Original article

Estimation of statistical parameters in candidate wheat genotypes for yield-related traits

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ARTICLE INFO

ABSTRACT

Background: The selection of genotypes in breeding programs relies on accurate estimates of heritability for variables relevant to yield. The better genotypes may be chosen rapidly using statistical estimate. Seventeen advanced breeding lines and three commercial bread wheat (*Triticum aestivum* L.) genotypes (used as checks) were assessed regarding their genetic characteristics for yield-related traits in the current study.
Methods: Grain yield's correlation with several possible qualities was investigated and compared to regional controls.
Results: The results showed that the peduncle length was positively correlated with the spike length, plant height, and total number of spikes. There was a favorable correlation between grain yield and spike count. The number of tillers per square meter was favorably connected with days to maturity but negatively correlated with grain weight, moisture percentage, and gluten content. The percentage of protein and gluten also declined with the increasing quantity of grains in each spike. Weight per 1000 grains was favorably connected with moisture percent and negatively correlated with days to maturity. Day of maturity was positively correlated with yield, whereas day of blooming was negatively correlated. The number of tillers m^{-2} had strong heritability and rapid genetic improvement. The number of grains per spike, plant height, 1000-grain weight, peduncle length, days to maturity, and protein percentage all demonstrated high broad sense heritability and moderate genetic advance, whereas spike length and starch percentage both displayed low heritability and poor genetic advance. The number of spikes per plant, plot yield, days to flowering, moisture%, and gluten% all showed moderate heritability with modest genetic progress.
Conclusion: Following from the above, it is recommended that plant features with high heritability and genetic advancement be given preference in selection, while qualities with a negative link to grain output be subjected to cautious selection.

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1. Introduction

Wheat (*Triticum aestivum* L.) is staple food in Pakistan and plays a key role in agricultural policies. Its contribution is 9.2 % in agriculture sector and 1.8 % towards GDP (GOP, 2020–21). To cope up with increasing population, sustainable wheat production is very crucial for food security (Braun et al., 2010). Globally, 280

million tons wheat is annually produced only in Asia continent, in which China (29 m hec) and India (26 m hec) are the largest wheat producers along with Pakistan. The world's 30 % wheat harvest and 36 % production belong to Pakistan, India, and China (FAO, 2018). Wheat is also good source of carbohydrate, protein, and vital amino acids (except lysine), vitamins Thiamine, Niacin, vitamin E and Riboflavin, minerals (Phosphorous, Iron, copper, Magnesium and Zinc (Khan and Zeb, 2007).

Wheat output is falling steadily because of inadequate resources. When compared to more established nations, emerging nations like Pakistan have far greater challenges. Since Pakistan's population is growing at a pace of 2.4 % annually, more wheat is needed to meet the rising demand for food. In Pakistan a huge yield gap is present between the wheat potential 7 metric ton and actual yield or average yield 2.5 metric tons per ha of wheat crop (Kirby et al., 2017).

The yield perspectives generally measured by the characteristics of the genotypes and biotic and abiotic factors like (temperature, light, radiations, CO_2 etc.). The possible significant increase in the yield in case of wheat crop belongs to plant height reduction which may help in equally provision of the proportion of carbon dioxide (CO_2) to the grains and at the same time may decreasing the yield risks majorly caused by the heavy lodging (Jiang et al., 2003). Wheat production is greatly influenced every year due to drastic changes in rainfall (Wolf, 2002). The significant increase in population requires increased production of cereals (wheat) to combat with the world food requirement. In this regard, the breeders can play their roles significantly in getting the maximum yield even under stressful environment, by developing the verities with strong and better genetic potential. The yield is imperative character which may contain numerous factors greatly influenced by the environment and genetic makeup of wheat genotypes (Samonte et al., 1998). To enhance yield potential of wheat breeders and making new crosses and developing high yielding varieties at farmer fields to reduce gap between the potential and actual yield. Wheat traits have high heritability which facilitates selection in early generations (Bisne et al., 2009).

Now breeders are trying to develop new ideotypes of wheat with increased characters that play crucial role in wheat yield. Heritability tells us about the extent of character under study to be transmitted in next generation (Baloch et al., 2003; Khan and Naqvi, 2011; Bisne et al., 2009). One of the most important and efficient technique used in breeding procedure is correlation which is used to determine genetic associations among yield contributing traits with ultimate objective to improve selection efficiency of wheat genotypes for better yield.

