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Combining ability analysis for seed yield and its attributing traits in Wheat (*Triticum aestivum* L.)

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Abstract

Ten lines, four testers and their 40 hybrids were analyzed for yield and its contributing traits in two different environmental conditions *i.e.*, timely sown and late sown. Crosses were made in line x tester mating design and data were recorded for 10 quantitative traits in both timely (E1) and late sown (E2) condition. ANOVA for combining ability analysis revealed that variances due to lines x testers showed highly significant differences for all the characters in E1 and E2 and pooled estimates except number of effective tillers per plant; Variance due to lines was also highly significant for days to maturity and test weight in E1, E2 and pooled estimate; whereas, variance due to testers were also highly significant for all the traits in both the environments as well as in pooled estimate except for test weight in E2 and harvest index in E1. The parental lines HD 2967 and among testers PBW 550 with high GCA effects were identified as superior donors for seed yield per plant, biological yield per plant, number of spikelet's per spike, number of grains per spike. The crosses HD 2824 X PBW 550, DBW 4 X Raj 3765 in timely sown, late sown and in pooled estimate showed significant & positive SCA effects for seed yield per plant as well as some other yield components.

Keywords: Wheat, GCA, SCA, ANOVA and Variance

Abbreviations: **DF:** days to 50% flowering, **DM:** Days to maturing, **PH:** plant height, **NETPP:** number of effective tillers per plant, **NSPS:** number of spikelet's per spike, **NGPS:** number of grains per spike, **BYP:** biological yield per plant, **HI:** harvest index, **SYP:** seed yield per plant

Introduction

Wheat (*Triticum aestivum* L., 2n = 42) ranks second as a staple food crop after rice in the world. It belongs to the Poaceae family (grass family), largest among all the plant families. The consumption of wheat is done in its various forms such as chapatti, bread, porridge, flour, suji and also whole grain after roasting. Wheat has high niacin and thiamine content. These amino acids contribute in formation of a very special type of protein known as "Gluten". This Gluten has the unique properties such as water absorption capacity, cohesiveness, viscosity and elasticity that make the wheat flour better for its bread making quality and baking quality. Wheat is adorned with the position of "King of Cereals" as it is next to rice in area, production and productivity in India as well as globally. Yield stability refers to how consistent an agricultural system yields from year to year. A high yielding agricultural system will produce roughly the same amount of food year after year and the world population increasing day by day and climatic conditions are going to be adverse for crop production, this will present an alarming situation of food security in upcoming years. Due to increasing population and rate of urbanization the agricultural land is decreasing very fast. Thus researchers must have to set a goal to boost up the crop productivity as well as production of wheat by employing recent technologies and to breed high yielding varieties to feed the burgeoning population effectively. Thus, keeping in the view of future goal researchers must have to develop high yielding wheat varieties which confer resistance to various biotic and abiotic stresses.

Study of combining ability helps in identifying the useful parental lines and the desirable specific cross combination which could be further exploited in development of improved varieties. Such studies are essential in choosing the appropriate breeding and selection methodologies for further improvement of crop. Combining ability analysis is frequently employed to identify the desirable parents and crosses. Therefore, it is urgently required to identify the best combiners and desirable crosses. Line x Tester analysis is an extension of top cross method in which several testers are used Kempthorne, (1957)^[2] which provides information about general and specific combining ability of parents and at the same time it is helpful in identifying best heterotic crosses.

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Materials and Methods

The experiment was conducted with 10 diverse lines and 4 broad genetic base testers and 40 crosses were made in line x tester fashion at Student's Instructional Farm of School of Agriculture, Career Point University Kota Rajasthan. The crosses were made during *Rabi* 2020-21 and evaluated in Randomized Block Design with three replications along with parental lines in *Rabi* 2021-22. Each line was grown in one row of 4 meter length. Row to row and plant-to-plant spacing was 30 cm and 10cm, respectively. Data were recorded on five randomly selected plants for plant height (cm), number of effective tillers per plant, number of spikelet's per spike, number of grains per spike, 1000-grain weight (g), biological yield per plant (g), seed yield per plant (g), harvest index (%) except days to 50% flowering and days to maturity which were recorded on plot basis.

