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Research Article

Assessment of genetic variability in newly developed rice (*Oryza sativa* L.) hybrids

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Abstract

The knowledge of genetic variability in a given crop species for characters under improvement is important in any plant breeding programme. Genetic parameters for yield and its correspondent characters in rice were estimated from a trial conducted at Rice Research Centre, Agricultural Research Institute, PJTSAU, Hyderabad during K*harif*, 2017. In the present study, four Cytoplasmic Male Sterility lines, eight male lines and thirty-two hybrids and four checks were evaluated. The analysis of variance showed highly significant differences among the genotypes for all the characters, indicated the presence of enormous amount of genetic variability. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for number of grains per panicle (26.55, 23.16) and grain yield per plant (21.67, 21.24) indicating that these characters could use as selection for crop improvement. High heritability coupled with high genetic gain as percentage of mean was observed for number of grains per panicle (70.26, 41.61) and 1000 grain weight (61.9, 29.52) which showed presence of additive gene action and thus the chances of fixing by selection will be more to improve such traits through pure line selection in the evaluated genotypes.

Key words
Genetic advance, Genetic variability, Heritability, Hybrids, Rice.

Introduction

Rice (*Oryza sativa* L.) is the most important cereal crop of the world and about 75 per cent of the people of Asia consume rice as staple food. In India rice is cultivated in an area of 43.8 million hectares with the production of 111.01 million tonnes with second in world rice production (*Indiastat*, 2016-17). Despite the age old human concerns about balancing population and food supplies, the world population is expected to continue to grow, possibly reaching 9-11 billion sometimes during 2030- 2050 (Shinde *et al*. 2015), to meet the growing population we need to increase rice production through development of high yielding varieties, which requires the knowledge of existing genetic variability.

The large spectrum of genetic variability in segregating population depends on the amount of the genetic variability among genotypes and offer better scope for selection. The magnitude of heritable variation in the traits studied has immense value in understanding the potential of the genotype for further breeding programme. Assessment of variability for yield and its component characters becomes absolutely essential before planning of an appropriate breeding strategy for genetic improvement. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm (Tomar *et al.*, 2016).

The genotypic coefficient of variation does not offer full scope to estimate the variation that is heritable or environmental and therefore, estimation of heritability becomes necessary. Narrow sense heritability is more effective than broad sense heritability because it considers additive genetic variability which is heritable hence more accurate towards selection (Tiwari *et al.*, 2011). Crop improvement depends on the magnitude of genetic variability and the extent to which the desirable characters are heritable.

High heritability is not enough to make efficient selection in segregating generation, unless the information is accompanied with substantial amount of genetic advance. The information on heritability alone may be misleading, when used in combination with genetic gain the utility of heritability estimate increases (Rahman *et al.*, 2014). With the above background information, the present investigation was undertaken to study the genetic parameters among the 48 rice genotypes for grain yield and yield contributing traits.

Materials and Methods

A field experiment was conducted with four CMS lines having the WA cytoplasmic background *viz*., CMS 23A, CMS 59A, CMS 64A and JMS 13A used as females and eight promising rice varieties *viz*., IET-19321, IET-26227, WGL 863, IET-26106, TP-30433, JGL 20649, JGL 5614 and JGL 21071 as males and their thirty-two hybrids generated adopting line x tester mating design in *Rabi*, 2016-17 and four checks (MTU 1010 and RNR 15048 as varietal checks, US 314 and 27-P-63 as hybrid checks). Details of 48 genotypes shown in table 1 and 2.

All the forty-eight genotypes were sown in Randomized Block Design (RBD) with two replications at Rice Research Centre, Agricultural Research Institute, PJTSAU, Hyderabad during K*harif*, 2017. A standard spacing of 30 cm x 15 cm was adopted for planting with a plot size of 1.2 m^2 each. Recommended packages of' practices were followed during the crop growth period. Observations were recorded for fourteen characters *viz*., days to 50% flowering, plant height (cm), panicle length (cm). number of productive tillers per plant, no. of grains per panicle, spikelet fertility %, 1000 grain weight (g), hulling per cent, milling per cent, head rice recovery (%), kernel length (mm), kernel breadth (mm), L/B ratio and grain yield per plant (g).

