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Short Communication

Genetic Analysis of Heterosis and Yield Traits Through Line × Tester Design in Bread Wheat (*Triticum aestivum* L.)

Hetvi G. Butani[1]*, A. G. Pansuriya[2], D. M. Vekaria[3] and Divijkumar R. Vaghasiya[1]

[1]*Research scholar, Dept. of Genetics and Plant breeding, Junagarh Agricultural University, Junagadh-362001, Gujarat, India*
[2]*Directorate of Research and Dean, PG Studies, Junagarh Agricultural University, Junagadh-362001, Gujarat, India*
[3]*Associate Research Scientist, Dept. of Genetics and Plant breeding, Junagarh Agricultural University, Junagadh-362001, Gujarat, India*
[4]*Assistant Research Scientist, Wheat Research Station, Junagarh Agricultural University, Junagadh-362001, Gujarat, India*

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****Corresponding author:*** *E-mail: hetvibutani111@gmail.com*

Wheat is staple food for majority of world's population. Global world population may be more than 9 billion warranting a major increase in the productivity and yield of major cereals including wheat food stability (Li *et al.*, 2020). Moreover, demand for wheat may rise by 50% from its current levels by 2050 (CIMMYT, 2024). Wheat is the major *Rabi* cereal in India and it was cultivated in area of 328.04 Lakh ha with production of 1179.45 Lakh Tonnes and yield of 3595 kg/ha during 2024-25 (Government of India, 2025).Among various states, Gujarat makes a substantial contribution in wheat production with an area, production and productivity of 14.73 lakh hectares, 48.55 lakh tonnes and 3,295 kg per hectare (Government of India, Ministry of Agriculture and Farmers Welfare, 2026). By 2050, India is predicted to have reached its wheat objective of 140 million tonnes due to its growing population and increasing demand (Anonymous, 2015). Heterosis breeding is an effective approach to attain high yields, facilitating the development of cultivars with broader genetic diversity and improved adaptability across diverse agroclimatic regions. Selection of appropriate parents for hybridization understanding inheritance of polygenic traits and to identify promising crosses combining ability studies. In this context, present studies were undertaken with the objective to evaluate the combining ability of selected genotypes to quantify the extent and orientation of heterosis for yield and its contributive traits. The experimental material comprised of 40 elite crosses developed by crossing 8 lines and 5 testers (Table 1) in line × teste mating design along with one standard check (GW 513) collected from Wheat Research Station, Junagadh Agricultural University, Junagadh. Heterosis and Standard heterosis were calculated following Fonseca and Patterson (1968) and Meredith and Bridge (1972), respectively.

During *rabi*, 2025–2026, the 54 entries comprising 13 parents, 40 F_1 crosses and one standard check (GW 513) were grown in RBD with 3 replications as a 2.5 m single row plot with row-to-row spacing 22.5 cm, respectively. The crop was attained following all cultural techniques and plant protection measures (Panse and Sukhatme, 1985; ICAR-AICRP Wheat & Barley Progress Report, 2025–26). The data were recorded for various yield and yield related traits i.e. days to heading (DH), days to anthesis (DA), grain filling period (GFP), days to maturity (DM), plant height(cm) (PH), number of effective tillers per plant (NET), length of main spike (cm) (LMS), number of spikelets per main spike (NSM), number of grains per

Table 1. List of genotypes used for crossing

Sr. No	Genotypes	Pedigree
		Line
1	DBW 166	BH 1146/DBW 16
2	RW 5	AKAW 4924/RW 5
3	RWP 2017-21	NAC/TH.AC//3*PVN/3/MIRLO/BVC/4/2*PASTOR/3/ KACHU/6/KACHU
4	DWAP 1608	HI 1544/GW 2013-513
5	GW 555	HI 1600/ HD 2987
6	GW 554	NIAW 2064/ GW 366
7	HD 2967	ALD/CUC//URES/HD2160M/HD2278
8	DBW 187	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU
		Tester
1	CG 1044	HW2045/LBPY4-2
2	DBW 443	NW 1014/7th HLBSN 21
3	NIAW4114	LO-62/NIAW 1689
4	DBW 110	KIRITATI/4/2*SERI1B*2/3/KAUZ*2/BOW//KAUZ
5	GW 543	WBLL1*2/BRAMBLING//WBLL1*2/BRAMBLING/3/2*BORL14
		Standard check
1	GW 513	PBW559/WR1873

main spike (NGM), 100-grain weight (g) (HGW), Grain yield per plant (g)(GYP), biological yield per plant (g) (BYP) and harvest index (%) (HI).The data analysis is done by using INDOSTAT software programme.