Data in each experiment of all entries was subjected to analysis of variance. Panse and Sukhatme, (1967) [3] for testing the significance of treatments. Combining ability analysis and the testing of significance of different genotypes was based on the procedure given by Kamphorne (1957).

Results and Discussion

The analyses of variance for combining ability for all the ten characters are given in Table 1. Partitioning of variance into lines x testers showed highly significant differences for all the ten characters except number of effective tillers per plant in both E1, E2 and pooled estimate, biological yield per plant in E1 and E2, harvest index in E2 and pooled estimate and seed yield per plant in E2 only, which were found non-significant; whereas, variance due to testers were also highly significant for all the traits in both the environments as well as in pooled estimate except for test weight in E2 and harvest index in E1. Variance due to lines was also highly significant for days to maturity and test weight in E1, E2 and pooled estimate, whereas plant height in E1 and E2, biological yield per plant and seed yield per plant in E1 only. While, days to 50% flowering in E1 and E2, biological yield per plant, harvest index and seed yield per plant in pooled estimate was found moderately significant. Whereas remaining characters due to line were found non-significant in both environments as well as in pooled estimate. Similar finding were reported by Raiyani *et al.* (2015) [5], Gupta *et al.* (2017) [6], Kumari *et al.* (2022) [10].

General combining ability: The GCA effects of the parents (Females + males) presented in the (Table-2) indicating GCA effects for almost all the characters. The significant and positive GCA effects among lines for seed yield per plant were exhibited HD 2967 in E1, E2 and pooled analysis, whereas HPW 355, HD 2824 and DBW 4 in E1 and pooled estimates. Among the testers the significant and positive GCA effect was exhibited by PBW 550 in E1, E2 and pooled analysis, whereas Raj 3765 in E2 and pooled estimate only.

On the basis of GCA effects and mean performance, [Table 3 (a), (b) and (c)] parent HD 2824 exhibited negative and highly-significant GCA effects in both, E1, E2 and pooled estimates; thus, found good general combiner for days to 50% flowering and days to maturity as early flowering and early maturity is desirable to escape the heat stress period and late sown condition. Short plant height is also desirable for wheat

regarding that parent KRL 99 was found good general combiner. High estimates of GCA and mean performance among lines was of HD 2967 found good general combiner for number of effective tillers per plant, number of spikelet's per spike, number of seeds per spike, biological yield per plant, harvest index and seed yield per plant in E1, E2 and pooled analysis; for increased 1000 seed weight Lok1 was found good general combiner. Whereas, among testers, PBW 550 was found good general combiner for early flowering and early maturity and for high number of effective tillers per plant, number of spikelet's per spike, number of seeds per spike, biological yield per plant, harvest index and seed yield per plant; for increased 1000 seed weight, HD 3226 was found good general combiner. Whereas, remaining lines and testers were found with moderate to low general combining ability for all the traits under study. Similar finding were reported by Raiyani *et al.* (2015) [5], Gupta *et al.* (2017) [6], Sharma *et al.* (2019), Kumari *et al.* (2022) [10], Chaudhary *et al.* (2022) [11].

Specific combining ability: The estimates of SCA effects of 40 crosses in E1, E2 and pooled analysis for 10 characters are given in (Table-4). Out of 40 crosses studied, the most promising crosses were *viz.*, HD 2824 X PBW 550 (0.97), PBW 343 X Raj 3765 (0.87), HPW 355 X DBW 16 (0.79), DBW 4 X Raj 3765 (0.65), DBW 4 X HD 3226 (0.55) in E1; DBW 4 X Raj 3765 (1.57), PBW 343 X Raj 3765 (1.39), HD 2967 X DBW 16 (1.32), NW 2036 X PBW 550 (1.30) in E2 and DBW 4 X Raj 3765 (1.11), HPW 355 X DBW 16 (0.93), HD 2967 X DBW 16 (0.80), HD 2824 X PBW 550 (0.80), PBW 343 X Raj 3765 (0.78) in pooled analysis showed significant & positive SCA effects for seed yield per plant as well as some other yield components. According to Kenga *et al.* (2004), cross-combinations with high means favorable SCA estimates and involving at least one of the parents with high GCA would likely enhance the concentration of favorable alleles to improve target traits. Similar finding were reported by Raiyani *et al.* (2015) [5], Gupta *et al.* (2017) [6], Abas *et al.* (2018), Tayade *et al.* (2020), Kalja *et al.* (2022), Kumari *et al.* (2022) [10].

