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Original Research Article

GENETIC EVALUATION OF INDIGENOUS AND EXOTIC WHEAT GERMPLASM BASED ON YIELD-RELATED ATTRIBUTES

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Abstract: *Wheat is a highly self-pollinated crop and the main staple food of the world. Yield is one of the main breeding objectives in the wheat crop. Plant breeders focus on developing new lines with increased yield, resistance against biotic and abiotic factors and more nutritional values. The current research aimed to identify acceptable crossings for further investigation by determining the type of gene action (genetic effects) and combining the ability of parental genotypes for morphological features. This approach was used to evaluate three lines, namely Ujala-2016, Johar-2016, Galaxy-2013 and four testers' viz. XJ22, XJ23, XJ24 and XJ25. Collected data were subjected to line × tester analysis. Johar-2016 found a good general combiner for studied traits among parents as lines genotype. While among testers XJ25 proved to be the best general combiner for studied traits. Similarly, cross combinations hybrid XJ25 × Galaxy-2013 performed best as a specific combiner. It was noticed that SCA variance was greater than GCA variance for all factors studied in wheat except for grains/spike. The superior genotypes and crosses can be further tested in yield to develop improved wheat varieties.*

Keywords: gene action, GCA, SCA, hybrid, biotic and abiotic stress

Introduction

Wheat, the most important crop in Pakistan, is given more importance in agricultural programs and occupies the greatest amount of land. It is a critical cereal crop for the great majority of the world's population in terms of productivity and nutrition (Azam & Shafique, 2017). Noodles, bread, cookies, and cakes are some of the most nutritious dishes containing its ingredients. It supplies 55% of the world's annual carbohydrate requirements and 20% of its annual calorie requirements (Serna-Saldivar, 2016). Wheat, along with rice and corn, is a critical cereal crop on a global scale. Wheat comes in two varieties: tetraploid (2n=4x=28 chromosomes) and hexapoloid (2n=6x=42 chromosomes). Anticipated to grow by 9.3 billion people by 2060 (Bahar *et al*., 2020). To feed the world's growing population, the primary goal is to increase food production. This goal and increasing agricultural productivity are critical for meeting both present and future food security goals (Stonawski *et al*., 2015). Grain accounts for a sizable portion of wheat output. Grain production can be increased by extending the wheat crop's photosynthetic cycle or grain-filling phase (Faralli & Lawson, 2020). Food security for the world's growing population depends on our ability to increase grain production, which depends on a number of yield-contributing traits (Ehrlich & Harte, 2015).

Wheat research has been intensive and ongoing for a long time to improve grain production and grain yield per unit area (Slafer *et al*., 2021). There is still tremendous room for progress to fulfill the increasing demands of a growing population, notably in efforts to contribute more to wheat genetic evolution. The most effective technique for increasing wheat productivity has shown to be genetic manipulation (Govindaraj *et al*., 2015). Genetic diversity is critical in plant breeding to take advantage of heterosis and develop viable recombinants (Ali *et al*., 2013; Ali *et al*., 2014ab; Ter Steeg *et al*., 2022).

[Citation: Ammar, A., Ghafoor, S., Akram, Q.U.A., Ashraf, W., Akhtar, S, Nawaz, M.S., Zaghum, M.J., Khan, M.Y., Aas, M.A., Shaheen, A., Khalid, M.N., Kashif, M. (2022). Genetic evaluation of indigenous and exotic wheat germplasm based on yield related attributes. *Biol. Clin. Sci. Res. J.*, **2022***: 104*. doi: https://doi.org/10.54112/bcsrj.v2022i1.104]

The selection of parents is critical to every breeding project. Therefore, understanding germplasm's genetic diversity and relatedness is, critical for agricultural improvement efforts. When genetic diversity decreases, crop sensitivity to disease and negative environmental changes increases (Varshney *et al*., 2021). To improve the genetics of this crop, diverse genotypes from accessible germplasm should be chosen and employed in subsequent breeding attempts. Plant breeders focus on producing high-yielding wheat cultivars by combining excellent general combining lines and selecting transgressive segregants for grain yield and other traits from the resulting hybrids (Mason & Batley, 2015). Some researchers concluded that general combining ability significantly influences grain production and other traits in parent selection for grain yield (Liu *et al*., 2020).

