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Studies on genetic parameters, correlation coefficient, and path analysis for yield and yield-contributing traits in bread wheat (*T. aestivum* L.)

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Abstract

The genetic variability, correlation, and path coefficient analysis of yield and yield contributing traits in 10 parents and 45 F₁ of wheat genotypes cultivated at B.R.D.P.G. college agricultural farms during 2019-2020, 2020-21, and 2021-2022 in rabi season were the subjects of this study. Significant genetic variation existed between genotypes regarding several grains per spike, grain weight per spike, number of effective tillers per plant, harvest index, and grain yield per spike. When genetic parameters were considered, the genotypic coefficient of variation (GCV) was found to be high for grain weight per spike, grain yield per plant, number of effective tillers per plant, and number of grains per spike, while it was low for days to maturity, plant height, and days to 50% flowering. Variances in phenotype were greater than those in genotype in every instance. High heritability and low genetic advancement in the percentage of mean were noted for days to maturity, and plant height, suggesting that non-additive gene action was involved in the expression of this trait and that selection for it might not be fruitful. High heritability and high genetic advance in the percentage of mean were found for grain weight per spike and grain yield per plant suggesting that these traits were subject to additive gene control and that selection for genetic improvement would be successful. There was a strong positive and significant correlation between grain yield per plant and harvest index and the number of spikelets per spike. Path coefficient analysis showed that the harvest index had the largest direct contribution to grain yield per plant, followed by the number of spikelets per spike. This data aids in assessing these traits' suitability as selection criteria for improved yield performance in breeding initiatives.

Keywords: Correlation coefficient, path analysis, seed yield, characters, wheat

Introduction

Wheat is one of the most significant staple crops in the world, referred to as the "king of cereals" and provides food for over 36% of the world's population. It is produced in 779.9 mt and cultivated in 222.17 mha worldwide (Anonymous, 2023) ^[1]. With a 31.13 mha area and 106.84 mt of production, it is the second most important cereal crop in India (Anonymous, 2022) ^[1]. Over the world, 36% of people get their food from wheat, which also provides 20% of food calories. In contrast to straw, which is used to feed animals, wheat is ground into flour, which is the main product of wheat used to make various foods like roti, pastries, cakes, sandwiches, and wafers. Wheat contains roughly 75% protein overall, with gluten being one of the main proteins in wheat grains. Around the world, around forty-four countries cultivate wheat because of its greater adaptability and the products made from its grains (Kumar *et al.*, 2017) ^[25]. Because of the expanding human population, many countries still struggle to increase wheat production and achieve stable yields like many other crops, due to biotic and abiotic stresses (Kumar *et al.*, 2023) ^[24]. The production of wheat can drop by 50 to 90 percent of its true yield potential in arid, or dry areas. Water shortages regularly affect about 20 million hectares of wheat and about half of all wheat grown worldwide experiences moisture stress. (Cossani and Reynolds 2012) ^[34]. The main element of breeding programs for expanding the gene pool of wheat and other crops is genetic variability for agronomic traits. The degree of genetic variability primarily determines the amount of genetic advancement under selection.

