Original Research Article

Study of combining ability in association with heterosis in rice (*Oryza sativa* L.)

Abstract

In the current investigation, eight lines KNM 12444, KNM 12469, KNM 12472, KNM 13449, KNM 13555, KNM 13568, KNM 14913 and KNM 14985 were crossed with four testers namely Aganni, IBT MRR 24, INRC 3021 and WGL 1119 in Line by Tester mating design during *rabi* season of 2021-22. The resultant 32 F_1'stogether with parents and two commercial checks, KNM 118 and KNM 1638 were evaluated for their combining ability and heterosis at Agricultural Research Station, Kunaram during *kharif* season, 2022.The analysis of variance for combining ability specified that significant differences were observed due to lines, testers, F_1' hybrids and various interactions indicating the existence of wider adaptability in the material examined. The ratio of *gca* to *sca* variances showed that non-additive gene action was predominant in the inheritance of panicle length, plant height, number of productive tillers/plants, grain yield per plant, kernel length, kernel L/B ratio and incidence of gall midge, whereas, preponderance of additive gene action was noticed for 1000 grain weight, days to 50% flowering, number of filled grains per panicle, kernel breadth, hulling percentage, milling percentage and head rice recovery. The *gca* effects of the parents revealed that, the line KNM 13555 and the testers Aganni, IBT MRR 24 were found to be the best general combiners for single plant yield and its components. Based on the significant *sca* effects, *per se* performance, standard heterosis and gall midge incidence, KNM 12469/Aganni followed by KNM 13555/INRC 3021, KNM 13568/IBT MRR 24, KNM 12472/Aganni and KNM 13449/Aganni were identified as promising for single plant yield, its components, quality traits and gall midge incidence. Hence, these parents and F_1 hybrids may be further tested for future crop improvement programme.

Key words: Combining ability, gca, heterosis, line x tester, rice, sca.

Introduction

Rice (*Oryza sativa* L.) is a staple food for over half of the world's population and essential crop for food security. Asia solitarily supplies more than 90% of the world's rice and 20% of the global dietary energy [1]. According to the USDA, approximately 503.3 million tonnes of milled rice has been produced globally during 2022-23 marketing year [3]. Notably, China leads as the largest rice producer, yielding 148.27 million tons of milled rice, followed by India (120.54 million tons), Indonesia (34.96 million tons), Bangladesh (34.77 million tons), and Vietnam (27.31 million tons [2]. Similarly, in terms of consumption, China ranked highest, with 150.62 million tons of milled rice, trailed by India (104.17 million tons), Bangladesh (36.10 million tons), Indonesia (35.51 million tons), and Vietnam (21.38 million tons) [3].

Climate change is projected to increase global rice production and consumption by 18% relative to 2010 and per capita land availability for rice cultivation is expected to decrease by 25% by 2050 [4]. Ensuring food security for a growing global population requires significantly increasing rice yield potential [5]. However, limited resources and the impact of biotic and abiotic stresses pose considerable challenges in rice production [6].

One of the key challenges faced by plant breeders in improving high-yielding varieties is selecting suitable parents and crosses [7]. In crop plant breeding, out of different genetic components estimations, the analysis of combining ability is an effective method to overcome this problem [8]. For estimating genetic components, the line × tester method proposed by Kempthorne in 1957 [16] is useful for obtaining precise measurements of general combining ability (*gca*) and specific combining ability (*sca*) and selecting parents for the hybridization program. This will aid in the assessment of *gca* and *sca* variances in addition to their effects and thus helps to deduce the nature of gene action responsible for the expression of economically important quantitative traits and to choose the plant breeding methods [9].

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Heterosis in rice was initially observed by Jones (1926) [10], who noted significant increases in culm number and grain yield in certain F_1 hybrids compared to their parents. Chinese scientists later demonstrated the commercial application of heterosis, achieving a yield increase of approximately 20% over semi-dwarf varieties [11]. Both negative and positive heterosis play vital roles in plant breeding, depending on the breeding objectives. Positive heterosis is sought after for enhancing yield, while negative heterosis is valuable for promoting early maturity [12]. Breeding strategies centered around exploitation of heterosis, necessitate high levels of specific combining ability and heterosis in crosses.

Rice is one of the most predominantly grown crops in Telangana state during rainy and post rainy seasons. Rice is being grown in an area of 41.89 lakh hectares with the production and productivity of 218 lakh tons and 5215 kg/ha, respectively [13]. In some parts of Telangana, major problem is high incidence of gall midge (Biotype 3) in *kharif* under early as well as late planting conditions. The Asian rice gall midge, *Orseolia oryzae* (Wood-Mason) is one of the important insect pests in Northern Telangana. More recently, gall midge incidence has been increased in almost all the rice growing states of India which results in considerable yield losses as affected tillers bear no panicles or grains. In contrast, the maggots fail to induce gall formation on the resistance varieties and perish in 2-4 days after hatching. Hence, breeding for gall midge resistant varieties has been important strategy with more yield [14].

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Hence, the present investigation was undertaken to study the combining ability of rice genotypes through Line x Tester design along with the estimation heterosis for yield, yield contributing characters, quality traits and incidence of gall midge.

Materials and methods

The present investigation was conducted at an experimental farm of Agricultural Research Station, Kunaram, Peddapalli District of Telangana state during the the rice-growing *kharif* season, 2022. The farm is geographically situated at 18.6^{o} N Latitude, 79^{o} E Longitude and an elevation of 231 m AMSL. The soil is silty loam with pH 7.43 and EC 0.26

dS m^{-1}.

This study was aimed at to evaluate the levels of combining ability between the lines and testers, and among the crosses, and to estimate the heterosis in order to identify superior crosses for yield and yield attributing traits, and quality traits along with incidence of gall midge.

A total of 12 parental genotypes, enlisted in Table 1, which were crossed in a Line-by-Tester fashion during the *rabi* season of 2021-22, resulting in 32 F_1 hybrids. The experimental material, consisting of 46 genotypes in total, including 32 F_1 hybrids, 12 parents, along with the inclusion of commercial checks KNM 118 and KNM 1638 were evaluated during the *kharif* season of 2022 in a randomized block design (RBD) with three replications for 14 various characters. Thirty-day-old seedlings were transplanted in the main field with a spacing of 20 cm x 15 cm between and within the rows, respectively. The experimental procedures followed the recommended agronomic and cultural practices to ensure optimal growth and development of the rice plants.