Objective

Yield is the main breeding objective of any crop because the population is increasing, and the production area is decreasing daily. The breeders focus on the traits that positively correlate with yield. This study will be conducted to get following objectives:

1. Determination of the genetic mechanism of yield-related traits in wheat.
2. To assess the effects of yield contributing traits in cross combination developed through line × tester design.

Materials and methods

This experiment was done to compare yield contributing parameters of Pakistani varieties, Chinese lines and their crosses by using line × tester analysis in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. The experimental material consisted of four lines or varieties of spring wheat, namely Ujala-2016, Johar 2016 and Galaxy 2013 that were used as lines and testers taken from China, namely XJ22, XJ23, XJ24 and XJ25 used in a field trial. These wheat lines and tester were crossed in line × tester method during the crop period in 2019-2020.

1. XJ22 × Ujala-2016
2. XJ22 × Johar-2016
3. XJ22 × Galaxy-2013
4. XJ23 × Ujala-2016
5. XJ23 × Johar-2016
6. XJ23 × Galaxy-2013
7. XJ24 × Ujala-2016
8. XJ24 × Johar-2016
9. XJ24 × Galaxy-2013
10. XJ25 × Ujala-2016
11. XJ25 × Johar-2016
12. XJ25 × Galaxy-2013

The F_1 seeds and seven parents were planted in the field during the third week of November 2019 using a randomized complete block design with three replications. The varieties/lines were arbitrarily assigned to experimental units within each block. Seven parents and twelve F1 crosses from each replication were put in a single three-meter-long row for the treatment. The plants and rows were separated by 10 cm and 30 cm, respectively. A dibbler was used for sowing two seeds into each hole, and each hole only had one seedling after germination. From germination until maturity, the experimental populations were cultivated under normal conditions. Additionally, efforts were made to develop good crops. Ten mature plants from each line that had been well-protected were chosen to collect data on the following traits:

PH: Plant height (cm), SL: Spike length (cm), SPS: Number of spikelets/spike, GPS: Number of grains/spike, PL: Peduncle length (cm), SD: Spike Density, GWPS: Grain weight per spike (g), GW: 1000 -grain weight (g), YPP: Yield per plant

Statistical analysis

Analysis of variance was done on the data of different characters to determine the genotypic differences using Statistics 8.1. Correlation analysis was calculated by Minitab 21. Line × tester analysis was calculated by DosBox software.

Results and discussion

Crop plant genetic architecture can be examined to boost productivity. Breeders should attempt to understand the genetic nature of yield and its associated qualities to develop new varieties with new genetic material and improve existing types. Superior plants with the desired features are selected from a segregating population and used to begin a breeding program (Borrill *et al*., 2019).

Analysis of variance (ANOVA)

In this investigation, analysis of variance was applied to yield data and other yield-related features. The differences between all genotypes in Table 1 were significant for all characteristics. Figure 1 displays the average performance for all analyzed characters overall lines, tests, and crossings.

Line × tester analysis

Line tester analysis was performed to calculate the impacts of GCA and SCA on significant data that

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had been determined through ANOVA. Mean squares were found for all characters using the line × tester analysis, as shown in table 2. It was revealed through line-tester analysis that the total sum of squares for all wheat genotypes was further broken down into its components, including genotypes, parents, lines, parent-versus-crosses, testers, crosses, and differences, some of which were highly significant, some of which were significant, and some of which were non-significant.

