dibbling method of seeding each in rows using Randomized complete block design.All recommended cultural practices were considered.The mean value was then determined for analysis over three replications figure in Table 2.

Comment [Ma14]: ????

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Comment [Ma16]: From 6 parents only 15 cross combination .. please verify??

Comment [Ma17]: Investigation (Table 1)

Comment [Ma18]: Do you have enough seed in F1 for establishing this layout ????? if yes HOW???

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Comment [Ma21]: (Table 2)

Data were recorded on five individual guarded plants chosen at random from each row. The studied characters were Days to heading, Days to maturity, Plant height (cm), Number of effective tillers/plant, Number of spikes/plant, Number of spikelets/spike, Spike length (cm), Spike weight (g), Number of grains/spike, Biological yield/plant (g), Harvest Index (%), 1000 Seed Weight (g) and Seed yield/plant (g).The List of wheat genotypes used in morphological assessment present in Table 1.

Comment [Ma22]: delete

The analysis of variance was carried out as per methods suggested by Panse and Sukhatme (1967). Genotypic coefficients of variation (GCV %) and phenotypic coefficients of variation (PCV %) were calculated by the method suggested by Burton (1952). In the present study the heritability was calculated in broad sense by the formula as suggested by (Hanson et al., 1956). The estimation of genotypic and phenotypic variances and heritability were used to determine the expected genetic advance as suggested by Johnson et al. (1955).

EstimatingofCorrelation

Comment [Ma23]: which software used for statistical analysis give reference also ..

Correlation coefficients among the characters in all possible combination were calculated with the help of procedure given by (Miller et al.,1958). The variance and covariance components were used to compute the correlation coefficients at genotypic and phenotypic level using the following formula.

$$\text{Phenotypic correlation (rp)} = \frac{\text{PCov. xy}}{\sqrt{\text{PVx.PVy}}}$$

Comment [Ma24]: type as below equations

$$\text{Genotypiccorrelation(rg)}= \frac{\text{GCov.xy}}{\sqrt{\text{GVx.GVy}}}$$

$$\text{rxy}=\frac{\text{Cov(x,y)}}{\sqrt{\text{V(x)}}\text{x}\sqrt{\text{V(y)}}}$$

Where,

r_{xy} =Correlation coefficientbetween character x and y
$Cov_{x,y}$=Co-varianceofcharacterxandy
V_x = Variance of character x, and
V_y=Varianceofcharactery
r_p = Phenotypic correlation
r_g = Genotypic correlation.

Estimation of PathAnalysis

Pathanalysissplitsthecorrelationcoefficientinto the measures of direct and indirect effects and measures contribution of each independent variableonthedependentvariableandestimates residualeffects.Ithelpsindeterminingtheyield andyieldcontributingcharacters.

Toestimatevariousdirectandindirecteffects, the following equations were used

$$r1y=P1y+r12P2y+r13P3y+\ldots+r1IPIy$$

$$r2y=r2yP1y+P2y+r23P3y+\ldots+r2IPIy$$

$$rIy=rI1P1y+rI2P2y+rI3P3y+\ldots+PIy$$

Where,

r_{1y}tor_{Iy}=Coefficientofcorrelationbetween factor 1 to I anddependent character y
$r_{12}$to$r_{I-1,I}$ =Coefficientofcorrelationamong causal factors themselves
P_{1y} to P_{Iy} = Direct effects of characters 1 to I on character y.

ResidualEffect

Residual effect, which measures the contribution of the characters was obtained by:

$$(\mathrm{PRY}) = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_{ij} P_i^{\,2} Y + 2 \sum_{\substack{i',j \\ i>j}} P_{iy} P_{jy} R_{ij}$$

EstimationofGAand GAM

Thegeneticadvance(GA)forselectionintensity(K)at5%wascalculatedbytheformulasuggested by Allard, 1960.

$$GA=(K)(\sigma_p)(H^2)$$

Where,

GA = Expected genetic advance at 5% selection intensity,
σ_p = Phenotypic standard deviation
H^2= Heritability and K = selection differential (K= 2.063 at 5% selection intensity).