Table 1. Details of genotypes

S.No	Genotypes	Source	Salient features
Lines			
1	KNM 12444	ARS, Kunaram	Early duration (125-130 days) with short slender and good quality grains.
2	KNM 12469	ARS, Kunaram	Long duration (145-150 days), medium slender rice variety.
3	KNM 12472	ARS, Kunaram	Long duration (145-150 days) with medium slender grain type.
4	KNM 13449	ARS, Kunaram	Short duration (125-130 days) coupled with short slender and good quality grains.
5	KNM 13555	ARS, Kunaram	Medium duration (130 days), long slender rice variety.
6	KNM 13568	ARS, Kunaram	Short duration (125-130 days) along with long slender rice grains.
7	KNM 14913	ARS, Kunaram	Early duration (125-130 days) with short slender and good quality grains.
8	KNM 14985	ARS, Kunaram	Short duration (125-130 days) along with long slender rice grains.
Testers			
1	Aganni	RARS, Jagtial	Long duration (160 days), medium slender and gallmidge resistant genotype.
2	IBT MRR 24	IBT, Rajendranagar	Early duration (120 days) long slender rice variety with gall midge resistance.
3	INRC 3021	IIRR, Rajendranagar	Short duration (120 days) long slender rice variety with gall midge resistance.

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4	WGL 1119	RARS, Warangal	Short duration (120 days) medium slender rice variety with gall midge resistance.
		Checks	
1	KNM 118	ARS, Kunaram	Short duration (120-125 days), long slender rice variety with resistance to leaf blast and moderately resistant to neck blast.
2	KNM 1638	ARS, Kunaram	Early duration (120-125 days), medium slender rice variety with moderately resistance to blast and gallmidge.

Observations were recorded for the following yield and yield-contributing traits, incidence of gall midge and quality traits for the five randomly selected plants (excluding border plants) from the middle of the row of each entry in every replication, except for days to 50% flowering which was recorded on a plot basis for statistical analysis. Data on days to 50 per cent flowering, plant height, panicle length, number of productive tillers per plant, number of grains per panicle, 1000-grain weight and grain yield per plant in addition to quality traits such as, hulling per cent, milling per cent, head rice recovery, kernel length, kernel breadth and kernel L/B ratio were recorded.The data recorded on the 32 F_1s crosses and 12 parents were subjected to study the variances among parents and their respective crosses by using statistical analysis INDOSTAT version 8.1. The means of all characters were subjected for variance analysis [15], combining ability [16] and estimation of the heterosis [17].

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Results and discussion

The analysis of variance for combining ability of all the traits under study has been presented in **Table 2**. The variance for combining ability due to parents, treatments and crosses was highly significant for all the characters under study. The variance due to parent vs. crosses was also found highly significant for most of the characters except number of filled grains per plant and hulling per cent. The variance due to lines was found significant for all the traits; whereas the variance due to testers was found non- significant for incidence of gall midge, milling per cent and head rice recovery per cent. When the crosses were partitioned into lines, testers and line x tester effects, the interaction effects (Lines x Testers) were found to be significant for most of the traits under study except hulling per cent indicating sufficient variability in the material used for study.

Similar works have been reported by Bagheri et al. (2010) [18], Rahimi et al. (2010) [7], Sarial (2014) [19], Devi et al. (2015) [20] and Bano et al. (2019) [21] for lines and Line x Tester interaction, Kumar et al. (2006) [22], Priyanka et al. (2014) [23], Sreelakshmi et al. (2018) [24], Deepika et al. (2019) [25], Ghidan et al. (2019) [26], Ambikabathy et al. (2019) [27], Mohan et al. (2021) [2], AnandaLekshmi et al. (2020) [28], Budhlakoti et al. (2020) [29] and Barhate et al. (2021) [30] and Azad et al. (2022) [31] for crosses, lines and Line x Tester interaction, Kour et al. (2019) [32], Keerthiraj et al. (2021) [33] and Bassuony [34] for

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treatments, hybrids, testers and Line x Tester effects, El-Hadi et al. (2020) [35], Singh et al. (2021) [36] and Yadav et al. (2021) [37] for treatments, lines and Line x Tester effects, Singh et al. (2020) [38], Neupane et al. (2022) [39] and You et al. (2022) [40], Nagamani et al. (2022) [41], Rahman et al. (2022) [42], Sakran et al. (2022) [43] and Ramakrishna et al. (2023) [44] for Line x Tester interaction in rice.

In general, general combining ability is associated with additive gene action, whereas specific combining ability is due to dominance and epistasis. It was found that *gca* variances were higher than *sca* variances for majority of the traits which indicated the predominance of additive gene action. Estimates of extremely significant *gca* and *sca* variance for some of the traits demonstrated the involvement of both additive and non-additive genes in the manifestation of the characters. The inheritance of several quantitative aspects in rice, including additive and non-additive gene effects, confirmed prior findings by Kargbo et al. (2019) [45], Fels et al. (2021) [46] and Mazal et al. (2021) [47]. **Table 3** also shows that variances of *gca*/*sca* ratios exceeded unity for the days to 50% flowering, 1000 grain weight, number of filled grains per panicle, hulling percentage, milling percentage, head rice recovery and kernel breadth, indicating that additive gene action is more important than non-additive gene action in controlling these features. Therefore, transgressive breeding is a superior option for these traits. Furthermore, other breeding methodologies such as biparental mating, reciprocal recurrent selection, or diallel selective mating may be reconstituted than 8 conventional pedigree method which would leave the unfixable components of genetic variances untapped for grain yield and its associated traits which were controlled mainly by additive along with non-additive gene action.

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In contrast, its ratio was less than unity for the characters plant height, panicle length, number of productive tillers/plants, grain yield per plant, incidence of gall midge, kernel length and kernel L/B ratio indicating predominance of nonadditive genetic variance, and hence, it gives a very good insights for exploitation of heterosis for crop improvement for these traits. The results were in accordance with the earlier findings of Mallikarjuna et al. (2014) [48] for culm length; and Mallikarjuna et al. (2014) [48] for panicle number plant per plant, spikelet fertility and panicle length; Patil et al. (2012) [49], Bano and Singh (2019) [21] and Ramakrishna et al. (2023) [44] for grain yield plant per plant in rice.

Degree dominance was more than unity for all the traits except days to 50% flowering, 1000 grain weight, number of filled grains/ panicle, hulling per cent, milling percent, head rice recovery, kernel length and kernel breadth which indicates over dominance, is the cause of heterosis.

