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Research Article

Assessment of genetic components and heterotic potential for panicle and yield related traits in rice (*Oryza sativa* L.)

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Abstract
Rice (*Oryza sativa* L.) is the staple food crop and it is cultivated under diverse ecological conditions. Understanding genetic effects and identifying superior hybrids are important steps in rice breeding to enhance yield. Six parents with varying numbers of grains per panicle were subjected to full diallel mating. Hayman's graphical approach was applied to compute various genetic parameters and better parental, mid parental and standard heterosis for panicle and yield related traits. The results revealed that, grain yield per plant and panicle related traits were governed by both additive and non-additive effects but the additive component was predominant for the number of filled grains per panicle and non-additive for grain yield per plant. The number of spikelets per panicle, the number of filled grains per panicle and the number of primary branches per panicle were mainly governed by recessive alleles present in the parents. The overdominance effect was found in the number of productive tillers, flag leaf area, panicle length, the number of primary branches per panicle, length of primary branches, thousand grain weight and grain yield per plant. The Vr-Wr graph depicted that the number of spikelets per panicle, the number of filled grains per panicle and the number of secondary branches per panicle were governed by partial dominance and grain yield per plant had over dominance effect and the low grain number parents, IET 28835 and ADT (R) 48 possessed more number of dominant alleles than other parents for all these traits. The promising cross combination BPT 5204 × CB12132 and its reciprocal hybrid exhibited high mid parental and standard heterosis for important panicle traits were adjudged as promising hybrids.

Keywords: Rice, diallel analysis, number of filled grains per panicle, heterosis

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important food crop in the world that directly feeds more than half of the world's population. It is the staple food in many countries and it occupies around twenty per cent of land area under cereal cultivation. The well-diversified nature of the crop makes it cultivable under wider ecological conditions. Due to the proliferating rate of population growth, it is required to feed globally 9 billion people by 2050. Therefore, the

first and foremost objective of rice breeders is to increase production thereby meeting the needs of the ever-increasing population (Hussain *et al*., 2022). The grain yield in rice depends on three major traits *viz.,* the number of panicles per plant, the number of grains per panicle and grain weight. Among these, the number of grains per panicle is the major contributor to yield which is in turn determined by panicle related traits *viz.,* the number of primary and secondary rachis, length of primary and secondary rachis *etc* (Mohapatra and Sahu, 2022).

Improvement of a trait value in rice breeding needs a proper understanding about various genetic parameters of targeted traits and the nature of inheritance of the traits. Hayman's diallel analysis provides all the valuable genetic information *viz.,* additive and dominance variances, over dominance effect, the proportion of dominant and recessive alleles in parents, group of genes governing a trait, heritability and presents graphical visualization using variance-covariance (Vr-Wr) graph. Hayman's diallel analysis was previously applied for yield related traits (Satheeshkumar *et al*., 2021), flag leaf characters (Bassuony and Zsembeli, 2021), biotic stress tolerance (Gunasekaran *et al.,* 2020), rice quality parameters (Bano and Singh, 2019; Hasanalideh *et al*., 2019) and salinity tolerance (Souleymane *et al*., 2017) in rice. Grain number per panicle and other panicle and yield related traits need more valuation using Hayman's diallel approach for understanding about the influence of various genetic parameters which will in turn increase the grain yield. To improve grain production in rice, breeding techniques like hybridization, selection, marker-assisted pyramiding of yield-related genes and heterosis breeding are employed. Utilizing heterosis is one of these effective methods, and research shows that hybrid rice varieties can increase yields by 15 to 30% compared to inbred varieties. (Gramaje *et al*., 2020).

The dominant gene effects play a major role in the determination of heterosis in hybrids. Previous reports revealed that the number of filled grains per panicle and panicle branching characters is governed by both additive (Kour *et al*., 2019) and non-additive gene effects (Paranthaman *et al*., 2019, Ananda Lekshmi *et al*., 2020; Kumar *et al*., 2020 and Buelah *et al*., 2021). The superior hybrids and parental combinations can be identified using standard heterosis, better parent and mid parental heterosis in diallel analysis. These superior hybrids and parental combinations could be utilized in heterosis breeding for the enhancement of grain yield in rice as reported by Huang *et al*. (2015), Sreewongchai *et al*. (2021) and Abd El-Aty *et al*. (2022). The present study attempted to assess the various gene effects that determine panicle and yield related traits and heterotic analysis for choosing of most appropriate breeding methods and identifying the promising hybrids. The information derived from this study would be useful for grain yield improvement in rice breeding.

MATERIALS AND METHODS

The six parents *viz.,* IET 28834 (low), IET 28835 (low), ADT (R) 48 (medium), BPT 5204 (medium), CB12132 (high) and IET 28749 (high) were selected for the full diallel mating design based on the number of filled grains per panicle. Genetically pure seeds were obtained and the experiment was conducted at Paddy Breeding Station, Department of Rice, TNAU, Coimbatore. Employing six parents in the full diallel mating design, 30 hybrids were developed. The six parents and 30 hybrids were evaluated in Randomized Block Design (RBD) in two replications during *kharif 2020* and the variety CO (R) 50 was used as the standard check. Standard agronomical practices were followed during the entire crop growth period. At the time of anthesis, the primary panicle of five plants in each replication were tagged and collected at the physiological maturity period for recording the observations *viz*., plant height (PH), the number of productive tillers (NPT), flag leaf area (FLA), panicle length (PL), the number of spikelets per panicle (NOSPP), the number of filled grains per panicle (NFGPP), the number of primary branches per panicle (NOPB), the number of secondary branches per panicle (NOSB), the number of secondary branches per primary branch (NOSBPB), the number of spikelets in primary branches (NOSIPB), the number of spikelets in secondary branches (NOSISB), length of primary branch (LOPB), thousand grains weight (TGW) and grain yield per plant (GYP). The collected mean data were subjected to Hayman's diallel analysis and heterosis analysis. The mid parental heterosis, better parental heterosis and standard heterosis were calculated using the following formula:

$$\text{BH (\%)} = \frac{\overline{F1} - \overline{BP}}{\overline{BP}} \times 100$$

$$\text{MH (\%)} = \frac{\overline{F1} - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{SH (\%)} = \frac{\overline{F1} - \overline{SP}}{\overline{SP}} \times 100$$

Where, BH- better parent heterosis (%), MH – Mid parental heterosis (%), SH – standard parent heterosis, $\overline{F}_1$ - mean value of hybrid, $\overline{MP}$ – average performance of parent 1 and 2, $\overline{BP}$ - meanvalue of the better parent, $\overline{SP}$ – standard parental value.