Data on days to 50% flowering recorded on plot basis at flowering stage. Five representative plants for each genotype were randomly selected to record observations on the quantitative characters under study. Data on plant height, panicle length, number of productive tillers per plant were recorded at physiological maturity and number of grains per panicle, spikelet fertility, 100-grain weight, hulling per cent, milling per cent, head rice recovery, kernel length, kernel breadth, L/B ratio and grain yield per plant were post-harvest estimates. Genotypic and phenotypic coefficients of variance, heritability and genetic advance were estimated for all fourteen characters by following standard procedures.

The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer (1981).

Heritability in the narrow sense refers to the proportion of additive variance to the total observed variance in the total population. Heritability (h^2) in the narrow sense was calculated according to the formula given by Lush (1945).

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the formula given by Burton (1952).

Results and Discussion

Variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. analysis of variance for different characters is presented in (Table-3). The treatment *i.e* mean sum of squares of genotypes showed significant differences to all 14 quantitative characters *viz*., days to 50% flowering, plant height, panicle length, number of productive tillers per plant, no. of grains per panicle, spikelet fertility, 1000 grain weight, hulling per cent, milling per cent, head rice recovery, kernel length, kernel breadth, L/B ratio and grain yield per plant shown presence of sufficient genetic variability for these traits. This indicates that there is an ample scope of selection in the present gene pool for yield and its components. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotype.

The mean values of genotypes presented in Table 4**.** The study revealed that in case of, days to 50 percent flowering showed range of 74 to 109 with a huge difference of 35 days. Among the males range varied from 82 (JGL 20649) to 109 days (IET 19321), 79 (CMS 23B) to 96 days (JMS 13B) in females and 74 (CMS 23B × JGL 20649) to 97 days (JMS13A × IET 19321) in hybrids.

The plant height ranged from 89.25 cm -131.25 cm with variation of 42 cm. The plant height for males ranged from 91.5 (JGL 20649) to 117.0 cm (IET 19321), while in the females, the range was from 89.3 (CMS 23B) to 113.3 cm (CMS 59B) and 100 (CMS23A × JGL 5614) to 131.3 cm (CMS 59A × IET19321) in hybrids.

Panicle length had variation from 22.8 (IET 26227) to 29.0 cm (IET 19321) in males, 22.3 (CMS 23B) to 25.8 cm (CMS 59B) in females and 22.3 (CMS23A × IET 26227) to 31.3 cm (CMS 59A × JGL 20649) in hybrids.

number of productive tillers per plant ranged from 12 (CMS 64B) to 16 (JMS 13B) in females, 11 (WGL 823) to 20 (JGL 5614) in males and 10 (JMS13A × JGL 20649) to 18 (CMS23A × JGL 20649) in hybrids.

No. of grains per panicle showed enormous variation from 138 (CMS 23B) to 296 (JMS 13A) in females, 114 (TP 30433) to 254 (WGL 823) in males and 140 (CMS 23A × IET 26106) to 323 (CMS 64A × WGL 823) in hybrids.

Spikelet fertility % ranged from 61.56 to 93.59 with difference of 32.03 %, 78.9 (CMS 64B) to 90.2 % (JMS 13B) in females, 80.8 (JGL 20649) to 93.0 % (IET 26106) in males and 61.6 (JMS 13A × IET 26106) to 93.6 % (JMS 13A × WGL 823) in hybrids.

1000 grain weight ranged from 12.64 g to 26.59 g with variation of 13.91 g, 17.71 (JMS 13B) to 22.22 g (CMS 59B) in females, 13.14 (WGL 823) to 25.60 g (TP 30433) in males and 13.37 (JMS 13A × WGL 823) to 26.59 g (CMS 23A × TP 30433) in hybrids.

Hulling per cent ranged from 75.42 % to 82.5 % with variation of 7.08 %, 79.2 (CMS 64B) to 80.4 % (JMS 13B) in females, 75.4 (WGL 823) to 81.3 % (JGL 5614, JGL 21071 and JGL 5614) in males,76.3 (JMS 13A × IET 26106) to 82.5 % (JMS 13A × JGL 20649) in hybrids.

Milling per cent ranged from 66.66 % to 75.41 % with variation of 8.75%, 66.7 (JMS 13B) to 75.4 % (CMS 23B) in females, 67.9 (WGL 823) to 72.5 % (IET 19321) in males and 67.1 ((CMS 64A × TP 30433) to 75.4 % (CMS 59A × IET 19321) in hybrids.