Table 2. Analysis of variance for combining ability (LinexTester) for yield, yield components, gall midge incidence and quality traits

Source of variation	d.f	Days to 50%flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers per plant	Grain yield per plant (g)	No. of filled grains per panicle	1000-grain weight (g)	Incidence of gall midge (%)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
Replicates	2	1.0	4.5	0.9	0.4	16.3	35.8	1.6	22.2*	1.31	5.8	8.3	0.0	0.0	0.0
Treatments	43	163.9**	674.9**	5.5**	7.6**	84.1**	5813.5**	72.8**	165.6**	7.71**	161.2**	87.8**	1.1**	0.2**	0.6**
Parents	11	272.4**	1510.6**	8.0**	8.8**	24.7**	13879.6**	134.4**	72.8**	11.62**	587.8**	46.8**	2.2**	0.4**	0.9**
Parents (Lines)	7	317.6**	230.1**	6.0**	3.6*	24.7**	12802.8**	165.5**	47.6**	11.55**	916.5**	56.6**	3.1**	0.2**	0.5**
Parents (Testers)	3	139.3**	4870.9**	14.9**	20.1**	31.4*	3131.7**	95.4**	15.2	6.30*	5.9	6.0	0.9**	1.0**	2.0**
Parents (L *vs* T)	1	355.6**	393.4**	0.8	11.7**	4.8	53660.9**	33.6**	422.4**	28.03**	32.3**	101.0**	0.0	0.6**	0.6**
Parents *vs* Crosses	1	11.5**	414.7**	27.4**	19.9**	1053.9**	1592.1	4.9**	423.6**	4.06	52.0**	46.1**	0.2**	0.5**	0.6**
Crosses	31	130.3**	386.8**	3.9**	6.8**	73.9**	3087.5**	53.2**	190.2**	6.45**	13.3**	103.7**	0.8**	0.2**	0.4**
Line effect	7	409.8**	146.0	6.1	6.7	96.9	9485.8**	167.1**	427.6*	9.84*	39.9**	409.1**	2.2**	0.3*	0.5
Tester effect	3	324.8**	837.6	4.1	9.3	145.9	2546.2	122.3**	106.9	18.50**	9.8	63.5**	1.7**	0.4**	1.1*
Line x Tester effect	21	9.4**	402.7**	3.1**	6.4**	55.9**	1032.0*	5.3**	122.9**	3.60	4.9**	7.6**	0.2**	0.1**	0.3**
Error	86	1.1	6.9	0.9	1.5	8.3	558.8	0.5	5.8	2.22	2.3	3.0	0.0	0.0	0.0
Total	131	54.5	226.1	2.4	3.5	33.3	2275.6	24.3	58.5	4.01	54.5	30.9	0.4	0.1	0.2

*Significant at 5 per cent level, ** Significant at 1 per cent level

Table 3. Estimates of general and specific combining ability, variance, proportionate gene action and degree of dominance.

S. No	Source of variation	$\sigma^2 gca$	$\sigma^2 sca$	$\sigma^2 gca$ / $\sigma^2 sca$	Degree of dominance = $\sqrt{\frac{\sigma^2 sca}{\sigma^2 gca}}$	Nature of gene action
1	Days to 50% flowering	40.69	2.76	14.74	0.26	Additive
2	Plant height	53.88	131.94	0.40	1.56	Non additive
3	Panicle length	0.46	0.72	0.63	1.25	Non additive
4	No. of productive tillers/ plant	0.72	1.65	0.44	1.50	Non additive
5	1000 grain weight	16.02	1.61	9.92	0.31	Additive
6	No. of filled grains/ panicle	606.35	157.74	3.84	0.51	Additive
7	Grain yield per plant	12.56	15.86	0.79	1.12	Non additive
8	Incidence of gall midge	29.04	39.02	0.74	1.15	Non additive
9	Hulling per cent	1.32	0.45	2.89	0.58	Additive
10	Milling per cent	2.50	0.86	2.89	0.58	Additive
11	Head rice recovery	25.92	1.53	16.87	0.24	Additive
12	Kernel length	0.21	0.06	3.39	0.54	Additive
13	Kernel breadth	0.03	0.02	1.49	0.81	Additive
14	Kernel L/B ratio	0.08	0.09	0.89	1.05	Non additive

The general combining ability (*gca*) effects of twelve parents *i.e.,* eight lines and four testers and specific combining ability effects (*sca*) of thirty two cross combinations were estimated according to the procedure described by Kempthorne, 1957 [16]. The character wise results of *gca* effects of the parents have been presented in the **Table 4** and *sca* effects of F_1 crosses are presented in **Table 5**. For traits like days to 50% flowering, plant height and incidence of gall midge, the negative significance is more desirable while in considering the traits like panicle length, number of productive tillers per plant, 1000-grain weight, number of filled grains per panicle, grain yield per plant, hulling per cent, milling per cent, head rice recovery per cent, kernel length, kernel breadth and kernel L/B ratio, the positive significance is much more appreciated.

The estimation of *gca* effects of the parents (**Table 4**) revealed that, none of the parental genotypes showed all the desirable traits under single roof. However, the line KNM 13555 and the testers Aganni, IBT MRR 24 were the strongest general combiners among all the parents. Since, KNM 13555 showed positive significance for grain yield per plant (1.6), 1000-grain weight (4.9), milling per cent (1.5), head rice recovery (3.0), kernel length (0.5) and kernel breadth (0.2). Whereas, Aganni reported positive significance for grain yield per plant (2.4), panicle length (0.5), number of productive tillers per plant (0.6), head rice recovery (1.6) and kernel breadth (0.06) coupled with desirable negative significance for incidence of gall midge (-1.3). The line, KNM 13568 was deemed as the best donor for grain yield per plant (5.0), panicle length (1.0), 1000-grain weight (4.7), milling per cent (0.9), head rice recovery (2.7), kernel length (0.4) and kernel L/B ratio (0.2). Moreover, tester IBT MRR 24 also showed positive significance for 1000-grain weight (2.8), hulling per cent (1.0), milling per cent (0.6), head rice recovery (1.0), kernel length (0.2) and kernel breadth (0.1).

Next to these lines, KNM 13449 was considered as good general combiner for days for 50 per cent flowering (-6.7), plant height (-4.6) and incidence of gall midge (-5.7) in addition to number of productive tillers per plant (0.8), number of filled grains per panicle (36.1) and head rice recovery (1.1); The tester, INRC 3021 showed good general combining ability towards days 50 per cent flowering (-5.1), plant height (-2.6) and incidence of gall midge (-2.2) along with kernel length (0.2) and kernel L/B ratio (0.2).

Kumar et al. (2006) [22], Priyanka et al. (2014) [23], Sreelakshmi et al. (2018) [24], Deepika et al. (2019) [25], Kour et al. (2019) [32], AnandaLekshmi et al. (2020) [28], El-Hadi et al. (2020) [35], Keerthiraj et al. (2021) [33], Singh et al. (2021) [37], Nagamani et al. (2022) [41] and Sakran et al. (2022) [43] also concluded similar results in their studies.

