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ASSESSMENT OF GENETIC AND COMBINING ABILITY ANALYSIS FOR SEED YIELD AND RELATED TRAITS IN BREAD WHEAT (*TRITICUM AESTIVUM L.*)

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ABSTRACT

The study was conducted during the Rabi season 2023–25 at Lovely Professional University, Punjab. Forty-four genotypes, including 32 F_1 hybrids derived from a line × tester design (8 lines × 4 testers) and 12 parents, were evaluated for twelve agronomic and physiological traits. Significant genetic variability was observed for all traits. High heritability and genetic advance in traits like 1000-seed weight, grain yield, and biological yield suggest additive gene action and potential for improvement through selection. Combining ability analysis revealed the involvement of both additive and non-additive gene actions. GS5052, IC55681, and GS3043 were identified as good general combiners, while crosses such as GS4055 × PBW824 and GS3043 × PBW803 showed significant specific combining ability effects. These results indicate promising genetic resources for enhancing yield and adaptability in wheat breeding programs.
***Keywords*:** Combining ability, variability, hybrids, selection

Introduction

Wheat (*Triticum aestivum* L.) is a staple crop that serves as a major food source for nearly one-third of the global population. It is one of the most widely cultivated cereal crops globally, owing to its extensive cultivation area, high yield potential, and vital role in international food grain markets. Its adaptability to a range of agro-climatic conditions, ease of grain storage, and versatility in processing into flour and various edible products contribute to its prominence. Wheat supplies about 20% of the world's dietary calories and plays a crucial role in human nutrition, offering approximately 12% protein, 1.8% fats, 1.8% ash, 2% reducing sugars, 59.2% starch, and 70% total carbohydrates, amounting to 314 kcal per 100 grams (Iqbal *et al.*, 2017).In India, wheat production for the year was projected at 112.92 million tonnes, cultivated over 31.78 million hectares, with an average yield of 36.15 quintals per hectare. The major wheat-producing states include Uttar Pradesh, Madhya Pradesh, Punjab, Haryana, and Rajasthan, with Uttar Pradesh leading in both area and output, contributing 35.43 million tonnes from 9.31 million hectares (ICAR-IIWBR, 2024). This research was undertaken to assess the nature and degree of genetic diversity, heritability, genetic gains, and the magnitude of economic heterosis across yield-related traits in wheat, aiming to boost productivity and profitability for farmers. One of the effective strategies to improve wheat yield and adaptability is the exploitation of heterosis. Heterosis refers to the phenomenon where hybrid offspring exhibit superior performance over their parents for traits such as yield, stress tolerance, and growth rate.

Materials and Methods

The present investigation titled "Genetic variability and heterosis analysis for seed yield and its components in wheat (*Triticum aestivum*)" was conducted during *Rabi* season of 2023-25 at Agriculture Farm, Department of Genetics and Plant breeding, Lovely Professional University, Phagwara, Kapurthala (Dist.), Punjab. Geographically, the experimental site is located between latitudes of 31.255˚N and longitude of 75,705˚E and at an altitude 180 m and 300 m above sea level. The climate of Punjab district is semi-arid with hot summer and cold winters. The experimental site had a sandy loam soil with low available nitrogen (N_2) moderately available phosphorusASWW21 and high availability of potash. The pH of the soil ranged from 7.8 to 8.5. the site experienced a humid subtropical climate characterized by cool winters from November to February and long, hot summers from April to June. During the summer, temperatures varied from average highs of around 38˚C (100.4˚F) to average lows of around 30˚C (86˚F). In winter, temperatures ranged from highs of 19˚C (66˚F) to lows of 7˚C (19˚F). The overall climate was dry, with an average annual rainfall of approximately 700m. The Experimental materials comprised of 44 treatments (12 parents and 32 hybrids) of wheat genotypes. These materials included 32 F_1 population developed in a line* tester by crossing 8 lines viz. GS 4055, *IC*78737, GS4021, HD2864, IC55681, GS5052, DBW303, GS3043) and 4 testers (DBW222, HTWYT43, PBW803, PBW824) .Five tagged plants from each plot were selected randomly and data were recorded on Days to 50% heading(DFH), Chlorophyll content (CC), Effective tillers per plant (ETPP), Plant height (PH), Flag leaf area (FLA), Thousand grain weight (TGW), Spike length (SL), Days to maturity (DM), Grain yield (GY), Biological yield (BY), Harvest index (HI)