The crosses showing significant and desirable SCA effects were associated with better *per se* performance for respective traits are given in the table 4(a), 4(b) and 4(c) for E1, E2 and pooled analysis, respectively.

In the present study the cross DBW 4 X Raj 3765 was emerged out as the most promising cross combination as it had high significant SCA effects for days to 50% flowering, number of spikelet's per spike, number of seeds per spike, biological yield per plant, seed yield per plant; PBW 343 X Raj 3765 for number of effective tillers per plant, number of spikelet's per spike, number of seeds per spike; PBW 343 X DBW 16, HD 2824 X HD 3226 and HD 2824 X PBW550 for plant height, days to 50% flowering and days to maturity; HD 2967 X HD 3226 for 1000 seed weight, plant height and days to maturity; HPW 355 X DBW 16 for harvest index, seed yield per plant, biological yield per plant and number of effective tillers per plant in both E1, E2 and pooled estimate. Similar finding were reported by Gupta *et al.* (2017) [6], Tayade *et al.* (2020), Kumari *et al.* (2022) [10], Chaudhary *et al.* (2022) [11], Kumari *et al.* (2022) [10].

Table 4(a): Five best crosses on the basis of SCA and *per se* performance in (E1)

S. No.	Number of spikelet's per spike			No. of grains per spike			1000 seed weight (g)			Biological yield per plant (g)			Grain yield per plant (g)		
	Crosses	per se	SCA	Crosses	per se	SCA	Crosses	per se	SCA	Crosses	per se	SCA	Crosses	per se	SCA
1	HD 2967 X DBW 16	20.67	1.70	DBW 4 X Raj 3765	55.33	5.64	HD 2967 X HD 3226	42.28	1.02	DBW 4 X Raj 3765	24.73	1.99	HD 2824 X PBW 550	12.63	0.97
2	PBW 343 X Raj 3765	18.67	1.73	PBW 343 X Raj 3765	52.00	5.31	HD 2824 X Raj 3765	39.47	0.82	NW 2036 X HD 3226	22.83	1.93	PBW 343 X Raj 3765	9.41	0.87
3	UP 2338 X DBW 16	19.33	1.53	UP 2338 X DBW 16	53.67	4.34	NW 2036 X DBW 16	40.92	0.82	HPW 355 X DBW 16	25.47	1.86	HPW 355 X DBW 16	11.68	0.79
4	DBW 4 X Raj 3765	20.67	2.48	HD 2967 X DBW 16	56.00	3.59	NW 2036 X PBW 550	40.52	0.78	DBW 4 X HD 3226	24.57	1.17	DBW 4 X Raj 3765	11.16	0.65
5	HD 2824 X DBW 16	16.00	1.12	NW 2036 X HD 3226	49.00	3.44	KRL 99 X Raj 3765	39.41	0.61	KRL 99 X DBW 16	20.63	1.10	DBW 4 X HD 3226	8.71	0.55

Table 4(b): Five best crosses on the basis of SCA and *per se* performance in (E2)