Analysis of Variance (ANOVA) for Hayman's diallel analysis and randomized block design (RBD) was calculated at a 5 % level of significance. The Hayman's diallel analysis and Vr-Wr graph were formed using the package "Diallel Analysis R" by R software version 4.2.0. The estimation of heterosis was done through the TNAUSTAT (Manivannan, 2014) statistical packages.

RESULTS AND DISCUSSION

Hayman's analysis of variance explained that the mean square value of both additive and non-additive components were significant for all the studied fourteen traits. The mean of dominance (b1) for nine traits, dominance determined by symmetrical distribution (b2) for eleven traits and residual dominance (b3) for all the traits were found significant. The maternal effect was significant for plant height, the number of primary branches per panicle, the number of secondary branches per primary branch, thousand grain weight and grain yield per plant (**Table 1**).

Various genetic components observed for the fourteen traits showed that the additive component value (D) was significant for all the traits except for the number of productive tillers (**Table 2**). The first dominance component (H_1) was observed to be significant in all the studied traits except flag leaf area, the number of secondary branches per primary branch and the number of spikelets in secondary branches and the second dominance component (H_2) showed significance for all the studied traits except flag leaf area. The magnitude of additive component (D) was higher than non-additive components (H_1 and H_2) in seven traits *viz.,* plant height, the number of spikelets per panicle, the number of filled grains per panicle, the number of secondary branches per panicle, the number of secondary branches per primary branch, the number of spikelets in primary branches and the number of spikelets in secondary branches. This emphasized the predominance of additive gene effect for the number of filled grains per panicle and other panicle traits. The traits with more additive components can be fixed in the early generation. The previous studies made by Bassuony and Zsembeli (2021) and Gunasekaran *et al*. (2020) supported the results on the role of both additive and non-additive genetic components essential for determining the number of filled grains per panicle.

The negative F value and lesser than one of $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}- F$ were observed in flag leaf area, the number of spikelets per panicle, the number of filled grains per panicle, the number of spikelets in primary branches, length of primary branches and thousand grain weight indicating that these traits were mainly controlled by a higher number of recessive genes. Kamboj *et al*. (2018) observed similar results of importance of many recessive genes on controlling grains per panicle in rice.

The amount of dominance effects revealed by $(H_1/D)^{1/2}$ was more than one for the number of productive tillers, flag leaf area, panicle length, the number of primary branches per panicle, length of primary branches, thousand grain weight and grain yield per plant confirming the presence of overdominance. Kamboj *et al.* (2018) and Bassuony and Zsembeli (2021) also reported overdominance for the above studied traits. The $H_2/4H_1$ value was recorded closer to 0.25 for flag leaf area

Table 1. ANOVA for 14 panicle and yield related traits of rice by Hayman's method

Source of variation	DF	PH	NPT	FLA	PL	NOSPP	NFGPP	NOPB	NOSB	NOSBPB	NOSIPB	NOSISB	LOPB	TGW	GYP
Replication	2	8	0.03	0.3	0.2123	5373	6815.	10.76.	113.4	0.009	8	5350.	0.3	0.16	9.3
Treatment	35	259**	20.66**	39.1**	0.2652**	27462**	24995**	21.78**	718.2**	1.35**	478**	22803**	4.65**	29.95**	67.8**
Additive	5	1510**	60.66**	173.8**	1.4376**	147116**	133984**	102**	4241.6**	7.771**	2515**	117269**	22.78**	169.73**	192.2**
Non-Additive	15	44293**	973.8**	3634.1**	11.3076**	299135**	275657**	887.04**	7809.5**	34.248**	21326**	172826**	495.74**	1868.32**	2157.8**
b1	1	74*	0.16	8.8	0.1517*	12473*	12990*	0.31	26.1	0.013	290*	16380**	3.87*	25.49**	207.7**
b2	5	129**	35.39**	40**	0.0392	8905**	7506*	22.01**	109.1.	0.169	164*	7901**	2.68**	8.18**	38.3**
b3	9	73741**	1603.32**	6033.6**	18.8073**	492225**	453815**	1466.13**	12952.3**	56.985**	35420**	281834**	824.32**	3106.49**	3552**
Maternal	5	38*	3.95	2.4	0.0195	3689	2880	13.43**	91.3	0.47*	148.	2977	1.35.	1.19*	32.3**
Reciprocal	10	66**	8.75	12.1	0.0411.	6478**	6198*	11.04**	156.7**	0.656**	261**	6966**	2.95**	2.84**	72.3**
Error	70	12	7.52	7.9	0.0221	1984	2216	3.04	52.1	0.15	60	1640	0.63	0.39	6.7

(DF- Degrees of freedom, *, ** and *** indicates significance at 5 %, 1 % and 0.1 % level)

PH : Plant height, NPT : Number of productive tillers, FLA : Flag leaf area, PL : Panicle length, NOSPP ; Number of spikelets per panicle, NFGPP : Number of filled grains per panicle ,NOPB:Number of primary branches per panicle, the number of secondary branches per panicle (NOSB), NOSBPB: Number of secondary branches per primary branch, NOSIPB: Number of spikelets in primary branches, NOSISB: Number of spikelets in secondary branches , LOPB: Length of primary branch, TGW: Thousand grains weight and GYP : Grain yield per plant

Table 2. Genetic components and genetic ratio for 14 panicle and yield related traits in rice

