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GENETIC ASSESSMENT OF FERTILITY RESTORER RICE LINES FOR YIELD AND YIELD CONTRIBUTING TRAITS

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ABSTRACT

For various yield and yield-contributing parameters, 98 rice fertility restorer lines were assessed for variability, heritability and genetic advance. The experimental material was collected from Rice Improvement Project, Department of Plant Breeding & Genetics, JNKVV, Jabalpur. During *Kharif* 2021, the experiment was conducted in the Seed Breeding Farm of the Department of Plant Breeding and Genetics at the College of Agriculture, J.N.K.V.V, Jabalpur (M.P.), India. The data was recorded on three randomly selected plants for various quantitative characters. The treatment, *i.e.* mean sum of squares due to genotypes showed significant differences for all the characters studied, indicating the presence of high genetic variability among the genotypes. Results revealed that the estimates of GCV were lower than the respective PCV, indicating the influence of environmental factors on the expression of the traits studied. Fertile spikelets per panicle, number of spikelets per panicle, sterile spikelets per panicle, flag leaf width, spikelet density and 1000 seed weight were found to have the highest GCV & PCV. High heritability accompanied with high genetic advance was exhibited by spikelet density, fertile spikelets per panicle, total spikelets per panicle, grain yield per plant, flag leaf width, 1000 seed weight, flag leaf length, panicle weight, stem thickness, biological yield per plant, harvest index, panicle length, number of tillers per plant, decorticated grain L/B ratio, Sterile spikelets per panicle, stem length and plant height which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility. High heritability accompanied with moderate genetic advance was depicted by grain breadth, head rice recovery, Panicle index, decorticated grain length, decorticated grain breadth, milling %, days to 50% flowering, days to maturity and grain length suggested the role of both additive and non-additive gene action in their inheritance.

Key words : Rice, Variability, GCV, PCV, Heritability, Genetic advance.

Introduction

The genus *Oryza*, which includes the rice species Oryza sativa and *Oryza glaberrima*, also includes 22 wild species. Out of 22 natural species, 14 are diploid (2n=2x=24) according to the current taxonomic information for this crop, while the remaining 8 are tetraploid (2n=4x=48). Diploid (2n=2x=24) species include *Oryza sativa* and *Oryza glaberrima*, which are grown for food. Oryza sativa, the Asian variety of cultivated rice, is planted on a large scale throughout the world, while *Oryza glaberrima*, the African variety, is only little produced in West Africa (Chang, 1976).

Over 50% of people in the planet eat rice (*Oryza sativa* L.) as a staple diet. One of the bright, useful, sustainable and environmentally friendly possibilities to breach the rice yield ceiling is hybrid rice technology. More than 50% of the land in China is used for the cultivation of hybrid rice, and other countries including Bangladesh, India, Vietnam, the Philippines and Myanmar are now using the same technology. The most popular CMS source is the WA-CMS system, which was found in China (Yuan 1977; Lin and Yuan 1980). To grow hybrid rice successfully, restorer line is crucial. For creating F1 hybrid rice seed, the cytoplasmic genetic male sterility (CGMS) caused by nuclear-cytoplasmic interaction has been commercially utilized. The CGMS system consists of three lines: the cytoplasmic male sterile (CMS) line,

the maintainer line and the restorer line, the latter of which (the R line) carries dominant genes that restore fertility. The resultant F_1 hybrid's fertility is restored when the R line is crossed with the CMS line.

Any breeding programme intended to improve quantitative traits must take genetic variability into account when planning and carrying out its breeding strategy. As a result, the success of plant breeding is dependent on the presence of genetic variability in desired traits and the plant breeder's ability to pick desirable qualities (Adhikari *et al.*, 2018). The genetically heritable portion of the overall phenotypic variance for a characteristic is known as heritability. The improvement in the mean genotypic values of the selected population relative to the original population from which these were chosen is referred to as genetic advance. When projecting genetic gain under selection, heritability projections in combination with genetic advancements are proven to be more accurate than heredity alone.

Materials and Methods

The experimental material consisted of 99 rice fertility restorer lines, collected from Rice Improvement Project, Department of Plant Breeding & Genetics, J.N.K.V.V., Jabalpur (Table 1). The experiment was carried out at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, J.N.K.V.V, Jabalpur (M.P.) during *Kharif* 2021. The Geographical co-ordinates of study sites are 23°12'44.4"N 79°56'48.6"E. Twenty-one-day old seedlings were transplanted in the experimental site. Each genotype was planted in furrows of five-meter length and spacing of 15×20 cm with one seedling per hill. These lines were planted in randomized complete block design with three replications.