The genetic advance as percent of the mean (GAM) was calculated by formula given by Johnson et al.Johnson et al., 1955

$$GAM= \frac{GA}{X} * 100$$

Where,

GAM = Genetic advance as percent of mean
GA=Geneticadvanceat5%selectionintensity
X= Population Mean

Heritability(H^2)wascomputedbyformuladeveloped by Dewey, 1959

$$H^2=\frac{\sigma 2g}{\sigma 2p} X\ 100$$

Where,
σ^2p= Phenotypic Variance
σ^2g= Genotypic Variance
H^2 = Heritability in broad sense

RESULTS AND DISCUSSION

Significant differences (P<0.01) were observed among the tested genotypes for all the traits investigated viz. Days to heading, Days to maturity, Plant height (cm), Number of

Comment [Ma25]: types again instead of pasting figure effective tillers/plant, Number of spikes/plant, Number of spikelets/spike, Spike length (cm), Spike weight (g), Number of grains/spike, Biological yield/plant (g), Harvest Index (%), 1000 Seed Weight (g) and Seed yield/plant (g)(Table 2). These findings indicate the presence of substantial variability among the genotypes, which can be harnessed through selection and hybridization. The significant differences observed among the genotypes for the studied characteristics justify conducting further genetic analysis (Chaudhary *et. al.*, 2023). The substantial genetic variation among the genotypes suggests that they exhibit genetic diversity, providing an excellent opportunity for breeders to select suitablegenotypesforspecifictraitsofinterestin variety development. A similar results reportedby Getachew*et. al.*, 2021, Ullah*et. al.*, 2021 and Yared *et. al.*, 2021 that the analysis of variance revealed significant genetic variability among all traits for the treatments. Table 3 presents the estimatedrange, minimum and maximum values, alongwith their corresponding genotypes, meanvalues, and corresponding standard errors forthe thirteen traits examined in wheat genotypes.

Comment [Ma26]: delete repetition

Variability,HeritabilityandGenetic Advance

Genetic variability parameters *viz.* GCV, PCV, Heritability (Broad sense), Genetic advance and genetic advance as 5 % of mean tabulated in Table4.PCV(Phenotypiccoefficientofvariance) is higher than GCV (Genotypic coefficient of variance) for all the characters that indicates an influenceofenvironmentontraits.Phenotypic coefficient of variation found moderate for Number of spikes/ plant, Seed yield /plant, Spike weight, Spike length and Biological yield/plant. The current findings are consistent withtheresultsreportedbyUpadhyay*etal.*, 2019,who also observed high PCV and GCV for Spike length and Biological yield/plant. Similarly, moderate PCV and GCV was recorded for Number of spikes/ plant, Spike weight, Seed yield /plant, Biological yield/plant and Spike length. Rajput et al., 2019, alsoreportedmoderatePCVandGCVNumber of spikes/ plant, Seed yield /plant and Spike lengthandlowPCVandGCVwere recorded for Days to heading Plant height, Days to maturity, Number of spikelets/spike and Harvest Index. The present result in agreement with Bayisa *et. al.*, 2020, Verma *et. al.*, 2013 and Bhanu *et. al.*,2018.

Comment [Ma27]: please add discussion on your cross combination/results

Heritability serves as a predictor of the traits that parentswillpass onto theiroffspring.Khanetal., 2013 found that selection processes become easier as heritability estimates increased. The heritability (H^2) revealed the extent to which quantitative traits inherited, but it fails to disclose the extent to which genetic gain may be attained bytheselectionoftheidealplant fromtheelitepopulations. Therefore, the combination of heritabilityand geneticadvanceisbeneficialthan either factor alone (Kumar *et. al.*, 2021). In the present investigation high heritability was observed for all the traits except harvest index (%). Upadhyay *et. al.*, 2019 and Rajput *et. al.*, 2029, documented similar result that high estimates of heritability. These traits exhibit a high degree of heritability, indicating that genetic factors have a strong influence on their expression. Consequently, environmental factors are likely to have a lesser impact on the development ofthese traits. Low heritability estimated for Harvest index only. Genetic advance as percent of mean (GAM) recorded highNumber of effective tillers/plant followed by 1000 grain seed weight, Number of grains per spike and Number of spikes/ plant. Moderate genetic advance as percentage of mean was recorded for Spike weight followed by Seed yield/plant, Spike length and Biological yield/plant. Low genetic advance as percentage of mean were noticed for Days to heading followed by Plant height, Days to maturity, Number of spikelets/spike and Harvest Index. Kumaret al., 2020,Upadhyay *et al.,* 2019, Rajput *et. al.,* 2019, Baye *et. al.,* 2020 Ayer *et. al.,* 2017 also found similar results.

