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Analysis of combining ability for yield and its component characters adopting line X tester analysis in wheat (*Triticum aestivum* L.)

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Abstract

An experiment has been conducted at the Agricultural Research Field of Department of Genetics and Plant Breeding, Rama University, Kanpur to estimate the extent of combining ability through the investigation of 18 F₁'s and 9 parents (six lines and 3 testers) in year 2022-23. The F₁s were generated by crossing 6 females (lines) by 3 males (testers) in a line x tester mating design during 2021-22. The trial has been conducted in randomized block design in three replication and the observations have been noted on the ten metric traits viz., days to 50% flowering, days to maturity, number of tillers per plant, plant height (cm), spike length (cm), number of grains per spike, biological yield per plant (g), 1000-grains weight (g), harvest index (%) and grain yield per plant (g). A perusal of the evidence that variances due to genotypes were found highly significant, which indicates the presence of genetic diversity among the genotypes for all the traits under study. For grain yield per plant, among female lines PBW677 (0.92) exhibited positive and significant GCA effects. Among female lines DBW110, DBW93 (1.80) and PBW677 (1.69) exhibited positive and significant GCA effects for number of grains per spike, however, among the male line MP3336 (2.74) showed significant positive GCA effects. Based on the magnitude of SCA effects for grain yield per plant cross combination DBW107×PBW343 (1.46) exhibited significant positive SCA effects. WH703 × PBD343 (4.59), DBW107 × MP3336 (4.26) and RUJ4037 × PBW343 (2.59) exhibited significant positive SCA effect for number of grains per ear, WH703 × PBW343 (1.18) and DBW110×MP3382 (0.77) exhibited significant positive SCA effects. Based on the present investigation it can be concluded that based on per se performance parents DBW110, PBW677 and PBW343 were identified as superior parents and crosses PBW677 x MP3382, DBW101 x MP3336, DBW107 x PBW343 and WH703 x MP3382 were identified superior for grain yield and other yield attributing characters.

Keywords: Wheat, *Triticum aestivum*, genetic variability, grain yield, GCA, SCA, combining ability

Introduction

Wheat (*Triticum aestivum* L.) is a self-pollinated crop and member belonging to the Poaceae family and it is one of the most leading cereals of the world. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. The term "Wheat" is derived from many different locations, specifically from the English, German and Welsh language.

The wheat is a hexaploid (allohexaploid) species ($2n = 6x = 42$) having AABBDD with A, B and D genomes. The species of bread wheat may be divided into diploid, tetraploid and hexaploid species with chromosome numbers $2n=14=AA$, $2n=14=BB$, $2n=28=AABB$ and $2n=42=AABBDD$ respectively with basic chromosome numbers (x) = 7 (Sleper and Poehlman, 2006) [13]. However, DNA studies revealed that *Triticum urartu* is diploid and has used as donor of A genome instead of *Triticum monococcum* (Dvorak *et al.*, 1993) [4] and *Aegilops speltoides* which is a wild diploid; has used as a possible donor of B genome. Wheat, a self-pollinating annual plant in the true grass family Gramineae (Poaceae) and genus *Triticum* is the world's most famous energy-rich cereal crop. It has been described as the "King of the cereals" because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. It is currently grown in approximately 225 mha Area globally, with an average productivity of 3 t/ha. It exhibits considerable variation between different agroecological zones (Singh *et al.*, 2008) [12]. It supplies about 25% of protein and 20% of the calories consumed by human beings in the daily diet. According to FAOSTAT, India is the second largest wheat producer in the world after China.

Total food grain production is estimated to rice 2.66% to a new record- 305.43 MT for 2020-21 crop year higher than 291.9 MT last year. In addition, India is set to harvest a record wheat production of 108.75 MT in the 2020-21 crop year on the back of food grain according to latest government of India. Wheat production is rising year on year and the previous record of 107.86 MT was achieved during the 2019-20 crop years (Source: www.livemint.com May, 2021) [14].

In a breeding programme for the development of genetically superior high-yielding wheat varieties, indigenous and exotic germplasm is the backbone of the successful breeding programme for improving yield and yield contributing traits. Selection and hybridization techniques are frequently used for improving genetic constitution of a genotype. The combining ability analysis provides useful information regarding the selection of better parents for the hybridization programme. Performances *per se* do not necessarily reveal which parents are good or poor combiners. To surmount this difficulty, it is necessary to gather information on the nature of gene actions. General combining ability is attributed to the additive type of gene effects, while specific combining ability is attributed to the non-additive type of gene actions. Non-additive gene type of action is not reliably fixable whereas additive type of gene actions or complementary type epistatic gene interactions are reliably fixable. The line x tester cross developed by Kempthorne (1957) [6] is a modified form of the top-cross scheme. This technique has been extensively used in almost all the major field crops to estimate GCA and SCA variances and effects, and to understand the nature of gene action for various quantitative traits. It however, fails to detect and estimate the epistatic variance. Combining ability analysis interprets the type and number of various types of gene actions governing the expression of these metric traits (Tarkeshwar, 2022) [15].