Components	PH	NPT	FLA	PL	NOSPP	NFGPP	NOPB
D	225.8351 ± 10.7965 **	2.1608 ± 1.3588	93.594± 48.1759*	17.8226 ± 4.3658**	21690.6895 ± 1261.5527**	19967.3848 ± 1210.6810 *	13.2947 ± 1.5803 *
F	15.0870 ± 26.3759	2.6269 ± 10.6485	-123.981± 117.6939	13.4123 ± 10.6656	-206.6147 ± 3081.9746	-251.7533 ± 2957.6951	3.0871 ± 3.8606
H_1	99.8067 ± 27.4080*	26.4523 ± 11.0652**	199.09± 122.299	27.1222 ± 11.0830**	12463.6475 ± 3202.5664 **	10492.6514 ± 3073.4241 *	13.8800 ± 4.0116 *
H_2	60.8236 ± 24.4842**	17.0959 ± 9.8848**	161.211± 109.2528	18.6404 ± 9.9007*	10187.9453 ± 2860.9326 **	8771.8291 ± 2745.5667*	7.6301 ± 3.5837 *
h^2	17.3175 ± 16.4795	-1.9888 ± 6.6531	-5.405± 73.5343	2.8831 ± 6.6638	2887.4390 ± 1925.5966	2957.2512 ± 1847.9475	-0.8199 ± 2.4121
E	5.9566 ± 4.0807	3.6580 ± 1.6475	12.471± 18.2088	1.4613 ± 1.6501	1038.9445 ± 476.8221	1171.9565 ± 457.5945	1.6295 ± 0.5973
$(H_1/D)^{1/2}$	0.6648	3.4989	1.459	1.2336	0.7580	0.7249	1.0218
$H_2/4_H1$	0.1524	0.1616	0.202	0.1718	0.2044	0.2090	0.1374
$(4DH_1)^{1/2}$+F/ $(4DH_1)^{1/2}$- F	1.1058	1.4205	0.375	1.8778	0.9875	0.9828	1.2564
h^2/H_2	0.2847	-0.1163	-0.034	0.1547	0.2834	0.3371	-0.1075
Heritability (%) NS	80.48	39.18	49.00	26.29	83.78	84.96	62.23
Components	**NOSB**	**NOSBPPB**	**NOSIPB**	**NOSISB**	**LOPB**	**TGW**	**GYP**
D	680.4407 ± 23.6776 *	1.5145 ± 0.0551**	329.5646 ± 24.3020**	17519.341 ± 1318.6355**	1.9985 ± 0.1946 **	13.898± 2.3771**	43.4423 ± 7.0450 **
F	0.9169 ± 57.8444	0.2514 ± 0.1346	-44.7425 ± 59.3699	317.9049 ± 3221.4280	-1.0090 ± 0.4753	-11.728± 5.8073**	23.0406 ± 17.2110
H_1	159.1130 ± 60.1078 *	0.1237 ± 0.1399	141.5396 ± 61.6929**	11610.4170 ± 3347.4763	2.1251 ± 0.4939**	14.365± 6.0345**	68.2531 ± 17.8844**
H_2	140.6774 ± 53.6958 *	0.1159 ± 0.1250**	106.4948 ± 55.1118**	9557.5527 ± 2990.3843**	1.4386 ± 0.4412**	11.767± 5.3908*	57.7524 ± 15.9766**
h_2	-7.6822 ± 36.1408	-0.0369 ± 0.0841	64.0989 ± 37.0939	4065.9397 ± 2012.7260	0.9040 ± 0.2970**	6.974± 3.6283	55.8081 ± 10.7533**
E	26.9014 ± 8.9493	0.0730 ± 0.0208	29.3889 ± 9.1853	871.4219 ± 498.3974	0.3093 ± 0.0735	0.193± 0.8985	3.3993 ± 2.6628
$(H_1/D)1/2$	0.4836	0.2858	0.6553	0.8141	1.0312	1.017	1.2534
$H_2/4H_1$	0.2210	0.2343	0.1881	0.2058	0.1692	0.205	0.2115
$(4DH_1)1/2$+F/ $(4DH_1)1/2$- F	1.0028	1.8184	0.8123	1.0225	0.6067	0.413	1.5367
$h2/H_2$	-0.0546	-0.3184	0.6019	0.4254	0.6284	0.593	0.9663
Heritability (%) NS	90.63	89.71	78.05	84.22	82.07	65.00	29.19

Where D - additive genetic variance, F- product of additive and dominant alleles, H_1, H_2 and h^2 dominant variance, E – environmental variance, $(H_1/D)1/2$ – degree of dominance, $H_2/4H_1$ – balance of positive and negative alleles, h^2/H_2 – number of effective factors, $(4DH_1)^{1/2}$+F/ $(4DH_1)^{1/2}$- F – proportion of dominant to recessive alleles.

PH : Plant height, NPT : Number of productive tillers, FLA : Flag leaf area, PL : Panicle length, NOSPP ; Number of spikelets per panicle, NFGPP : Number of filled grains per panicle ,NOPB:Number of primary branches per panicle, the number of secondary branches per panicle (NOSB), NOSBPB: Number of secondary branches per primary branch , NOSIPB: Number of spikelets in primary branches, NOSISB: Number of spikelets in secondary branches , LOPB: Length of primary branch, TGW: Thousand grains weight and GYP : Grain yield per plant

(0.202), the number of spikelets per panicle (0.2044), the number of filled grains per panicle (0.2090), the number of secondary branches per panicle (0.2210), the number of secondary branches per primary branch (0.2343), the number of spikelets in secondary branches (0.2058), thousand grain weight (0.205) and grain yield per plant (0.215) revealing the symmetrical distribution of genes on parents and rest of the traits recorded higher deviation from 0.25 ensuring asymmetrical distribution of recessive and dominant genes in parents (**Table 2**). Both symmetrical and asymmetrical distribution of genes present in the parents for the number of filled grain, the number per panicle and other yield related traits have been reported previously by Gunasekaran *et al.* (2020), Ashfaq *et al*. (2012) and Bassuony and Zsembeli (2021). The high narrow sense heritability (> 60 %) recorded

in plant height (80.48 %), the number of spikelets per panicle (83.78 %), the number of filled grain per panicle (84.96 %), the number of primary branches (62.23 %), the number of secondary branches per panicle (90.63 %), the number of secondary branches per primary branch (89.71 %), the number of spikelets in primary branches (78.05 %), the number of spikelets in secondary branches (84.22 %), length of primary branch (82.07 %) and thousand grain weight (65 %). This indicated the most of the panicle traits exhibited high heritability and showed that a high fraction of additive gene action and the selection will be rewarded on these traits efficiently. The other traits recorded low heritability values *viz.,* the number of productive tillers (39.18 %), flag leaf area (49 %), panicle length (26.29 %), and grain yield per plant (29.19 %) which may be due to a high fraction of non-additive components and this suggested that in segregated generations, selection may be less effective. As a result, advanced generations of recurrent and pedigree selection may be recommended for improving these low heritable traits. The similar low and high heritability of panicle and yield related traits were observed by Gunasekaran *et al.* (2020), Haghighi *et al.* (2017) and Bassuony and Zsembeli (2021).