The genetic coefficient of variation combined with the heritability estimate gives the best indication of the amount of progress that can be expected from selection. Environmental factors are known to affect most quantitatively inherited agronomically significant traits. For such challenging traits, phenotypic selection would be challenging. These traits are often difficult to manipulate in breeding programs because they are indirectly controlled by several inter-componential traits (Hittalmani *et al.*, 2003) [18]. One important statistical method that wheat breeders can use to choose lines that will maximize yield is the correlation coefficient. In wheat, the literature showed positive differences between grain yield and yield-associated traits like i.e. no of spikelets per plant, plant height (Mohamad, 1999) [32], and 1000-grain weight. At both the genotypic and phenotypic levels, Nabi *et al.* (1998) [31] and Shah *et al.* (1999) [17] reported positive variations in grain yield depending on plant height, number of effective tillers per plant, no of grains per spike, spike length, and 1000-grain weight. It has been documented that various wheat yield-related traits exhibit variability, correlation coefficients, and path analysis (Meles, 2017; Zerga *et al.*, 2016) [26, 44]. Genotypic variability, correlation coefficient, path analysis, heritability in general, and various traits were used in the current experiment to identify possible offspring that might be used in upcoming wheat breeding initiatives. Correlation in grouping with path analysis would improve comprehension of the cause-and-effect relationship between different character pairs, claim Jayasudha and Sharma (2010) [20]. In order to establish plant selection guidelines, it is essential to comprehend the correlation between yield and the contributing characteristics. Selection becomes more efficient when the total correlation is split into direct and indirect effects using path coefficient analysis (Priya and Joel, 2009) [33]. The correlations between genotype, phenotype, and environment typically determine the current associations between traits. Estimates of heritability are crucial for the current crop breeding strategy because they provide information on the transmission index of the quantitative trait of commercial importance. With the help of genetic advancement, progenies can be accurately represented and separated for likely selection in the next generation. Maximum values approve the possibility of choosing probable new lines with desired features of broad sense heritability combined with high genetic advance (GA) (Ajmal *et al.*, 1995) [3]. Heritability and genetic advancement are very important factors to consider when calculating genetic progress in a breeding program (Gite *et al.*, 2018) [14]. For effective crop improvement, genetic diversity is essential. Several studies have reported patterns of genetic variety loss due to modern breeding methods (Russell *et al.*, 2000; Fu *et al.*, 2005) [35, 13]. Therefore, it seems crucial to understand the levels and distribution of genetic variability in the existing crop gene pools to develop strategies for resource management and utilization. Path analysis is therefore crucial to any plant breeding program to select superior genotypes and improve any trait, genetic variability, character association, and path are prerequisites for improving any crop, including rice (Krishnaveni *et al.*, 2006) [22]. Path analysis's main benefit is that it allows the correlation coefficient to be divided into its constituent parts. The path coefficient, which quantifies the direct impact of a predictor variable on its response variable, is one of these parts. The other part is the indirect effect or effects of a predictor variable on the response variable via another predictor variable (Dewey and Lu, 1959) [11]. Plant breeders have utilized path analysis in agriculture to help them find traits that can be used as selection criteria to increase crop yield (Surek

and Beser, 2003) [37]. Breeders can identify yield components and comprehend the cause of the association between two variables by using path coefficient analysis, which quantifies the direct and indirect contributions of independent variables on dependent variables. Since direct selection is ineffective for low heritable traits like yield, the data gathered from path coefficient analysis aids in indirect selection for genetic yield improvement. A breeder must therefore estimate heritability and genetic advancement to comprehend the extent, character, and interplay of genotype and environmental variation in the traits. Therefore, it is useful to estimate yield variability and yield-related traits before establishing a suitable breeding plan for genetic improvement (Kumar *et al.*, 2019) [23].

Materials and Methods

Experimental site

The experiment was conducted at the Agriculture Research Farm, B.R.D.P.G. College, Deoria, Uttar Pradesh in the Rabi season of 2019-2020, 2020-21, and 2021-2022. The farm is situated in the North-Eastern part of the city at 26° 51' North latitude and 83° 77' East longitude at an elevation of 70 m above the mean sea level. The site lies in a sub-tropical climate under the agro-ecological zone of the Eastern plains. Soil pH ranged from 6.0-8.5. Genetically pure and physically healthy seeds of 10 diverse genotypes of wheat were collected from the wheat research group of the Department of Genetics and Plant Breeding, SHUATS, Prayagraj, NDUAT, India.

Experimental materials and design

The experimental material used in the study was derived from the crossing of 10 lines with two checks of wheat. Following that, 55 genotypes consisting of 45 F₁+10 parents, and third-year 10 parents + 45 F₁ + 45 F₂ will be evaluated in a Randomized Complete Block Design with three replications. The individual plot was 3 m × 2 m in size. The distance between row to row and plant to plant was 22 cm and 10 cm, respectively. Recommended agronomic packages and practices were applied to raise a healthy crop. Data were recorded on various parameters: days to 50% flowering, days to maturity, plant height (cm), No. of effective tillers per plant, flag leaf area (cm), spike length (cm), No. of spikelet per spike, peduncle length (cm), No. of grains per spike, grain weight per spike (g), test weight (g), biological yield per plant (g), harvest index (%), and grain yield per plant (g).

Statistical analysis

For statistical analysis, the mean data from five plants of each genotype were averaged replication-wise. The coefficient of variation (CV), mean, and range were also calculated. Burton (1952) [8] estimated the genotypic and phenotypic coefficients of variation (GCV and PCV); Burton and Devane (1953) [9] estimated the heritability in broad-sense (h²B); Johnson *et al.* (1955) [21] calculated the genetic advance (GA) and genetic advance as a percentage of mean (GAPM); Robinson *et al.* (1951) [36] calculated the correlation coefficient analysis; and Dewey and Lu (1959) [11] accessed the path coefficient analysis.