Keeping the above facts in view the present investigation has been carried out to understand the pattern of general and specific combining ability present among elite wheat genotypes.

Materials and Methods

Experimental site and weather

Kanpur is situated in the central part of Uttar Pradesh at an elevation of 126.49 meters from mean sea level in gangetic plain and lies between latitude and longitude 26°33'0" north and 80°13'28" east respectively. This tract enjoys a subtropical climate with occasional showers in winter. The meteorological data during the crop period as recorded in the meteorological laboratory of the Rama University Mandhana Kanpur U.P. are presented below in the table and represented by the summers are hot and dry, May and June are the hottest months. December and January constitute the cooler months of the year. The maximum temperature goes up to 34.4 °C during summer and the minimum goes as low as 4.6 °C during winter. The seasonal rainfall of about 629.5 mm was received mostly from IInd Fortnight of June or first Fortnight of July to mid-October with a few showers in winter season.

Experimental materials and methods

The experimental material for the present study includes 18 F₁ crosses derived by crossing and 9 parents (six lines *viz.*, RUJ 4037, DBW107, WH703, PBW 677, DBW 110 and DBW 93; and 3 testers *viz.*, PBW343, MP3336 and MP3382) in a line x tester mating design. The genotypes were collected from the

genetic stock available in "Department of Genetics and Plant Breeding, Rama University, Mandhana, Kanpur. The experiment was sown in randomized block design with three replications at the experimental field. Each plot consists two rows of 2.5 m spacing of 5cm plant to plant with in the row and 20 cm between the rows. Fertilizer was applied at the rate of 120 kg N, 60 kg P and 40 kg K. The crosses were made during rabi 2021-22 and these accessions along with their parents were raised and followed recommended packages and practices during *Rabi* season, 2022-23 to grow a healthy crop.

Observations recorded

The observation on 10 quantitative characters *viz.*, days to 50% flowering, days to maturity, number of tillers per plant, plant height (cm), spike length (cm), number of grains per spike, biological yield per plant (g), 1000-grains weight (g), harvest index (%) and grain yield per plant (g) were recorded to estimate extent of general and specific combining ability.

Statistical analyses

The experimental data collected the respect of 10 characters on total 27 wheat genotypes (18 F₁'s and 9 parents) were compiled by taking the mean values of selected plants in each plot and subjected for following statistical analyses: Analysis of variance (Panse and Sukhatme, 1988) [7] and Combining ability variances and their effects (Kempthorne, 1957) [6].

Results and Discussion

Analysis of variance for experimental design

Before subjecting the data for various genetic analysis, the analysis of variance for design of experiment was done for all the characters for testing the significance of differences among the genotypes. Mean squares due to replications, genotypes and error for ten quantitative traits during year 2022-23 are presented in (Table 1). A perusal of the evident that variances due to genotypes were found highly significant, which indicates the presence of genetic diversity among the genotypes for all the traits under study.

Combining ability variances and their effects

The combining ability analysis provides useful information regarding the selection of better parents for hybridization programme. Performances *per se* do not necessarily reveal which parents are good or poor combiners. To surmount this difficulty, it is necessary to gather information on the nature of gene actions. General combining ability is attributed to additive type of gene effects, while specific combining ability is attributed to non-additive type of gene actions. Non-additive gene type of action is not reliably fixable whereas additive type of gene actions or complementary type epistatic gene interactions are reliably fixable. The line x tester cross is a modified form of the top-cross scheme. This technique has been extensively used in almost all the major field crops to estimate GCA and SCA variances and effects, and to understand the nature of gene action for various quantitative traits. It however, fails to detect and estimate the epistatic variance. Combining ability analysis interprets the type and number of various types of gene actions governing the expression of these metric traits.

Analysis of combining ability variances

A perusal of the Table 2 evident that variances due to crosses, lines, testers and line x testers were found highly significant,

which indicates the presence of genetic diversity among the crosses, lines, testers and line \times testers for all the traits under study. The variances due to lines were found significant for all the characters except for 1000 seed weight. For L(P) \times T(P) all the characters were found significant except for days to 50% flowering.