The purpose of this research was to examine the relationship between grain yield and yield-related variables in genetically isolated populations. The information gathered would help wheat breeders for developing high yielding wheat varieties in future. It was hypothesized that the studied traits would have significant association with yield. The traits having positive association with yield could be used in the breeding programs to improve yield.

2. Materials and methods

The current research was carried out to investigate the relationship between grain yield and yield contributing parameters in advanced bread wheat genotypes. The 17 advanced breeding lines, together with three checks, were employed as experimental material and evaluated at the College of Agriculture, University of Sargodha's research area. The experiment was carried out in triplicate using a randomized full block design with a plot size of 1.8x5m and a row to row spacing of 30 cm. Table 1 shows the genotypes of wheat in detail.

Table 1
List of advanced bread wheat genotypes along with commercial checks.

Sr. #	Name/Parentage of wheat genotype	Sr. #	Name/Parentage of wheat genotype
1	BAV-92/Pastor	11	ND643/PRULA//INQ-91
2	Attila/BCN/Pastor	12	MNV/BAV-92//ND6432
3	ND643/WBLLI	13	CM6553/PRL//KACHU
4	Inq-91/Australian donor-1	14	WBLII/INQ-91//BABAX
5	Inq-91/Australian donor-2	5	FRET2/FISCAL//ND643/3/BRAMBLING
6	Milan//Akuri//S87230	6	SA42/PRLLU26/NAC
7	OASIS/BCN//BORL93	17	LU26/NAC
8	BCN/KRIIAII//ND6432	18	Punjab-2011(Check)
9	ND6432/WBLLI//F2004	19	Faisalabad-2008 (Check)
10	SB73230/WBLII//KRIIAII	20	Galaxy-2013 (Check)

Plant height, days to flowering, days to maturity, number of productive tillers per meter square, peduncle length, number of spikes per plant, number of grains per spike, 1000-grain weight, plot yield, gluten%, starch, and moisture content were all measured separately from five randomly chosen plants of each genotype in each plot in each replication. The means for each characteristic were determined, and the data were then submitted to (ANOVA) analysis of variance to discover genotypic differences (Steel et al., 1997). The importance of features and application of the biometrical technique were determined using the statistical programs Statistix 8.1 and SPSS 25.0. Genotypic and phenotypic variances were computed from the ANOVA table following the formula given by Burton and Devane (1952).

Genotypic variance V_g = (MSSg-MSSe)/r.

Phenotypic variance V_P = Vg + Ve.

Environmental variance V_e = EMS.

Broad sense heritability (h^2_{BS}) was calculated following the method suggested by Singh and Chaudhary (1985).

Heritability (h^2_{BS}) = V_g / V_P × 100 (%).

Where, V_g = genotypic variance of respective accessions, and V_P = phenotypic variance.

Genetic advance (GA) was predicted to observe expected gain by using the formula provided by Poehlman and Sleeper (1995).

GA = $h^2_{BS} \times (Vp)^{1/2} \times i$.

Where, h^2_{BS} = Heritability in broad sense, V_p = phenotypic variance of the trait, and i = selection intensity which is 1.732 at 10 %.

3. Results and discussion

3.1. Genetic variability

The fundamental need for choosing genotypes with superior performance is the availability of genetic heterogeneity in any wheat germplasm. Table 2 displays the mean square values for each attribute under investigation. The findings indicated that all wheat genotypes, except for starch percentage, had extremely significant differences among themselves for the stated attributes. Additionally, for several morphological features, Mecha et al. (2017) revealed extremely significant variations across the wheat genotypes. Hood-Niefer et al. (2012) reported non-significant result for starch % among different chickpea varieties. While Saleem et al. (2008) reported significant difference among maize genotypes for starch %. The highly significant differences among genotypes displayed occurrence of hereditary variability which could be used for selection. The maximum plant height observed in SA42/PRL (106.33 cm) while minimum in BCN/KRIIAII//ND6432 (87 cm) Table 4. Regarding the spike length, the maximum length was observed in Pb-11 (Local check) (14.33 cm) followed by LU26/NAC (13.67) and the minimum was calculated in Inq-91/Australian donor-1 (10.33 cm). The maximum peduncle length was found in MNV/BAV-92//ND6432 (52.0 cm) while the

Table 2
Mean squares values of wheat genotypes for grain yield and related traits.