Comment [Ma28]: please add discussion on your cross combination/results

EstimationofCorrelation

Assessment of the genotypic and phenotypic correlation between various traits tabulated in Table 5a & 5b. The seed yield or economic yield in almost all the crops is referred to as super character, which results from multiplicative interactions of several other characters that are termed as yield components. Thus, genetic architecture of seed yield per plant in wheat as well as other crops is based on the balance or overall net effect produced by various yield components directly or indirectly by interaction with one another. Therefore, identification of important yield components and information about their association with yield and also with each other is very useful for developing efficient selection strategy for evolving high-yielding varieties. The correlation coefficient which provides the measurement of degree of symmetrical association between two variables or characters helps in understanding the nature and magnitude of association among yield and yield components. The phenotypic and genotypic correlations were computed among thirteen characters using data of all the wheat genotypes. In general, the genotypic correlation coefficient values were higher than the phenotypic values. This indicated that how much of phenotypic correlation coefficients are influenced by environment. In the present study, all possible correlation coefficient at genotypic and phenotypic levels among thirteen traits themselves and with seed yield per plant were estimated.

Comment [Ma29]: Reduce para for Genotypic/phenotypic importance

At genotypic level significant positive correlation of seed yield with Biological yield/plant, 1000 Seed Weight and Number of grains/spike. Additionally, there is a positive but non-significant correlation with Harvest Index, Number of spikelets/spike, Number of effective tillers/plant, Spike weight, Spike length and Days to maturity. At Phenotypic level significant positive correlation found with Biological yield/plant, 1000 Seed Weight and Number of grains/spike. Additionally, there is a positive but non-significant correlation with Harvest Index, Number of spikelets/spike, days to maturity, Spike length and Spike weight. Positive correlation values indicates that the values of both variables tend to increase together. These findings corroborate with those of Ullah *et al.,* (2021), Allah *et al.,* (2021), Kumar *et al.,* (2020), Rajput *et al.,* (2019), Verma *et al.,* (2019) and Baye *et al.,* (2020) reportedsimilarresults,wherethegenotypic correlation coefficients (r_g) were found to be higher than the corresponding phenotypic correlation coefficients (r_p) for most of the character combinations. This suggests that the observed correlations between traits are predominantly influenced by genetic factors rather than environmental factors. Genotypic correlations provide valuable insights into the underlying genetic relationships between traits, which can be useful for plant breeders in selecting desirablecombinations of traits for crop improvement programs. Indirect selection is more effective than direct selection procedure when the attribute in question has low heritability and/or is not easily and precisely measured. The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because selection for one or more traits results in correlated response for several other traits (Searle, 1965), and the pattern of variation will also be changed (Waddington and Robertson, 1966). Therefore, knowledge of genetic correlation existing between yield and its components is essential.

Phenotypic correlation may be of genotypic and/or environmental origin and provides information about association observed between two characters. For selection purpose phenotypic correlation is of little practical values unless genetic and environmental correlations between pairs of characters are in the same direction when they are estimated separately. Genetic correlation provides a measure of genetic association between characters and is used in selection of one character for the improvement of other, and provides information by themselves (Miller *et. al.,* 1958) and will be helpful to the breeder since they are based on transmissible genetic variance (Jerome *et. al.,* 1956). Genetic correlation is the net effect of all segregating genes that affects the characters; some are causing positive and negative correlations. The major causes underlying genetic correlation are pleiotropy, linkage and developmentally induced relationship (Adams, 1967; Stebbins, 1950).

Comment [Ma30]: Instead of writing for Genotypic/phenotypic importance etc etc.. kindly elaborate your results and discussion over it

PathAnalysis

Comment [Ma31]: Comments Same as above.