Head rice recovery (%) had values from 55 % to 70.42 % with variation of 15.42 %, 55.0 % (JGL 20649) to 67.5 % (JGL 5614) in males 58.8 (CMS 64B) to 64.5 % (CMS 23B) in females and 58.3 (CMS 23A × IET 26227) to 70.4 % (CMS 59 × TP 30433) in hybrids.

Genotypes exhibited variation of 2.67 mm with range of 5.43 to 8.10 for kernel length, 5.49 (JGL 5614) to 8.1 mm (JGL 20649) in males, 6.46 (CMS 23B) to 7.64 mm (CMS 64B) in females and 5.43 (JMS 13A × JGL 20649) to 7.87 mm (CMS 59A × IET 19321 and CMS 59A × JGL 20649) in hybrids.

Kernel breadth ranged from1.63 mm to 2.59 mm with difference 0.96 mm, 1.76 (JGL 20649) to 2.58 mm (JGL 5614) in males, 2.03 (CMS 64B) to 2.47 mm (CMS 23B) in females and 1.78 (CMS 64A × JGL 20649) to 2.51 mm (CMS 23A × JGL 5614) in hybrids.

L/B ratio displayed from range of 2.13 to 4.62 with variation of 2.49, 2.13 (JGL 5614) to 4.61 (JGL 20649) in males, 2.62 (CMS 23B) to 3.77 (CMS 64B) in females and 2.24 (CMS 23A × JGL 5614) to 3.93 (CMS 64A × JGL 20649) in hybrids.

Grain yield per plant recorded 38.6 g variation with range 18.5 to 57.1 g, 27.35 (CMS 64B) to 31.45 g (JMS 13A) in females, 23.00 (JGL 20649) to 35.20 g (IET 26227) in males and 18.50 (JMS 13A × IET 26106) to 57.10 g (CMS 64A × IET 19321) in hybrids. The study revealed that, the presence of monstrous variability in experimental material for all the traits, therefore simple selection was effective for these characters.

The extent of variability present in the genotypes was measured in terms of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), it is shown in Table 5.

The genotypes were highly variable for number of grains per panicle and grain yield per plant as indicated by the estimates of PCV & GCV (> 20 %) and revealed the existence of wide range of genetic variability in the genotypes for these traits. This also indicated broad genetic base and less environmental influence. High GCV and PCV for number of grains per panicle was in accordance with Shekawat *et al.* (2015) and Devi *et al.* (2016), high GCV and PCV for grain yield per plant was in accordance with Thippeswamy *et al.* (2016) and Lakshmi *et al.* (2017).

The genotypes were moderately variable for number of productive tillers, 1000 grain weight, kernel length and length/breadth ratio for GCV and PCV values (10.1-20 per cent). The similar results of moderate variability for number of productive tillers were reported by Dhurai *et al.* (2014), Shekawat *et al.* (2015) and Devi *et al.* (2016), 1000 grain weight by Devi *et al.* (2016), kernel length by Shekawat *et al.* (2015) and Devi *et al.* (2016) and for length/breadth ratio with moderate GCV and PCV values reported by Dhurai *et al.* (2014) and Devi *et al.* (2016), While, the genotypes were less variable for days to fifty percent flowering, plant height, panicle length, spikelet fertility, milling per cent, hulling per cent, head rice recovery and kernel breadth with low GCV & PCV values (<10). Low variability for fifty percent flowering, plant height head, rice recovery and kernel breadth observed by Rahman *et al.* (2014), Suresh *et al.* (2014) and Mohan *et al.* (2016), spikelet fertility by Shekawat *et al.* (2015), panicle length, milling per cent by Rahman *et al.* (2014), Devi *et al.* (2016) and Mohan *et al.* (2016), and low variability for hulling per cent reported by Shekawat *et al.* (2015) and Suresh *et al.* (2014).

Heritability and genetic advance are important parameters that directly affect the response to selection. Heritability is a measure of genetic relationship between parent and progeny has been widely using to assess the degree to which a character may be transmitted from parent to offspring. It also indicated that relative importance of heritability and environment in the expression of characters. The heritability is a combination with intensity of selection variability present *i.e.* the population influences the grain to be obtained from selection. If heritability of a character is very high selection would be fairly easy and effective because characters having high heritability values could be improved directly through selection as they less affected by environment (Thippeswamy *et al*., 2016).