Plant traits	Genotypes (G-1) 99	Replications (R-1) 1	Error (G-1)(R-1) 99
Plant height (cm)	93.03**	4.12	1.924
Peduncle length (cm)	2.35**	2.12	1.26
Spike length (cm)	48.58**	0.27	3.32
Number of spikes per plant	3.91**	16.20	1.24
Number of grains per spike	4728.53**	12.20	163.62
Number of tillers m^{-2}	247.24**	0.12	10.64
1000-grain weight (g)	102.44**	16.35	6.37
Plot yield (kg)	0.32**	0.0039	0.11
Days to flowering	6.77**	13.95	2.28
Days to maturity	20.63**	0.27	0.37
Protein (%)	0.72**	0.25	0.06
Moisture (%)	0.57**	0.0042	0.18
Starch (%)	1.06^{NS}	0.11	0.96
Gluten (%)	6.18**	0.12	2.78

Here, **= Significant at 99 probability, NS = non-significant.

minimum length was observed in the Inq-91/Australian donor-2 (37.67 cm). Results depicted that the maximum spikelets/spike were counted in BAV-92/Pastor, Milan/Akuri//S87230, and Galaxy-13 (21.33), and the minimum was computed in Inq-91/Australian donor-1 (17.33). The maximum number of tillers per m^2 were observed in BAV-92/Pastor (332) and the minimum tillers per m^2 were found in the SB73230/WBLII//KRIIAII (163.33). The number of grains per spike were found maximum in the Milan/Akuri//S87230 (72.0) while the minimum was found in Inq-91/Australian donor-1 (38.33). In the case of 1000 grains mass, the maximum 1000 grains mass was computed (57.67 g) in CM6553/PRL//KACHU and the minimum was in Pb-11 (33.0). In case of yield per plot, the maximum yield per plot (3.13 kg) was attained by OASIS/BCN//BORL93 while the minimum yield per plot (1.86 kg) was reported inFRET2/FISCAL//ND643/3/BRAMBLING. In the days to flowering, the duration was maximum (105.67 days) in Inq-91/Australian donor-1 and the minimum (100.33 days) in OASIS/BCN//BORL93. The genotype ND643/PRULA//INQ-91 required 137.33 days to become mature and declared as late maturing genotype and BAV-92/Pastor found early maturing with 129.33 days. The maximum protein % (12.17 %) was recorded from ND643/WBLLI and MNV/BAV-92//ND6432 while the minimum protein % (10.67 %) recorded from genotype Fsd-08 (local check). The genotype OASIS/BCN//BORL93 and MNV/BAV-92//ND6432 showed maximum moisture (10.17 %) while Galaxy-13 (Local check) showed minimum moisture (8.83 %). The maximum starch was (57.33 %) observed in genotype SB73230/WBLII//KRIIAII, while the minimum (55.00 %) was recorded from genotype Inq-91/Australian donor-2. The maximum gluten (20.67 %) was recorded in MNV/BAV-92//ND6432 and the minimum (15.0 %) was in

OASIS/BCN//BORL93. Hence, the remarkable genetic variation was found in the studied wheat breeding lines regarding yield contributing characters. Therefore, the selection of high yielding genotypes could be based on these traits. Further, at the time of genotype selection, these parameters should be considered in segregating populations. The results are in-line with Sharaan et al. (2017), Ghallab et al. (2016), Ghuttai et al. (2015), Tripathi et al. (2015), Yahaya (2014), Tahmasebi et al. (2013), Khan et al. (2015), Birhanu et al. (2016), and Khokhar et al. (2019). They all found similar type of results in wheat genotype as reported above.

3.2. Correlation coefficients

Table 3 displays the correlation matrix between grain yield and associated variables in bread wheat genotypes. The findings showed that plant height exhibited positive or negative but non-significant associations with all other investigated variables, but only showed a substantially positive link with peduncle length. Spike length also exhibited significantly positive relationship only with peduncle length and number of spikes per plant. (Siahbidi et al., 2013; Hussain et al., 2014) There was a positive correlation among spike and peduncle length and number of spikelets over spikes (Khan and Naqvi, 2012), Sokoto et al. (2012) and Çifci, 2012). Gluten % and peduncle length displayed significant and positive correlation with one another while significantly negative with number of tillers. Plot yield showed significantly positive interrelationship with days to maturity but negative with days to flowering (Ajmal et al., 2009).