Result and Discussion

Analysis of Variance for Yield and Yield Attributing Traits

The analysis of variance (ANOVA) performed on the 44 genotypes demonstrated highly significant differences across all evaluated traits, reflecting substantial genetic variability within the study material. Traits such as days to 50% flowering (DFF), chlorophyll content (CC), effective tillers per plant (ETPP), plant height (PH), flag leaf area (FLA), days to maturity (DM), number of grains per spike (NGPS), 1000-seed weight (1000SW), biological yield per plant (BYPP), grain yield per plant (GYPP), and harvest index (HI) exhibited significant treatment mean squares, underscoring the presence of wide genetic diversity essential for hybrid development. Significant variation among parents for traits like DFF, CC, PH, FLA, DM, NGPS, and BYPP confirmed the genetic divergence among the selected lines and testers. Further partitioning of parental variance revealed significant differences between lines and testers, notably for PH, FLA, and GYPP, indicating notable variation between these two groups. Additionally, significant differences in the parents versus crosses comparison for traits such as DFF, FLA, NGPS, and HI pointed to the existence of heterosis and the enhanced performance of hybrids over their parents. The crosses exhibited highly significant differences for most traits, highlighting the potential of hybrid combinations. Significant line × tester interactions for traits like CC, DM, NGPS, 1000SW, GYPP, and HI suggested the predominance of non-additive gene action in their inheritance. Overall, the results demonstrate the contribution of both additive and non-additive gene effects in trait expression, offering a strong genetic foundation for wheat improvement through hybrid breeding. Comparable patterns were also reported by Roy *et al*. (2023), Gautham *et al*. (2024), and Singh *et al*. (2022).

Table 1: ANOVA for 12 parents and 32 hybrids

Characters	df	DFF	CC	ETPP	PH	SL	FLA	DM	NGPS	1000SW	BYPP	GYPP	HI
Replicates	2	25.520**	9.007	0.346*	10.054	0.86	5.218*	53.964**	77.598**	0.979	16.511	0.914	27.685
Treatments	43	4.222*	21.140**	0.278**	38.476**	2.413**	4.714**	0.474	13.696**	25.707**	44.805**	5.401**	17.199*
Parents	11	3.768	6.148	0.073	8.647	0.161	2.588	0.309	4.687	2.968	17.054*	1.529*	17.616
Parents (Line)	7	3.345	3.273	0.076	9.693	0.177	1.904	0.225	5.409	1.5	11.705	2.191*	7.938
Parents (Testers)	3	0.902	7.011	0.083	5.325	0.01	1.531	0.599	0.205	6.704	27.950*	0.475	37.658*
Parents (L vs T)	1	15.327*	23.690**	0.02	11.289	0.5	10.549**	0.023	13.082*	2.037	21.802	0.053	25.241
Parents vs Crosses	1	3.96	570.139**	5.400**	1148.185**	60.068**	127.999**	6.153**	357.159**	866.808**	1337.752**	183.424**	16.198
Crosses	31	4.392*	8.750**	0.186**	13.264**	1.353**	1.491	0.349	5.813**	6.644**	12.944	1.032	17.083*
Line Effect	7	7.988*	17.983*	0.532**	36.710**	1.659	1.782	0.4	8.523	14.192*	24.729*	1.21	7.152
Tester Effect	3	7.87	5.305	0.205	10.265	0.68	1.017	0.64	5.312	1.953	20.153	3.252**	37.056
Line * Tester Eff.	21	2.697	6.165*	0.068	5.877	1.347**	1.462	0.29	4.981*	4.798*	7.986	0.655	17.54
Error	86	2.621	3.263	0.087	4.591	0.556	1.495	0.405	2.593	2.848	8.224	0.797	10.624
Total	131	3.496	9.219	0.154	15.797	1.17	2.609	1.245	7.382	10.323	20.358	2.31	13.042

Table 2 : Estimates of general combining *(gca)* effects of parents in wheat for twelve yield attributes