For the study of quantitative characters, three competitive plants from each replication were randomly selected and tagged for recording various quantitative characters *viz.*, Days to 50% flowering, Days to maturity, Number of tillers per plant, Number of productive tillers per plant, Plant height(cm), Stem length (cm), Flag leaf length (cm), Flag leaf width (cm), Panicle length of main axis (cm), Panicle weight per plant (g), Stem thickness (cm), Number of spikelets per panicle, Fertile spikelets per panicle, Sterile spikelets per panicle, Spikelet fertility (%), Spikelet density, Thousand (1000) seed weight (g), Grain yield per plant (g), Number of panicles per plant, Panicle index (%), Biological yield per plant (g) and Harvest index (%). The mean performance of individual genotypes was embayed for statistical analysis.

Methodology

Days to 50% flowering : The number of days taken from sowing to 50% flowering was recorded.

Days to maturity : The number of days taken from sowing to physiological maturity of plot was recorded as days to maturity.

Number of tillers per plant : Tillers were counted for each randomly selected five plants at the end of active tillering stage.

Number of productive tillers per plant : Out of the total number of tillers per plant, ear-bearing tillers were counted at maturity.

Plant height (cm) : Plant height was measured in centimeter from ground level to the tip of the panicle of main stem excluding awns if any at the time of maturity. It can also be calculated from the following formula:

Plant height (cm) = Stem length (cm) + Panicle length (cm)

Stem length (cm) : Culm length was measured in centimeter from ground level to the neck node of the panicle.

Flag leaf length (cm) : The upper leaf attached to panicle base was measured in centimeter from the base of leaf to its tip.

Flag leaf width (cm) : Flag leaf width was measured in centimeter from the middle of flag leaf in the standing crop.

Panicle length of main axis (cm) : Panicle length was measured in centimeter from neck node of the panicle to the tip of the uppermost spikelet, excluding awns if any.

Panicle weight per plant (g) : Total weight in grams of panicle was recorded after two days of sun drying.

Stem thickness (cm) : Stem thickness was measured in centimeter from the base of plant by the use of Verniercalliper.

Number of spikelets per panicle : It was counted by random selection of the panicles from each of the plant selected for observation.

Fertile spikelets per panicle : Total number of filled spikelet (filled grain) of main, average and smallest panicle for randomly selected plants was counted and average taken.

Sterile spikelets per panicle : One panicle from each plant was selected randomly and the total numbers of sterile spikelets were counted in number.

Spikelet fertility (%) : The spikelet fertilityper cent was calculated as follows

$$\text{Spikelet fertility \%} = \frac{\text{Total number of filled spikelet per panicle}}{\text{Number of spikelet per panicle}} \times 100$$

Spikelet density : It is calculated by using the following formula:

Table 1 : List of 99 rice lines used in the study programme.