S. No.	Spikelets per spike			No. of grains per spike			1000 seed weight (g)			Biological yield per plant (g)			Grain yield per plant (g)		
	Crosses	per se	SCA	Crosses	per se	SCA	Crosses	per se	SCA	Crosses	per se	SCA	Crosses	per se	SCA
1	DBW 4 X Raj 3765	17.67	1.78	DBW 4 X Raj 3765	50.67	5.44	HD 2967 X HD 3226	41.53	1.03	DBW 4 X Raj 3765	40.60	2.99	DBW 4 X Raj 3765	11.05	1.57
2	NW 2036 X HD 3226	14.67	1.18	UP 2338 X DBW 16	44.33	3.41	NW 2036 X PBW 550	39.81	0.86	HD 2967 X DBW 16	39.87	2.67	PBW 343 X Raj 3765	10.78	1.39
3	PBW 343 X Raj 3765	16.00	1.28	PBW 343 X Raj 3765	45.00	3.36	NW 2036 X DBW 16	40.30	0.80	PBW 343 X Raj 3765	41.15	2.63	HD 2967 X DBW 16	9.37	1.32
4	UP 2338 X DBW 16	15.67	1.17	NW 2036 X HD 3226	41.33	3.22	KRL 99 X Raj 3765	39.55	0.75	NW 2036 X PBW 550	39.81	2.09	NW 2036 X PBW 550	11.53	1.30
5	HD 2824 X PBW 550	17.33	0.80	HD 2967 X DBW 16	44.33	2.66	KRL 210 X HD 3226	41.89	0.60	HPW 355 X DBW 16	40.63	1.76	HPW 355 X DBW 16	8.32	1.07

Table 4(c): Five best crosses on the basis of SCA and *per se* performance in pooled analysis

S. No.	Spikelet's per spike			No. of grains per spike			1000 seed weight (g)			Biological yield per plant (g)			Grain yield per plant (g)		
	Crosses	per se	SCA	Crosses	per se	SCA	Crosses	per se	SCA	Crosses	per se	SCA	Crosses	per se	SCA
1	DBW 4 X Raj 3765	18.17	2.13	DBW 4 X Raj 3765	50.00	5.54	HD 2967 X DBW 16	40.33	1.02	DBW 4 X Raj 3765	21.93	2.04	DBW 4 X Raj 3765	9.77	1.11
2	PBW 343 X Raj 3765	17.00	1.51	PBW 343 X Raj 3765	47.83	4.33	NW 2036 X DBW 16	41.08	0.76	PBW 343 X Raj 3765	21.22	1.81	HPW 355 X DBW 16	10.44	0.93
3	UP 2338 X DBW 16	17.33	1.35	UP 2338 X DBW 16	48.83	3.87	NW 2036 X PBW 550	39.75	0.72	HPW 355 X DBW 16	22.48	1.56	HD 2967 X DBW 16	9.31	0.80
4	HD 2967 X DBW 16	17.83	1.22	NW 2036 X HD 3226	42.67	3.33	HD 2824 X Raj 3765	39.27	0.69	HD 2967 X DBW 16	19.99	1.24	HD 2824 X PBW 550	10.09	0.80
5	NW 2036 X HD 3226	15.17	1.06	HD 2967 X DBW 16	49.33	3.12	KRL 99 X Raj 3765	39.35	0.68	NW 2036 X PBW 550	19.22	1.19	PBW 343 X Raj 3765	9.43	0.78

Conclusion

The extent GCA was higher than SCA for nearly all the traits in both E1, E2 and pooled estimates indicates towards existence of genetic variability in the parental lines included in the present study and involvement of both additive and non-additive gene effects in the inheritance of these traits. The study on the general combining ability effects of parents showed their ability to transmit additive genes in the desirable direction for all the traits under study. Among the 10 lines HD 2967, HPW 355, HD 2824 and DBW 4 were the best general combiners exhibited high GCA effects each in desirable direction for most of the characters in both environments as well as in pooled analysis. Among the testers (male parents), PBW 550 was found good general combiner for early flowering and early maturity and for high number of effective tillers per plant, number of spikelet's per spike, number of seeds per spike, biological yield per plant, harvest index and seed yield per plant; for increased 1000 seed weight, HD 3226 was found good general combiner in timely sown, late sown

and pooled estimates showed significant & positive SCA effects. In most of the cases significantly higher SCA effects were associated with high heterosis for different characters. This study provided combining ability information on tested inbred lines. The promising lines have to be maintained and used in hybridization program. The promising single crosses could be tested across locations and seasons to fix the desirable characters through advanced selection generations.

Abbreviations

E₁, Timely Sown Environment; E₂, Late Sown Environment; GCA, General Combining Ability; SCA, Specific Combining Ability; m. ha, Million hectare; Kg/ha, Kilogram per hectare.

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