Result and Discussion

Analysis of variance (ANOVA)

According to the analysis of variance, the average sum of squares for different characters such as, days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, flag leaf area, spike length, number of spikelets per spike, peduncle length, number of grains per spike, grain weight per

spike, test weight, biological yield per plant, harvest index, and grain yield per plant are significant for treatment, parent, F_1 and PVF_1 indicating that there is enough variation among the pre-breeding lines chosen for the investigation. For all yield and yield-related traits, combined analyses of the variance of every year were performed (Table 1). For each trait, the ANOVA revealed highly significant differences ($p < 0.001$) between the parents, F_1 , and PVF_1 genotypes of wheat that were tested. Similar findings of substantial variability among wheat genotypes have been reported by other researchers (Bayisa *et al.*, 2020)^[7], suggesting that there is sufficient genetic variability for growth and yield attributes. This is due to the existence of additive gene action, which may allow selection to produce variability and be successful for a variety of quantitative traits, including crossing programs.

Genetic variability at the genotype and phenotype level

The mean, genotypic, and phenotypic coefficients of variability, along with the predictable regions, are shown in Table 2. Current research indicates that the genotypic coefficient of variance (GCV) value for grain weight per spike and days to maturity ranged from 19.97% to 2.05%, while the phenotypic coefficient of variance (PCV) value for yield and yield-related traits for the combined subsequent year ranged from 21.08% for grain weight per spike to 2.10% for days to maturity. The grain yield per plant showed at both genotypic and phenotypic coefficients of variance of 15.53% and 15.94%. The others who conducted research reported similar GCV and PCV values (Bayisa *et al.*, 2020)^[7]. To measure the variability between given genotypes and help us choose better-performing varieties and start a breeding program, the two most crucial parameters are the genotypic and phenotypic coefficients of variation. The grain weight per spike character showed a high value of GCV and PCV alone, indicating that a significant amount of variation for this character among the lines was due to the environment alone. Meanwhile, grain yield per plant, harvest index, biological yield per plant, number of grains per spike, peduncle length, flag leaf area, spike length, and number of effective tillers per plant, showed moderate values of GCV and PCV, while days to 50% flowering, days to maturity, plant height showed lowest values. The higher GCV and PCV values found among the tested traits imply greater variability among genotypes. Previous studies on wheat (Monpara, 2011, Singh *et al.*, 2012, and Tsegaye *et al.*, 2012)^[27, 38, 43] also found comparable outcomes. Grain yield showed higher genotypic and phenotypic coefficients of variance, which is consistent with findings from Hassani *et al.*, (2022)^[16], Fellahi *et al.*, (2013)^[12], and Bayisa *et al.*, (2020)^[7]. According to Deshmukh *et al.* (1986)^[10], the GCV and PCV values can be classified as low (<10%), moderate (10%-20%), and high (>20%).

Genetic heritability and genetic advance analysis

Heritability estimation is divided into four categories: very high (>85%), moderately high (75% - 85%), moderate (60%-75%) and low (less than 60%). The result showed that the heritability in the broadest sense ranged from 48.58 to 96.33 percent, with the highest heritability of days to 50% flowering, grain yield per plant, days to maturity, number of grains per spike, peduncle length, and grain weight per spike weight, coming in second and third, respectively shown in table 2. The current results are consistent with Singh *et al.*, (2012)^[38] and Monpara (2011)^[27]. The result shown in Table 2, clearly identifies that the highly moderate variables are test weight, spike length, and several effective tillers. The following variables showed moderate

heritability: plant height, flag leaf area, number of spikelets per spike, and harvest index, while biological yield per plant had the lowest heritability. The majority of traits had higher to moderate heritability overall, suggesting that selection for the majority of the traits may work well for those genotype sets. Therefore, phenotypic variations that can be passed down to the following generation and section would be useful for future crop improvement. Hassani *et al.*, (2022)^[16] and Bayisa *et al.*, (2020)^[7] have both reported the same outcome. For every trait that is being studied, the estimated GA values are shown in Table 2. GA is the improvement in the genotypic value of traits for the new population compared to the base. The population is described by Singh *et al.*, (2001)^[41] for a single selection cycle at a particular selection intensity. The predicted genetic gain from a single selection cycle must be predicted (Hamdi *et al.*, 2003)^[15]. Heritability alone cannot result in the appropriate degree of genetic improvement when selecting individual breeding materials. Understanding heritability in conjunction with genetic advancements is more important in this regard. The results showed that the character grain weight per spike had the highest expected genetic advance, reaching 98.96%. The expected genetic advance over the mean ranged from 4.10% to 38.96%. Grain yield per plant, number of effective tillers, number of grains per spike, spike length, harvest index, and peduncle length were the next highest expected genetic advances. Sharma *et al.*, (2006)^[42] reported similar results for wheat tillers plant-1, grain yield, and number of grains ear-1, while Singh *et al.*, (2012)^[38] found little genetic advancement for spike length, tillers m-1, and 1000 grain weight. Hassani *et al.*, 2022^[16] found that grain per spike, grain yield, and biological yield had higher GAM values. Days to maturity, plant height, number of spikelets per spike, number of productive tillers, and thousand kernel weights all show low genetic advance as a percentage of the mean, which is consistent with the results of Hassani *et al.*, (2022)^[16] for days to maturity, number of kernels per spike, and number of spikelets per spike. The traits with moderate genetic advancement as a percentage of the mean and high heritability values were collected for the days to heading and grain-filling period, suggesting that these characters may be satisfactorily selected for improvement. This outcome is consistent with earlier researchers' findings. This suggests that no additive gene action plays a bigger part in their inheritance. The expression of economically important characteristics through additive gene action makes selection for crop improvement rewarding and can be confirmed by recording a high value of broad sense heritability along with high genetic advance as a percentage of the mean.