The information regarding *sca* effects of F$_1$s (**Table 5**) provided insights that, no individual cross combination expressed all the traits of objective. Among all the crosses, seven crosses expressed significant and positive *sca* effects for grain yield per plant. KNM 14985/IBT MRR 24 which expressed itself as good specific combiner for grain yield per plant (7.3), incidence of gall midge (-13.6) and plant height (-5.3), followed by KNM 13555/INRC 3021 (grain yield per plant, 1000-grain weight along with incidence of gall midge) and KNM 13449/IBT MRR 24 (grain yield per plant, panicle length and incidence of gall midge). Including for grain yield per plant, KNM 12469/Aganni reported better desirable *sca* effects for panicle length, number of productive tillers per plant coupled with incidence of gall midge but it had undesirable *sca* effect for plant height (9.7). KNM 12444/INRC 3021 and KNM 13449/Aganni were next best performers for grain yield per plant with respect to *sca* effects.

Similarly, the crosses KNM 12469/INRC 3021 (plant height and number of filled grains per panicle), KNM 12472/INRC 3021 (days to 50 per cent flowering and plant height), KNM 12472/WGL 1119 (grain yield per plant, days to 50 per cent flowering and hulling per cent), KNM 13449/IBT MRR 24 (grain yield per plant and panicle length), KNM 14913/WGL 1119 (panicle length and kernel length) and KNM 14985/Aganni (hulling per cent, head rice recovery per cent) were also exhibited as good specific combiners.

In their research, Bagheri et al. (2010) [18], Devi et al. (2015) [20], Bano et al. (2019) [21], Ghidan et al. (2019) [26], Budhlakoti et al. (2020) [29], Barhate et al. (2021) [30], Bassuony et al. (2021) [34], Yadav et al. (2021) [37] , Rahman et al. (2022) [42] and Ramakrishna et al. (2023) [44] also found the matching outcomes for the present study.

The *sca* effects of hybrids and the *gca* effects of their parents do not always show a direct relationship. High or low *sca* values can result from parents with either high or low *gca* values, indicating the presence of various gene interactions, such as dominance × dominance, additive × additive and additive × dominance interactions. The crosses, KNM 14913/WGL 1119, KNM 14913/Aganni and KNM 13568/Aganni have low x low, low x high, high x high *gca* effects respectively.The superior crosses identified with high x high *gca* effects can be exploited through pedigree breeding method and the better crosses with high x low and low x high *gca e*ffects can be improved through biparental mating and recurrent selection methods**.**

Table 4. Estimates of general combining ability (*gca*) effects for lines and testers for yield, yield components and quality traits in rice.

Source	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers per plant	1000 grain weight (g)	No. of filled grains per panicle	Grain yield per plant (g)	Incidence of gall midge (%)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
LINES														
KNM 12444	-0.6*	0.2	0.0	-0.8*	-2.0**	30.1**	-1.6	-6.0**	-0.01	1.3**	1.8**	-0.01	0.06 **	-0.1**
KNM 12469	6.0**	-5.1 **	-0.73**	-0.4	-2.2**	4.2	0.08	-2.0**	0.3	0.8*	2.4**	-0.2**	-0.2**	0.3**
KNM 12472	9.9**	2.8**	0.7**	0.01	-2.5**	21.0**	0.9	-1.3	0.4	0.009	3.0**	-0.2**	-0.09**	0.02
KNM 13449	-6.7**	-4.6**	-0.5*	0.8*	-3.8**	36.1**	0.5	-5.7**	-0.1	-0.1	1.1*	-0.5**	-0.1**	-0.04
KNM 13555	1.6**	-0.8	0.4	-0.07	4.9**	-36.1**	1.6*	7.6**	0.5	1.5**	3.0**	0.5**	0.2**	-0.09*
KNM 13568	-0.1	3.7**	1.0***	-0.6	4.7**	-28.0**	5.0**	9.5**	0.04	0.9*	2.7**	0.4**	-0.004	0.2**
KNM 14913	-3.9**	3.6**	-0.6*	-0.1	-2.6**	0.2	-4.5**	-4.3**	0.9*	-0.4	-0.05	-0.4**	0.01	-0.2**
KNM 14985	-6.1 **	0.1	-0.3	1.3**	3.6**	-27.5**	-2.1*	2.3**	-2.0**	-4.1**	-14.2**	0.4**	0.1**	-0.05
TESTERS														
Aganni	2.5**	7.6**	0.5**	0.6**	0.2	5.8	2.4**	-1.3**	-1.0**	0.4	1.6**	-0.2**	0.06**	-0.2**
INRC 3021	-5.1**	-2.6**	0.0	-0.0	-0.5**	-11.7*	0.7	-2.2**	-0.2	-0.4	-1.8**	0.2**	-0.05**	0.2**
IBT MRR 24	2.8**	1.0	-0.2	0.1	2.8**	-5.0	0.2	2.0**	1.0**	0.6*	1.0**	0.2**	0.1**	-0.1**
WGL 1119	-0.2	-6.1**	-0.3	-0.8**	-2.5**	10.9*	-3.42**	1.5**	0.3	-0.6	-0.7*	-0.2**	-0.1**	0.1**

*Significant at 5 per cent level, ** Significant at 1 per cent level

Table 5. Estimates of specific combining ability (*sca)* effects for yield, yield components and quality traits in rice.

