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Half diallel analysis for combining ability and gene action of yield and yield contributing traits in bread wheat (*Triticum aestivum* L.)

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Abstract

The experiment was evaluated at the Student Instructional farm, Peeli Kothi, Tilak Dhari Post Graduate College, Jaunpur, Uttar Pradesh, during the Rabi season 2024-25 in randomized block design with three replications. Gene action and combining ability was carried out for all fourteen characters and to identify the superior parent and hybrids. Analysis of variance for GCA and SCA of all traits observed highly significant findings and the ratio of GCA and SCA was less than one in all fourteen traits. The positive significant of GCA effects, among the parents DBW18, HD2967, Lok-1 and DBW88 were found as good general combiners for grain yield per plant. Among the crosses, the positive significant of SCA effect, eighteen out of forty-five crosses was found as good specific combiners for grain yield per plant. The cross of good specific combiners include such as DBW88 x PBW 527, PBW 723 x PBW 343, DBW 187 x Lok -1, HD 2967 x PBW 833, WH 147 x HPBW 01, DBW88 x Lok-1, DBW 187 x PBW 833, HD 2967 x HPBW 01, PBW 527 x HPBW 01, Lok -1 x HPBW 01, PBW 527 x Lok -01, HD 2967 x PBW 723, PBW 833 x PBW 723, Lok -1 x PBW 833, PBW 833 x HPBW 01, WH 147 x PBW 343, PBW 723 x HPBW 01 and PBW 527 x WH 147. Conclusively that parents and hybrids can be effectively utilized in multiple-cross breeding programs to enhance grain yield. Their inclusion is likely to facilitate the development of transgressive segregants and the creation of populations with a wider genetic base, thereby contributing to sustained yield improvement in wheat.

Keywords: Wheat, half diallel, general combining ability, specific combining ability

1. Introduction

Wheat (*Triticum aestivum* L., $2n=6x=42$, AABBDD) plays a vital role in maintaining global food security, contributing for nearly 30% of total grain production and accounting about half of the grain traded across international markets. It is a primary staple crop in more than 40 countries and serves as a significant source of dietary energy and protein for a large portion of the world's population. With the global population expected to reach approximately 9.1 billion by 2050, the demand for wheat is projected to increase substantially, indicating the urgent need to improve its productivity and overall production to fulfill for future food requirements (Maity *et al.*, 2024) ^[10]. Wheat is rich essential nutrient and noted a high content of important components like as carbohydrates (60-80%), proteins (8-15%), fats (1.5-2%), dietary fiber (about 2.2%), as well as vitamins like as B and E, and various amino acids. Furthermore, the presence of gluten makes wheat particularly suitable for food processing. Owing to its unique gluten properties, wheat is widely used in the preparation of high-quality bread, with gluten content in bread wheat typically ranging from 30 to 35% (Aziz *et al.*, 2019) ^[2]. Improving the nutritional quality of wheat along with its agronomic performance require the identification of genetically superior parents and a thorough understanding of the genetic architecture governing yield and quality characters, like as protein, iron (Fe), and zinc (Zn) content. Combining ability analysis offers an effective method to assess the relative contribution of additive and non-additive gene actions and to select suitable parental combinations for hybrid development as well as selection-based breeding program. Among various methods, diallel mating designs are widely utilized for estimating general combining ability (GCA), specific combining ability (SCA), heterosis, and for knowledge of genetic basis of characters inheritance (Jaiswal *et al.*,

2013, Owusu *et al.*, 2020) [6, 12].

General combining ability (GCA) offers valuable insight into the performance of genotypes across various hybrid combinations, thereby enhancing effective phenotypic selection (Longin *et al.*, 2013) [9]. Specific combining ability (SCA) indicates the variation reported in particular cross combinations arising due to dominance and epistatic gene interactions. It is therefore useful in identifying superior hybrid combinations and plays a key role in the exploitation of heterosis (Kumari *et al.*, 2015) [7]. The present study the results of gene action, general combining ability, and specific combining ability in 45 F₁s crosses developed by 10 wheat varieties. The goal was to identification superior genotypes with strong GCA and crosses with the potential to significantly improve wheat yields in the future.

2. Materials and Methods

The present investigation was evaluated at Student Instructional farm, Peeli Kothi, Tilak Dhari Post graduate College, Jaunpur, Uttar Pradesh, during rabi season 2024-2025 in randomized block design with three replications. The experiment was carried out with 10 parents and 45 hybrids using half diallel mating design. Ten genetically diverse genotypes, exhibited silent features like disease resistance, yield potential, abiotic stress tolerance and quality parameters were selected as parents for hybridization (Table 1). Observations of fourteen traits viz., days to heading, days to anthesis, days to maturity, Grain filling duration, plant height (cm), Effective tillers per plant, chlorophyll content, spike length (cm), number of spikelets per spike, number of grains per spike, 1000-grain weight (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%). Biometrical analysis: The gene action and combining ability estimation have been done using Griffing's (1956) [5] Method 2 Model I.