Parents	Days to 50% heading	Chlorophyll content	Effective tillers	Plant height (cm)	Spike length	Flag leaf area	Days to maturity	No of grains per spike	1000 seed weight	Grain yield / plant (g)	Biological yield / plant (g)	Harvest index (%)
GS 4055	-1.125 *	-1.425 **	-0.354 ***	-3.736 ***	-0.518 *	-0.816 *	-0.121	-1.418 **	-2.342 ***	-2.464 **	-0.418	0.410
*IC*78737	0.508	-0.875	-0.237 **	-0.775	-0.431 *	0.330	-0.365	0.514	0.149	-0.517	0.160	-0.308
GS4021	-0.475	-0.413	-0.121	1.484 *	0.044	0.444	0.014	0.073	0.656	-0.833	0.242	0.868
HD2864	-0.675	-0.165	0.096	0.236	0.384	-0.125	0.030	0.452	0.255	1.762 *	0.235	-0.961
IC55681	0.342	1.997 ***	0.079	1.846 **	0.315	-0.034	0.125	-0.576	0.017	-0.013	-0.310	0.262
GS5052	1.342 **	1.596 **	0.146	0.446	-0.256	-0.085	-0.033	1.227 *	0.352	-0.692	-0.400	0.167
DBW303	0.558	0.236	0.212 *	-0.409	0.446 *	0.101	0.231	-0.690	-0.476	1.451	0.158	-1.228
GS3043	-0.475	-0.951	0.179 *	0.908	0.015	0.183	0.119	0.417	1.388 **	1.306	0.333	0.792
DBW222	0.633 *	-0.083	-0.062	-0.621	-0.217	0.102	0.115	-0.685	-0.288	0.474	-0.511 **	-1.361 *
HTWYT 43	0.208	0.577	-0.038	0.826*	0.129	-0.136	-0.173	0.283	-0.024	-1.085	0.025	-1.557 **
PBW803	-0.725 *	-0.564	-0.037	0.210	-0.050	-0.204	-0.104	0.331	-0.080	-0.377	0.126	0.314
PBW824	-0.117	0.070	0.137*	-0.415	0.137	0.238	0.162	0.071	0.392	0.988	0.359 *	-0.510

Table 3 : Estimates of specific combining ability (*sca*) effects for crosses in wheat for twelve yield attributes