The variance for genotypes was divided into components related to parents, crosses and the comparison between parents and crosses (Table 2). The differences amongst the parents and crosses were significant for all of the test traits. The mean squares due to parents *vs.*crosses contrast were significant for: DH, DA, GFP, NET, NGM and HGW, indicating difference in performance of parents and crosses as a group and as individual. These variations among crosses may be significant due to the genes recombination from diverse parental sources, resulting in a distribution of variability for various traits. This indicated the presence of overall heterosis and the potential for major modifications among crosses and parents regarding these traits.

The analysis of variance revealed that mean squares due to lines were significant across all traits when tested against error mean squares, indicating a substantial contribution of lines to the gca variance components for every trait studied. Traits such as DH, DA, GFP, NSM and HSW were found significant when tested against line × tester interaction mean squares. The mean squares due to testers were significant for all attributes, indicating their good contribution to GCA variance components. The mean squares due to lines exceeded those of testers for all traits (except NET, LMS and HI). Furthermore, line × tester interaction mean squares were significant for all traits (except PH) when tested against error mean squares, revealing their important role in hybrid production.

In the current research, the top 4 crosses *viz.,* RW 5 × CG 1044, HD 2967 × GW 543, GW 555 × DBW 110 and RWP 2017-21 × CG 1044 showed significant heterobeltiosis and standard heterosis for grain yield per plant. These crosses also exhibited desirable heterobeltiosis as well as standard heterosis for grain yield and its associated traits including DH, DA, GFP, DM, PH, NET, LMS, NSM, NGM, HSW, GYP, BYP and HI.

Comparisons between heterobeltiosis and standard heterosis revealed that most of the preferred crosses were DBW 187 × GW 543 for DH(-5.39 and 6.76); DBW 166 × DBW 110 for DA (-11.39 and 9.82); DBW 166 × GW 543 for GFP (-20.00 and -27.27); HD 2967 × CG 1044 for

DM (-4.04 and -3.3); GW 554 × GW 543 for PH (-12.92 and -11.20); RWP 2017-21 × CG 1044 for NET (32.31 and -6.52); RWP 2017-21× CG 1044 for LMS (5.21 and 21.63); GW 555 × DBW 110 for NSM (11.07 and 1.10); GW 555 × DBW 110 for NGM (33.62 and 20.16); GW 555 × DBW 110 for HGW (24.41 and 13.92); RW 5 × CG 1044 for GYP (48.24 and 18.59); GW 555 × NIAW 4114 for BYP (57.24 and 18.35) and RW 5 × CG 1044 for HI (53.32 and 43.37).

The present results are in conformity with the findings of Kalhoro *et al.* (2015), Dedaniya *et al.* (2018), Bhagya Shree. (2021), Kumar *et al.* (2021), Dudhat *et al.* (2022), Dahiya *et al.* (2023), Elwasef *et al.* (2023), Fouad and Mahdy (2023), Fareed *et al.* (2024), Bubuche *et al.* (2025), Jeel *et al.* (2025), Puri *et al.* (2025), Raza *et al.* (2025) and Vikash *et al.* (2025)

For grain yield, heterobeltiosis varied from –29.74% (DBW 166 × CG 1044) to 48.24% (RW 5 × CG 1044). The highest desirable heterobeltiosis was observed in cross RW 5 × CG 1044 (48.24%), followed by HD 2967 × GW 543 (34.76%) and GW 555 × DBW 110 (33.78%). Out of the crosses studied, eleven exhibited significant and positive heterosis over the better parent (Table 4).