Correlation co-efficient analysis at genotypic and phenotypic level

The correction coefficient, which measures the relationship between the two attributes, is used to quantify the strength of the association whose limits fall between minus one and one. A positive relationship exists when an increase in one variable causes another to rise; a negative relationship occurs when an increase in one causes another to fall. Two variables are considered uncorrelated if changes in one do not impact the other. Correlation information is very important to a plant breeder because all phenotypic features are the result of the interaction of several genetic elements with one another as well as with environmental factors both individually and in combination. Plant breeders can use correlation to help them figure out the best way to improve a trait that cannot be improved by direct selection and therefore requires indirect

selection. It also details how the connection has become inevitable. It also provides information on the corresponding response to directional selection, which can be used as selection indices for more effective selection and to predict genetic advancement. Correlations may be phenotypic, genotypic, and environmental. Phenotypic correlation is a relationship between metrics that are directly measured on individuals and includes both genetic and non-genetic effects. Genomic correlation considers only genetic factors, such as pleiotropy, linkage, or gene frequency disequilibrium. At the phenotypic level, correlation coefficients showed a highly significant positive relationship between the harvest index, plant height, number of effective tillers per plant, flag leaf area, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike test weight, biological yield per plant, and grain yield per plant. At the genotypic level, the correlation values were also at or above the phenotypic level (Table 3). Therefore, it can be concluded that increasing these qualities by selection, either separately or together, will increase wheat production. The current study found a highly significant positive correlation between the harvest index and grain yield per plant, which could be due to the association of the genes controlling these traits. In contrast, the character days to 50% flowering and days to maturity showed a negative and significant correlation with grain yield per plant, suggesting that direct selection for this character might not be beneficial for increasing yield; instead, indirect selection will need to be carried out using number of grains per spike and grain weight per spike. The current results support those of Ahmed *et al.*, (2010)^[5] and Singh *et al.*, (2012)^[38], which demonstrated a strong correlation between yield and component traits such as tillers per meter, grain weight per spike, and grains per spike. This suggests that maximizing the expression of spike length, spikes per plant, number of grains per spike, and grain weight per spike, among other traits, can effectively increase grain yield potential. Among the characteristics that contribute to yield, the number of effective tillers per plant had shown a positively significant association with character flag leaf area (0.302), spike length (0.500), number of spikelets per spike (0.419), no of grain per spike (0.288), grain weight per spike (0.463), test weight (0.636), biological yield (0.428), suggesting that if selection is applied to increasing the effective number of tillers, all these traits take into account. The association between effective tiller number and peduncle length (-0.097) is negative and non-significant, so when applying selection for tiller numbers, peduncle length may impair these characters' performance in and of themselves. In a positive direction, character number of spikelets per spike strongly correlates with biological yield (0.949), grain weight per spike (0.798), test weight (0.745), number of grains per spike (0.693), harvest index (0.557), and peduncle length (0.223). According to studies by Sharma *et al.* (2006)^[42], Ahmed *et al.* (2007)^[4], Monpara and Kalariya (2009)^[28], Singh *et al.*, (2010)^[38], Sakhare and Ghawat (2011)^[39], and Singh *et al.*, (2012)^[38], there is a stronger or weaker correlation between wheat yield and yield component traits. These studies also suggested that increasing the expression of yield-contributing characters that show a stronger association in a desired direction can effectively increase the grain yield potential of wheat crops.