S. no.	Variety	S. no.	Variety	S. no.	Variety
1.	Mahamaya	34.	RP5219-9-6-7-3-2-1-1	67.	NPT-3821
2.	R-548	35.	MTU1153	68.	E-TP-1001
3.	R-650	36.	UPR2628-9-1-1	69.	E-TP-1008
4.	R-704	37.	MTU11320-41-2-1	70.	E-TP-1014
5.	Abhya	38.	P-3123	71.	E-TP-1018
6.	R-321	39.	MC-13	72.	E-TP-1019
7.	R-296	40.	TRC2013-2	73.	E-TP-1021
8.	R-712	41.	VNR-212	74.	E-TP-1023
9.	R-710	42.	CR3424-2-2-5	75.	E-TP-1054
10.	R-304	43.	HRI-183	76.	E-TP-1062
11.	JR -503	44.	NP-9165	77.	E-TP-1064
12.	Sugandha-3	45.	CR3703-11-1	78.	IME-1101
13.	NPT-10	46.	RP5911-52-13-3-2-2-1	79.	E-TP-1124
14.	NPT-13-01	47.	CR2829-PLN-32	80.	IE-TP-2
15.	NPT-15	48.	CANP-318	81.	PS-5
16.	NPT-29	49.	ANP-526	82.	NPT-704
17.	NPT-35-01	50.	ANP-553	83.	NPT-710
18.	NPT-37	51.	Johar	84.	NPT-86
19.	NPT-65	52.	PR35766-B-24-3-18	85.	RYT-3378
20.	NPT-70	53.	IR838614-678-8	86.	PRR-812
21.	NPT(S) 81	54.	HRT-181	87.	PRR-815
22.	JNPT809	55.	JNPT-81	88.	CBSN 168
23.	NP-72	56.	JNPT-782	89.	JR(SF)-21
24.	NP-1024	57.	NPT14-12	90.	WGL-32183
25.	NP-8421	58.	JNPT767	91.	WGL-23985
26.	PSP-456	59.	JR-81	92.	NPT-82
27.	Gemini	60.	NPT-3803	93.	JAGTIAL SANALU
28.	Laxmi-144	61.	NPT-3804	94.	WGL-32100
29.	IR09N26	62.	NPT-3805	95.	JGL-3828
30.	IR-79854-38-2-4	63.	NPT-3806	96.	RPHR-612
31.	IR-79854-48-2-1	64.	NPT-3810	97.	SUREKHA
32.	AD02207	65.	NPT-3817	98.	JR-206
33.	PAU-3832-79-4-3-1	66.	NPT-3820	99.	KRANTI

$$\text{Spikelet density} = \frac{\text{Total number of spikelet per panicle}}{\text{Length of panicle (cm)}} \times 100$$

Thousand (1000) grain weight (g) : One thousand sound filled grains were sun dried up to 12% moisture level and were weighted in grams.

Grain yield per plant (g) : Individual plant was hand threshed, cleaned, dried up to 12% moisture level and weighed in grams.

Number of panicles per plant : Number of panicles for each plant is counted by the randomly selection of 5 plant in each replication.

Panicle index (%) : It was calculated by using the following formula

$$\text{Panicle index} = \frac{\text{Grain yield per plant (g)}}{\text{Panicle weight per plant (g)}} \times 100$$

Biological yield per plant (g) : Weight in grams of sun dried plants of each line after harvested from ground level (excluding roots) was recorded in grams.

Harvest index (%) : It was worked out by using the following formula:

$$\text{Harvest index} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}}$$

The data on quantitative characters were statistically analyzed based on model described by Cochran and Cox (1950) for randomized complete block design. To test

the significance of treatments, critical difference was computed (Fisher and Yates, 1963). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the method suggested by Burton (1952). Heritability for the present study was calculated in broad sense by adopting the formula as suggested by Hanson *et al*. (1956) and expected genetic advance was calculated by the method suggested by Johnson *et al*. (1955).

Results and Discussion

Genetic variability

The term "variability" describes the existence of phenotypic variations among the members of a plant population. The genotypic coefficient of variation (GCV) is a tool for quantifying the amount of genetic diversity contained in a crop species as well as the amount of variability present in certain traits. The manifestation of a character's genotypes, environment and interactions between the genotypes and environment is known as the phenotypic coefficient of variation (PCV). A successful breeding plan to develop superior cultivars depends critically on the nature and extent of GCV and PCV present in the crop species.

Results of analysis of variance indicated that, the mean sums of squares due to genotypes were highly significant for all the traits, suggesting presence of sufficient variation among the genotypes for these traits (Table 2). The outcome was consistent with the findings of Barde *et al*. (2021), Dhavaleshvar *et al.* (2019), Tiwari *et al*. (2019), Pratab *et al*. (2018) and Ranjith *et al.* (2018). Total spikelets per panicle showed the greatest variation, followed by fertile spikelets/panicle and stem length.

In the current study, it was discovered that for all traits across both the environments, the phenotypic coefficient of variation was larger in size than the genotypic coefficient of variation (Table 3). As a result, selection for such traits based solely on phenotype could also be fruitful. However, in the current study, the difference between PCV and GCV is very small, indicating that there is negligible influence of extraneous factors. This indicates that the apparent variation is not only due to genotypes, but also due to the influence of environment.