S.No.	Crosses	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers per plant	1000 grain weight (g)	No. of filled grains per panicle	Grain yield per plant (g)	Incidence of gall midge (%)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
1	KNM 12444 × AGANNI	-0.6	2.6	0.4	-1.7*	1.1**	2.4	-1.2	5.0**	-0.8	-0.03	-0.6	0.09*	0.2**	-0.3**
2	KNM 12444 × IBT MRR 24	0.6	-11.5**	-1.1*	0.2	-0.2	2.4	-5.1**	0.3	-0.5	1.04	-0.1	-0.1**	-0.07	0.03
3	KNM 12444 × INRC 3021	0.6	2.5	0.7	1.7*	0.1	-15.8	5.0**	-2.0	1.5	-0.07	0.1	0.1**	0.003	0.04
4	KNM 12444 × WGL 1119	-0.5	6.3 **	-0.0	-0.2	-1.1**	10.9	1.3	-3.3*	-0.1	-0.9	0.6	-0.04	-0.1**	0.2**
5	KNM 12469 × AGANNI	0.9	9.7**	1.1*	2.9**	-0.9*	1.6	5.0**	-10.2**	-0.3	-0.3	-0.2	-0.1**	-0.1**	0.1
6	KNM 12469 × IBT MRR 24	-0.0	17.5**	1.0	-0.7	1.9**	-25.3	-3.9*	8.0**	0.9	0.9	0.5	-0.0	0.03	-0.05
7	KNM 12469 × INRC 3021	-1.3*	-16.9**	-1.1*	-2.2**	-1.7**	49.1**	-1.1	0.9	0.4	-1.2	-0.3	0.1**	-0.04	0.1
8	KNM 12469 × WGL 1119	0.4	-10.4**	-1.0	0.07	0.7	-25.3	-0.02	1.2	-1.0	0.7	0.1	0.05	0.1**	-0.2**
9	KNM 12472 × AGANNI	5.7**	7.8 **	0.3	3.0**	-0.6	19.2	3.2	-8.0**	0.2	0.1	-0.4	-0.02	-0.07	0.06
10	KNM 12472 × IBT MRR 24	-1.3*	-8.6 **	-0.6	-1.8**	0.5	14.4	-4.9**	4.1**	-0.7	-0.05	0.5	-0.1**	0.01	-0.06
11	KNM 12472 × INRC 3021	-1.9**	-21.3 **	-0.3	-0.76	-1.1**	-28.2*	-2.2	1.0	-1.4	-0.2	-0.8	0.01	-0.007	0.02
12	KNM 12472 × WGL 1119	-2.5***	22.1 **	0.6	-0.4	1.2**	-5.4	3.9*	2.8*	1.9*	0.1	0.6	0.1**	0.06	-0.02
13	KNM 13449 × AGANNI	-1.8**	-1.2	-0.7	-0.09	1.3**	-2.3	3.5*	-3.6*	-1.0	-1.7	-2.2*	-0.01	-0.4**	1.0**
14	KNM 13449 × IBT MRR 24	0.1	0.9	1.2*	0.2	0.4	-11.5	5.1**	-5.5***	0.9	-0.8	-0.3	0.2**	0.1**	-0.2*
15	KNM 13449 × INRC 3021	1.1	7.7 **	1.0	0.07	-1.0*	4.5	-4.2*	7.6***	-0.9	1.5	1.6	-0.4**	0.1**	-0.5**
16	KNM 13449 × WGL 1119	0.5	-7.4 **	-1.5**	-0.2	-0.7	9.3	-4.4**	1.6	1.1	1.06	0.9	0.1**	0.1**	-0.2**

S.No.	Crosses	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers per plant	1000 grain weight (g)	No. of filled grains per panicle	Grain yield per plant (g)	Incidence of gall midge (%)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
17	KNM 13555 × AGANNI	-1.5**	-4.7**	0.6	-1.5*	-2.1**	-9.9	-3.8*	1.9	0.09	0.1	-0.3	0.3**	0.1**	-0.04
18	KNM 13555 × IBT MRR 24	0.6	9.4**	-0.7	1.5*	-0.3	6.7	1.1	6.4**	-0.3	0.3	0.1	0.1**	0.01	0.03
19	KNM 13555 × INRC 3021	0.07	0.1	0.1	-0.6	2.5**	2.5	5.5**	-4.4**	-0.1	-0.9	-0.5	-0.05	0.06	-0.1
20	KNM 13555 × WGL 1119	0.8	-4.8**	-0.0	0.6	0.01	0.7	-2.9	-4.0**	0.4	0.5	0.7	-0.4**	-0.2**	0.1
21	KNM 13568 × AGANNI	-1.1	-10.6**	-0.8	-1.5*	-1.02*	-8.2	-4.1*	7.0***	-0.08	-0.4	-0.7	0.08	0.03	-0.08
22	KNM 13568 × IBT MRR 24	0.1	-2.0	0.9	0.4	-0.09	18.4	1.6	1.3	0.2	-0.4	0.5	-0.08	0.00	-0.02
23	KNM 13568 × INRC 3021	0.4	10.0 **	-0.6	0.9	1.3**	-4.8	-0.3	-6.8***	0.2	0.9	0.5	0.1*	-0.08	0.2*
24	KNM 13568 × WGL 1119	0.5	2.7	0.4	0.2	-0.2	-5.2	2.8	-1.5	-0.4	-0.05	-0.3	-0.1*	0.03	-0.09
25	KNM 14913 × AGANNI	-0.6	0.5	-0.1	-0.4	1.4***	14.8	-0.9	3.3*	0.2	3.3**	0.09	-0.3**	0.1**	-0.4**
26	KNM 14913 × IBT MRR 24	0.2	-0.4	-1.4*	0.2	-1.2**	-7.3	-1.2	-1.1	-0.7	-1.2	1.4	-0.05	-0.1*	0.1*
27	KNM 14913 × INRC 3021	-0.6	7.5 **	0.2	0.07	-0.2	-7.3	0.8	0.1	1.2	0.1	0.6	-0.07	-0.08*	0.1
28	KNM 14913 × WGL 1119	1.0	-7.6**	1.2*	0.07	0.1	-0.08	1.2	-2.3	-0.7	-2.2*	-2.2*	0.5**	0.06	0.1*
29	KNM 14985 × AGANNI	-0.7	-4.0*	-0.8	-0.5	0.7	-17.4	-1.7	4.6**	1.8*	-0.9	4.6**	0.007	0.1**	-0.2**
30	KNM 14985 × IBT MRR 24	-0.4	-5.3**	0.6	-0.2	-0.8*	2.2	7.3**	-13.6**	0.1	0.2	-2.7**	0.08	-0.04	0.1
31	KNM 14985 × INRC 3021	1.5*	10.2**	-0.0	0.9	0.1	0.06	-3.5*	3.5*	-0.9	-0.09	-1.2	0.1**	-0.03	0.1
32	KNM 14985 × WGL 1119	-0.3	-0.8	0.3	-0.09	-0.08	15.2	-2.0	5.5 **	-1.1	0.7	-0.6	-0.2**	-0.08*	0.01

*Significant at 5per cent level, ** Significant at 1 per cent level

Heterosis for a trait could be both positive and negative while the desired value of heterosis is dependent on the nature of the particular trait. The positive heterosis in general is used for yield whereas heterosis in negative is desired for earliness. The present study investigated heterosis over mid parent (relative heterosis), over better parent (heterobeltiosis) and over standard checks (standard heterosis) was estimated in 32 crosses for 14 characters to search out the best combination of parents giving high degree of useful heterosis and characterization of parents for their prospects for future use in breeding programme. The standard checks used were KNM 118 and KNM 1638.The estimation of heterosis aided in understanding that none of the crosses exhibited all the traits in desirable direction.