Path coefficient analysis at the genotypic and phenotypic level

We can better understand the relationships between the characteristics and develop efficient selection strategies by using path coefficient analysis to divide the observed correlation

coefficient into the direct and indirect effects of the yield components. In contrast to simple correlations, which only evaluate the mutual relationship while ignoring the causation, path analysis highlights the causes and their relative importance. Wright (1921) developed the concept of the path coefficient to critically evaluate each component's true contribution to the complex result at hand, such as yield, and statistically analyze the cause and effect in linked variables. The path coefficient analysis was performed using the methodology suggested by Dewey and Lu (1959)^[11]. To represent the direct and indirect effects of each feature on grain yield, the correlation coefficients of the many research characters were split using the route coefficient analysis. The path coefficient analysis was performed on both the genotypic and phenotypic paths. The dependent variable in this study was grain yield per plant, while the other thirteen attributes served as independent or contributing variables (Table 4). Table 4 presents the findings of a path-coefficient analysis at the genotypic level using basic correlation coefficients among thirteen quantitative characters. The highest positive direct effect on grain yield per plant was observed by harvest index (0.6187), biological yield (0.4867), and other characters had considerable positive direct contributions towards grain yield per plant while number of spikelets per spike (0.0477), days to maturity (0.0437), spike length (0.0388), flag leaf area (0.0129), number of grains per spike (0.0105). The direct effect of the remaining characters' grain weight per spike (0.0022), peduncle length (0.0006), found to be too low to be considered any consequence and days to 50% flowering, plant height, number of effective tillers per plant, test weight showed considerable negative direct effect on grain yield per plant. At the phenotypic level, the harvest index (0.7783) showed the highest order of direct positive influence on grain yield per plant, followed by biological yield per plant (0.06811), spike length (0.0160), grain weight per spike (0.0148), days to maturity (0.0083), peduncle length (0.0033), plant height (0.0029) and remaining agronomical characters showed negative direct effect on grain yield per plant represented in table 4. Similar results were also reported in wheat by Sharma *et al.*, (2006)^[42], Ahmed *et al.*, (2007)^[4], Singh *et al.*, (2009)^[30]. The harvest index also demonstrated a strong correlation with grain yield per plant (0.722) at phenotypic level and the greatest positive direct effect on grain yield (0.894) at the genotypic level. Singh *et al.*, (2009)^[30] found that in a range of conditions, there was a positive and significant correlation between grain yield and tiller number, grains spike-1, 1000 grain weight, and plant height. At both the genotypic and phenotypic levels, the contribution of residual effects influencing grain yield was very low, suggesting that the characters included in the current study were adequate to explain the variability in the dependent character, or grain yield per plant. The harvest index, biological yield per plant, grain weight per plant, spike length, days to maturity, and peduncle length all had a direct high or moderately positive impact on grain yield, according to an analysis of the aforementioned results. Therefore, it would be worthwhile to focus on these traits to implement an appropriate selection program for increasing wheat grain yield. The character's indirect influence on other component traits is the main factor contributing to the traits' indirect contribution. It would also be beneficial to increase yield through indirect selection using traits that have a high or moderately positive impact on grain yield. According to Mohammad *et al.*, (2005)^[6], D75%M had a significant negative genotypic correlation with harvest index and grain yield and a negative genotypic correlation with biological yield, and grain yield at both the genotypic and phenotypic

levels. With harvest index and grain yield, plant height displayed a negative genotypic and phenotypic correlation. According to

Mohsin *et al.* (2009) [30], grain yield was positively impacted by both spike length and grains per spike.

Table 1: Combined analysis of variance (ANOVA) for parent and hybrids F1 for fourteen traits in wheat genotypes

Source of variation	DF	Days to 50% flowering	Days to maturity	Plant Height (cm)	No of effective tillers per plant	Flag leaf area (cm)	Spike length (cm)	No.of spikletes per spike	Peduncle length (cm)	No of grains per spike	Grain Weight per spike(g)	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
REP	2	0.36	1.03	31.32	0.72	5.58	0.78	2.94	1.34	9.14	0.06	12.83	1.33	5.99	0.02
Treat	54	36.21**	18.56**	37.97**	0.591**	13.41**	5.67**	10.43**	34.98**	49.14**	0.932**	19.30**	12.59**	59.06**	7.75**
PAR	9	29.80**	10.32**	22.47**	0.45**	10.57**	1.15**	9.50**	9.64**	47.31**	0.30**	10.60**	9.61**	37.82**	4.45**
F ₁	44	37.04**	20.53**	30.37**	0.69**	14.35**	4.31**	8.95**	16.72**	50.02**	0.91**	20.75**	13.35**	58.22**	8.13**
PVF ₁	1	56.58**	7.15**	309.99**	2.95**	286.14**	11.74**	83.95**	62.18**	358.76**	7.41**	77.46**	150.92**	2.85	32.14**
ERROR	108	0.46	0.33	3.89	0.06	1.73	0.47	1.58	1.04	1.28	0.03	0.97	3.28	10.07	0.13