3. Results

Analysis of variance findings revealed that both general combining ability (GCA) and specific combining ability (SCA) was highly significant for all the fourteen traits. Grain yield, being a complex trait, indicate significant contributions from both general combining ability (4.2696**) and specific combining ability (2.2686**) sources of variation. Similarly, 1000-seed weight, an important yield-contributing trait, also

showed significant general combining ability (18.7885**) and specific combining ability (16.7728**) effects. The predominance of non-additive gene action was demonstrate by the GCA/SCA variance ratio being less than one, suggesting that SCA variance was higher than GCA variance (Table 2). Overall, the findings suggest the involvement of both additive and non-additive gene actions in the inheritance of the traits, similar result were reported by Kumar *et al.*, (2015) [8], Bharat Bhushan *et al.*, (2018) [3] Ranjitha *et al.*, (2018) [14], Ramadan *et al.*, (2018) [13], Ahmad *et al.*, (2024) [1], Chaudhary *et al.*, (2025) [4]. Similarly, other important findings, such as the GCA/SCA variance ratio being less than one for the all fourteen traits, this indicates the predominance of non-additive gene action, which can be effectively exploited in heterosis breeding. Similar findings align with found by Nageshwar *et al.*, (2021) [11], Ahmad *et al.*, (2024) [1], Chaudhary *et al.* (2025) [4].

The general combining ability (GCA) of a parental line arises primarily due to additive gene action and reflects its potential to contribute favorable genes in hybrid combinations. The GCA analysis showed that, among the ten parents evaluated, DBW187, HD2967, Lok-1 and DBW88 were identified as good general combiners for grain yield per plant. In the case of 1000-seed weight, the parents Lok-1 (1.9015**), DBW 187 (1.5815**), HD 2967 (1.0368**) and PBW 527 (0.4984*) exhibited significant GCA effects (Table 3).

Specific combining ability (SCA) serves as an important criterion for identifying superior parental combinations in crop improvement programs aimed for enhancing yield. A high GCA effect in parents does not necessarily result in high SCA in all hybrid combinations; therefore, the estimation of SCA is essential. SCA refers to the performance of a specific cross that is either superior or inferior relative to its parents. Crosses exhibiting high SCA effects indicate the predominance of non-additive gene action. the Top three parents in grain yield with the highest GCA estimates were DBW187 (1.1148 **), HD2967 (0.5582**) and Lok-1 (0.5265**) and among the crosses, the top three hybrids in grain yield with the highest SCA estimates were DBW88 x PBW 527 (2.8080 **), PBW 723 x PBW 343 (2.6311**) and DBW 187 x Lok 1 (2.3503) presented in (Table-4.). The SCA estimates for all traits across the 45 crosses further provide valuable interpretations into hybrid performance and gene action.

Table 1: Parents details using hybridization programme.

Name	Pedigree	Developed	Special features
DBW88	KAUZ//ALTR84/AOS/3/MILAN/ KAUZ/4/HUITES	IIWBR, Karnal Haryana	Resistance to yellow and brown rust
DBW-187	NAC/TH.AC//3*P VN/3/MIRLO/BUC /4/2*PASTOR/5/KACHU/6/KACHU	ICAR-IIWBR, Karnal	Resistance to yellow and brown rust, good biscuit spread factor (8.6cm), High Fe content (43.1 ppm)
HD2967	ALD/CUC//URES/HD2160/HD2278	IARI, New Delhi	Wider adaptability and resistance to yellow and brown rust
PBW527	PBW-175/PBW-389	PAU, Ludhiana	Resistance to yellow and brown rust
LOK-1	S308/S331	Lok Bharti, Sanosara	Wider adaptability and good for chapatti quality
PBW 833	BWL0762/PBW62 1//HD3086	PAU, Ludhiana	Highly resistant to leaf rust, good chapatti quality (score 8.2) and protein content (12.9%)
WH-147	E 4870/C286/C2 73 /4/S339/PV18	CCSHAU, HISAR	High protein (>13%) content
PBW723	PBW343+Lr57/Yr40+ Lr37/Yr17	PAU, Ludhiana	Resistant to yellow and brown rust
HPBW 01	T.DICOCCON/CI9309/ AE.SQUARROSA(409)/3/MILAN/S87230//BAV92/4/ 2*MILAN/S87320//BAV92	PAU, Ludhiana	Zinc (40.6 ppm) rich wheat variety, resistance to yellow and brown rust
PBW 343	ND/VG9144//KAL/BB/3/YACO'S' /4/VEE#5 'S'	PAU, Ludhiana	Double dwarf variety with profuse tillering and stiff straw