Merely examining correlations does not offer a comprehensive understanding of how each specific trait contributes to the overall picture. Path analysis, on the other hand, provesvaluable in evaluating variables by quantifying their respective contributions and distinguishing between partially indirect and direct sources of association. This analytical approach enables a comparative assessment of variables based on the magnitude of their influences. On the basis of genotypic path, results indicate that biological yield per plant, 1000-seed weight, and harvest index are the most important traits with strong direct effects on seed yield per plant. These traits should be prioritized in breeding programs for yield improvement. Traits like plant height and spike length have minor direct effects, while days to heading and maturity negatively impact yield, indicating a need to select for early-maturing genotypes. While on the basis of phenotypic path, the biological yield per plant, 1000-seed weight, and harvest index have the strongest direct positive effects on seed yield, making them the key selection criteria in breeding programs. Traits like days to heading and days tomaturity have negative direct effects, suggesting that earlier heading and maturity should be prioritized for higher productivity (table 6a & 6b).This result in agreement with Ayer*et. al.,* (2017), Meles*et. al.,* (2017), Chimdesa *et. al.,* (2017), Getachew*el. al.,* (2021), Rajput *et. al.,* (2019) and Kumar *et. al.,* (2020).

Table1. Parents and crosses of wheat used in the experiment

Comment [Ma32]: Are they ramdomly crossed/blind crosses or targeted crosses based on traits. Kindly write para in M&M

Parents			
S. No.	**Germplasm**	**S. No.**	**Germplasm**
1	CWYT-614	4	GS-2031
2	HI-1633	5	HI-1634
3	CWYT-644	6	HI- 8777
Cross Combinations			
S. No.	**Combinations**	**S. No.**	**Combinations**
1	CWYT-614xCWYT-644	9	CWYT-644xHI-1633
2	CWYT-614xHI-1634	10	HI-1634x GS-2031
3	CWYT-614xGS-2031	11	HI-1634xHI-8777
4	CWYT-614xHI-8777	12	HI-1634xHI-1633
5	CWYT-614xHI-1633	13	GS-2031xHI-8777
6	CWYT-644 x HI -1634	14	GS-2031xHI-1633
7	CWYT-644 xGS -2031	15	HI-8777xHI-1633
8	CWYT- 644 x HI- 8777		

Table2. ANOVA for different quantitative traits over (two) environments studied in Wheat (*Triticum aestivum* L.)

Comment [Ma33]: Explain environments. No such environmental study is mention in M & M or objectives/aims

Source of Variation	df	Days to heading	Days to maturity	Plant height (cm)	Number of effective tillers/ plant	Number of spikes/ plant	Number of spikelets/ spike	Spike length (cm)
Environments	**1**	62051.28**	6143.70**	7020.51**	5644.12**	7.2**	813.24**	412.4**
Replications	**2**	2339.1**	105.4**	4402.56**	472.5**	10.92**	329.62**	182.25**
Genotypes	**20**	6432.45**	159.87**	323.36**	1289.42**	6.88**	694.14**	65.03**
Parents	**5**	4445.45**	245.59**	258.33**	2744.3**	3.4**	833.60**	91.91**
F1 hybrids	**14**	2365.43**	122.76**	304.55**	866.82**	6.5**	652.25**	40.64**
Parents Vs Hybrids	**1**	6645.69**	1629.13**	2261.6**	3754.91**	71.25**	1883.08**	1355.01**
Error	**70**	48.19	0.59	14.9	1.68	0.59	41.08	2.07
Environment	**df**	**Spike weight (g)**	**Number of grains/spike**	**Biological yield/plant (g)**	**Harvest Index (%)**	**1000 Seed Weight (g)**	**Seed yield/plant (g)**	
Replication	**1**	3243.27**	275.83**	6.20*	8525.28**	1453.85**	221.78**	
Genotypes	**2**	988.91**	62.40**	14.68**	1339.10**	988.91**	81.00**	
Parents	**20**	3590.61**	1652.03**	41.78**	2475.04**	719.98**	148.86**	
F1 hybrids	**5**	4588.9**	801.30**	39.17**	3396.97**	209.10**	74.66**	
Parents Vs Hybrids	**14**	3444.5**	1550.33**	42.7**	2304.62**	756.17**	163.70**	
Error	**1**	2107.05**	5620.77**	11.14*	3412.82**	3987.11**	0.46	
	70	40.87	1.18	1.11	48.19	40.87	6.5	

Comment [Ma34]: Very strange to note that in 2 environments all quantitative traits are highly significant in first cross combination. Please verify..

Comment [Ma35]: Recheck col and rows

Table3.Meanofparentandcrossesforthirteen traitswithCV,CD.