Estimates of GCA and SCA effects

Table 3 displayed the findings for general combining ability (GCA) effects. Among lines, positive GCA effects were found for Ujala-2016 (0.75) and Galaxy-2013 (0.50), whereas negative GCA effects were observed for Johar-2016 (-1.25) for 1000-grain weight. Among testers, XJ23, XJ24 and XJ25 exhibited positive GCA effects (0.78, 0.44 and 1.78), respectively, while negative GCA effects were observed in tester XJ22 (-3.00). Ujala-2016 and Johar-2016 showed significant GCA effects, while XJ22, XJ23 and XJ25 proved good general combiners for 1000-grain weight. Positive GCA effects were found for Galaxy-2013 (0.78), whereas negative GCA for Johar-2016 (-0.34) and Ujala-2016 (-0.44) for yield per plant. XJ22 showed positive GCA effects (0.78), while negative GCA effects were exhibited in tester XJ23, XJ24 and XJ25 (-0.38, -0.07 and -0.30), respectively. These results were accorded with observations of Ahmad *et al*. (2017), Farooq *et al*. (2019) and Istipliler *et al*. (2015). The most extreme and positive SCA impacts were found among crosses for XJ25 × Ujala-2016 (1.22) and XJ23 × Galaxy-2013 (1.09). Negative SCA impacts were seen in XJ25 × Johar-2016 (-- 0.07) trailed by XJ24 × Ujala-2016 (- 0.12) for yield per plant (Table 4). These observations were likewise expressed by Parveen *et al*. (2018); Sharma *et al*. (2019); Sarwar *et al*., 2021; Soughi *et al*. (2019) and Tomar *et al*. (2020).

Genetic variances

GCA variance, SCA and GCA to SCA ratio and their dominance evaluation for all characters studied in wheat genotypes are given in table 5. It was noticed that SCA variance was greater than GCA variance for all factors studied in wheat except for grains/spike as revealed in table 5. The GCA/SCA ratio exposed that genes that were non-additive in their activities were more prominent than additive genetic effects for all attributes studied. Ali *et al*., (2014ab); Ali *et al*., (2013); Din *et al*. (2020) and Kamara *et al*. (2021) also observed the similar results. At the same time, Abro *et al*. (2021); Farooq *et al*., (2011); Farooq *et al*. (2019); Hassan *et al*. (2021), and Patel *et al*. (2020) observed the involvement of both types of gene action for the traits under investigation.

Table 1: Mean square ANOVA for traits studied in wheat using RCBD design

SOV	D.F	PH	SL	SPS	GPS	PL	SD	GWPS	GW	YPP
Genotype	18	96.03**	5.56**	8.51**	173.98^{ns}	14.62**	0.01**	0.43^{ns}	24.51^{ns}	2.77**
Block	2	59.80	0.68	5.42	64.54	12.33	0.00	0.90	75.22	4.56
Error	36	17.27	1.22	1.88	276.54	5.46	0.003	0.51	25.22	1.02

** = Significant at 5% probability level, ns = Non-significant, Abbreviations are in material and method section

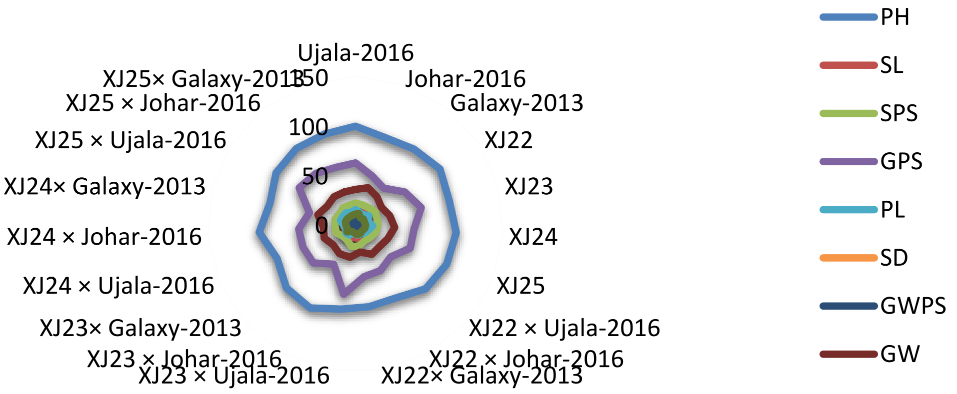

Fig 1: Mean performance of all lines, tester and crosses

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Table 2: Mean square ANOVA of line × tester analysis for traits studied in wheat