Heritability is measure of extent of phenotypic variance caused by the actions of genes. The magnitude of heritability ranged from 12.42 % to 78.46 %. Heritability estimates were high (>60%) for days to fifty percent flowering, plant height, panicle length, number of grains per panicle and 1000 grain weight, which showed, these traits are under the control of additive genes and hence there is a good scope for the further improvement of these characters through selection. High heritability for days to fifty percent flowering and 1000 grain weight were reported by Rahman *et al*. (2014), Hasan *et al.* (2015) and Thippeswamy *et al*. (2016), plant height by Pandey *et al.* (2012) and Hasan *et al.* (2015), number of grains per panicle by Thippeswamy *et al*. (2016) and high heritability for panicle length reported by Pandey *et al.* (2012).

Moderate heritability (30-60%) was observed for kernel length, length/breadth ratio, head rice recovery and kernel breadth. Rahman *et al*. (2014) and Hasan *et al.* (2015) were also reported moderate heritability for length/breadth ratio and kernel breadth. Moderate heritability for kernel length by Pandey *et al.* (2012) and moderate heritability for head rice recovery by Hasan *et al.* (2015) and Thippeswamy *et al*. (2016). Low heritability (<30%) observed for number of productive tillers, spikelet fertility, milling percent, hulling percent and grain yield per plant. Low heritability for number of productive tillers, hulling per cent and grain yield per plant were reported by Sharma and Sharma (2007), milling per cent and grain yield per plant by Pandey *et al.* (2012) and Hasan *et al.* (2015) and spikelet fertility by Thippeswamy *et al*. (2016) and Rahman *et al*. (2014). Which implied that the environmental effects constitute a major portion of the total phenotypic variation and hence, direct selection for these traits will be less effective.

Crop improvement depends on the magnitude of genetic variability and the extent to which the desirable characters are heritable. High heritability is not enough to make efficient selection in segregating generation unless the information is accompanied with substantial amount of genetic advance. Heritability and genetic advance, when calculated together, would prove more useful in predicting the resultant effect of selection on phenotypic expression, without genetic advance the estimation of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability.

In the present study, the value of genetic advance as percentage of mean ranged from 2.03 to 42.96%. High heritability coupled with high genetic gain (>20%) as percentage of mean was observed for number of grains per panicle (41.61%) and 1000 grain weight (29.52%).

High heritability and high genetic advance for 1000 grain weight reported by Thippeswamy *et al*. (2016) and Mohan *et al*. (2016) and for number of grains per panicle by Babu *et al*. (2012), Hasan *et al*. (2015). The knowledge of heritability along with genetic advance estimates provide a better picture of genetic improvement through selection. Heritability is due to additive gene effects and thus the chances of fixing by selection will be more to improve such traits through pure line selection in the evaluated genotypes.

However, few characters like kernel length (20.95%), length/breadth ratio (29.83%) and grain yield per plant (42.96%) had moderate heritability with high genetic advance (>20%). Rahman *et al*. (2014) and Hasan *et al.* (2015) reported moderate heritability and high genetic advance for kernel length and grain yield per plant, which attributes that genetic advance is due to additive gene action and heritability was influenced by environmental factors thus the selection may be effective. These results are in accordance with Hulling percent and milling percent had low heritability and low genetic advance (<10%). Shekawat *et al.* (2015) and Mohan *et al.* (2016) reported similar results for low heritability coupled with low genetic advance as percent of mean for hulling percent and milling percent. Selection would be ineffective due to low expected gain or improvement in the next generation by these traits. Therefore, priority should be given to those traits which showed higher estimates of genetic advance as percent mean while deciding selection strategies and selection based on these characters may be useful in realizing better gain by selection.

Based on the present results it may be concluded that high heritability coupled with high genetic advance was recorded for number of grains per panicle and 1000 grain weight indicating the major role of additive gene action in the inheritance of these characters. Thus, these characters could be improved through simple selection methods. The characters showing high heritability with low genetic advance indicated the presence of non-additive gene action. Hence selection could be postponed for these characters or these characters could be improved by intermating of superior genotypes of segregation population from recombination breeding.