Crosses	Days to 50 % heading	Chlorophyll content	Effective tillers	Plant height (cm)	Spike length	Flag leaf area	Days to maturity	No of grains per spike	1000 seed weight	Grain yield/ plant (g)	Biological yield / plant (g)	Harvest index (%)
GS4055× DBW222	-0.58	-1.36	0.11	-0.64	-0.88	0.95	-0.06	-3.34 **	-1.01	0.71	0.37	0.68
GS4055× HTWYT 43	-0.03	-0.46	-0.11	-0.62	0.08	-0.18	-0.59	-0.12	-0.42	-2.35	-1.14 *	1.47
GS4055× PBW803	1.71	-0.31	0.09	-1.22	-0.13	-0.09	0.09	1.63	-0.19	2.14	0.25	-2.89
GS4055× PBW824	-1.10	2.13 *	-0.09	2.48 *	0.94 *	-0.68	0.56	1.83 *	1.62	-0.50	0.52	0.74
IC78737×DBW222	0.12	0.99	0.06	0.17	0.39	0.03	-0.08	-0.01	1.07	1.00	0.09	0.41
IC78737×HTWYT 43	-0.06 ns	-2.02 *	-0.10	0.08	-0.27	0.40	0.47	0.08	-0.11	1.01	-0.02	-1.14
IC78737×PBW803	-0.92	1.79	-0.10	0.10	-0.39	0.57	-0.12	0.17	-0.31	-1.35	-0.36	-1.65
IC78737×PBW824	0.87	-0.75	0.13	-0.35	0.27	-0.99	-0.26	-0.24	-0.64	-0.66	0.30	2.38
GS4021×DBW222	1.03	0.06	0.21	0.02	-0.04	0.97	-0.13 ns	0.69	0.61	-1.18	-0.49	1.30
GS4021×HTWYT 43	0.06	0.83	-0.01	0.79	1.21 *	-0.43	0.26	-0.19	-1.93	0.78	0.32	-0.75
GS4021×PBW803	-1.14	0.53	-0.01	1.01	-0.65	-0.07	0.13	-0.10	1.91	0.90	0.73	0.42
GS4021×PBW824	0.05	-1.42	-0.19	-1.82	-0.53	-0.47	-0.26	-0.40	-0.59	-0.49	-0.55	-0.98
HD2864×DBW222	-0.97	-1.52	-0.00	1.96	0.25	-1.35 *	-0.01 ns	0.18	-0.59	-1.33	0.29	3.00
HD2864×HTWYT 43	-0.07	1.87 *	-0.10	-0.06	0.13	0.85	-0.05 ns	-0.23	1.21	0.27	-0.32	-2.43
HD2864×PBW803	0.93	-1.17	0.17	-1.34	-0.31	0.24	0.25 ns	0.56	-0.43	1.03	-0.00	-0.07
HD2864×PBW824	0.12	0.83	-0.07	-0.56	-0.07	0.26	-0.19 ns	-0.51	-0.19	0.04	0.04	-0.50
IC55681×DBW222	-1.32	0.70	-0.25	0.52	0.10	-0.78	-0.02 ns	-0.81	0.07	2.68	-0.08	-3.56
IC55681×HTWYT 43	1.31	-0.59	0.12	1.33	-0.78	-0.41	0.05	0.76	-0.80	-0.23	-0.06	-0.14
IC55681×PBW803	0.71	-0.54	0.05	-0.83	-0.21	0.04	-0.42	0.20	-0.52	-1.91	-0.05	3.18
IC55681×PBW824	-0.70	0.43	0.08	-1.03	0.89	1.15	0.40	-0.14	1.25	-0.54	0.19	0.52
GS5052×DBW222	0.62	1.60	-0.19	-0.83	-0.13	0.22	0.04	-0.02	0.77	-0.72	-0.13	-0.40
GS5052×HTWYT 43	-0.56	1.43	0.12	1.39	-0.24	-0.06	-0.31	-0.50	1.56	-2.23	0.18	4.20 *
GS5052×PBW803	-0.96	-0.17	-0.08	-1.24	0.93	-0.23	0.00	0.23	0.35	1.31	-0.07	-1.98
GS5052×PBW824	0.90	-2.85 **	0.15	0.68	-0.56	0.06	0.27	0.29	-2.68 *	1.63	0.02	-1.82
DBW303×DBW222	1.07	-0.58 ns	-0.12	0.10	0.54	0.33	0.17	1.91 *	-0.55	0.33	0.18	0.12
DBW303 × HTWYT 43	-0.64	-0.74	0.19	-1.33	-0.69	0.07	0.19	1.15	1.31	0.02	0.62	1.80
DBW303×PBW803	-0.11	0.24	-0.08	1.13	0.78	-0.73	-0.13	-1.49	-1.17	-0.25	-0.21	-1.25
DBW303×PBW824	-0.32	1.09	0.01	0.10	-0.63	0.33	-0.23	-1.57	0.42	-0.10	-0.58	-0.67
GS3043×DBW222	0.03	0.12	0.18	-1.30	-0.23	-0.38	0.10	1.42	-0.36	-1.48	-0.22	-1.55
GS3043×HTWYT43	-0.01	-0.30	-0.11	-1.58	0.56	-0.23	-0.01	-0.95	-0.81	2.74	0.43	-3.01
GS3043×PBW803	-0.21	-0.37	-0.05	2.38 *	-0.02	0.28	0.19	-1.20	0.37	-1.88	-0.28	4.24 *
GS3043×PBW824	0.18	0.55	-0.02	0.50	-0.31	0.34	-0.28	0.74	0.81	0.62	0.06	0.32

Combining ability

The analysis of combining ability revealed the presence of both additive and non-additive gene actions governing various yield and yield-related traits in wheat. Among the parents, GS 4055 exhibited significantly negative GCA effects for key traits such as days to 50% heading (-1.125), chlorophyll content (-1.425), plant height (-3.736), spike length (-0.518), and grain yield per plant (-2.464), indicating its potential utility in crosses aiming for earliness and reduced plant stature. In contrast, GS5052 recorded significantly positive GCA effects for early flowering (1.342), chlorophyll content (1.596), and number of grains per spike (1.227), suggesting its role as a promising general combiner for physiological and grain traits. IC55681 was also identified as a good general combiner for chlorophyll content (1.997) and plant height (1.846), while GS3043 showed significant positive effects for 1000-seed weight (1.388) and biological yield, indicating its potential in yield enhancement. The analysis of specific combining ability (*sca*) effects among the wheat hybrids revealed substantial non-additive gene action governing various agronomic and physiological traits. For chlorophyll content, the highest significant positive SCA effect was observed in the cross GS4055 × PBW824 (2.13*), followed by HD2864 × HTWYT43 (1.87*), GS5052 × HTWYT43 (1.43), and GS5052 × DBW222 (1.60), indicating superior photosynthetic efficiency in these combinations. On the other hand, GS5052 × PBW824 (–2.85**) and IC78737 × HTWYT43 (–2.02*) showed significantly negative SCA values, suggesting lower chlorophyll content and potential limitations in photosynthetic performance.