Table 2: Analysis of variance of 14 traits for GCA and SCA in wheat

Source of variance	d.f.	Mean sum of square													
		DTH	DTA	DM	GFD	PH	ETP	CC	SL	NSPS	NGPS	TGW	GYP	BYP	HI
GCA	9	14.2638**	3.1300**	4.3206**	5.1128**	61.5668**	1.8747**	52.9454**	4.3748**	5.4642**	60.1762**	18.7885**	4.2696**	17.5518**	6.3067**
SCA	45	3.6988**	1.7585**	4.8833**	4.7069**	31.7390**	1.1835**	26.4109**	0.8736**	2.4334**	29.5087**	16.7728**	2.2686**	12.6698**	24.3439**
Error	108	1.1358	0.5995	0.6210	0.9868	0.4621	0.0661	0.5990	0.1211	0.1459	2.8751	0.5332	0.0189	0.0430	0.4851
GCA var.	1.09	0.21	0.31	0.34	5.09	0.15	4.36	0.35	0.44	4.77	1.52	0.35	1.45	0.48	1.09
SCA var.	2.56	1.16	4.26	3.72	31.28	1.12	25.81	0.75	2.29	26.63	16.24	2.24	12.62	23.85	2.56
GCA /SCA ratio	0.42	0.18	0.07	0.09	0.16	0.13	0.16	0.47	0.19	0.17	0.09	0.15	0.11	0.02	0.42

df, Degrees of freedom; DTH, Days to heading; DTA, Days to anthesis; DTM, Days to maturity; GFD, Grain filling duration Grain PH, Plant height; ETP, Effective tillers per plant plant; SL, Spike length; NSPS, Numbers of spikelet per spike; NGPS, Number of grains per spike; TGW, 1000-grain weight; GY, Grain yield per plant; BYP, Biological yield per plant; HI, Harvest index; GCA, General combining ability; SCA, Specific combining ability; GCA var., General combining ability variance; SCA var., Specific combining ability variance **, * indicates significant at 1% and 5% level of significance.

Table 3: Representation of GCA effects of the ten parents using in the hybridization

Parents	Traits													
	DTH	DTA	DTM	GFD	PH	ETP	CC	SL	NSPS	NGPS	TGW	GYP	BYP	HI
DBW88	2.1222**	0.2944	1.2167**	0.9111**	0.8272**	-0.0348	0.0867	0.7621**	0.7979**	2.7653**	-0.1810	0.4196**	1.4067**	-0.5191**
DBW 187	-0.1278	-1.1778**	0.2722	1.3278**	3.5583**	0.7316**	3.4317**	-1.0258**	-1.0302**	-2.8844**	1.5815**	1.1148**	1.6642**	1.3754**
HD2967	-1.0444**	0.1278	0.1056	-0.0333	1.6919**	0.4358**	1.6414**	0.0822	-0.1612	0.4692	1.0368**	0.5582**	0.8276**	0.8717**
PBW527	-0.8778**	0.4611*	0.4667*	-0.0056	0.5155**	-0.1639*	-1.7881**	-0.0395	0.0852	0.2825	0.4984*	-0.3974**	-0.4580**	-0.8579**
LOK-1	-1.4056**	-0.1222	-0.3667	-0.2556	2.1783**	0.4524**	3.0611**	0.2308*	0.1619	0.5528	1.9015**	0.5265**	1.3626**	-0.2888
PBW833	0.4833	0.4889*	-0.3944	-0.7556**	-2.0392**	-0.3873**	-2.4119**	-0.6928**	-0.5908**	-2.1192**	-1.2313*	-0.4524**	-1.3313**	0.4767*
WH-147	0.5389	-0.1778	-0.2833	-0.1167	-0.2745	-0.2356**	-0.7678**	0.8110**	0.9568**	3.0286**	-0.6579**	-0.4210**	-0.8377**	-0.1566
PBW723	1.0389**	-0.0389	-0.2000	-0.0611	-3.2548**	-0.3478**	-2.3606**	-0.0226	0.4228**	1.6511**	-1.8610**	-0.6082**	-1.6116**	0.2573
HPBW 01	-0.8500**	-0.3444	-1.0056**	-0.7000*	-0.0201	-0.1248	-0.0681	-0.5232**	-0.9091**	-3.4783**	0.0112	-0.2960**	-0.3241**	-0.5905**
PBW 343	0.1222	0.4889*	0.1889	-0.3111	-3.1826**	-0.3256**	-0.8244**	0.4179**	0.2668*	-0.2675	-1.0982**	-0.4441**	-0.6983**	-0.5683**

df, Degrees of freedom; DTH, Days to heading; DTA, Days to anthesis; DTM, Days to maturity; GFD, Grain filling duration Grain PH, Plant height; ETP, Effective tillers per plant plant; SL, Spike length; NSPS, Numbers of spikelet per spike; NGPS, Number of grains per spike; TGW, 1000-grain weight; GY, Grain yield per plant; BYP, Biological yield per plant; HI, Harvest index; GCA, General combining ability; SCA, Specific combining ability. **, * indicates significant at 1% and 5% level of significance

Table 4: List of top three best general and specific combiners for fourteen traits in wheat.