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Table 1. List of genotypes used for evaluation

Genotypes	Source	Features
CMS 23B	IRRI, Philippines	Maintainer line
CMS 59B	IRRI, Philippines	Maintainer line
CMS 64B	IRRI, Philippines	Maintainer line
JMS 13B	RARS, Jagital	Maintainer line
JGL 20649	RARS, Jagital	Short duration, long slender grain
JGL 21071	RARS, Jagital	Short duration, long slender grain
JGL 5614	RARS, Jagital	Medium duration, medium bold grain
IET 19321	IIRR, Hyderabad	Medium duration, medium bold grain, high yield
IET 26227	IIRR, Hyderabad	Medium duration, long bold grain
WGL 823	RARS, Warangal	Medium duration
IET 26106	IIRR, Hyderabad	Mid early duration, dwarf, medium slender grain
TP 30433	IRRI, Philippines	Short duration, long bold grain
RNR-15048	RRC, R'Nagar	Short slender grain, short duration
MTU-1010	RARS, Maruteru	Long slender grain, short duration
US-314	Private company (Seed works)	Medium slender, Short duration
27-P-63	Private company (Pioneer)	Medium slender, Medium duration

Table 2.List of experimental hybrids evaluated during *Kharif*, 2017.

Sl. No.	Crosses	Sl. No.	Crosses
1	CMS 23A × IET 19321	17	CMS 64A × IET 19321
2	CMS 23A × IET 26227	18	CMS 64A × IET 26227
3	CMS 23A × WGL 863	19	CMS 64A × WGL 863
4	CMS 23A × IET 26106	20	CMS 64A × IET 26106
5	CMS 23A × TP 30433	21	CMS 64A × TP 30433
6	CMS 23A × JGL 20649	22	CMS 64A × JGL 20649
7	CMS 23A × JGL 5614	23	CMS 64A × JGL 5614
8	CMS 23A × JGL 21071	24	CMS 64A × JGL 21071
9	CMS 59A × IET 19321	25	JMS 13A × IET 19321
10	CMS 59A × IET 26227	26	JMS 13A × IET 26227
11	CMS 59A × WGL 863	27	JMS 13A × WGL 863
12	CMS 59A × IET 26106	28	JMS 13A × IET 26106
13	CMS 59A × TP 30433	29	JMS 13A × TP 30433
14	CMS 59A × JGL 20649	30	JMS 13A × JGL 20649
15	CMS 59A × JGL 5614	31	JMS 13A × JGL 5614
16	CMS 59A × JGL 21071	32	JMS 13A × JGL 21071

Table 3. Analysis of variance for 14 different characters in rice

Source of Variation	DF	DFF	PH	PL	PT	GP	SF	GW	H	M	HRR	KL	KB	LBR	GYP
Replications	1	4.59	32.90	1.30	1.63	1502.29	0.023	0.04	0.02	0.35	0.33	0.00001	0.000001	0.000009	5.75
Treatments	47	122.97**	184.72**	11.77**	6.95**	6165.94**	82.86**	20.74**	3.96**	7.35**	22.39**	0.98**	0.072**	0.42**	102.83**
Error	47	1.84	16.74	0.42	2.59	834.44	11.31	1.26	1.38	1.84	4.81	0.03	0.0007	0.01	1.93

*Significant at P=0.05 level **Significant at P=0.01 level

DFF= Days to fifty percent flowering **PH** = Plant height **PL**= Panicle length **PT** =No of productive tillers
GP = No. of grains per panicle **SF** = Spikelet fertility **GW** = 1000 grain weight **H** =Hulling
M = Milling **HRR** =Head rice recovery **KL** =Kernel length **KB** = Kernel breadth
LBR = Length/breadth ratio **GYP** = grain yield per plant **DF =** degrees of freedom

Table 4. Mean values of genotypes for yield and yield contributing characters in rice