The days to maturity and tiller numbers showed strong positive association with one another. Negative association was recorded with grains weight, percentage of moisture contents and gluten percentage (Bagrei and Bybordi, 2015). Correlation estimates depicted that 1000-grainsweight had positive correlation with moisture content however there was negative correlation in days to maturity. Negative association showed inverse relationship for earliness traits and yield which would be beneficial under stresses like drought and terminal heat. Similar results were reported by Mecha et al. (2017) during his work on wheat. Correlation estimate show that percentage of starch was negatively correlated with duration to flowering while protein% is positively correlated with gluten%. Results are in consistency with Ashfaq, (2002) who reported similar results in bread wheat.

3.3. Genetic variability, broad sense heritability(h^2_{BS}) and genetic advance (GA)

The findings demonstrated substantial heritability and genetic progress for the examined plant characteristics of wheat genotypes (Table 5). High heredity was evident in the plant height, number of

Table 3
Correlation coefficients of grain yield and related traits in bread wheat genotypes.

	PH	SL	PL	NSP	NT	GPS	GW	PY	DF	DM	P%	M%	S%
SL	−0.002												
PL	0.341**	0.435**											
NSP	0.117	0.296**	0.122										
NT	−0.188	−0.072	−0.256*	0.018									
GPS	0.203	0.009	−0.313	0.318*	0.095								
GW	0.160	−0.009	0.141	−0.062	−0.346**	−0.057							
PY	0.082	−0.141	−0.120	0.061	0.247	−0.016	−0.053						
DF	0.073	0.082	0.091	−0.049	0.066	−0.004	−0.200	−0.273*					
DM	0.252	0.058	0.080	0.134	0.356**	0.252	−0.403**	0.356**	0.019				
P%	−0.162	0.067	0.106	−0.194	−0.136	−0.181	0.067	0.010	−0.051	−0.120			
M%	0.057	0.189	0.214	−0.074	−0.298*	−0.258*	0.322**	−0.072	−0.261	−0.204	0.187		
S%	−0.050	−0.069	0.183	−0.028	−0.031	−0.044	−0.146	0.123	−0.264*	0.231	−0.044	0.021	
G%	−0.101	0.028	0.369**	−0.185	−0.315*	−0.337**	0.133	−0.091	−0.084	−0.120	0.372**	0.064	0.251

Here; Plant height (PH, cm), spike length (SL, cm), peduncle length (PL, cm), number of spikes per plant (NSP), number of tillers m^{-2} (NT), 1000-grain weight (1000-GW, g), number of grains per spike (GPS), plot yield (PY, kg), days to maturity (DM), days to flowering (DF), protein % (P%), moisture % (M%), Starch % (S%) and Gluten % (G%).

Table 4
Mean values of grain yield and related traits in bread wheat genotypes.