The standard heterosis for grain yield per plant ranged from –41.65% (DBW 187 × NIAW 4114) to 18.59% (RW 5 × CG 1044 and HD 2967 × GW 543). The crosses HD 2967 × GW 543 (18.59%), RW 5 × CG 1044 (18.59%), and GW 555 × DBW 110 (13.63%) showed significant positive heterosis over the check. In all, four crosses demonstrated desirable standard heterosis for this attribute (Table 4). Comparisons of standard heterotic crosses and their performance for grain yield per plant relative to other yield contributing traits. It was evident that the significant, high and desirable heterosis for grain yield per plant in these crosses was not associated with any specific trait. Moreover, these crosses also exhibited positive desirable heterosis for several yieldcontributing component traits.

Five crosses *viz.*,RW 5 × CG 1044, HD 2967 × GW 543, GW 555 × DBW 110, RWP 2017-21 × CG 1044 and RWP 2017-21 × DBW 443 showed significant heterobeltiosis and standard heterosis for grain yield per plant (except in RWP 2017-21 × DBW 443 and RWP 2017-21 × CG 1044 for standard heterosis). These crosses also exhibited desirable heterobeltiosis as well as standard heterosis for grain yield and its associated traits, including heading time, flowering time, grain filling duration, maturity period, plant stature, productive tiller count, spike length, spikelet number, grain count per spike, test weight, perplant yield, biological yield and harvest index.

The evaluation of heterotic crosses revealed several combinations with superior grain yield and desirable associated traits. Among them, RW 5 × CG 1044 and HD 2967 × GW 543 produced the highest grain yield per plant (16.80 g), exhibiting significant positive heterosis over both the standard check and their respective better parents. These crosses also showed improvements in key traits such as GFP, NET, HI and BYP, indicating their potential for yield enhancement. The cross GW 555 × DBW 110 recorded a grain yield of 16.10 g per plant, with notable heterosis for PH, NGP, HGW and BYP, suggesting its usefulness in improving spike architecture and grain productivity. Moderate yields were observed in RWP 201721 × CG 1044 (15.53 g) and RWP 201721 × DBW 443 (14.97 g), yet both displayed significant heterotic effects for specific traits such as PH, NGP, NET and BYP. Overall, the results highlight that certain crosses not only enhanced grain yield but also contributed positively to multiple yield attributing traits, underscoring their importance for future wheat improvement programs.

The graphical analysis of heterobeltiosis (%) for grain yield per plant revealed wide variation among the evaluated crosses. Certain combinations such as RW 5 × CG 1044 (48.24) and HD 2967 × DBW 1443 (34.76) expressed high positive heterobeltiosis, indicating their superiority over the better parent in terms of yield potential. In contrast, some crosses showed negative heterobeltiosis, reflecting reduced performance compared to the better parent, which is expected in genetic studies where not all combinations result in favourable heterotic effects. This variation highlights the importance of specific parental combinations in exploiting heterosis for yield improvement.

Similarly, the graphical analysis of standard heterosis (%) for grain yield per plant demonstrated fluctuations across different crosses when compared with the standard check variety. Positive standard heterosis was observed in crosses such as RW 5 × CG 1044 (18.59), HD 2967 × DBW 1443 (18.59) and GW 555 × DBW 110 (13.63), suggesting their potential to outperform the check in practical cultivation. On the other hand, several crosses exhibited negative standard heterosis, indicating lower yield relative to the

Table 2. Analysis of variance (mean squares) for grain yield and its contributing traits in the test wheat genotypes

Source of variation	d.f.	Days to heading	Days to anthesis	Days to maturity	Grain filling period	Plant height (cm)	Number of effective tillers per plant	Length of main spike (cm)	Number of spikelets per main spike	Number of grains per main spike	100-grain weight	Grain yield per plant (g)	Biological yield per plant (g)	Harvest index
Replications	2	0.03	1.53	0.65	0.27	18.88	0.91	0.24	2.03	8.33	0.04	1.54	10.30*	49.58 *
Genotypes	52	25.25**	25.31**	21.56**	14.34**	43.73*	3.97**	1.88**	2.13**	84.81**	0.40**	14.11**	100.43 **	99.91**
Parents	12	40.32**	38.75**	33.29**	17.95**	68.46**	5.50**	4.23**	3.16**	89.88**	0.41**	4.96**	69.16**	68.34**
Crosses	39	20.25**	19.39**	18.44**	32.60**	36.92**	3.46**	1.20**	1.86**	82.76*	0.37**	17.24**	112.38**	112.12**
Parents *vs* Crosses	1	39.41**	95.03**	2.58	58.91**	12.63	5.76**	0.02	0.35	104.26**	1.48**	1.89	9.23	2.66
Error	104	1.51	0.94	1.07	2.51	15.73	0.69	0.23	0.67	3.71	0.12	0.68	3.26	11.76