Fertile spikelets per panicle, number of spikelets per panicle, sterile spikelets per panicle, flag leaf width, spikelet density, and 1000 seed weight were determined to have the highest GCV & PCV (Table 3). As a result, these traits ought to be considered during the selection process. For a 1000 seed weight, this result did not agree with Barde *et al*. (2021). Similar findings were obtained from Dhavaleshvar *et al*. (2019), Ranjith *et al*. (2018),

Pratab *et al*. (2018) for no. of fertile spikelet and Dhavaleshvar *et al*. (2019) for no. of total spikelet; Dhavaleshvar *et al*. (2019), Tiwari *et al*. (2019), Lamichhane and Mohini (2015) for 1000 seed weight; Abebe *et al*. (2017) for number of unfilled grain per panicle; Srujana *et al*. (2017) for flag leaf width.

While medium GCV & PCV were found traits no. of tillers per plant, no. of effective tillers per plant, stem length, flag leaf length, panicle length, panicle weight, stem thickness, panicle no., biological yield per plant, harvest index, grain breadth, DGL, DGB, DG L/B and grain yield per plant (Table 3). Similar results found by Dhavaleshvar *et al*. (2019), Srujana *et al*. (2017) for grain yield; Pragnya *et al*. (2018), Lamichhane and Mohini (2015) for panicle length; Srujana*et al*. (2017) for harvest index and No. of tillers; Srujana *et al*. (2017), Lamichhane and Mohini (2015) for flag leaf length; Lamichhane and Mohini (2015) for grain width, L/B ratio and decorticated seed breadth.

Low GCV and PCV values were found for the following traits *viz.*, days to 50% flowering, days to maturity, plant height, spikelet fertility, panicle index, grain length, hulling%, milling%, and head rice recovery (Table 3). These results were like those of Pragnya *et al*. (2018), Lamichhane and Mohini (2015) for the traits of days to 50% flowering; Pragnya *et al*. (2018) for days to maturity days to maturity; Lamichhane and Mohini (2015) for hulling% and milling%.

Heritability and genetic advance

The estimations of heritability aid plant breeders in selecting elite genotypes from a diverse genetic population and serve as a reliable indicator of how traits are passed down from one generation to the next.

When compared to the base population, genetic advance shows the improvement in individual's genotype. The attribute specifically enhancing or advancing the generation is also important for genetic improvement in crop productivity and cannot be considered when choosing an elite genotype. To categorize those features that could be used as the foundation for the selection of prospective genotypes, both are therefore paired.

High heritability was expressed by 1000 seed weight, stem length, plant height, flag leaf length, days to maturity, spikelet density, total spikelets per panicle, 50% flowering days, fertile spikelets per panicle, head rice recovery, panicle weight, milling %, grain yield per plant, harvest index, panicle length, panicle index, hulling %, sterile spikelets per panicle, flag leaf width, biological yield per plant, spikelet fertility percent, stem thickness, grain length, decorticated grain length, number of tillers per plant and decorticated grain L/B ratio. This findings was in consonance with days to 50% flowering shown by

Table 2 : ANOVA for yield and quality attributing traits in fertility restorer lines.

Source of variation	d.f.	Mean sum of squares									
		DTF	DTM	NOT	NOET	PH (cm)	SL (cm)	FLL (cm)	FLW (cm)	PL (cm)	PW (g)
Replication	2	7.73	1.35	0.33	0.81	0.79	1.34	1.06	0.001	0.24	0.083
Genotype	97	128.78***	248.61***	7.31***	6.90***	408.03***	516.26***	164.05***	0.23***	35.34***	36.12***
Error	194	1.65	2.30	1.18	1.28	2.58	2.90	1.17	0.012	0.92	0.85

Source of variation	d.f.	Mean sum of squares									
		ST (mm)	TSPP	FSPP	SSPP	SF (%)	SD	1000 SW (g)	PI (%)	PN	BYPP (g)
Replication	2	0.46	154.71	141.69	2.52	0.70	0.45	0.19	5.74	0.81	0.83
Genotype	97	3.03***	13133.06***	10274.19***	388.63***	34.83***	29.24***	93.50***	129.49***	6.90***	207.54***
Error	194	0.39	166.75	138.95	18.66	3.35	0.35	0.25	5.08	1.28	17.57

Source of variation	d.f.	Mean sum of squares									
		HI (%)	GL (mm)	GB (mm)	DGL (mm)	DGB (mm)	DG L/B ratio	H (%)	M (%)	HRR (%)	GYPP (g)
Replication	2	1.63	0.19	0.028	0.15	0.08	0.237	0.44	0.65	1.62	0.32
Genotype	97	148.76***	2.23***	0.46***	1.74***	0.205***	0.956***	36.77***	64.77***	79.23***	28.06***
Error	194	3.76	0.32	0.089	0.27	0.051	0.155	1.73	1.59	1.54	0.70