The Vr-Wr graph showed that, for the number of spikelets per panicle, the number of filled grains per panicle and the number of secondary branches per panicle, the regression line passed above the origin, proving that these traits were governed by partial dominance and for grain yield per plant the regression line passed below the origin showed the existence of over dominance effect (**Fig. 1**). The parents IET 28834, IET 28835 and ADT (R) 48 plotted near the origin for a number of spikelets per panicle, the number of filled grains per panicle and the number of secondary branches per panicle indicated that it had a higher proportion of dominant alleles, whereas, the parents BPT 5204, CB12132 and IET 28749 plotted farthest from the origin exhibiting the higher proportion of recessive alleles present in these parents. In the case of grain yield per plant, IET 28835 and ADT (R) 48 plotted near the origin indicated a higher number of dominant alleles and IET 28749 and IET 28834 plotted farthest from origin showed the presence of higher number of recessive alleles in the parents. This finding was supported by Ashfaq *et al*. (2012), Priyanka and Jaiswal (2017) and Satheeshkumar *et al.* (2021).

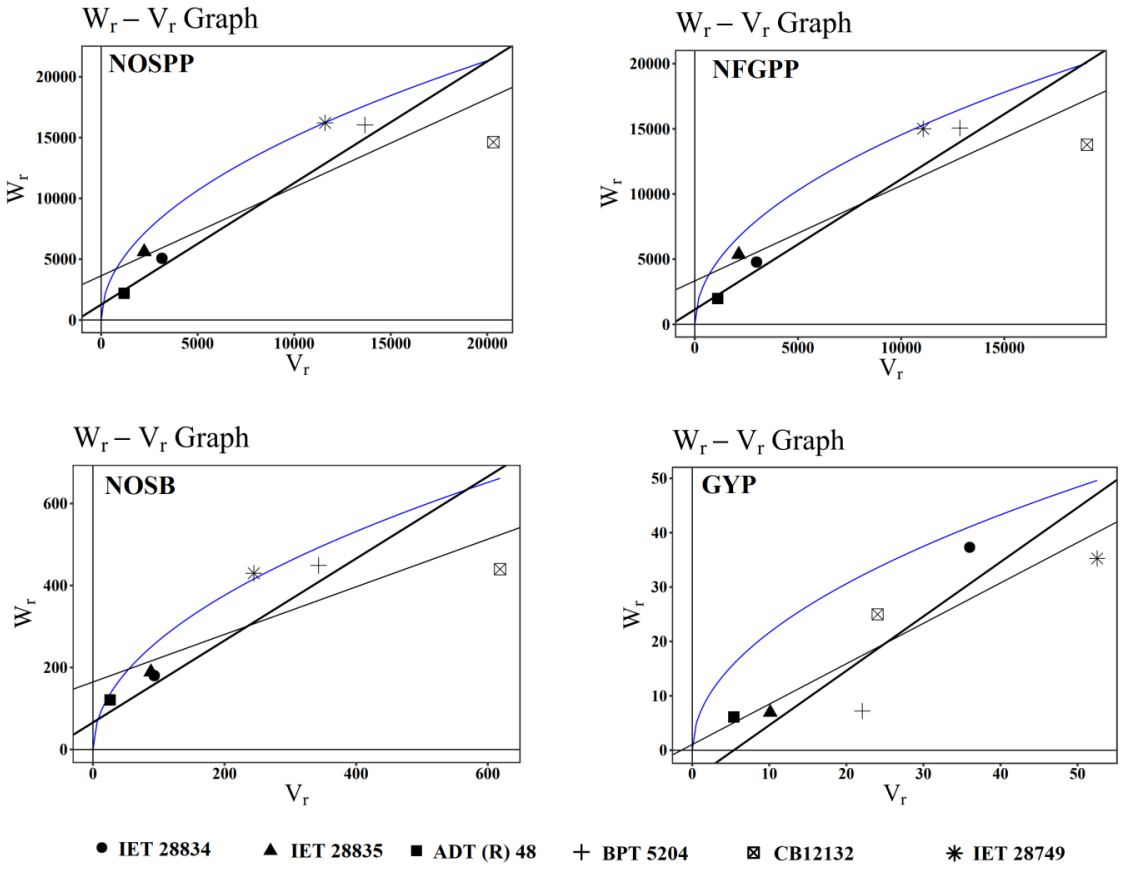

Fig. 1. Vr – Wr graph for number of spikelets per panicle, number of filled grains per panicle, number of secondary branches per panicle and grain yield per plant
(IET28834, 2- IET28835, 3- ADT (R) 48, 4- BPT 5204, 5 – CB12132, 6- IET28749)

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Table 3. Mid parental heterosis of 30 hybrids for 14 panicle and yield related traits in rice