Estimates of general combining ability effects

The estimates of combining ability (GCA) for all the 10 characters in respect to 9 parents (6 females, 3 males) are presented in table 3. The character-wise results are presented below:

Days to 50% flowering

For days to 50% flowering negative GCA effects are desirable. Among female lines, only PBW677 (-1.24) exhibited negative and significant GCA effects. However, none of the male line showed significant negative GCA effects.

Days to maturity

For days to maturity negative GCA effects are desirable. Among female lines DBW110 (-1.26) and PBW677 (-1.04) exhibited negative and significant gca effects. However, among the male lines only MP3366 (-1.20) showed significant negative GCA effects.

Plant height

For plant height negative GCA effects are desirable. Among female lines only PBW677 (-1.16) exhibited negative and significant gca effects. However, none of the male line showed significant negative GCA effects.

Number of productive tillers per plant

For number of productive tillers per plant positive GCA effects are desirable. Among female lines DBW110 (0.79) and PBW677 (0.67) exhibited positive and significant gca effects. However, none of the male line showed significant positive GCA effects.

Spike length

For spike length positive GCA effects are desirable. Among female lines DBW93 (1.13) and DBW110 (1.12) exhibited positive and significant gca effects. However, none of the male line showed significant positive GCA effects.

Number of grains per ear

For number of grains per ear positive GCA effects are desirable. Among female lines DBW110, DBW93 (1.80) and PBW677 (1.69) exhibited positive and significant gca effects. However, among the male line MP3336 (2.74) showed significant positive GCA effects.

Biological yield per plant

For biological yield per plant positive GCA effects are desirable. None of the female or male lines exhibited positive and significant gca effects.

Harvest Index

For harvest index positive GCA effects are desirable. Among female lines only PBW677 (1.96) exhibited positive and significant gca effects. However, among the male lines MP3382 (1.20) showed significant positive GCA effects.

Grain yield per plant

For grain yield per plant positive GCA effects are desirable. Among female lines PBW677 (0.92) exhibited positive and significant GCA effects. However, none of the male line showed significant positive GCA effects.

Significant values of GCA indicated the importance of additive or additive \times additive gene action. As a result, these parents provided optimum opportunity for the production of enhanced wheat lines through the hybridization program. From the present experiment it could be suggested that to enhance wheat yield one should breed for superior combining ability for the component attributes with ultimate goal of increasing the rate of genetic improvement. Abro *et al.* (2016)^[1], Ahmad *et al.* (2017)^[3], Rajput *et al.* (2018)^[9], Patel *et al.* (2020)^[8], Kamara *et al.* (2021)^[5] and Yang *et al.* (2022)^[16] have also observed and supported significant gca for most the traits as well as genotypes earlier.

Estimates of specific combining ability effects

The SCA effects which are supposed to be manifestation of non-additive components of genetic variance are highly valuable for identification of crosses for their genetic worth as breeding material. Normally SCA effects do not contribute tangibly to the improvement of self-pollinated crop like wheat. Therefore, breeders interest rests in obtaining transgressive segregants through crosses by producing more potent homozygous lines.

Specific Combining Ability for ten characters are presented in Table 4 and described as character-wise hereunder:

Days to 50% flowering

Based on magnitude of SCA effects for days to 50% flowering none of the cross combination exhibited significant SCA effect.

Days to maturity

Based on magnitude of SCA effects for days to maturity cross combinations PBW677 \times MP3382 (-2.35), WH703 \times PBW343 (-2.19) and RUJ4037 \times PBW343 (-2.07) exhibited significant negative SCA effects.

Plant height

Based on magnitude of SCA effects for plant height cross combination DBW110 \times MP3382 (-2.00) exhibited significant positive SCA effects.

Number of productive tillers per plant

Based on magnitude of SCA effects for number of productive tillers cross combination WH703 \times PBW343 (1.18) and DBW110 \times MP3382 (0.77) exhibited significant positive SCA effects.

Spike length

Based on magnitude of SCA effects for spike length cross combination WH703 \times PBW343 (1.49) exhibited significant positive SCA effects.

Number of grains per ear

Based on magnitude of SCA effects for number of grains per ear cross combinations WH703 \times PBD343 (4.59), DBW107 \times MP3336 (4.26) and RUJ4037 \times PBW343 (2.59) exhibited significant positive SCA effect.

Test weight

Based on magnitude of SCA effects for test weight cross combinations DBW107 × PBW343 (2.08) and DBW93 × MP3336 (1.27) exhibited significant positive SCA effects.