*, ** significant at 5% and 1% level, respectively

Table 2: Range, Mean, and variability parameters for fourteen different traits in wheat genotypes

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to 50% flowering	77.89	71.84	84.44	11.92	12.37	96.33	6.98	8.96	4.43	4.52
Days to maturity	120.49	116.52	123.46	6.07	6.41	94.69	4.94	4.10	2.05	2.10
Plant Height (cm)	106.61	104.96	111.12	11.31	15.35	73.68	5.95	5.58	3.15	3.67
No of effective tillers per plant	3.35	2.51	4.10	0.18	0.24	75.48	0.75	22.55	12.60	14.51
Flag leaf area (cm)	21.78	19.44	26.71	3.84	5.73	67.02	3.30	15.18	9.00	10.99
Spike length (cm)	14.66	13.55	16.97	1.71	2.24	76.33	2.36	16.06	8.93	10.22
No.of spikletes per spike	25.98	25.27	29.40	2.95	4.53	65.05	2.85	10.98	6.61	8.20
Peduncle length (cm)	42.13	38.99	45.58	11.31	12.36	91.56	6.63	15.74	7.98	8.34
No of grains per spike	39.23	35.77	45.71	15.96	17.23	92.61	7.92	20.18	10.18	10.58
Grain Weight per spike(g)	2.74	2.37	3.85	0.30	0.33	89.74	1.07	38.96	19.97	21.08
Test weight (gm)	45.51	39.08	50.78	6.06	7.17	84.52	4.66	10.25	5.41	5.89
Biological yield per plant (g)	24.82	22.65	29.24	3.10	6.38	48.58	2.53	10.19	7.10	10.18
Harvest index (%)	41.44	37.62	45.43	16.33	26.40	61.85	6.55	15.80	9.75	12.40
Grain yield per plant (g)	10.26	9.20	13.02	2.54	2.67	95.01	3.20	31.19	15.53	15.94

Table 3: Analysis of the correlation coefficient of fourteen characters of wheat germplasm at genotypic (g) and phenotypic (p) level

Parent/Hybrids	Days to 50% flowering	Days to maturity	Plant Height (cm)	No of effective tillers per plant	Flag leaf area (cm)	Spike length (cm)	No. of spikletes per spike	Peduncle length (cm)	No of grains per spike	Grain Weight per spike(g)	Test weight (gm)	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)	
Days to 50% flowering	g	1.000	0.756**	-0.654**	-0.600**	-0.559**	-0.659**	-0.600**	0.082	-0.570**	-0.580**	-0.769**	-0.541**	-0.636**	-0.684**
	p	1.000	0.726**	-0.549**	-0.526**	-0.470**	-0.554**	-0.477**	0.075	-0.540**	-0.538**	-0.685**	-0.395**	-0.472**	-0.649**
Days to maturity	g		-0.605**	-0.499**	-0.585**	-0.807**	-0.753**	-0.062	-0.591**	-0.585**	-0.739**	-0.633**	-0.724**	-0.782**	
	p		-0.512**	-0.433**	-0.491**	-0.672**	-0.583**	-0.059	-0.559**	-0.538**	-0.668**	-0.460**	-0.530**	-0.735**	
Plant Height (cm)	g			0.394**	0.908**	0.916**	0.894**	0.050	0.755**	0.761**	0.726**	0.919**	0.499**	0.795**	
	p			0.294**	0.665**	0.599**	0.654**	0.042	0.587**	0.638**	0.575**	0.583**	0.326**	0.663**	
No of effective tillers per plant	g				0.302**	0.500**	0.419**	-0.097	0.288**	0.463**	0.636**	0.428**	0.338**	0.436**	
	p				0.277**	0.412**	0.281**	-0.070	0.239**	0.382**	0.510**	0.283**	0.244**	0.391**	
Flag leaf area (cm)	g					0.825**	0.903**	0.227**	0.698**	0.784**	0.760**	0.873**	0.469**	0.754**	
	p					0.669**	0.632**	0.183*	0.612**	0.648**	0.603**	0.551**	0.347**	0.655**	
Spike length (cm)	g						0.996**	0.069	0.782**	0.799**	0.885**	0.885**	0.582**	0.831**	
	p						0.619**	0.028	0.653**	0.645**	0.668**	0.530**	0.381**	0.673**	
No.of spikletes per spike	g							0.223**	0.693**	0.798**	0.745**	0.949**	0.557**	0.850**	
	p							0.165*	0.530**	0.586**	0.573**	0.619**	0.312**	0.673**	
Peduncle length (cm)	g								0.177*	0.025	0.075	0.407**	-0.019	0.196*	
	p								0.162*	0.021	0.049	0.303**	-0.031	0.183*	
No of grains per spike	g									0.679**	0.713**	0.772**	0.416**	0.666**	
	p									0.615**	0.619**	0.558**	0.298**	0.624**	
Grain Weight per spike(g)	g										0.754**	0.851**	0.425**	0.714**	
	p										0.637**	0.574**	0.338**	0.670**	
Test weight (gm)	g											0.799**	0.451**	0.704**	
	p											0.561**	0.283**	0.612**	
Biological yield per plant (g)	g												0.524**	0.849**	
	p												-0.092	0.620**	
Harvest index (%)	g													0.894**	
	p													0.722**	
Grain yield per plant (g)	g													1.000	
	p													1.000	