Hybrids	PH	NPT	FLA	PL	NOSPP	NFGPP	NOPB	NOSB	NOSBPB	NOSIPB	NOSISB	LOPB	TGW	GYP
IET 28834 × IET 28835	3.41	-27.66	-18.97	2.18 **	50.75	49.62	33.62	58.63	19.83	45.98	54.87	3.55	4.66**	-10.60
IET 28834 × ADT (R) 48	1.00	59.14	-14.76	0.60	-29.75	-31.13	-13.95	23.53	39.55	4.22	-45.80	-8.33	9.24**	-16.40
IET 28834 × BPT 5204	7.34	42.86 *	-11.85	3.54	26.87	27.13	75.56 **	23.21	-19.27	42.62 **	17.84	12.60	10.99**	3.92
IET 28834 × CB12132	-4.52	23.40	-34.71**	-6.98	-43.05 **	-42.51 **	-5.66	-39.72 *	-27.07	1.17	-57.31 **	-0.23	14.21**	27.69 **
IET 28834 × IET 28749	5.99 *	-5.26	-14.71	8.45	-13.07	-13.56	22.22	2.36	-5.41	30.59 *	-22.99	8.59	22.18**	11.94
IET 28835 × IET 28834	-11.19	-31.91	-5.11	-69.34 **	20.65	19.18	9.08	36.64	25.90	5.73	33.54	0.44	12.63**	-10.84
IET 28835 × ADT (R) 48	1.05	-4.27	-7.01	7.96	-41.51	-41.80	-22.14	-16.48	3.52	-7.15	-60.22	-13.47	13.33**	-30.47 **
IET 28835 × BPT 5204	7.67	0.87	-12.34	-4.52	0.42	-1.29	20.43	-13.93	-24.70	24.24	-18.22	30.38 *	13.25**	-24.46
IET 28835 × CB12132	-6.63	-28.81	-21	-7.43	-40.56 *	-40.40 *	-6.84	-42.76 **	-30.85 *	-5.06	-54.26 **	18.51	17.89**	-8.78 **
IET 28835 × IET 28749	7.86 **	-39.50	-5.68	22.67 **	-18.56	-17.71	4.26	2.45	7.59	24.14 *	-14.56	3.64	19.41**	-37.40 **
ADT (R) 48 × IET 28834	-1.00	22.58	-13.75	7.23	-25.02	-25.49	-11.63	9.80	20.08	22.29	-64.24	-16.67	6.87**	-33.37
ADT (R) 48 × IET 28835	-2.26	-0.85	-18.71	3.20	-41.86	-43.24	-22.14	-2.85	18.31	-0.77	-59.47	-1.93	16.45**	-37.23 **
ADT (R) 48 × BPT 5204	-3.87	61.40 **	-17.77	15.21	-47.06 *	-47.44 *	-23.08 *	-24.30	0.99	-20.87	-56.90 *	4.76	3.81	-14.91 *
ADT (R) 48 × CB12132	-9.07	-2.56	-24.85*	3.98	-52.20 *	-52.74	-33.33 *	-50.72	-17.45	-6.58	-63.48 *	6.19 *	12.54	-25.60
ADT (R) 48 × IET 28749	5.10	-33.90 *	-17.12	34.04 **	-56.41 **	-56.77 **	-31.15 **	-33.10	11.68	3.00	-69.68 **	-7.84	26.17**	-44.13 **
BPT 5204 × IET 28834	2.45	51.65 *	-20.3	2.67	6.12	3.51	17.78 **	14.29	4.41	18.44 **	-0.94	7.40	10.16**	29.84 **
BPT 5204 × IET 28835	1.75	14.78	9.34	3.73	2.80	3.44	7.29	12.81	9.96	3.86	2.22	5.77 *	14.92**	6.92
BPT 5204 × ADT (R) 48	-0.65	42.11 **	-24.83	8.35	-38.75 *	-38.78 *	-25.00 *	-18.69	12.41	-11.30	-49.06 *	7.62	3.23	-30.03 *
BPT 5204 × CB12132	6.12	-2.61	30.42**	19.90 **	27.19 **	26.30 *	6.45	19.06	1.15	-0.93	35.82 **	24.68 **	-7.37	-19.29
BPT 5204 × IET 28749	15.86 **	6.90	30.22*	14.38 *	3.73	4.74	3.17	7.58	4.95	12.73	1.16	9.63	-13.37**	-5.37
CB12132 × IET 28834	-4.98	-2.13	-25.9**	-4.65	-45.42 **	-45.15 **	-15.09	-27.32 *	-0.86	-19.07	-53.92 **	-10.96	9.02**	-35.46
CB12132 × IET 28835	-2.77	-18.64	-14.41	-1.68	-28.99 *	-29.38 *	0.61	-29.79 **	-21.13 *	4.05	-39.41 **	6.20	7.63**	-40.60 **
CB12132 × ADT (R) 48	-0.28	2.56	-30.95*	0.00	-2.77 *	-1.43	-16.67 *	10.14	38.09	9.47	-5.80 *	23.71 *	-1.17	-2.37
CB12132 × BPT 5204	4.85	-9.57	41.07**	11.84 **	35.75 **	36.85 *	19.35	20.77	4.01	1.87	46.15 **	22.14 **	-7.37	-59.02 **
CB12132 × IET 28749	9.85 **	-9.24	29.89**	9.66	-18.71	-17.80	-1.41	-3.70	-2.30	24.23	-28.13	20.05 *	-7.9**	-19.09 *
IET 28749 × IET 28834	6.75 *	1.05	-7.16	14.87	-17.41	-17.64	-6.19	-6.63	12.77	18.00 *	-27.84	-0.36	18.19**	-5.60
IET 28749 × IET 28835	12.38 **	-19.33	-6.43	20.00 **	-13.37	-13.70	9.75	-4.59	-5.69	32.16 *	-26.49	-3.03	18.87**	-22.46 **
IET 28749 × ADT (R) 48	3.50	-32.20 *	-8.95	32.49 **	-43.00 **	-41.48 **	-24.59 **	-23.34	14.72	2.54	-53.17 **	10.87	28.15**	-47.66 **
IET 28749 × BPT 5204	20.11 **	8.62	27.19*	18.13 *	19.19	1.79	22.22	29.58	6.81	18.17	19.48	18.05	-19.46**	-8.34
IET 28749 × CB12132	13.89 **	-9.24	64.2**	11.75	4.39	3.75	-7.04	0.00	7.81	-3.41	6.10	10.53 *	-17.31**	-18.31 *

(* and ** indicates significance at 5 % and 1 % level)

PH : Plant height, NPT : Number of productive tillers, FLA : Flag leaf area, PL : Panicle length, NOSPP ; Number of spikelets per panicle, NFGPP : Number of filled grains per panicle ,NOPB:Number of primary branches per panicle, the number of secondary branches per panicle (NOSB), NOSBPB: Number of secondary branches per primary branch , NOSIPB: Number of spikelets in primary branches, NOSISB: Number of spikelets in secondary branches , LOPB: Length of primary branch, TGW: Thousand grains weight and GYP : Grain yield per plant

Table 4. Better parent heterosis of 30 hybrids for 14 panicle and yield related traits in rice