Table 3. Per cent heterosis over better parent (H_1) and standard check (H_2) for DH, DA, GFP, DM, PH, NET, LMS and NSM

Sr. No.	Crosses	DH		DA		GFP		DM		PH		NET		LMS		NSM	
		H_1	H_2	H_1	H_2	H_1	H_2	H_1	H_2	H_1	H_2	H_1	H_2	H_1	H_2	H_1	H_2
1	RW 5 × CG 1044	-9.25**	6.08**	-7.98**	6.13**	1.69	-9.09**	2.09*	-0.68	-2.20	-1.15	27.69**	-9.78	-15.03**	-1.77	-7.21	-8.06*
2	HD 2967 × GW 543	6.83**	16.22**	6.25**	14.72**	0.83	-7.58*	4.04**	4.75**	-4.79	-1.07	15.38*	-10.33	-7.32*	3.19	1.28	1.65
3	GW 555 × DBW 110	-2.52	4.73*	-2.26	6.13**	-1.46	2.27	2.67**	4.41**	-11.81**	-13.92**	23.63**	-1.90	9.23*	0.71	11.07**	1.10
4	RWP-2017-21 × CG 1044	1.16	18.24**	1.06	16.56**	-6.31	-21.21**	2.44**	-0.34	0.53	1.61	32.31**	-6.52	5.21	21.63**	-3.96	-2.20
5	RWP-2017-21 × DBW 443	6.25**	14.86**	6.32**	13.50**	6.31	-10.61**	6.32**	2.71**	-5.72	-3.01	31.71**	-11.96*	-9.62*	-6.74	-8.63*	-6.96
6	DWAP 1608 × GW 543	9.55**	16.22**	6.25**	14.72**	-19.51**	-25.00**	-3.38**	-3.05**	-1.91	-0.49	15.38*	-10.33	-8.50*	-4.61	-6.42	-9.16*
7	HD 2967 × CG 1044	-0.58	16.22**	-0.53	14.72**	-19.01**	-25.76**	-4.04**	-3.39**	-12.72**	-9.30*	16.15*	-17.93**	-12.88**	0.71	2.74	3.11
8	GW 554 × DBW 443	-1.27	5.41**	0.01	6.75**	-6.30*	-9.85**	-1.01	-0.68	-10.76**	-8.19*	19.35*	-19.57**	-1.03	2.13	-5.12	-8.42*

9	GW 555 × NIAW 4114	-1.89	5.41**	0.58	6.75**	0.01	3.79	3.67**	5.42**	-1.62	-5.15	-9.51	-14.67**	-2.67	-9.57**	-2.87	-13.19**
10	RWP-2017-21 × NIAW 4114	0.62	8.78**	1.15	7.98**	9.82**	-6.82*	4.91**	1.36	4.18	0.45	-6.63	-11.96*	8.66*	6.74	-8.81*	-7.14
Range of heterosis		-12.22 to 10.76	3.38 to 22.30	-11.39 to 9.20	3.07 to 20.86	-24.48 to 9.82	-27.27 to 3.79	-8.60 to 6.32	-3.39 to 5.42	-12.92 to 4.18	-13.92 to 4.24	-27.95 to 32.31	-37.50 to -1.90	-26.16 to 13.46	-9.57 to 21.63	-12.84 to 11.07	-13.19 to 3.11
No. of crosses with significant and desirable heterosis		13	0	13	0	22	36	18	15	11	8	9	0	6	5	2	0

Table 4. Per cent heterosis over better parent (H_1) and standard check (H_2) for NGM, HGW, GYP, BYP and HI