Parents	DFF	PH	PL	PT	GP	SF	TW	HP	MP	HRR	KL	KB	LBR	GYP
FEMALES														
CMS 23 B	79	89.3	22.3	13	138	79.7	21.45	80.0	75.4	64.5	6.46	2.47	2.62	31.1
CMS 59 B	94	113.3	25.8	15	176	80.8	22.22	79.6	69.2	63.3	7.52	2.20	3.42	30.20
CMS 64 B	94	93.3	24.5	12	167	78.9	20.22	79.2	69.2	58.8	7.64	2.03	3.77	27.35
JMS 13 B	96	109.0	24.0	16	296	90.2	17.71	80.4	66.7	60.8	6.86	2.08	3.30	31.45
MALES														
IET 19321	109	117.0	29.0	14	196	91.3	22.12	78.8	72.5	66.3	6.00	2.37	2.53	34.40
IET 26227	99	111.5	22.8	16	184	92.3	21.62	80.0	71.3	65.4	6.87	2.29	3.00	35.20
WGL 823	94	100.0	24.8	11	251	85.3	13.14	75.4	67.9	60.4	5.56	1.90	2.93	25.40
IET 26106	90	101.3	24.5	14	191	93.0	23.49	79.2	69.2	60.0	6.12	2.39	2.56	31.30
TP 30433	87	107.5	25.5	14	114	82.3	25.60	78.8	69.6	55.4	6.58	2.27	2.90	28.90
JGL 20649	82	91.5	24.8	14	183	80.8	17.59	81.3	70.0	55.0	8.10	1.76	4.61	23.00
JGL 5614	105	100.5	23.8	20	188	82.0	21.05	81.3	71.7	67.5	5.49	2.58	2.13	31.00
JGL 21071	92	108.3	26.5	14	211	92.2	18.19	81.3	70.8	62.5	6.79	1.98	3.42	31.90
Hybrids														
CMS 23A × IET 19321	86	112.5	24.0	14	202	91.0	21.54	80.4	74.6	67.1	5.75	2.33	2.46	40.40
CMS 59A × IET 19321	96	131.3	29.8	16	263	86.4	24.82	80.0	75.4	69.6	7.87	2.10	3.76	36.25
CMS 64A × IET 19321	96	113.3	24.3	13	231	84.5	22.49	80.4	70.8	67.1	7.20	2.13	3.38	57.10
JMS 13A × IET 19321	97	121.0	26.8	17	233	85.4	20.82	79.6	71.3	65.3	6.21	1.99	3.12	36.40
CMS 23A × IET 26227	77	102.8	22.3	13	193	80.6	21.26	81.0	70.8	58.3	6.97	2.12	3.29	25.50
CMS 59A × IET 26227	82	118.5	24.5	14	215	81.7	22.67	80.8	70.8	61.3	6.90	2.17	3.18	28.60
CMS 64A × IET 26227	96	105.0	23.8	13	238	78.0	20.93	81.3	70.4	58.8	7.23	2.07	3.50	35.00
JMS 13A × IET 26227	97	109.8	23.8	12	279	82.4	20.11	81.7	70.4	60.8	6.91	2.17	3.19	38.50
CMS 23A × WGL 823	77	103.8	24.0	13	160	77.0	21.92	78.8	69.2	62.9	6.92	2.15	3.21	27.20
CMS 59A × WGL 823	81	107.5	23.0	14	292	90.4	18.57	79.6	70.0	61.7	6.31	2.17	2.91	35.90
CMS 64A × WGL 823	85	107.5	24.8	14	323	92.9	17.32	80.4	69.6	63.3	6.24	2.02	3.09	42.90
JMS 13A × WGL 823	97	119.3	22.5	17	281	93.6	13.37	81.8	73.0	66.4	5.89	1.97	3.00	43.15
CMS 23A × IET 26106	84	100.8	22.9	13	140	84.5	21.07	81.0	68.5	58.8	6.44	2.20	2.93	27.00
CMS 59A × IET 26106	94	106.3	26.8	13	148	88.3	24.32	80.0	70.8	68.8	7.41	2.22	3.33	30.90
CMS 64A × IET 26106	95	104.5	24.0	13	205	85.1	22.84	80.8	70.0	64.6	7.12	2.13	3.35	33.10