Hybrids	PH	NPT	FLA	PL	NOSPP	NFGPP	NOPB	NOSB	NOSBPB	NOSIPB	NOSISB	LOPB	TGW	GYP
IET 28834 × IET 28835	-0.70 *	-42.37 *	-22.86	-1.23 **	35.57 **	35.42 **	31.23	41.58 **	8.09	41.18	31.32	-2.44	3.37*	-25.07 *
IET 28834 × ADT (R) 48	-17.52 **	27.59	-33.74*	-14.36	-47.01	-47.79	-26.00	12.50	11.69	-3.89	-64.18 *	-19.51 **	3.6	-26.34 *
IET 28834 × BPT 5204	-2.57	16.07	-14.53	-2.56	-13.53	-13.31	46.30	-17.86	-39.61 *	12.99	-25.63	0.24	-9.21**	-17.22
IET 28834 × CB12132	-5.29	-1.69	-45.61**	-14.89 *	-65.71 **	-65.31 **	-28.57 **	-64.21 **	-50.35 **	-22.16 **	-75.99 **	-6.22	-6.07**	-1.44 **
IET 28834 × IET 28749	-2.80	-25.00	-27.52*	-4.62	-47.25 **	-47.39 **	-8.33	-36.93 **	-31.00 *	7.12	-56.59 **	7.67	3.37	-19.96 **
IET 28835 × IET 28834	-14.72 *	-45.76 *	-9.66	-70.36 **	8.50	7.87	7.12	21.95	13.58	2.25	13.23	-5.37	11.24*	-25.28 *
IET 28835 × ADT (R) 48	-14.72 **	-5.08	-24.98	-5.38	-52.14 *	-52.36	-32.00 *	-31.31	-23.24	-16.95	-70.91 *	-19.75	8.76**	-34.39 **
IET 28835 × BPT 5204	1.52	-1.69	-18.96	-7.14	-26.96	-28.48	1.85	-38.69	-39.13 *	0.97	-43.70	22.72	-6.45	-29.10
IET 28835 × CB12132	-11.03 **	-28.81	-36.72**	-17.87 *	-62.69 **	-62.59 **	-28.57 *	-64.55 **	-49.88 **	-25.15 *	-73.02 **	5.36	-2.07*	-17.71 **
IET 28835 × IET 28749	2.79	-40.00	-23.02*	11.21	-48.38 **	-47.83 **	-20.83	-33.61 **	-15.50	4.63	-49.46 **	-3.12	2.07	-48.79 **
ADT (R) 48 × IET 28834	-19.16 **	-1.72	-32.96*	-8.72	-43.45	-43.51	-24.00	0.00	-3.90	12.78	-76.36 *	-26.83 **	1.35	-41.30 *
ADT (R) 48 × IET 28835	-17.51 **	-1.69	-34.42	-9.56	-52.42 *	-53.54	-32.00 *	-20.10	-12.27	-11.24	-70.36 *	-9.05	11.75**	-40.76 **
ADT (R) 48 × BPT 5204	-14.61 **	58.62 *	-37.47*	3.49	-54.63 **	-55.20 *	-25.93 *	-51.79 **	-34.46 *	-40.91 **	-60.89 *	3.13	-11.28**	-24.34 **
ADT (R) 48 × CB 12132	-26.21 **	-3.39	-48.54**	-17.70 **	-66.51 **	-66.90 **	-42.86 **	-71.57 **	-49.77 **	-32.04 **	-74.65 **	-11.59	-3.26**	-36.25 **
ADT (R) 48 × IET 28749	-7.56 *	-35.00	-42.49**	29.05 **	-69.04 **	-69.29 **	-41.67 **	-60.17 **	-28.76 *	-20.64	-78.83 **	-19.66	11.78**	-56.30 **
BPT 5204 × IET 28834	-7.01	23.21	-22.73	-3.38	-27.67	-29.42	-1.85	-23.81	-21.90 *	-6.17	-37.48	-4.39	-9.89**	3.43
BPT 5204 × IET 28835	-4.06	11.86	1.09	0.88	-25.23	-25.05	-9.26	-19.64	-11.11 *	-15.58	-29.63	-0.44	-5.07	0.36
BPT 5204 × ADT (R) 48	-11.75 **	39.66 *	-42.84*	-2.67	-47.51 **	-47.82 *	-27.78 *	-48.21 **	-27.05 *	-33.77 **	-53.78 *	5.94	-11.78**	-37.78 **
BPT 5204 × CB 12132	-4.37	-5.08	11.45	3.83	-0.69	-0.95	-5.71	-7.02	-12.56	-4.79	0.28	5.15	-8.01	-41.82 **
BPT 5204 × IET 28749	14.57 **	3.33	13.6	6.40	-17.60	-16.38	-9.72	-8.71	1.04	7.79	-24.84	-3.12	-16.88**	-18.38 *
CB12132 × IET 28834	-5.75	-22.03	-38.27**	-12.77 *	-67.14 **	-66.90 **	-35.71 **	-56.86 **	-32.51 **	-37.72 **	-74.08 **	-16.31	-10.34**	-50.18 **
CB12132 × IET 28835	-7.36 **	-18.64	-31.44**	-12.77 *	-55.43 **	-55.67 **	-22.86 *	-56.52 **	-42.84 **	-17.96 *	-64.27 **	-5.58	-10.6*	-46.42 **
CB12132 × ADT (R) 48	-19.08 **	1.69	-52.72**	-20.85 **	-31.89 **	-30.97 **	-28.57 **	-36.45 **	-15.96 **	-20.36 **	-34.60 **	3.00	-15.04**	-16.35 **
CB12132 × BPT 5204	-5.52	-11.86	20.56	-3.15	6.00	7.33	5.71	-5.69	-10.09	-2.10	7.91	3.00	-8.01	-60.73 **
CB12132 × IET 28749	0.00	-10.00	26.79**	-10.64	-20.57	-19.74	-2.78	-13.04	-12.68	14.37	-28.81	13.73	-11.04**	-27.55 **
IET 28749 × IET 28834	-2.10	-20.00	-21.11*	1.03	-49.88 **	-49.88 **	-29.64	-42.46 **	-17.73 *	-3.20	-59.32 **	-1.20	0	-32.50 **
IET 28749 × IET 28835	7.11	-20.00	-23.64*	8.79	-45.09 **	-45.29 **	-16.67	-38.17 **	-25.93	11.39	-56.52 **	-9.35	1.61	-36.57 **
IET 28749 × ADT (R) 48	-8.96 *	-33.33	-36.81**	27.57 **	-59.52 **	-58.44 **	-36.11 **	-54.36 **	-26.83 *	-21.00	-67.31 **	-3.36	13.53**	-59.06 **
IET 28749 × BPT 5204	18.77 **	5.00	10.96	9.88	-5.33	-18.73	6.94	9.96	2.83	12.99	-11.23	4.32	-22.73**	-20.94 *
IET 28749 × CB12132	3.68	-10.00	60.28**	-8.94	2.00	1.30	-8.33	-9.70	-3.64	-11.08	5.08	4.72	-20.13**	-26.85 **