Sr. No.	Crosses	NGM		HGW		GYP		BYP		HI	
		H_1	H_2	H_1	H_2	H_1	H_2	H_1	H_2	H_1	H_2
1	RW 5 × CG 1044	-21.90**	-17.05**	2.06	2.31	48.24**	18.59**	-6.97	-17.20**	53.32**	43.37**
2	HD 2967 × GW 543	2.65	-10.08**	8.47	11.13	34.76**	18.59**	0.01	10.20**	-4.17	7.75
3	GW 555 × DBW 110	33.62**	20.16**	24.41**	13.92*	33.78**	13.63**	30.13**	12.94**	-3.25	0.68
4	RWP-2017-21 × CG 1044	39.00**	7.75*	-4.89	-4.66	32.39**	9.65*	17.84**	0.29	8.10	9.57
5	RWP-2017-21 × DBW 443	-15.63**	-16.28**	4.42	1.53	27.56**	5.65	6.51	-5.76	10.49	11.99
6	DWAP 1608 × GW 543	25.49**	-0.78	26.46**	4.66	18.45**	4.24	-7.16*	2.30	27.14**	1.92
7	HD 2967 × CG 1044	5.31	-7.75*	3.30	5.84	30.18**	3.53	-6.67	-20.57**	16.03*	30.45**
8	GW 554 × DBW 443	1.56	0.78	2.91	6.26	22.95**	2.12	37.27**	21.45**	-27.05**	-15.77*
9	GW 555 × NIAW 4114	-24.63**	-21.71--	3.61	-5.11	11.43*	-8.24	57.24**	18.35**	-29.10**	-22.42**
10	RWP-2017-21 × NIAW 4114	-28.36**	-25.58**	14.99*	-1.29	11.36*	-7.76	2.60	-16.13**	0.78	10.27
Range of heterosis		-32.79 to 52.04	-36.43 to 20.16	-32.27 to 26.46	-32.11 to 13.92	-29.74 to 48.24	-41.65 to 18.59	-47.47 to 57.24	-43.09 to 21.45	-38.82 to 53.32	-33.05 to 43.37
No. of crosses with significant and desirable heterosis		9	4	5	1	11	4	7	6	5	5

number of grains per main spike (NGM), 100-grain weight (g) (HGW), Grain yield per plant (g)(GYP), biological yield per plant (g) (BYP) and harvest index (%) (HI).

check. Together, these results emphasize that while some crosses hold promise for enhancing grain yield through heterosis, others may not be suitable for direct utilization, thereby guiding breeders toward the most effective parental combinations for wheat improvement.

Conclusion

The analysis of variance revealed significant differences among genotypes for all studied traits, confirming substantial genetic variability among parents. Traits such as DH, DA, GFP, NET, NGM and HGW showed highly significant mean squares for parents, crosses and their interactions, highlighting the genetic basis of inheritance and heterosis expression. Desirable heterobeltiosis was observed for grain yield per plant, ranging from –29.74% to 48.24%, with RW 5 × CG 1044 (62.72%) recording the highest value, followed by HD 2967 × GW 543 (34.76%) and GW 555 × DBW 110 (33.78%). Crosses also exhibited significant heterobeltiosis for yield-contributing traits including PH, LMS, NSM, BYP and HI. Standard heterosis estimates for grain yield ranged from –41.65% to 18.59%, with HD 2967 × GW 543 and RW 5 × CG 1044 showing the highest positive values (18.59%), followed by GW 555 × DBW 110 (13.63%). These crosses also displayed significant standard heterosis for DM, NET, LMS and GYP. Notably, high heterotic crosses also demonstrated superior mean performance, suggesting that selection based on either heterotic effects or mean yield performance would be equally effective.

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Author contributions

Conceptualization of research (Hetvi G. Butani and A. G. Pansuriya); Designing of the experiments (Hetvi G. Butani, A. G. Pansuriya and D. M. Vekaria); Contribution of experimental materials (Hetvi G. Butani, A. G. Pansuriya, M. H. Sapovadiyaand D. M. Vekaria); Execution of field/lab experiments and data collection (Hetvi G. Butani, Divijkumar R. Vaghasiya); Analysis of data and interpretation (Hetvi G. Butani, A. G. Pansuriya); Preparation of the manuscript (Hetvi G. Butani, A. G. Pansuriya, D. M. Vekaria and Divijkumar R. Vaghasiya).

Conflict of interest statement

The authors declare that there is no conflict of interest

Ethical Approval

The article doesn't contain any study involving ethical approval.

Use of Generative AI or AI assisted technologies

No

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