Source	D.F	PH	SL	SPS	GPS	PL	SD	GWPS	GW	YPP
Replication	02	59.80	0.15	11.52	9.98	0.08	0.00	0.09	1.33	0.25
Genotype	18	96.03	3.77	19.90	79.63	7.46	0.00	1.05	18.16	2.93
Crosses	11	85.44	3.81	21.48	71.09	5.71	0.01	1.16	23.75	3.33
Line (C)	03	97.29	.33	14.76	64.38	14.08	0.02	0.32	38.88	2.42
Tester (C)	02	29.36	2.08	9.36	50.97	1.51	0.00	4.06	14.25	5.48
L (C) × T (C)	06	98.21	2.63	28.87	81.15	2.92	0.00	0.62	19.36	3.06
Parents	06	35.76	4.15	4.07	107.62	7.40	0.00	0.99	7.00	2.67
Line (P)	03	12.55	1.44	1.33	178.22	9.97	0.00	0.92	4.75	1.85
Tester (P)	02	33.77	10.11	2.11	43.87	4.27	0.00	1.58	13.00	5.23
L (P) × T (P)	01	109.34	0.39	16.25	23.32	5.94	0.00	0.01	1.75	0.01
C × P	01	574.13	1.08	97.42	5.62	27.05	0.01	0.20	23.57	0.12
Error	36	17.27	0.86	9.08	19.90	0.47	0.00	0.16	1.12	0.22

Table 3: GCA effects of lines and testers for morphological related traits in wheat

Genotypes (parents)	PH	SL	SPS	GPS	PL	SD	GWPS	GW	YPP
Ujala-2016	-0.86^{ns}	0.00^{ns}	-0.94^{ns}	-2.60^{ns}	-0.29 ^{ns}	0.00^{ns}	0.45**	0.75*	-0.44*
Johar-2016	1.81^{ns}	-0.42^{ns}	0.14 ^{ns}	2.40^{ns}	-0.1 ^{ns} 1	-0.01*	0.20^{ns}	-1.25**	-0.34^{ns}
Galaxy-2013	-0.94^{ns}	0.42^{ns}	0.81 ^{ns}	-2.01^{ns}	0.40^{ns}	0.01*	-0.66**	0.50^{ns}	0.78**
XJ22	-3.50*	-0.22^{ns}	-1.86 ^{ns}	2.21^{ns}	-0.99**	-0.01^{ns}	0.20^{ns}	-3.00**	0.75**
XJ23	0.50^{ns}	-0.56^{ns}	0.58 ^{ns}	1.18^{ns}	-1.09**	-0.00^{ns}	-0.24^{ns}	0.78*	-0.38^{ns}
XJ24	-1.28^{ns}	-0,56^{ns}	1.03 ^{ns}	-2.38^{ns}	0.59*	-0.05**	0.09^{ns}	0.44^{ns}	-0.07^{ns}
XJ25	4.28**	1.33**	0.25 ^{ns}	1.20^{ns}	1.48**	0.07**	-0.06^{ns}	1.78**	-0.30^{ns}