Treatments	Days to heading	Days to maturity	Plant height (cm)	Number of effective tillers/plant	Number of spikes/plant	Number of spikelets/spike	Spike length (cm)	Spike weight (g)	Number of grains per spike	Biological yield/plant (g)	Seed yield / plant (g)	1000 grain seed weight (g)	Harvest Index (%)
Parents													
CWYT-614	80.85	122.55	63.65	9.03	13.50	20.90	12.15	4.78	85.05	127.03	59.52	46.48	46.96
CWYT- 644	79.00	121.50	83.75	5.00	10.50	21.07	10.40	4.50	72.80	114.81	56.22	49.75	48.97
HI -1634	74.10	114.85	75.10	6.00	12.00	21.33	12.55	5.25	90.00	121.83	58.50	45.52	48.02
GS -2031	83.80	122.50	86.40	8.00	13.50	18.00	14.50	5.47	71.50	110.34	54.30	47.98	49.22
HI- 8777	66.95	106.00	70.65	10.00	12.00	18.50	7.55	4.42	34.00	88.19	39.50	53.42	44.79
HI -1633	66.70	106.00	82.70	12.50	10.50	19.43	15.50	4.64	39.50	100.67	50.50	45.62	50.17
Mean	**75.23**	**115.57**	**77.04**	**8.42**	**12.00**	**19.87**	**12.11**	**4.84**	**65.48**	**110.48**	**53.09**	**48.13**	**48.02**
Min	**66.70**	**106.00**	**63.65**	**5.00**	**10.50**	**18.00**	**7.55**	**4.42**	**34.00**	**88.19**	**39.50**	**45.52**	**44.79**
Max	**83.80**	**122.55**	**86.40**	**12.50**	**13.50**	**21.33**	**15.50**	**5.47**	**90.00**	**127.03**	**59.52**	**53.42**	**50.17**
CV	**5.04**	**3.35**	**3.16**	**3.79**	**5.96**	**2.84**	**2.88**	**8.54**	**1.71**	**6.14**	**5.59**	**2.75**	**6.04**
$CD_{0.05\%}$	**1.32**	**1.38**	**2.74**	**2.20**	**1.22**	**1.37**	**0.88**	**4.06**	**0.15**	**0.92**	**1.83**	**1.94**	**1.93**
Crosses													
CWYT-614 x CWYT-644	80.90	120.55	87.50	6.50	13.00	20.80	15.30	5.40	57.10	54.71	26.31	11.05	48.10
CWYT-614 x HI -1634	81.85	120.50	90.00	7.00	10.00	21.30	10.25	3.64	51.75	88.37	43.09	44.61	48.75
CWYT-614 x GS -2031	80.85	121.75	94.55	14.00	14.50	17.83	12.50	4.51	67.50	108.82	53.58	49.76	49.24
CWYT-614 x HI- 8777	89.88	131.00	84.00	17.30	12.00	18.67	13.60	4.30	75.20	70.43	34.17	18.83	48.51
CWYT-614 x HI -1633	82.65	124.00	89.10	13.03	13.00	19.63	17.55	5.61	72.85	109.04	53.14	45.50	48.74
CWYT- 644 x HI -1634	81.98	122.50	93.50	12.55	14.00	18.60	12.40	4.76	66.80	113.42	55.76	53.53	49.16
CWYT- 644 x GS -2031	80.95	121.50	96.60	13.55	16.00	20.83	12.60	5.10	68.20	110.43	54.04	49.91	48.93
CWYT- 644 x HI- 8777	80.18	120.50	84.75	9.00	13.00	20.60	12.35	5.54	66.45	96.66	47.16	40.87	48.79
CWYT- 644x HI -1633	79.78	123.00	94.80	15.35	11.50	21.47	14.55	4.14	81.85	107.17	52.46	39.66	48.95
HI -1634 x GS -2031	83.73	125.50	88.60	11.23	10.50	19.20	13.45	4.34	74.15	115.90	56.90	49.77	49.09
HI -1634 x HI- 8777	79.63	121.00	88.72	14.32	14.50	21.30	11.60	3.21	50.50	94.22	46.04	51.56	48.87
HI -1634 x HI -1633	75.06	116.09	88.50	14.60	13.50	19.70	13.65	3.54	76.00	109.33	55.50	46.65	50.77
GS -2031 x HI- 8777	84.06	125.01	82.29	10.01	11.00	20.73	11.55	3.43	80.85	117.41	57.66	46.58	49.11
GS -2031 x HI -1633	64.90	105.90	88.00	11.05	13.00	19.90	13.30	3.33	53.10	94.73	46.26	49.46	48.83
HI- 8777 x HI -1633	61.05	103.05	82.73	17.57	15.00	17.87	11.45	3.63	43.00	104.49	54.00	55.81	51.68
Mean	**79.16**	**120.12**	**88.91**	**12.47**	**13.57**	**19.90**	**13.07**	**4.30**	**65.69**	**99.67**	**49.07**	**43.57**	**49.17**
Min	**61.05**	**103.05**	**82.29**	**6.50**	**10.50**	**17.83**	**10.25**	**3.21**	**43.00**	**54.71**	**26.31**	**11.05**	**48.10**
Max	**89.88**	**131.00**	**96.60**	**17.57**	**15.00**	**21.47**	**17.55**	**5.61**	**81.85**	**117.41**	**57.66**	**55.81**	**51.68**
CV	**0.99**	**3.08**	**0.71**	**7.85**	**15.96**	**6.66**	**3.24**	**2.18**	**2.16**	**3.36**	**7.77**	**5.48**	**4.32**
$CD_{0.05\%}$	**1.75**	**6.83**	**1.72**	**6.93**	**6.35**	**4.14**	**0.32**	**1.10**	**0.59**	**0.31**	**4.07**	**0.09**	**1.64**