*, ** significant at 5% and 1% level, respectively

Table 4: Analysis of direct and indirect effects of different traits on grain yield per plant at genotypic (g) and phenotypic (p) level

Parent/Hybrids		Days to 50% flowering	Days to maturity	Plant Height (cm)	No of effective tillers per plant	Flag leaf area (cm)	Spike length (cm)	No.of spikelets per spike	Peduncle length (cm)	No of grains per spike	Grain Weight per spike(g)	Test weight (gm)	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
Days to 50% flowering	g	-0.0308	0.0330	0.0300	0.0003	-0.0072	-0.0255	-0.0286	0.0001	-0.0060	-0.0013	0.0086	-0.2632	-0.3933	-0.684**
	p	-0.0100	0.0060	-0.0016	0.0001	0.0039	-0.0089	0.0018	0.0002	0.0004	-0.0080	0.0034	-0.2692	-0.3671	-0.649**
Days to maturity	g	-0.0233	0.0437	0.0277	0.0002	-0.0075	-0.0313	-0.0359	0.0000	-0.0062	-0.0013	0.0083	-0.3082	-0.4479	-0.782**
	p	-0.0073	0.0083	-0.0015	0.0001	0.0041	-0.0108	0.0022	-0.0002	0.0004	-0.0080	0.0033	-0.3135	-0.4124	-0.735**
Plant Height (cm)	g	0.0201	-0.0264	-0.0459	-0.0002	0.0117	0.0355	0.0427	0.0000	0.0079	0.0017	-0.0081	0.4474	0.3086	0.795**
	p	0.0055	-0.0043	0.0029	-0.0001	-0.0055	0.0096	-0.0025	0.0001	-0.0004	0.0094	-0.0029	0.3973	0.2534	0.663**
No of effective tillers per plant	g	0.0185	-0.0218	-0.0181	-0.0004	0.0039	0.0194	0.0200	-0.0001	0.0030	0.0010	-0.0071	0.2084	0.2092	0.436**
	p	0.0053	-0.0036	0.0009	-0.0002	-0.0023	0.0066	-0.0011	-0.0002	-0.0002	0.0056	-0.0025	0.1925	0.1900	0.391**
Flag leaf area (cm)	g	0.0172	-0.0256	-0.0416	-0.0001	0.0129	0.0320	0.0431	0.0001	0.0073	0.0017	-0.0085	0.4247	0.2903	0.754**
	p	0.0047	-0.0041	0.0020	-0.0001	-0.0083	0.0107	-0.0024	0.0006	-0.0004	0.0096	-0.0030	0.3750	0.2702	0.655**
Spike length (cm)	g	0.0203	-0.0352	-0.0420	-0.0002	0.0106	0.0388	0.0475	0.0000	0.0082	0.0018	-0.0101	0.4309	0.3603	0.831**
	p	0.0056	-0.0056	0.0018	-0.0001	-0.0055	0.0160	-0.0023	0.0001	-0.0004	0.0095	-0.0033	0.3613	0.2962	0.673**
No.of spikelets per spike	g	0.0185	-0.0329	-0.0410	-0.0002	0.0116	0.0386	0.0477	0.0001	0.0073	0.0018	-0.0083	0.4620	0.3447	0.850**
	p	0.0048	-0.0048	0.0019	-0.0001	-0.0052	0.0099	-0.0037	0.0005	-0.0003	0.0087	-0.0029	0.4218	0.2429	0.673**
Peduncle length (cm)	g	-0.0025	-0.0027	-0.0023	0.0000	0.0029	0.0027	0.0107	0.0006	0.0019	0.0001	-0.0008	0.1981	-0.0120	0.196*
	p	-0.0008	-0.0005	0.0001	0.0000	-0.0015	0.0005	-0.0006	0.0033	-0.0001	0.0003	-0.0002	0.2066	-0.0242	0.183*
No of grains per spike	g	0.0176	-0.0258	-0.0346	-0.0001	0.0090	0.0303	0.0331	0.0001	0.0105	0.0015	-0.0080	0.3755	0.2573	0.666**
	p	0.0054	-0.0047	0.0017	0.0000	-0.0051	0.0105	-0.0020	0.0005	-0.0007	0.0091	-0.0031	0.3798	0.2323	0.624**
Grain Weight per spike(g)	g	0.0179	-0.0255	-0.0349	-0.0002	0.0101	0.0310	0.0381	0.0000	0.0071	0.0022	-0.0084	0.4141	0.2631	0.714**
	p	0.0054	-0.0045	0.0019	-0.0001	-0.0054	0.0103	-0.0022	0.0001	-0.0004	0.0148	-0.0032	0.3908	0.2629	0.670**
Test weight (gm)	g	0.0237	-0.0323	-0.0333	-0.0003	0.0098	0.0351	0.0355	0.0000	0.0075	0.0017	-0.0112	0.3887	0.2790	0.704**
	p	0.0069	-0.0056	0.0017	-0.0001	-0.0050	0.0107	-0.0022	0.0002	-0.0004	0.0094	-0.0050	0.3818	0.2200	0.612**
Biological yield per plant (g)	g	0.0167	-0.0277	-0.0422	-0.0002	0.0112	0.0343	0.0453	0.0002	0.0081	0.0019	-0.0089	0.4867	0.3240	0.849**
	p	0.0040	-0.0038	0.0017	-0.0001	-0.0046	0.0085	-0.0023	0.0010	-0.0004	0.0085	-0.0028	0.6811	-0.0713	0.620**
Harvest index (%)	g	0.0196	-0.0316	-0.0229	-0.0001	0.0060	0.0226	0.0266	0.0000	0.0044	0.0009	-0.0051	0.2549	0.6187	0.894**
	p	0.0047	-0.0044	0.0010	0.0000	-0.0029	0.0061	-0.0012	-0.0001	-0.0002	0.0050	-0.0014	-0.0624	0.7783	0.722**