*Significant at 5% level, ** Significant at 1% level

Where, TSPP-Total spikelets /panicle, FSPP-fertile spikelets / panicle, SSPP-Sterile spikelet / panicle, PH -Plant height, SSPP-Sterile spikelet / panicle, SL-stem length, BYPP -Biological Yield/ plant, PI %- Panicle index%, FLL -Flag leaf length, DTM-days to maturity, DTPI-Days to panicle initiation, PW-Panicle weight, PN-panicle no, HRR %- Head rice recovery %, M %-Milling %, GYPP -Grain yield / plant, 1000 SW- Thousand seed weight, SF%-Spikelet fertility%, H%-Hulling %, SD-Spikelet density, PL-Panicle length, NOT-Number of tillers /plant, NOET-Number of effective tillers / plant, DGL-Decorticated grain length, GL (mm)-Grain length, ST (mm)-Stem thickness, DG L/B ratio-Decorticated length/breadth ratio, GB-Grain Breadth, DGB -Decorticated grain breadth, FLW- Flag leaf width, HI -Harvest index.

Manjunatha *et al*. (2019), Longjam *et al*. (2019), Adhikari *et al*. (2018),Kumar *et al*. (2018) and Manjunatha *et al*. (2019); Plant height by Adhikari *et al*. (2018), Kumar *et al*. (2018) and Manjunatha *et al*. (2019); Manjunatha *et al*. (2019) for panicle index; Longjam (2019) and Kumar *et al*. (2018) for panicle length and number of tillers per plant; 1000 seed weight by Sarkar *et al*. (2019), Kumar *et al*. (2018), Adhikari *et al*. (2018) and Longjam*et al*. (2019); Days to maturity by Sarkar *et al*. (2019),Kumar *et al*. (2018) and Adhikari *et al*. (2018); Spikelet fertility by Longjam *et al*. (2019) and Kumar *et al*. (2018); Total spikelet per panicle, harvest index, L/B ratio by Kumar *et al*. (2018); Grain yield by Manjunatha *et al*. (2019), Kumar *et al*. (2018) and Sterile spikelet per panicle by Longjam *et al*. (2019).

High heritability accompanied with high genetic advance was exhibited by spikelet density, fertile spikelets per panicle, total spikelets per panicle, grain yield per plant, flag leaf width, 1000 seed weight, flag leaf length, panicle weight, stem thickness, biological yield per plant, harvest index, panicle length, number of tillers per plant, decorticated grain L/B ratio, Sterile spikelets per panicle, stem length and plant height (Table 3). These findings were in proximity with plant height by Manjunatha *et al*. (2019), Rajesh *et al*. (2016) and Devi *et al*. (2017); Longjam *et al*. (2019) show in number of tillers per plant and Sterile spikelets per panicle; Devi *et al*. (2017) show for flag leaf length, fertile spikelets per panicle,1000 seed weight, grain yield per plant and decorticated grain L/B ratio; Rajesh *et al*. (2016) for number of tillers per plant, panicle weight, total number of filled grains per panicle, total

Table 3 : Genetic parameter of variability for yield and its component traits.