Comment [Ma36]: Mention date of sowing in M & M . Its seems very low value of days to heading and maturity while all the crosses have late heading and maturity. Which one is desirable???

Comment [Ma37]: What is the need for spike weight

Comment [Ma38]: Kindly convert in Kg/hac according to lot size

Comment [Ma39]: Too much HI in relation to plant height

Comment [Ma40]: Too much dwarf

Table4.Variability(GCV&PCV),Heritability(broadsense),Geneticadvanceas percentage of mean (GAM)at5%inwheat

Characters	GCV (%)	PCV (%)	Heritability (%) (Broad sense)	Genetic advance as % of mean 5%
Days to heading	9.23	9.71	95.06	18.07
Days to maturity	5.92	7.00	84.57	10.31
Plant height (cm)	9.15	9.61	95.21	17.96
Number of effective tillers/ plant	32.05	33.28	96.30	65.57
Number of spikes/ plant	18.50	18.98	97.47	37.54
Number of spikelets/spike	5.62	6.69	84.01	9.73
Spike length (cm)	16.45	16.96	96.99	33.37
Spike weight (g)	17.17	17.62	97.45	34.47
Number of grains per spike	23.38	24.58	95.12	47.73
Biological yield/plant	16.47	16.82	97.92	33.22
1000 grain seed weight	23.91	25.11	95.22	48.86
Harvest Index (%)	2.14	3.62	59.12	2.62
Seed yield /plant	16.92	18.17	93.12	34.34

Table5a.Genotypic correlation coefficient analysis for yield and its contributing traits in Wheat genotypes

Characters	Days to heading	Days to maturity	Plant height (cm)	Number of effective tillers/ plant	Number of spikes/ plant	Number of spikelets/ spike	Spike length (cm)	Spike weight (g)	Number of grains/ spike	Biological yield/ plant (g)	Harvest Index (%)	1000 Seed Weight (g)	Seed yield/ plant (g)
Days to heading	1.0000	0.9255 **	0.2379	-0.0840	0.2505	0.0223	0.2303	0.3053	0.618 **	-0.0057	-0.1717	-0.4081	-0.0253
Days to maturity		1.0000	0.3182	-0.1004	0.2000	-0.0973	0.2106	0.1316	0.6181 **	0.0413	0.0980	-0.3519	0.0036
Plant height (cm)			1.0000	0.2357	0.0490	-0.1046	0.3179	-0.1741	-0.0487	-0.1370	0.5605 **	-0.0263	-0.0649
Number of effective tillers/plant				1.0000	0.6505 **	0.0392	0.2559	-0.2003	-0.0653	-0.0362	0.1374	0.0869	0.0568
Number of spikes/plant					1.0000	0.0809	0.1417	0.1104	0.1117	-0.3220	-0.0713	-0.3315	-0.282
Number of spikelets/spike						1.0000	0.1366	0.3272	0.1918	0.0797	-0.3467	0.0724	0.0908
Spike length (cm)							1.0000	0.4076	0.3024	-0.0583	0.2295	-0.4004	0.0092
Spike weight (g)								1.0000	0.3019	0.0290	-0.4607 *	-0.2663	0.0153
Number of grains/spike									1.0000	0.4957 *	-0.0883	-0.1532	0.4840 *
Biological yield/plant (g)										1.0000	0.1282	0.7204 **	0.9851 **
Harvest Index (%)											1.0000	0.1342	0.1876
1000 Seed Weight (g)												1.0000	0.7176 **
Seed yield/plant (g)													1.0000