Sr. No.	Traits	Good general combiners (parents)	Good specific combiners (Hybrids)
1	Days to heading	Lok-1 (-1.4056**) PBW 527 (-0.8778**) HPBW 01 (-0.8500**)	DBW88 x HPBW 01 (-4.1995**) WH 147 x PBW 723 (-3.8384**) DBW 187 x HD 2967 (-2.7551**)
2	Days to anthesis	DBW 187 (-1.1778**) WH 147 (-0.1778) Lok-1 (-0.1222)	DBW88 x HPBW 01 (-3.0530**) DBW88 x WH 147 (-1.5530*) DBW 187 x PBW 723 (-1.5530*)
3	Days to maturity	HPBW 01 (-1.0056**) PBW 723 (-0.2000) WH 147 (-0.2833)	Lok -1 x PBW 343 (-4.4646**) PBW 723 x PBW 343 (-3.2980**) PBW 833 x PBW 343 (-2.7702**)
4	Grain filling duration	PBW 833 (-0.7556**) HPBW 01 (-0.7000*) PBW 343 (-0.3111)	PBW 723 x PBW 343 (-5.1793**) Lok -1 x PBW 343 (-3.9848**) PBW 833 x PBW 343 (-2.4848**)
5	Plant height	PBW 723 (-3.2548**) PBW343 (-3.1826**) PBW833 (-2.0392**)	PBW 833 x PBW 723 (8.6536**) HPBW 01 x PBW 343 (8.4122**) PBW 527 x PBW 343 (7.4134**)
6	Effective tillers per plant	DBW187 (0.7316**) Lok-1 (0.4524**) HD2967 (0.4358**)	HD 2967 x HPBW 01 (2.2511**) DBW 187 x PBW 723 (2.2049**) Lok -1 x PBW 833 (2.0502**)
7	Chlorophyll content	DBW187 (3.4317**) Lok-1 (3.0611**) HD2967 (1.6414**)	PBW 527 x PBW 343 (8.4340**) Lok -1 x PBW 833 (7.3390**) PBW 833 x PBW 723 (7.3073**)

8	Spike length	WH147 (0.8110 **) DBW88 (0.7621**) PBW343 (0.4179 **)	DBW88 x DBW 187 (2.3944 **) HD 2967 x Lok-1 (1.5935 **) PBW 527 x PBW 833 (1.4087 **)
9	Number of spikelets per spike	WH147 (0.9568 **) DBW88 (0.7979**), PBW723 (0.4228**)	DBW 187 x PBW 723 (3.4760 **) Lok -1 x HPBW 01 (3.0815 **) PBW 527 x PBW 833 (2.4733 **)
10	Number of grain per spike	WH147 (3.0286**) DBW 88 (2.7653**) PBW 723 (1.6511**)	DBW 187 x PBW 723 (11.7700 **) Lok -1 x HPBW 01 (10.9522 **) DBW88 x DBW 187 (7.5092 **),
11	1000- grain weight	Lok-1 (1.9015**), DBW187 (1.5815**), HD2967 (1.0368 **)	DBW 187 x PBW 723 (6.8544**) PBW 527 x PBW 343 (6.5114**) Lok -1 x PBW 833 (6.3281**)
12	Grain yield per plant	DBW187 (1.1148 **) HD2967 (0.5582**) Lok-1 (0.5265**)	DBW88 x PBW 527 (2.8080 **) PBW 723 x PBW 343 (2.6311**) DBW 187 x Lok 1 (2.3503 **)
13	Biological yield per plant	DBW187 (1.6642 **) DBW88 (1.4067**), Lok-1 (1.3626**)	DBW 187 x HD 2967 (10.0516**) PBW 833 x PBW 343 (10.0516 **) DBW88 x HD 2967 (7.2991**)
14	Harvest index	DBW187 (1.3754**) HD2967 (0.8717**) PBW833 (0.4767*)	HD 2967 x WH 147 (9.5149 **) PBW 527 x PBW 343 (8.5596 **) DBW88 x PBW 343 (8.2008 **)

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