For the trait days to 50 per cent flowering, KNM 13449/IBT MRR 24 coupled with KNM 14985/IBT MRR 24 and KNM 13449/IBT MRR 24 showed standard heterosis over two checks KNM 118 and KNM 1638 respectively. Similar finding has also been reported by Faiz et al. [8] et al. (2006), Sarial (2014) [19], Ambikabathy et al. (2019) [27], Vange and Ladan (2020) [50], Azad et al. (2022) [31] and Parimala et al. (2022) [51] indicating the possibility of exploiting heterosis for earliness. For plant height, the cross KNM 12469 X WGL 1119 exploited the lowest standard heterosis over KNM 118 and KNM 1638. Utharasu et al. (2013) [52], Vange and Ladan (2020) [50], Ambikabathy et al. (2021) [53] and Islam et al. (2022) [54] also emphasized the importance of negative significant heterosis for plant height to develop dwarf plant types, in contrary to Vadivel et al. (2018) [55], Azad et al. (2022) [31] and You et al. (2022) [40] who reported positive significant heterosis for plant height. With regard to single plant yield, highest standard heterosis recorded in KNM 12469/Aganni followed by KNM 13555/INRC 3021, KNM 13568 / IBT MRR 24, KNM 12472/Aganni, KNM 13449/Aganni over KNM 118 and KNM 12469/Aganni followed by KNM 13555/INRC 3021, KNM13568/IBT MRR 24, KNM 12472/Aganni, KNM 13449/Aganni and KNM 13449/IBT MRR 24 over KNM 1638. The findings are in consonance with earlier reports Faiz et al. [8] et al. (2006), Rahimi et al. (2010) [7], Utharasu et al. (2013) [52], Vange and Ladan (2020) [50], Ambikabathy et al. (2021) [53] , Mohan et al. (2021) [2], Manivelan et al. (2022) [56], Neupane et al. (2022) [40], Parimala et al. (2022) [51], You et al. (2022) [40] and Ramakrishna et al. (2023) [44] (**Table 6**).

The significant positive standard heterosis was observed in KNM 12472/WGL 1119 for hulling percentage. Similar results are reported by Sarial (2014) [19], Sundaram et al. (2019) [57], Awad-Allah (2020) [58], Nandita et al. (2021) [59], Islam et al. (2022) [54] and Devi et al. (2022) [60]. For milling percentage, none of the crosses had significant positive heterobeltiosis or over KNM 118 and KNM 1638. The results are in agreement with the findings of Rahimi et al. (2010) [7], Utharasu et al. (2013) [52], Vadivel et al. (2018) [55], Vange and Ladan (2020) [50], Mohan et al. (2021) [2], Neupane et al. (2022) [39] and Ramakrishna et al. (2023) [41]. None of the crosses exhibited positive significant heterobeltiosis and standard heterosis over KNM 118 and KNM 1638 for head rice recovery. These results are in conformity with the findings of Singh et al. (2020) [38], Rasheed et al. (2021) [5], Azad et al. (2022) [31], Parimala et al. (2022) [51] and You et al. (2022) [40].

Table 7 depicts that based on the significant *sca* effects, *per se* performance, standard heterosis and gall midge incidence, the best cross identified were KNM 12469/Aganni, KNM 13555/INRC 3021, KNM 13568/Aganni, KNM 12472/Aganni and KNM 13449/Aganni (**Table 7**). Further these crosses may be successfully employed in breeding programme for development of gall midge resistance varieties along with high yield and good grain quality traits.

Summary and Conclusion

The current study was carried out to assess the combining ability and to estimate heterosis of rice genotypes and their crosses. The research thus concluded that, significant differences were observed among lines, testers, crosses, and interactions indicating the existence of wider adaptability in the material under study. The line KNM 13555 and the testers Aganni, IBT MRR 24 were performed as the best general combiners among the parents. On the whole, it can be emphasized that the crosses KNM 12469/Aganni followed by KNM 13555/INRC 3021, KNM 13568/IBT MRR 24, KNM 12472/Aganni and KNM 13449/Aganni were identified as promising for single plant yield, its components, quality traits and gall midge incidence. Hence, these parents and F_1 hybrids may be further tested for future crop improvement programmes.

Table 6. Estimates of heterosis over check for yield, yield components and quality traits in rice.

S.No.	Crosses	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers / plant	1000 grain weight (g)	No. of filled grains per panicle	Grain yield per plant (g)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
CHECK KNM 118														
1	KNM 12444 × AGANNI	12.4 **	18.9 **	8.9 **	-37.1 **	-25.2 **	45.7 **	12.2	-2.5	-0.9	-1.2	-14.5 **	-3.5	-11.0 **
2	KNM 12444 × IBT MRR 24	4.5 **	-4.7 *	0.5	-25.7 **	-33.8 **	34.8 **	-11.1	-1.1	-0.7	-5.9 *	-11.3 **	-23.1 **	15.3 **
3	KNM 12444 × INRC 3021	14.4 **	12.4 **	6.6 *	-11.4	-19.3 **	27.7 *	29.6 **	2.9	-0.6	-0.8	-7.8 **	-10.0 **	2.6
4	KNM 12444 × WGL 1119	9.0 **	9.1 **	2.9	-37.1 **	-45.1 **	54.1 **	-1.3	0.1	-3.4 *	-2.8	-17.0 **	-30.5 **	19.3 **
5	KNM 12469 × AGANNI	22.6 **	20.6 **	8.2 *	5.7	-34.0 **	29.2 *	46.2 **	-1.5	-1.8	0.5	-20.9 **	-33.5 **	19.5 **
6	KNM 12469 × IBT MRR 24	11.9 **	18.1 **	6.0	-31.4 **	-26.1 **	1.7	1.0	1.1	-1.4	-4.0	-13.0 **	-32.0 **	27.9 **
7	KNM 12469 × INRC 3021	20.1 **	-11.6 **	-4.3	-42.8 **	-27.2 **	51.8 **	11.0	2.1	-2.7	-0.7	-10.5 **	-26.1 **	21.3 **
8	KNM 12469 × WGL 1119	18.5 **	-12.3 **	-4.3	-31.4 **	-38.4 **	15.7	0.0	-0.6	-1.8	-2.8	-18.6 **	-32.0 **	19.5 **
9	KNM 12472 × AGANNI	33.3 **	26.5 **	11.3 **	11.4	-34.4 **	50.5 **	42.1 **	-0.6	-2.3	1.2	-19.5 **	-24.5 **	6.5
10	KNM 12472 × IBT MRR 24	15.2 **	0.6	5.4	-37.1 **	-33.0 **	36.6 **	0.1	-0.8	-3.8 *	-2.9	-13.7 **	-26.0 **	16.6 **
11	KNM 12472 × INRC 3021	24.2 **	-8.1 **	5.1	-25.7 **	-26.0 **	14.4	10.0	-0.2	-2.6	-0.4	-12.6 **	-17.8 **	6.4
12	KNM 12472 × WGL 1119	19.7 **	26.9 **	8.7 **	-31.4 **	-38.0 **	38.4 **	20.1 *	3.1 *	-3.7 *	-0.9	-17.7 **	-28.3 **	14.8 **
13	KNM 13449 × AGANNI	3.2 **	10.3 **	1.3	-8.6	-31.3 **	46.5 **	41.9 **	-3.0	-5.0 **	-4.8 *	-24.3 **	-43.9 **	35.1 **
14	KNM 13449 × IBT MRR 24	-3.7 **	2.6	7.5 *	-11.4	-38.1 **	29.9 *	41.2 **	0.4	-5.0 **	-7.5 **	-13.1 **	-20.9 **	9.7 **