JMS 13A × IET 26106	93	110.5	23.8	16	194	61.6	17.70	76.3	67.9	62.5	6.68	2.32	2.88	18.50
CMS 23A × TP 30433	82	102.5	25.5	16	161	93.4	26.59	81.3	70.8	62.5	7.18	2.19	3.28	36.50
CMS 59A × TP 30433	89	114.3	24.8	15	163	91.2	26.42	81.3	73.3	70.4	6.89	2.33	2.96	37.00
CMS 64A × TP 30433	96	113.5	27.5	12	200	77.4	20.98	79.6	70.8	62.5	7.20	2.27	3.18	24.95
JMS 13A × TP 30433	90	109.0	27.0	13	206	72.1	19.21	78.8	67.1	60.4	5.50	2.26	2.43	27.85
CMS 23A × JGL 20649	86	112.5	24.0	14	202	91.0	21.54	80.4	74.6	67.1	5.75	2.33	2.46	40.40
CMS 59A × JGL 20649	96	131.3	29.8	16	263	86.4	24.82	80.0	75.4	69.6	7.87	2.10	3.76	36.25
CMS 64A × JGL 20649	96	113.3	24.3	13	231	84.5	22.49	80.4	70.8	67.1	7.20	2.13	3.38	57.10
Hybrids														
JMS 13A × JGL 20649	80	105.0	28.5	10	286	87.5	19.85	82.5	70.8	62.5	5.43	1.96	2.77	29.50
CMS 23A × JGL 5614	83	100.0	26.5	18	171	76.6	23.30	82.1	70.4	66.3	5.62	2.51	2.24	39.60
CMS 59A × JGL 5614	91	107.8	24.0	13	201	84.1	23.33	77.5	69.2	63.8	7.24	2.17	3.34	25.60
CMS 64A × JGL 5614	89	105.8	22.8	13	195	83.2	26.34	79.8	71.0	64.2	7.15	2.10	3.40	28.45
JMS 13A × JGL 5614	90	103.5	22.5	15	320	82.0	18.99	82.1	72.9	65.8	5.59	2.38	2.35	46.90
CMS 23A × JGL 21071	80	120.3	29.5	13	229	79.9	19.33	80.0	69.6	60.4	6.21	2.28	2.72	33.80
CMS 59A × JGL 21071	85	127.5	29.0	16	254	83.2	20.06	80.4	70.0	61.3	6.66	2.16	3.08	37.55
CMS 64A × JGL 21071	89	126.8	28.8	13	265	87.3	20.20	80.4	71.3	63.8	5.79	2.20	2.63	40.15
JMS 13A × JGL 21071	91	130.0	27.0	14	290	88.9	17.90	82.3	73.3	65.1	5.58	1.94	2.88	40.50
Range Lowest	74	89.3	21.5	10	114	61.6	12.68	75.4	66.7	55.0	5.43	1.63	2.13	18.50
Range Highest	109	131.3	31.3	20	323	93.6	26.60	82.5	75.4	70.4	8.10	2.59	4.62	57.10

DFF = Days to 50% flowering
PH = Plant height (cm)
PL = Panicle length (cm)
PT = No of productive tillers per plant
GP = No. of grains per panicle
SF = Spikelet fertility (%)
TW = 1000 grain weight (g)
HP = Hulling percent
MP = Milling percent
HRR = Head rice recovery (%)
KL = Kernel length (mm)
KB = Kernel breadth (mm)
LBR = Kernel length breadth ratio
GYP = grain yield per plant (g)

Table 5. Variability, heritability and genetic advance as percent mean.

Character	Range lowest	Range highest	Range variation	Coefficient of variation		Heritability (%) (Narrow sense)	Genetic advance as percent mean at 5%
				Genotypic	Phenotypic		
Days to 50% flowering	74	109	35	8.71	8.84	78.46	17.67
Plant height (cm)	89.25	131.25	42	8.32	9.11	74.79	15.65
Panicle length (cm)	21.5	31.25	9.75	9.36	9.7	61.30	18.61
Number of productive tillers	10	19	9	10.53	15.57	12.52	14.67
Number of grains per panicle	114	322	208	23.16	26.55	70.26	41.61
Spikelet fertility (%)	61.56	93.59	32.03	7.03	8.07	20.45	12.63
1000 grain weight (gm)	12.68	26.59	13.91	15.23	16.18	61.90	29.52
Hulling (%)	75.42	82.50	7.08	1.42	2.04	3.71	2.03
Milling (%)	66.66	75.41	8.75	2.34	3.02	12.65	3.74
Head rice recovery (%)	55.00	70.42	15.42	4.73	5.85	34.84	7.87
Kernel length (mm)	5.43	8.10	2.67	10.50	10.83	57.25	20.95
Kernel breadth (mm)	1.63	2.59	0.96	8.83	8.89	51.53	17.99
Length/Breadth ratio	2.13	4.62	2.49	14.82	15.17	48.66	29.83
Grain yield per plant (g)	18.5	57.1	38.6	21.24	21.67	20.95	42.96