Biological yield per plant

Based on magnitude of SCA effects for biological yield per plant none of the cross combination exhibited significant positive SCA effects.

Harvest index

Based on magnitude of SCA effects for harvest index cross combination DBW107 × PBW343 (2.98), DBW93 × MP3336 (2.77) and RUJ4037 × PBW343 (2.61) exhibited significant positive SCA effects.

Grain yield per plant

Based on magnitude of SCA effects for grain yield per plant cross combination DBW107×PBW343 (1.46) exhibited significant positive SCA effects.

The results demonstrated that the crossing with high order significant and desirable SCA effects for distinct traits had parents with a multitude of GCA effects such as high x high, high x average, high x low and low x low. For the characters studied, the above observations suggested that here was no association between positive and significant SCA effects of crosses and GCA effects of their parents and supported by previous workers in wheat Adel *et al.*, (2013) [2], Ahmad *et al.* (2017) [3], Rajput *et al.*, (2018) [9], Sharma *et al.*, (2019) [11], Shamyarira *et al.*, (2021) [10] and Yang *et al.* (2022) [16].

Table 1: Anova for the design of experimental of wheat

Characters	Replication	Genotypes	Error
df	2	26	52
Days to 50% flowering	2.75	9.15**	1.93
Days to maturity	1.12	23.33**	2.05
Plant height (cm)	1.81	26.19**	1.88
Number of productive tillers per plant	0.37	3.31**	0.37
Spike length (cm)	0.63	6.89**	0.34
No of grains per ear	3.37	33.80**	3.92
Test weight	0.87	4.82**	0.96
Biological yield per plant	3.23	14.94**	6.06
Harvest Index	9.89	18.51**	3.72
Grain yield per plant (g)	1.8	8.86**	0.85

Table 2: ANOVA for combining ability of line x tester design

Characters	Replication	crosses	Lines	Testers	L x T	Error	Total
df	2	17	5	2	10	34	53
Days to 50% flowering	2.57	4.57**	5.57**	5.69**	3.84	2.36	3.08
Days to maturity	0.24	11.56**	7.59**	19.69**	11.93**	1.46	4.65
Plant height (cm)	4.05	6.15**	5.47**	7.39**	6.24**	2.12	3.49
Number of productive tillers/plant	0.84	2.77**	5.98**	2.18**	1.29**	0.42	1.19
Spike length (cm)	0.49	6.58**	11.38**	13.07**	2.88**	0.33	2.34
No of grains per ear	0.3	45.16**	37.17**	128.30**	32.52**	3.36	16.65
Test weight	0.09	4.27**	1.39	12.43**	4.09**	1.01	2.02
Biological yield/plant	0.37	9.61**	3.38**	26.01**	9.44**	5.43	6.58
Harvest Index	4.58	19.12**	12.75**	34.31**	19.27**	3.48	8.54
Grain yield per plant (g)	1.4	3.78**	4.12**	4.38**	3.50**	0.97	1.89

Table 3: General Combining Ability effects for parents in line x tester design of wheat

S.N.	Parents	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers/plant	Spike length (cm)	No of grains per ear	Test weight	Biological yield/plant	Harvest Index	Grain yield per plant (g)
Lines											
1	RUJ 4037	0.200	0.520	0.620	-0.72 **	-0.94 **	-2.65 **	0.010	-0.350	-0.370	-0.360
2	DBW107	0.540	0.520	0.99 *	-0.250	-1.48 **	-0.650	-0.400	0.150	-1.26 *	-0.77 *
3	WH703	0.760	0.300	0.180	-1.13 **	-0.49 *	-1.98 **	-0.210	0.050	-0.990	-0.610
4	PBW 677	-1.24 *	-1.04 *	-1.16 *	0.64 **	0.67 **	1.69 **	0.74 *	-0.850	1.96 **	0.92 **
5	DBW 110	-0.690	-1.26 **	-0.090	0.79 **	1.12 **	1.80 **	-0.060	0.000	0.740	0.480
6	DBW 93	0.430	0.96 *	-0.540	0.66 **	1.13 **	1.80 **	-0.090	1.000	-0.080	0.340
Testers											
1	PBW343	0.650	0.520	0.650	-0.32 **	-0.98 **	-2.59 **	-0.77 **	1.050	-1.51 **	-0.57 *
2	MP3336	-0.350	-1.20 **	-0.630	0.37 *	0.50 **	2.74 **	0.88 **	0.260	0.310	0.310
3	MP3382	-0.300	0.69 *	-0.020	-0.060	0.48 **	-0.150	-0.120	-1.31 *	1.20 **	0.260
	SE(gca line)	0.512	0.402	0.486	0.216	0.190	0.611	0.336	0.777	0.622	0.328
	SE(gca tester)	0.362	0.285	0.344	0.153	0.135	0.432	0.237	0.549	0.440	0.232
	SE(bet gca line)	0.724	0.569	0.687	0.305	0.269	0.864	0.475	1.098	0.880	0.464
	SE(bet gca tester)	0.512	0.402	0.486	0.216	0.190	0.611	0.336	0.777	0.622	0.328