(* and ** indicates significance at 5 % and 1 % level)

PH : Plant height, NPT : Number of productive tillers, FLA : Flag leaf area, PL : Panicle length, NOSPP ; Number of spikelets per panicle, NFGPP : Number of filled grains per panicle ,NOPB:Number of primary branches per panicle, the number of secondary branches per panicle (NOSB), NOSBPB: Number of secondary branches per primary branch, NOSIPB: Number of spikelets in primary branches, NOSISB: Number of spikelets in secondary branches, LOPB: Length of primary branch, TGW: Thousand grains weight and GYP : Grain yield per plant

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Table 5. Standard heterosis of 30 hybrids for 14 panicle and yield related traits in rice

Hybrids	PH	NPT	FLA	PL	NOSPP	NFGPP	NOPB	NOSB	NOSBPB	NOSIPB	NOSISB	LOPB	TGW	GYP
IET 28834 × IET 28835	14.25	-26.09	-54.04 **	-6.50 **	-46.84 **	-46.33 **	36.11	-32.21	-50.18 **	-12.26 *	-59.76 **	-36.91 **	4.66 **	-11.89
IET 28834 × ADT (R) 48	-5.11	60.87	-60.53 **	-18.93 *	-67.37 **	-67.52 **	2.78	-57.72 **	-58.60 **	-44.19 **	-76.27 **	-47.95 **	4.89	-23.13 *
IET 28834 × BPT 5204	12.10 *	41.30	-45.79 **	-7.77	-25.44 *	-23.49	119.44 **	-7.38	-54.87 **	12.26	-39.52 *	-35.17 **	-8.08 **	10.98
IET 28834 × CB12132	10.75 **	26.09	-51.35 **	-2.91	-47.37 **	-46.15 **	38.89	-28.19	-49.10 **	-16.13 *	-59.04 **	-31.07 **	-4.89 *	44.14
IET 28834 × IET 28749	11.83 **	-2.17	-38.27 **	-9.71	-22.72	-22.20	83.33 **	2.01	-44.28 **	-2.90	-27.35	-29.18 **	4.66	47.99 *
IET 28835 × IET 28834	-1.88	-30.43	-46.18 **	-71.94 **	-57.46 **	-57.25 **	11.11	-41.61	-47.65 **	-36.45 *	-65.30 **	-38.80 **	12.63 **	-12.12
IET 28835 × ADT (R) 48	-9.68 **	21.74	-59.59 **	-16.41 **	-70.53 **	-70.37 **	-5.56	-67.11 **	-64.62 **	-48.39 **	-80.72 **	-54.10 **	7.39 **	-22.84
IET 28835 × BPT 5204	7.53	26.09	-48.59 **	-17.96 *	-37.02 *	-36.88 *	52.78 *	-30.87	-54.51 **	0.32	-54.22 *	-29.81 **	-7.62 *	-4.95
IET 28835 × CB12132	4.03	-8.70	-43.39 **	-6.31	-42.72 *	-41.93 *	38.89 *	-28.86	-48.62 **	-19.35	-53.98 *	-22.56 **	-3.30 *	20.34
IET 28835 × IET 28749	8.87 **	-21.74	-34.43 **	-1.75	-24.39	-22.84	58.33 **	7.38	-31.77 **	-5.16	-15.42	-36.28 **	0.80	-5.32
ADT (R) 48 × IET 28834	-6.99	23.91	-60.06 **	-13.59 *	-65.18 **	-64.86 **	5.56	-62.42 **	-64.38 **	-34.52 **	-84.34 **	-52.68 **	2.62	-38.74 *
ADT (R) 48 × IET 28835	-12.63 **	26.09	-64.68 **	-20.10 **	-70.70 **	-71.10 **	-5.56	-61.74 **	-59.57 **	-44.84 **	-80.36 **	-47.98 **	10.35 **	-30.34
ADT (R) 48 × BPT 5204	-19.89 **	100.00 **	-60.33 **	-13.59 *	-60.88 **	-60.46 **	11.11	-45.64 *	-51.02 **	-41.29 **	-68.19 **	-47.95 **	-19.45 **	1.44
ADT (R) 48 × CB 12132	-13.71 *	23.91	-53.97 **	-6.12	-48.60	-48.62	11.11	-42.95	-48.50 **	-26.77 *	-56.75	-35.02 **	-12.17 **	-6.78
ADT (R) 48 × IET 28749	-11.29 **	-15.22	-51.01 **	-7.28	-54.65 **	-54.59 **	16.67	-35.57	-42.48 **	-28.06 **	-64.58 **	-47.16 **	1.48	-19.20
BPT 5204 × IET 28834	6.99 *	50.00	-50.98 **	-8.54	-37.63 *	-37.71	47.22 **	-14.09	-41.64 **	-6.77	-49.16 *	-38.17 **	-8.76 **	38.66
BPT 5204 × IET 28835	1.61	43.48	-35.88 **	-10.87 *	-35.53 *	-33.85 *	36.11 *	-9.40	-33.57 **	-16.13	-42.77 *	-43.06 **	-6.26 *	34.54
BPT 5204 × ADT (R) 48	-17.20 **	76.09 **	-63.74 **	-18.74 *	-54.74 **	-53.94 **	8.33	-41.61 *	-45.49 **	-34.19 **	-62.41 **	-46.53 **	-19.91 **	-16.59
BPT 5204 × CB 12132	11.83 **	21.74	-0.30	18.45 *	52.46 **	53.76 **	83.33 **	86.58 **	-10.35	2.58	71.08 **	-22.71 **	-39.93 **	-14.92 *
BPT 5204 × IET 28749	9.95 **	34.78	-3.24	-11.17	20.70	23.67	80.56 **	47.65 **	-18.41	7.10	25.78	-36.28 **	-41.75 **	50.92 **
CB12132 × IET 28834	10.22 **	0.00	-44.78 **	-0.49	-49.56 **	-48.62 **	25.00	-13.42	-30.81 **	-32.90 *	-55.78 **	-38.49 **	-9.22 *	-27.15
CB12132 × IET 28835	8.33	4.35	-38.67 **	-0.49	-31.58 *	-31.19 *	50.00 *	-12.75	-41.40 **	-11.61	-39.04 *	-30.60 **	-11.72 *	-21.64
CB12132 × ADT (R) 48	-5.38 *	30.43	-57.71 **	-9.71	4.56	7.16	38.89	27.52	-13.84 **	-14.19 *	11.57	-24.29 **	-22.87 **	22.33
CB12132 × BPT 5204	10.48 **	13.04	7.84	10.49 *	62.72 **	66.61 **	105.56 **	89.26 **	-7.82	5.48	84.10 **	-24.29 **	-39.93 **	-42.57 *
CB12132 × IET 28749	16.94 **	17.39	13.41 *	1.94	21.93 *	24.59 *	94.44 **	74.50 **	-10.47	23.23	21.45 *	-16.40 **	-37.66 **	33.95 *
IET 28749 × IET 28834	12.63 **	4.35	-32.81 **	-4.37	-26.58	-25.87	40.72 **	-6.94	-33.57 **	-12.26	-31.93	-35.02 **	1.25	24.81 *
IET 28749 × IET 28835	13.44 **	4.35	-34.95 **	-3.88	-19.56	-19.08	66.67 **	0.00	-40.19 **	0.97	-27.23	-40.38 **	0.34	17.28
IET 28749 × ADT (R) 48	-12.63 **	-13.04	-46.18 **	-8.35	-40.70 **	-38.53 **	27.78	-26.17	-40.91 **	-28.39 **	-45.30 **	-36.44 **	3.07	-24.30
IET 28749 × BPT 5204	13.98 **	36.96	-5.49	-8.25	38.68	20.18	113.89 **	77.85 **	-16.97	12.26	48.55	-31.39 **	-45.85 **	46.18 **
IET 28749 × CB12132	21.24 **	17.39	43.37 *	3.88	56.58 *	57.25 *	83.33 **	81.21 **	-1.20	-4.19	79.28 *	-23.03 **	-44.03 **	35.26 *