Genotypes	PH	SL	PL	NSP	T	GPS	1000-GW	PY	DF	DM	P%	M%	S%	G%
BAV-92/Pastor	92.33	13.33	49.33	21.33	332.00	56.00	38.33	2.39	102.33	129.33	11.17	10.00	56.00	18.00
Attila/BCN/Pastor	98.00	13.00	43.33	20.33	219.33	44.33	40.67	2.75	102.33	131.67	12.17	10.00	56.00	20.33
ND643/WBLLI	93.00	12.33	43.33	17.67	219.67	42.00	43.67	2.64	102.00	130.67	12.17	9.17	56.00	20.33
Inq 91/Australian donor-1	91.67	10.33	38.67	17.33	261.33	38.33	34.67	2.05	105.67	131.67	11.17	9.50	57.00	19.00
Inq-91/Australian donor-2	99.33	11.33	37.67	19.00	243.00	70.33	44.67	2.56	104.67	132.67	11.17	9.00	55.00	17.00
Milan/Akuri//S87230	91.33	12.33	45.00	21.33	234.33	72.00	44.00	3.01	102.67	136.67	11.83	10.00	57.00	17.33
OASIS/BCN//BORL93	100.33	12.00	42.00	21.00	269.67	59.00	40.33	3.13	100.33	135.00	11.17	10.17	56.33	15.00
BCN/KRIIAII//ND6432	87.00	12.33	44.00	19.33	234.00	58.67	46.00	2.89	101.00	134.33	12.10	9.00	56.33	20.33
ND6432/WBLLI//F2004	89.33	13.00	44.33	21.00	202.33	50.00	38.67	2.95	101.33	135.67	11.00	9.83	56.33	19.00
SB73230/WBLII//KRIIAII	101.67	13.00	49.33	20.00	163.33	54.33	48.00	2.58	104.33	134.67	12.00	10.00	57.33	20.33
ND643/PRULA//INQ-91	101.00	12.67	49.00	19.67	272.33	65.33	44.33	2.39	101.00	137.33	11.17	9.83	57.00	19.00
MNV/BAV-92//ND6432	91.67	12.67	52.00	19.33	220.00	49.67	39.67	2.65	102.33	130.33	12.17	10.17	57.00	20.67
CM6553/PRL//KACHU	102.33	13.00	51.67	21.00	205.00	55.00	57.67	2.34	104.33	130.67	11.17	10.00	56.00	19.00
WBLII/INQ-91//BABAX	89.67	12.67	44.00	20.33	216.33	61.00	53.00	2.66	101.00	130.33	10.83	9.83	57.00	18.00
FRET2/FISCAL//ND643/3/BRAMBLING	90.00	13.00	47.33	20.67	183.33	63.33	42.33	1.86	102.00	130.33	11.83	9.83	57.00	19.33
SA42/PRL	106.33	13.00	51.67	20.33	178.00	64.33	41.67	2.69	102.67	136.33	11.17	9.83	57.00	19.33
Pb-11 (local check)	92.00	14.33	48.67	21.00	262.33	58.67	33.00	2.52	105.00	136.67	11.17	9.17	57.00	17.67
LU26/NAC	99.33	13.67	47.33	20.33	180.67	61.00	44.33	2.22	102.67	130.33	11.17	9.83	56.00	17.67
Fsd-08 (local check)	92.33	11.33	46.00	20.67	218.00	63.00	38.00	2.36	104.00	132.67	10.67	9.17	57.00	18.67
Galaxy-13 (local check)	101.67	12.00	46.67	21.33	245.00	66.00	37.00	2.92	103.33	134.33	11.17	8.83	57.00	17.33
LSD Value	**3.97**	**5.22**	**3.21**	**3.19**	**9.31**	**36.62**	**7.23**	**0.95**	**4.32**	**1.74**	**0.70**	**1.21**	**2.81**	**4.77**

Here; Plant height (PH, cm), spike length (SL, cm), peduncle length (PL, cm), number of spikes per plant (NSP), number of tillers m^{-2} (NT), 1000-grain weight (1000-GW, g), number of grains per spike (GPS), plot yield (PY, kg), days to maturity (DM), days to flowering (DF), protein % (P%), moisture % (M%), Starch % (S%) and Gluten % (G%).

Table 5
Genetic variability, heritability, and genetic advance of bread wheat genotypes.

Plant Traits	V_G	V_p	H_{bs}^2 (%)	GA
Plant height (cm)	30.37	32.29	94	9.25
Peduncle length (cm)	0.365	1.622	22.50	0.496
Spike length (cm)	15.08	18.41	81.9	6.085
Number of spikes per plant	0.892	2.13	41.93	1.059
Number of grains per spike	1521.63	1685.25	90.29	64.194
Number of tillers m^{-2}	78.865	89.51	88.11	14.437
1000-grain weight (g)	32.02	38.39	83.40	8.95
Plot yield (kg)	0.068	0.18	37.78	0.278
Days to flowering	1.494	3.78	39.54	1.331
Days to maturity	6.752	7.12	94.79	4.382
Protein (%)	0.218	0.28	77.58	0.627
Moisture (%)	0.127	0.31	40.96	0.395
Starch (%)	0.032	0.99	3.229	0.055

grains per spike, 1000-grain weight (g), days to maturity, protein percentage, peduncle length, and number of tillers per square meter. This showed that the manifestation of these qualities has a stronger genetic preponderance than environmental influences, therefore selection in the early generation would be advantageous to create genotypes with high yields. However, plot yield (kg), days to flowering, moisture%, and gluten% displayed significant heredity whereas spike length and starch% revealed low heritability. With the aforementioned factors in mind, choosing wheat genotypes for traits with high heritability might provide better results. Our findings are consistent with According to Sharaan et al. (2017), Ghallab et al. (2016), Ghuttai et al. (2015), Tripathi et al. (2015), Yahaya. (2014), Zeeshan et al. (2014), Azimi et al. (2017), Afiah et al. (2000), and Danda and Sethi (2003).

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

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