Traits	Mean	Range		cv	H²(bs) (%)	Genetic advance	Genetic advance as % of mean	GCV%	PCV%
		Max	Min						
DTF	98.59	113.67	85.33	1.31	0.96	13.16	13.34	6.60	6.73
DTM	124.73	142.67	108.00	1.22	0.97	18.41	14.76	7.26	7.37
NOT	9.34	12.73	5.44	11.65	0.63	2.34	25.08	15.30	19.23
NOET	7.24	10.76	4.57	15.64	0.59	2.17	30.03	18.92	24.55
PH (cm)	118.34	147.30	94.71	1.36	0.98	23.72	20.05	9.82	9.92
SL (cm)	88.88	131.03	62.78	1.92	0.98	26.72	30.07	14.72	14.84
FLL (cm)	38.37	57.39	22.92	2.82	0.98	15.02	39.14	19.21	19.41
FLW (cm)	1.37	2.12	0.78	8.06	0.86	0.52	38.01	19.91	21.48
PL (cm)	25.28	32.01	17.91	3.80	0.93	6.71	26.56	13.40	13.93
PW (g)	27.29	38.50	19.47	3.39	0.93	6.82	24.99	12.56	13.02
ST (mm)	5.53	8.14	3.67	11.32	0.69	1.61	29.09	16.98	20.40
TSPP	217.58	405.33	59.00	5.94	0.96	132.89	61.08	30.22	30.79
FSPP	189.23	371.00	53.33	6.23	0.96	117.35	62.01	30.72	31.34
SSPP	28.35	60.00	5.67	15.24	0.87	21.32	75.21	39.18	42.04
SF (%)	86.96	94.70	79.33	2.11	0.76	5.81	6.68	3.73	4.28
SD	8.79	20.26	2.36	6.76	0.97	6.28	71.43	35.30	35.95
1000 SW(g)	23.02	42.27	11.35	2.18	0.99	11.44	49.69	24.22	24.32
PI (%)	79.91	93.07	62.53	2.82	0.89	12.52	15.67	8.06	8.54
PN	7.24	10.76	4.57	15.64	0.59	2.17	30.03	18.92	24.55
BYPP (g)	51.77	76.90	31.12	8.10	0.78	14.50	28.02	15.37	17.38
HI (%)	41.50	57.80	24.35	4.68	0.93	13.79	33.23	16.75	17.39
GL (mm)	8.82	11.04	7.07	6.47	0.66	1.34	15.17	9.05	11.13
GB (mm)	2.78	3.74	1.93	10.79	0.58	0.55	19.91	12.69	16.66
DGL (mm)	7.74	9.89	6.04	6.78	0.64	1.15	14.88	9.03	11.30
DGB (mm)	2.17	3.30	1.58	10.42	0.50	0.33	15.26	10.46	14.77
DG L/B ratio	3.64	5.56	2.21	10.82	0.63	0.85	23.23	14.19	17.84
H (%)	77.05	87.48	63.25	1.71	0.87	6.57	8.53	4.44	4.75
M (%)	70.96	83.37	56.00	1.78	0.93	9.12	12.85	6.47	6.71
HRR(%)	64.29	73.86	49.90	1.93	0.94	10.18	15.84	7.92	8.15
GYPP(g)	21.77	32.47	14.27	3.85	0.93	6.00	27.53	13.87	14.40

Where,
DTPI-Days to panicle initiation, DTM-days to maturity, FLL-flag leaf length, FLW-flag leaf width, NOT-Number of tillers per plant, NOET- Number of effective tillers per plant ,ST-Stem thickness, SL-Stem length, PH-Plant height, PL- Panicle length, PW-Panicle weight, PN- panicle no., FSP-fertile spikelets per panicle, TSPP-Total spikelets per panicle, SSP-Sterile spikelet per plant, SF%-Spikelet fertility percentage, SD%-Spikelet density %, 1000 SW-thousand seed weight, GL-Grain length, GW-grain breadth, DGL-Decorticated grain length, DGW-Decorticated grain breadth, DG L/B ratio- Decorticated length to breadth ratio, H%-Hulling percentage, M%-Milling pergentage HRR%- Head rice recovery, BYPP-Biological yield per plant, PI%-Panicle index, HI%-Harvest index, GYPP-Grain yield per plant.

spikelets per panicle and grain yield per plant.

High heritability accompanied with moderate genetic advance was depicted by grain breadth, head rice recovery, Panicle index, decorticated grain length, decorticated grain breadth, milling %, days to 50% flowering, days to maturity and grain length (Table 3). This finding was supported by Sreedhar *et al.* (2017) for days to 50% flowering.

Conclusion

All the major yield attributing traits showed significant variation for all characters. High GCV and PCV was observed in spikelet density, fertile spikelets per panicle, total spikelets per panicle, grain yield per plant, flag leaf width, stem thickness and thousand seed weight. Therefore, these characters should be considered in selection programme for the crop improvement programme to develop the diverse morphological breeding

lines for further utilization. High heritability coupled with high genetic advance was observed for spikelet density, fertile spikelets per panicle, total spikelets per panicle, grain yield per plant, flag leaf width, thousand seed weight, flag leaf length, panicle weight, stem thickness, biological yield per plant, harvest index, panicle length, number of tillers per plant, decorticated grain L/B ratio, stem length and plant height. This finding indicates that there is prevalence of additive gene action in inheritance of these characters.

Acknowledgement

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