(* and ** indicates significance at 5 % and 1 % level)
PH : Plant height, NPT : Number of productive tillers, FLA : Flag leaf area, PL : Panicle length, NOSPP ; Number of spikelets per panicle, NFGPP : Number of filled grains per panicle ,NOPB:Number of primary branches per panicle, the number of secondary branches per panicle (NOSB), NOSBPB: Number of secondary branches per primary branch, NOSIPB: Number of spikelets in primary branches, NOSISB: Number of spikelets in secondary branches , LOPB: Length of primary branch, TGW: Thousand grains weight and GYP : Grain yield per plant

Among the 30 hybrids, positive significant relative heterosis was observed in BPT 5204 × CB 12132 and CB12132 × BPT 5204 for both numbers of spikelets per panicle and the number of filled grains per panicle (**Table 3**). Also, these two hybrids recorded significant positive heterosis for flag leaf area, panicle length, the number of spikelets in secondary branches and length of primary branch. In the case of grain yield per plant the hybrids, IET 28834 × CB12132 and BPT 5204 × IET 28834 recorded significant positive mid parental heterosis among the thirty hybrids. While observing mid parental heterosis for the other major traits, there were four hybrids with a positive significant value for the number of productive tillers and eight hybrids for plant height, and twenty hybrids for thousand grain weight was identified.

Better parent heterosis was insignificant for most of the panicle related traits under this study. The hybrid, IET 28834 × IET 28835 showed significant positive better parental heterosis for the number of spikelets per panicle, the number of filled grains per panicle and the number of secondary branches per panicle (**Table 4**). Two hybrids each for plant height (BPT 5204 × IET 28749 and IET 28749 × BPT 5204), the number of productive tillers (ADT (R) 48 × BPT 5204 and BPT 5204 × ADT (R) 48) and flag leaf area (CB12132 × IET 28749 and IET 28749 × CB12132) and six hybrids for thousand grain weight showed significant positive better parental heterosis. The lack of better parental heterosis for panicle traits might be due to the higher fraction of additive components present in it Naik *et al*. (2021) observed a very low number of better parental heterosis for grain number per panicle which was similar to the present study. None of the hybrids showed significant positive better parental heterosis for grain yield per plant.

While comparing the performance of hybrids with the standard check variety CO (R) 50, four hybrids *i.e.,* BPT 5204 × CB12132, CB12132 × BPT 5204, CB12132 × IET 28749 and IET 28749 × CB12132 exhibited significant positive standard heterosis for number of spikelets per panicle, the number of filled grains per panicle, the number of primary branches per panicle, the number of secondary branches per panicle and the number of spikelets in secondary branches (**Table 5**). The six hybrids, IET 28834 × IET 28749, BPT 5204 × IET 28749, CB12132 × IET 28749, IET 28749 × IET 28834, IET 28749 × BPT 5204 and IET 28749 × CB12132 exhibited significant positive standard heterosis for grain yield per plant. Two hybrids for flag leaf area (CB12132 × IET 28749 and IET 28749 × CB12132), number of productive tillers (ADT (R) 48 × BPT 5204 and BPT 5204 × ADT (R) 48) and panicle length (BPT 5204 × CB 12132 and CB12132 × BPT 5204) displayed significant positive heterosis for the respective traits. Vadivel (2018) studied the performance of rice hybrids by comparing it with IR 64 check variety and identified 11 hybrids out of 28 hybrids expressing significant positive standard heterosis for grain number per panicle.

It can be concluded that both additive and non-additive gene effects contributed to the panicle and yield related traits, which the additive gene effect was predominant in panicle traits and the majority of non-additive gene effects contributed to grain yield per plant. Two hybrids, BPT 5204 × CB12132 and CB12132 × BPT 5204 recorded higher significant positive standard heterosis for panicle traits and in the case of grain yield per plant, the hybrids IET 28834 × CB12132, BPT 5204 × IET 28749 and IET 28749 × BPT 5204 exhibited high standard heterosis. Hence, these hybrids could be utilised for heterosis breeding as well as recombination breeding, where the selection can be deferred to later generations.

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