S.No.	Crosses	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers / plant	1000 grain weight (g)	No. of filled grains per panicle	Grain yield per plant (g)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
15	KNM 13449 × INRC 3021	7.4 **	12.7 **	5.2	-11.4	-30.5 **	44.0 **	0.0	-0.3	-0.3	0.6	-24.1 **	-10.0 **	-15.3 **
16	KNM 13449 × WGL 1119	2.8 **	**	-6.0	-22.8 **	-50.4 **	56.8 **	-16.6	1.4	-2.7	-3.6	-21.5 **	-25.8 **	5.8
17	KNM 13555 × AGANNI	13.9 **	10.7 **	10.9 **	-28.5 **	-11.1 **	-2.8	15.3	-0.7	-0.4	1.3	-2.2 *	-1.2	-0.8
18	KNM 13555 × IBT MRR 24	7.4 **	14.5 **	3.8	-8.6	-7.3 **	-3.4	29.1 **	-0.3	-1.3	-3.5	2.3 *	-12.0 **	16.2 **
19	KNM 13555 × INRC 3021	16.4 **	9.0 **	5.6	-25.7 **	17.1 **	-1.9	45.9 **	1.6	-1.5	0.0	-2.1 *	-0.6	-1.4
20	KNM 13555 × WGL 1119	13.5 **	-2.7	4.7	-22.8 **	-13.6 **	6.9	-5.5	1.4	-1.2	-0.8	-15.3 **	-26.6 **	15.3 **
21	KNM 13568 × AGANNI	12.3 **	9.4 **	7.6 *	-34.2 **	-7.6 **	3.2	27.9 **	-1.5	-1.9	0.3	-8.3 **	-15.1 **	8.0 *
22	KNM 13568 × IBT MRR 24	4.5 **	7.8 **	13.3 **	-22.8 **	-7.1 **	8.8	45.4 **	-0.1	-3.0	-3.4	-3.6 **	-22.5 **	24.3 **
23	KNM 13568 × INRC 3021	14.8 **	23.0 **	5.3	-17.1 *	11.7 **	-1.4	34.8 **	1.5	0.3	1.5	-1.7	-17.1 **	18.6 **
24	KNM 13568 × WGL 1119	11.1 **	9.0 **	9.2 **	-31.4 **	-15.4 **	8.2	32.9 **	-0.2	-2.7	-2.9	-11. **	-25.4 **	18.6 **
25	KNM 14913 × AGANNI	8.2 **	20.1 **	3.2	-20.0 *	-26.7 **	34.9 **	1.6	0.0	1.3	-3.0	-27.9 **	-10.3 **	-19.5 **
26	KNM 14913 × IBT MRR 24	0.0	9.3 **	-3.7	-20.0 *	-40.2 **	10.3	-7.0	-0.2	-5.9 **	-6.4 **	-15.7 **	-26.5 **	14.6 **
27	KNM 14913 × INRC 3021	8.6 **	20.5 **	1.5	-20.0 *	-22.9 **	14.5	0.0	3.7 *	-2.6	-2.9	-16.9 **	-16.4 **	-0.5
28	KNM 14913 × WGL 1119	7.0 **	-1.1	5.4	-28.5 **	-42.7 **	28.8 *	-14.1	0.5	-7.3 **	-10.6 **	-14.6 **	-23.4 **	11.4 **
29	KNM 14985 × AGANNI	5.3 **	12.3 **	1.5	-8.6	-4.9 *	-2.2	8.0	-1.6	-9.3 **	-18.5 **	-8.4 **	-1.4	-7.0
30	KNM 14985 × IBT MRR 24	-3.7 **	1.1	5.9	-11.4	-14.3 **	-0.9	39.2 **	-2.7	-8.8 **	-36.0 **	-0.1	-16.8 **	20.0 **

S.No.	Crosses	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers / plant	1000 grain weight (g)	No. of filled grains per panicle	Grain yield per plant (g)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
31	KNM 14985 × INRC 3021	8.6 **	19.6 **	1.4	0.0	3.1	1.9	-8.4	-2.5	-7.8 **	-28.8 **	0.4	-7.0 *	8.2 *
32	KNM 14985 × WGL 1119	2.4 *	2.1	2.7	-17.1 *	-19.1 **	21.1	-17.7	-3.6 *	-8.3 **	-30.8 **	-12.8 **	-23.2 **	13.4 **
CHECK KNM 1638														
1	KNM 12444 × AGANNI	0.7	19.8 **	12.6 **	-15.4	22.1 **	-11.6	8.7	-3.8 **	-2.6	-0.7	2.5 *	16.5 **	-11.6 **
2	KNM 12444 × IBT MRR 24	-6.2 **	-4.0	4.0	0.0	8.2 *	-18.2 *	-13.9	-2.5	-2.3	-5.48 *	6.4 **	-7.0 *	14.6 **
3	KNM 12444 × INRC 3021	2.5 **	13.3 **	10.3 **	19.2	31.8 **	-22.5 **	25.6 *	1.5	-2.3	-0.3	10.6 **	8.7 **	1.9
4	KNM 12444 × WGL 1119	-2.2 *	10.0 **	6.5	-15.4	-10.3 **	-6.5	-4.4	-1.3	-5.0 **	-2.3	-0.4	-16.0 **	18.6 **
5	KNM 12469 × AGANNI	9.9 **	21.5 **	12.0 **	42.3 **	7.8 *	-21.5 **	41.6 **	-2.9	-3.4 *	1.0	-5.0 **	-19.7 **	18.8 **
6	KNM 12469 × IBT MRR 24	0.4	19.0 **	9.6 **	-7.7	20.6 **	-38.3 **	-2.2	-0.3	-3.0	-3.5	4.3 **	-17.8 **	27.1 **
7	KNM 12469 × INRC 3021	7.7 **	-10.9 **	-0.9	-23.0 *	18.9 **	-7.9	7.5	0.7	-4.3 **	-0.2	7.4 **	-10.8 **	20.5 **
8	KNM 12469 × WGL 1119	6.2 **	-11.6 **	-1.0	-7.7	0.6	-29.8 **	-3.1	-2.0	-3.4 *	-2.3	-2.3 *	-17.8 **	18.8 **
9	KNM 12472 × AGANNI	19.5 **	27.5 **	15.2 **	50.0 **	7.2	-8.7	37.7 **	-2.0	-3.9 *	1.8	-3.3 **	-8.7 **	5.8
10	KNM 12472 × IBT MRR 24	3.3 **	1.4	9.0 **	-15.4	9.4 *	-17.1 *	-3.0	-2.2	-5.4 **	-2.4	3.6 **	-10.6 **	15.9 **
11	KNM 12472 × INRC 3021	11.4 **	-7.4 **	8.7 *	0.0	20.8 **	-30.5 **	6.5	-1.6	-4.1 *	0.1	4.9 **	-0.7	5.7
12	KNM 12472 × WGL 1119	7.3 **	27.9 **	12.5 **	-7.7	1.3	-16.0 *	16.4	1.7	-5.3 **	-0.4	-1.3	-13.4 **	14.0 **
13	KNM 13449 × AGANNI	-7.3 **	11.2 **	4.8	23.0 *	12.2 **	-11.1	37.4 **	-4.3 **	-6.6 **	-4.4	-9.1 **	-32.2 **	34.3 **