Table 4: SCA effects of crosses for yield and its related traits in wheat

Genotypes (crosses)	PH	SL	SPS	GPS	PL	SD	GWPS	GW	YPP
XJ22 × Ujala-2016	8.75**	0.22^{ns}	-4.06^{ns}	-2.73^{ns}	0.35^{ns}	0.02^{ns}	0.43*	1.25*	-0.85*
XJ22 × Johar-2016	-5.58*	-1.36*	1.19^{ns}	-5.84^{ns}	-0.42^{ns}	-0.04**	-0.20^{ns}	-0.75^{ns}	0.51^{ns}
XJ22× Galaxy-2013	-3.17^{ns}	1.14^{ns}	2.86^{ns}	8.57*	0.07^{ns}	0.03*	-0.23^{ns}	-0.50^{ns}	0.34^{ns}
XJ23 × Ujala-2016	-4.92^{ns}	-0.11^{ns}	4.50*	1.93^{ns}	-0.48^{ns}	-0.07**	-0.01^{ns}	0.47^{ns}	-0.25^{ns}
XJ23 × Johar-2016	1.75^{ns}	0.97^{ns}	-1.58^{ns}	0.94^{ns}	0.31^{ns}	0.05**	-0.20^{ns}	0.14^{ns}	-0.84*
XJ23× Galaxy-2013	3.17^{ns}	-0.86^{ns}	-2.92^{ns}	-2.87^{ns}	0.17^{ns}	0.03*	0.21^{ns}	-0.61^{ns}	1.09**
XJ24 × Ujala-2016	-3.81^{ns}	-0.11^{ns}	0.06^{ns}	1.57^{ns}	-0.83^{ns}	0.00^{ns}	-0.67**	-4.19**	-0.12^{ns}
XJ24 × Johar-2016	4.86^{ns}	-0.03^{ns}	-0.03^{ns}	1.23^{ns}	-0.33^{ns}	0.00^{ns}	0.57*	1.81**	0.39^{ns}
XJ24× Galaxy-2013	-1.06^{ns}	0.14^{ns}	-0.03^{ns}	-2.80^{ns}	1.16*	-0.01^{ns}	0.10^{ns}	2.39**	-0.27^{ns}
XJ25 × Ujala-2016	-0.03^{ns}	-0.00^{ns}	-0.50^{ns}	-0.77^{ns}	0.95*	0.05**	0.25^{ns}	2.47**	1.22**
XJ25 × Johar-2016	-1.03^{ns}	0.42^{ns}	0.42^{ns}	3.68^{ns}	0.44^{ns}	-0.01^{ns}	-0.17^{ns}	-1.19*	-0.07^{ns}
XJ25× Galaxy-2013	1.06^{ns}	-0.42^{ns}	0.08^{ns}	-2.91^{ns}	-1.40**	-0.04**	-0.08^{ns}	-1.28*	-6.00^{ns}

Table 5: Estimates of GCA variance, SCA variance, additive and dominance variance

Genetic components	PH	SL	SPS	GPS	PL	SD	GWPS	GW	YPP
Cov. H. S. lines	-0.10	0.52	-1.56	12.77	1.23	0.00	-0.03	2.16	-0.07
Cov. H. S. testers	-5.73	-0.04	-1.62	-0.75	-0.11	-0.00	0.28	-0.42	0.20
Cov. H. S. average	-0.55	0.05	-0.31	1.28	0.12	0.00	0.02	0.18	0.01
Cov. F. S.	18.78	0.99	1.52	-25.06	1.84	0.00	0.50	7.68	1.14
б^{2}GCA	-0.55	0.05	-0.31	1.28	0.12	0.00	0.02	0.18	0.01
б^{2}SCA	26.35	0.55	5.15	-36.30	0.80	0.00	0.16	6.14	0.90
When F=0, б^{2}A	-2.20	0.20	-1.27	5.12	0.48	0.00	0.09	0.75	0.04
When F=1, б^{2}A	-1.10	0.10	-0.63	2.56	0.24	0.00	0.04	0.37	0.02
When F=0, б^{2}D	105.42	2.21	20.61	-145.58	3.21	0.00	0.66	24.59	3.61
When F=1, б^{2}D	26.35	0.55	5.15	-36.39	0.80	0.00	0.16	6.14	0.90