*,** Significant at 5% and 1% level of probability respectively.

Table 4: General Combining Ability effects for parents in line x tester design of wheat

S. N.	Hybrids	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers/ plant	Spike length (cm)	No of grains per ear	Test weight	Biological yield/plant	Harvest Index	Grain yield per plant (g)
1	RUJ 4037 × PBW343	-1.20	-2.07 **	-1.43	0.07	0.65	2.59 *	-0.78	-1.65	2.61 *	1.06
2	RUJ 4037 × MP3336	1.13	0.65	1.77 *	-0.25	-0.45	-3.74 **	-0.01	2.26	-1.80	-0.28
3	RUJ 4037 × MP3382	0.07	1.43 *	-0.34	0.18	-0.20	1.15	0.79	-0.61	-0.81	-0.77
4	DBW107 × PBW343	0.13	-1.41 *	-0.02	-0.03	0.36	-1.07	2.08 **	-1.33	2.98 **	1.46 *
5	DBW107 × MP3336	-0.87	0.31	-0.30	0.48	0.19	4.26 **	-1.62 **	1.56	-3.52 **	-1.72 **
6	DBW107 × MP3382	0.74	1.09	0.32	-0.46	-0.55	-3.19 **	-0.46	-0.24	0.55	0.27
7	WH703 × PBW343	-1.09	-2.19 **	-0.51	1.18 **	1.49 **	4.59 **	0.05	-1.51	1.08	0.13
8	WH703 × MP3336	0.57	1.54 *	0.64	-0.57	-1.43 **	-2.41 *	0.70	0.08	-0.09	-0.01
9	WH703 × MP3382	0.52	0.65	-0.12	-0.61	-0.06	-2.19 *	-0.74	1.42	-1.00	-0.12
10	PBW 677 × PBW343	0.57	2.48 **	0.84	-0.45	-0.99 **	-2.74 *	-0.79	1.46	-2.88 *	-1.28 *
11	PBW 677 × MP3336	0.57	-0.13	-1.65	0.16	0.65	0.59	-0.05	-0.99	1.39	0.53
12	PBW 677 × MP3382	-1.15	-2.35 **	0.81	0.29	0.34	2.15 *	0.84	-0.47	1.50	0.75
13	DBW 110 × PBW343	1.35	2.37 **	0.83	-0.41	-1.26 **	-1.19	-0.16	1.20	-1.80	-0.71
14	DBW 110 × MP3336	-0.31	-1.24	1.17	-0.36	0.60	-0.52	-0.29	-0.56	1.25	0.59
15	DBW 110 × MP3382	-1.04	-1.13	-2.00 *	0.77 *	0.66	1.70	0.46	-0.64	0.55	0.12
16	DBW 93 × PBW343	0.24	0.81	0.29	-0.37	-0.25	-2.19 *	-0.38	1.82	-1.98	-0.65
17	DBW 93 × MP3336	-1.09	-1.13	-1.63	0.54	0.44	1.81	1.27 *	-2.36	2.77 *	0.90
18	DBW 93 × MP3382	0.85	0.31	1.33	-0.17	-0.20	0.37	-0.89	0.54	-0.78	-0.24
	SE(sca effects)	0.887	0.697	0.841	0.374	0.330	1.058	0.581	1.345	1.078	0.568
	SE(bet sca effects)	1.254	0.985	1.190	0.528	0.466	1.496	0.822	1.902	1.524	0.803

*,** Significant at 5% and 1% level of probability respectively.

Conclusion

Based on the present investigation it can be concluded that based on per se performance parents DBW110, PBW677 and PBW343 were identified as superior parents and crosses PBW677 x MP3382, DBW101 x MP3336, DBW107 x PBW343 and WH703 x MP3382 were identified superior for grain yield and other yield attributing characters. These promising crosses merit further testing and evaluation in different location evaluation and their utilization in breeding programs aimed at developing high-yielding superior varieties.

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