Resi- 0.00100 (g)

Resi-0.00346 (p)

*, ** significant at 5% and 1% level, respectively

Conclusion

The main objective must be to discover and choose superior genotypes with desirable characteristics from a wide range of breeding materials to properly harness the available variability. In the current study, the phenotypic and genotypic correlation coefficients among fourteen characters were evaluated. The results of the correlation study showed that harvest index, number of spikelets per spike, spike length, biological yield, and the number of effective tillers per plant were strongly positively correlated with grain yield per plant. According to the association studies, choosing genotypes with better performances for the aforementioned traits can increase wheat grain yield. Selecting for low plant height would ultimately contribute to higher grain yield.

Although the number of tillers per meter 2, days to heading, spike length, and chlorophyll content all directly impacted yield negatively, while days to 50% flowering, and days to maturity had a negative direct effect on yield, the path-coefficient analysis showed that harvest index had the largest positive direct effect, followed by the number of spikelets per spike, biological yield per plant, and spike length. As a result, path analysis indicates that harvest index, number of effective tillers per plant, number of spikelets per spike, spike length, grain weight per

spike, and number of grains per spike, could all be useful selection criteria for breeding programs aimed at increasing yield. Knowledge of the interactions between grain yield and yield components is necessary to achieve this. Studying the correlation coefficient will help you create a good selection criterion by allowing you to assess the degree of relationships between various features. The overall effect of the gene that influences both features is pleiotropy or correlation coming from linkage, where other factors boost one and reduce the other of positive correlation or negative correlation.

Author contributions

Mohit Yadav: Conceptualization; data curation; formal analysis; methodology; validation; visualization; writing-original draft; Vishwajeet Yadav: formal analysis; methodology; software; visualization; writing-original draft; writing-review and editing, S.N. Singh: Conceptualization; data curation; formal analysis; investigation; supervision; validation; visualization; writing-original draft; review and editing. U.P. Singh: Conceptualization; investigation; methodology; resources; supervision; validation; visualization; review and editing.

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Conflict of interest statement

The authors declare no conflicts of interest.

Data availability statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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