Comment [Ma41]: Reproductive or effective

Table 5b: Phenotypic correlation coefficient analysis for yield and its contributing traits in Wheat genotypes

Characters	Days to heading	Days to maturity	Plant height (cm)	Number of effective tillers/plant	Number of spikes/plant	Number of spikelets/spike	Spike length (cm)	Spike weight (g)	Number of grains/spike	Biological yield/plant (g)	Harvest Index (%)	1000 Seed Weight (g)	Seed yield/plant (g)
Days to heading	1	0.9849 **	0.3219 *	0.2163	0.4042 **	-0.1274	0.1896	0.0316	0.4509 **	-0.0423	0.2263	-0.3072 *	-0.0006
Days to maturity		1	0.3221 *	0.2484	0.3874 **	-0.1398	0.1966	0.0065	0.5265 **	0.0247	0.2228	-0.284	0.0641
Plant height (cm)			1	0.4981 **	0.2304	-0.0906	0.4124 **	-0.0142	-0.1177	-0.1835	0.5166 **	0.0139	-0.0622
Number of effective tillers/plant				1	0.6719 **	-0.1725	0.444 **	-0.178	-0.0905	-0.1055	0.5175 **	0.0653	-0.0122
Number of spikes/plant					1	0.0162	0.3697 *	-0.0561	0.0966	-0.2551	0.4754 **	-0.2063	-0.1836
Number of spikelets/spike						1	0.0139	0.0023	0.2179	0.1675	0.0006 NS	0.1188	0.1487
Spike length (cm)							1	0.2645	0.199	-0.0596	0.6703 **	-0.2614	0.0623
Spike weight (g)								1	0.1299	0.0418	-0.0986	-0.1378	0.0317
Number of grains/spike									1	0.5728 **	0.1094	-0.0665	0.5706 **
Biological yield/plant (g)										1	0.1156	0.7244 **	0.9845 **
Harvest Index (%)											1	0.1691	0.2796
1000 Seed Weight (g)												1	0.7248 **
Seed yield/plant (g)													1

Table 6a. Genotypic path matrix of thirteen traits in wheat for seed yield

Comment [Ma42]:

Comment [Ma43]: Explain a and b table in text and discuss

Traits	**Days to heading**	**Days to maturity**	**Plant height (cm)**	**Number of effective tillers/plant**	**Number of spikes/plant**	**Number of spikelets/spike**	**Spike length (cm)**	**Spike weight (g)**	**Number of grains/spike**	**Biological yield/plant (g)**	**Harvest Index (%)**	**1000 Seed Weight (g)**	**Seed yield/plant (g)**
Days to heading	0.14194	-0.17628	0.01959	0.00075	-0.00444	0.00691	0.00003	0.00056	0.00689	-0.07358	0.00247	0.02062	-0.0253
Days to maturity	0.13966	-0.17917	0.01971	0.00102	-0.00425	0.00709	-0.00001	0.00142	0.00812	0.00042	0.00334	0.01906	0.0036
Plant height (cm)	0.0404	-0.05133	0.06882	0.00299	-0.00202	0.00494	-0.00066	0.0018	-0.00224	-0.21586	0.04791	0.00101	-0.0649
Number of effective tillers/plant	0.01653	-0.02854	0.03209	0.00642	-0.008	0.0109	-0.00032	0.01013	-0.00241	-0.17001	0.02607	0.00017	0.0568
Number of spikes/plant	0.04517	-0.05469	0.00996	0.00369	-0.01394	0.00758	0.00019	0.0069	0.00064	-0.3954	0.00442	0.02062	-0.2823
Number of spikelets/spike	-0.03857	0.04994	-0.0134	-0.00275	0.00416	-0.02542	0.00081	0.0028	0.00298	0.14658	-0.04624	-0.00333	0.0908
Spike length (cm)	-0.00262	-0.00148	0.02806	0.00129	0.00164	0.01276	-0.00162	-0.00728	0.00278	-0.2099	0.01619	0.03298	0.0092
Spike weight (g)	-0.0038	0.01204	-0.0059	-0.00308	0.00456	0.00337	-0.00056	-0.02109	0.00298	0.04467	-0.0523	0.0161	0.0153
Number of grains/spike	0.06247	-0.09291	-0.0099	-0.00099	-0.00057	-0.00484	-0.00029	-0.00402	0.01565	0.59078	0.0031	0.0048	0.4840
Biological yield/plant (g)	-0.01005	-0.00007	-0.0143	-0.00105	0.0053	-0.00358	0.00033	-0.00091	0.00889	0.93957	0.00533	-0.04054	0.9851
Harvest Index (%)	0.0043	-0.00736	0.04055	0.00206	-0.00076	0.01446	-0.00032	0.01357	0.0006	0.0682	0.08131	-0.00419	0.1876
1000 Seed Weight (g)	-0.05209	0.06077	-0.0012	-0.00002	0.00511	-0.00151	0.00095	0.00604	-0.00134	0.7501	0.00607	-0.05619	0.7176