Correlation Analysis

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Plant height was significantly and positively correlated with spike length (0.29), grains per spike (0.16), peduncle length (0.76) and spike density (0.37), while it showed a negative correlation with spikelets/spike (-0.19), grain weight per spike (-0.38), 1000-grain weight (-0.00) and yield per plant (-0.07). Spike length positively correlated with all traits other than grains' weight per spike. Spikelets per spike negatively correlated with peduncle length, and spike density, while it positively correlated with other remaining morphological traits. The number of grains per spike correlated negatively with spike density and thousand-grain weights, while it correlated positively with peduncle length and yield per plant. Peduncle length indicated a positive correlation with grain yield. It showed a positive correlation with 1000 grain weight while negatively correlated with grain weight per spike. Spike density exhibited a significant positive correlation with 1000-grain weight. It had a highly significant positive correlation with peduncle length followed by spike length. Grain weight per spike and 1000-grain weight also exhibited a positive correlation yield per plant (Fig 2). At both genotypic and phenotypic levels, including spike length at phenotypic levels, Baye *et al*. (2020) found a significant positive correlation between grain yield and days to maturity, grain-filling period, plant height, kernels per spike, thousand seed weight, biomass yield, and harvest index. According to Kanwar *et al*., (2020) the length of the spike, the number of spiklets per spike, the number of seeds per spike, and the number of seeds per plant were all positively connected with the number of seeds that were produced in each plot. According to Pour-Aboughadareh *et al*. (2020), grain yield was significantly and favorably correlated with the number of spikes per plant, biomass, and harvest index.

Conclusion

In this study, all lines, tests, and their cross combinations showed significant differences. It was obvious that the non-additive type of gene action was significantly connected with the inheritance of the studied parameters since the variance of the SCA was greater than the variance of the GCA. Among the parental lines, Genotype Johar-2016 found a good general combiner for the investigated attributes. The best general combiner among testers appeared from the characteristics assessment as XJ25. As a specific combiner, the hybrid XJ25 Galaxy-2013 cross-combinations performed well. In order to considerably increase spring wheat yield and its related attributes, numerous crosses should make by use of parental genotypes with high GCA and certain cross combinations with high SCA. The inclusion of both types of gene activity thus opens a new chapter in the debate. The choice of paternal and maternal lines exhibiting the best specific combiners should be used for yield enhancement in the following generation since dominant type of gene activity was significant for yield-related characteristics.

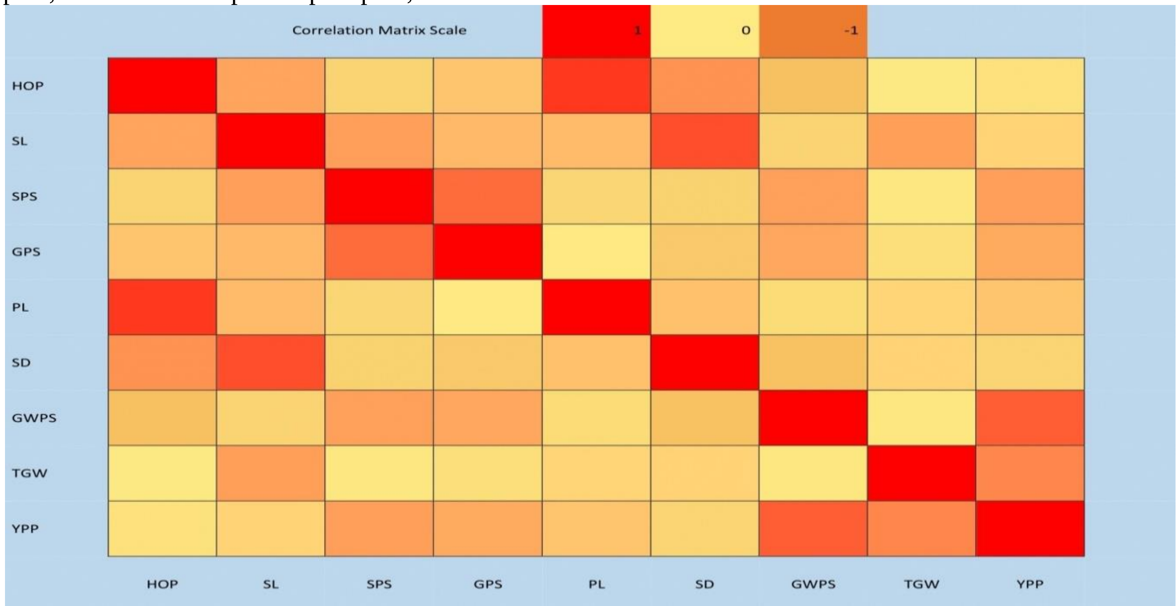

Fig 2: Correlation between different morphological traits of wheat

Conflict of interest

The authors declared absence of conflict of interest.

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