In terms of grain yield per plant, GS4055 × PBW803 (2.14), GS3043 × HTWYT43 (2.74), and GS5052 × PBW824 (1.63) exhibited superior positive SCA effects, suggesting these combinations are promising for yield improvement. GS4021 × PBW803 (0.90) and IC55681 × DBW222 (2.68) also contributed positively to biological yield, while GS3043 × PBW803 (4.24*) and IC55681 × PBW803 (3.18) showed the highest significant SCA effects for harvest index, reflecting better biomass partitioning to economic yield. Conversely, crosses such as GS5052 × HTWYT43 (–2.23) and GS4055 × HTWYT43 (–2.35) exhibited significantly negative SCA effects for grain yield, which could be due to suboptimal hybrid combinations or negative interactions between parental lines. Regarding plant height, positive SCA effects were evident in crosses such as GS4055 × PBW824 (2.48*), HD2864 × DBW222 (1.96), and GS3043 × PBW803 (2.38*), suggesting these combinations may be suitable for improving plant stature and biomass accumulation. In contrast, negative SCA effects were recorded in GS4021 × PBW824 (–1.82) and GS3043 × HTWYT43 (–1.58), which could be advantageous for developing semi-dwarf varieties. For spike length, the cross GS4021 × HTWYT43 (1.21*) and GS4055 × PBW824 (0.94*) were among the top performers, indicating the potential for longer spikes, which may correlate positively with grain number. Similarly, crosses such as HD2864 × PBW803 (0.93) and GS5052 × PBW803 (0.93) also showed enhanced spike length, though not all were statistically significant. SCA effects for number of grains per spike were significantly positive in crosses such as DBW303 × DBW222 (1.91*) and GS3043 × DBW222 (1.42), while GS4055 × DBW222 (–3.34**) and GS3043 × HTWYT43 (–0.95) displayed significant negative SCA values. These results indicate considerable variation in genetic potential for grain number per spike across different cross combinations. Overall, the study highlights the crossesGS4055 × PBW824, GS3043 × PBW803, HD2864 × HTWYT43, and GS5052 × HTWYT43 as promising for multiple traits, while combinations like GS4055 × HTWYT43 and GS5052 × PBW824 showed trait-specific weaknesses. These insights can be utilized in wheat hybrid development programs for selecting superior hybrids based on specific trait combinations and maximizing heterosis. similar findings were also given by Ahmed *et al*.,(2024)

Conclusion

The present investigation on combining ability analysis in wheat revealed significant variation among genotypes for both general combining ability (GCA) and specific combining ability (SCA), indicating the role of both additive and non-additive gene actions in the expression of yield and its component traits. Among the parents, GS5052 was identified as a superior general combiner for early flowering, chlorophyll content, and number of grains per spike; IC55681 for chlorophyll content and plant height; and GS3043 for 1000-seed weight and biological yield, making them valuable for inclusion in hybridization programs aimed at improving physiological efficiency and yield potential.Specific cross combinations also showed remarkable SCA effects for various traits. Notably, GS4055 × PBW824 exhibited significant positive SCA effects for chlorophyll content, plant height, spike length, and number of grains per spike, suggesting its potential to improve physiological and reproductive traits. Similarly, GS3043 × PBW803 recorded significant SCA effects for plant height and harvest index, while GS5052 × HTWYT 43 was superior for harvest index, and DBW303 × HTWYT 43 for 1000-seed weight and number of grains per spike.

These findings underscore the importance of selecting both efficient general combiners and specific cross combinations to enhance earliness, photosynthetic efficiency, plant architecture, and grain yield in wheat breeding programs targeting yield improvement and adaptability under varying environments.

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