Chelk2	Chelk2	Chelk2	Chelk2

S.No.	Crosses	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers / plant	1000 grain weight (g)	No. of filled grains per panicle	Grain yield per plant (g)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
14	KNM 13449 × IBT MRR 24	-13.6 **	3.4	11.2 **	19.2	1.1	-21.1 **	36.7 **	-1.0	-6.6 **	-7.05 **	4.2 **	-4.5	9.03 *
15	KNM 13449 × INRC 3021	-3.6 **	13.6 **	8.8 **	19.2	13.5 **	-12.6	-3.1	-1.7	-2.0	1.1	-8.8 **	8.7 **	-15.9 **
16	KNM 13449 × WGL 1119	-7.7 **	-8.2 **	-2.8	3.9	-18.9 **	-4.9	-19.2	0.0	-4.2 **	-3.1	-5.7 **	-10.4 **	5.2
17	KNM 13555 × AGANNI	2.2 *	11.5 **	14.8 **	-3.9	45.3 **	-41.0 **	11.7	-2.1	-2.1	1.8	17.4 **	19.3 **	-1.4
18	KNM 13555 × IBT MRR 24	-3.6 **	15.4 **	7.3 *	23.0 *	51.4 **	-41.4 **	25.0 *	-1.7	-3.0	-3.0	22.8 **	6.3	15.4 **
19	KNM 13555 × INRC 3021	4.4 **	9.9 **	9.2 **	0.0	91.5 **	-40.4 **	41.4 **	0.1	-3.1	0.5	17.5 **	20.1 **	-2.0
20	KNM 13555 × WGL 1119	1.9	-1.9	8.3 *	3.9	41.1 **	-35.1 **	-8.5	0.0	-2.8	-0.3	1.6	-11.3 **	14.6 **
21	KNM 13568 × AGANNI	0.7	10.2 **	11.4 **	-11.5	51.0 **	-37.3 **	23.9 *	-2.9	-3.5 *	0.8	10.1 **	2.6	7.3 *
22	KNM 13568 × IBT MRR 24	-6.2 **	8.6 **	17.2 **	3.9	51.9 **	-34.0 **	40.8 **	-1.5	-4.6 **	-2.9	15.7 **	-6.3	23.5 **
23	KNM 13568 × INRC 3021	2.9 **	24.0 **	8.9 **	11.5	82.7 **	-40.2 **	30.6 **	0.1	-1.4	2.0	18.0 **	0.2	17.8 **
24	KNM 13568 × WGL 1119	-0.4	9.8 **	13.0 **	-7.7	38.1 **	-34.3 **	28.7 **	-1.6	-4.3 **	-2.4	6.2 **	-9.8 **	17.8 **
25	KNM 14913 × AGANNI	-2.9 **	21.1 **	6.8 *	7.7	19.8 **	-18.1 *	-1.6	-1.4	-0.4	-2.5	-13.4 **	8.3 *	-20.1 **
26	KNM 14913 × IBT MRR 24	-10.3 **	10.1 **	-0.4	7.7	-2.3	-33.0 **	-10.0	-1.6	-7.4 **	-5.93 *	1.1	-11.1 **	13.8 **
27	KNM 14913 × INRC 3021	-2.5 **	21.5 **	5.1	7.7	25.9 **	-30.5 **	-3.1	2.3	-4.2 *	-2.4	-0.2	0.9	-1.2
28	KNM 14913 × WGL 1119	-4.0 **	-0.3	9.0 **	-3.9	-6.3	-21.8 **	-16.8	-0.9	-8.9 **	-10.23 **	2.5 *	-7.4 *	10.7 **
29	KNM 14985 × AGANNI	-5.5 **	13.2 **	5.0	23.0 *	55.4 **	-40.6 **	4.6	-3.0 *	-10.8 **	-18.10 **	9.9 **	19.1 **	-7.6 *

S.No.	Crosses	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers / plant	1000 grain weight (g)	No. of filled grains per panicle	Grain yield per plant (g)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
30	KNM 14985 × IBT MRR 24	-13.6 **	1.9	9.5 **	19.2	40.0 **	-39.8 **	34.8 **	-4.0 **	-10.3 **	-35.76 **	19.9 **	0.6	19.2 **
31	KNM 14985 × INRC 3021	-2.5 **	20.6 **	4.9	34.6 **	68.5 **	-38.1 **	-11.3	-3.9 **	-9.3 **	-28.49 **	20.4 **	12.2 **	7.5 *
32	KNM 14985 × WGL 1119	-8.1 **	2.9	6.2	11.5	32.2 **	-26.5 **	-20.3 *	-5.0 **	-9.9 **	-30.53 **	4.6 **	-7.26 *	12.6 **

*Significant at 5 percent level, ** Significant at 1 per cent level

Table 7. The five top F_1 crosses identified based on overall performance.

S. No.	Crosses	Average heterosis (%)	Heterobeltiosis (%)	Standard Heterosis		Mean performance of grain yield per plant (g)	*sca* effect	Gall midge reaction
				KNM 118	KNM 1638			
1	KNM 12469 X Aganni	48.32	39.93	46.24	41.61	34.70	5.04	Resistant
2	KNM 13555 X INRC 3021	48.51	47.81	45.91	41.42	34.62	5.55	Highly Resistant
3	KNM 13568 X IBT MRR 24	71.12	60.32	45.43	40.80	34.53	1.63	Highly Resistant
4	KNM 12472 X Aganni	47.33	36.04	42.13	37.72	33.72	3.20	Moderately Resistant
5	KNM 13449 X Aganni	66.94	35.80	41.92	37.43	33.62	3.55	Moderately Resistant

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