Table6b.Genotypicpathmatrixofthirteentraitsinwheatforseed yield

Traits	Days to heading	Days to maturity	Plant height (cm)	Number of effective tillers/plant	Number of spikes/plant	Number of spikelets/ spike	Spike length (cm)	Spike weight (g)	Number of grains/ spike	Biological yield/plant (g)	Harvest Index (%)	1000 Seed Weight (g)	Seed yield/ plant (g)
Days to heading	0.0664	-0.0832	0.0148	0.0037	-0.0102	0.0015	-0.0019	0.0001	0.0032	-0.0422	0.0362	0.0111	-0.0006
Days to maturity	0.0654	-0.0845	0.0148	0.0043	-0.0098	0.0016	-0.0020	0.0000	0.0037	0.0247	0.0356	0.0103	0.0641
Plant height (cm)	0.0214	-0.0272	0.0460	0.0086	-0.0058	0.0010	-0.0042	0.0000	-0.0008	-0.1831	0.0826	-0.0005	-0.0622
Number of effective tillers/plant	0.0144	-0.0210	0.0229	0.0172	-0.0170	0.0020	-0.0045	-0.0006	-0.0006	-0.1053	0.0828	-0.0024	-0.0122
Number of spikes/plant	0.0268	-0.0327	0.0106	0.0115	-0.0253	-0.0002	-0.0038	-0.0002	0.0007	-0.2546	0.0760	0.0075	-0.1836
Number of spikelets/spike	-0.0085	0.0118	-0.0042	-0.0030	-0.0004	-0.0115	-0.0001	0.0000	0.0016	0.1672	0.0001	-0.0043	0.1487
Spike length (cm)	0.0126	-0.0166	0.0190	0.0076	-0.0093	-0.0002	-0.0102	0.0009	0.0014	-0.0595	0.1072	0.0094	0.0623
Spike weight (g)	0.0021	-0.0005	-0.0007	-0.0031	0.0014	0.0000	-0.0027	0.0033	0.0009	0.0417	-0.0158	0.0050	0.0317
Number of grains/spike	0.0299	-0.0445	-0.0054	-0.0016	-0.0024	-0.0025	-0.0020	0.0004	0.0071	0.5716	0.0175	0.0024	0.5706
Biological yield/plant (g)	-0.0028	-0.0021	-0.0084	-0.0018	0.0064	-0.0019	0.0006	0.0001	0.0041	0.9980	0.0185	-0.0262	0.9845
Harvest Index (%)	0.0150	-0.0188	0.0238	0.0089	-0.0120	0.0000	-0.0068	-0.0003	0.0008	0.1154	0.1599	-0.0061	0.2796
1000 Seed Weight (g)	-0.0204	0.0240	0.0006	0.0011	0.0052	-0.0014	0.0027	-0.0005	-0.0005	0.7229	0.0270	-0.0361	0.7248

CONCLUSION

Comment [Ma44]: Rewrite conclusion according to objectives and outcome

Correlation reveals the degree and direction of association at phenotypic and genotypic levels btw the yield and its contributing traits. However, it should be noted that the correlation could sometimes fail to give accurate insights into the individual impact of each character on the dependent character.

COMPETINGINTERESTS

Authors have declared that no competing interests exist.

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Comment [Ma45]: Cross check all references again and convert according to journal instructions plz.

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