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Genetic evaluation of rice restorer lines through variability, heritability and genetic advance analysis

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Abstract
Restorer lines of rice are utilized in hybrid breeding programme to meet the demand of growing population by enhancing the productivity through assessment of variability. With the aim of determining the genetic parameters of variability, the present investigation was carried out among 90 genotypes of rice plotted in randomized block design under rice improvement project at seed breeding farm, JNKVV, Jabalpur during Kharif season 2018. The 21 quantitative and 8 quality traits were observed and revealed significant difference among them through analysis of variance. Superior genotype ANP 526 based on mean yield, CBSN 168 based on quality parameters and PRR 828 based on fertile and total spikelet per panicle. The narrow magnitude of difference between GCV and PCV indicated efficient selection as less influenced by environment. The high estimate of GCV and PCV showed scope of improvement through direct selection and high heritability with high genetic advance expressed simple inherited trait along with preponderance of additive gene action. Thus, total spikelet per panicle, fertile spikelet per panicle, and spikelet density percentage were found to be high in almost all genetic parameters of variability such as mean, range, genetic advance, GCV and PCV, which could be considered in future rice breeding programme for obtaining better restorer. While, lowest GCV and PCV was exhibited for traits hulling percentage, milling percentage and head rice recovery percentage indicates need of creation of variability. None of the traits exhibited low heritability. High heritability coupled with high genetic advance was high for trait total spikelet per panicle, fertile spikelet per panicle and spikelet fertility percentage indicates that these characters are largely controlled by additive gene action, and improvement is possible through mass selection and progeny selection.

Keywords: Genetic variability, mean, range, heritability, genetic advance, GCV and PCV

Introduction
In India, rice is the staple food for 90% of Asiatic population. India secures first position in acreage with total cultivated area of 44.80 million hectare and second in production with 109.7 million tonnes. As per 2nd advance estimates, released by Department of Agriculture, Cooperation and Farmers Welfare, India's rice production has increased at 1.2 percent from last five year while area under rice cultivation remained same substantially during this period. Although, holding great rank, the average productivity of rice is low compare to other countries. With much of the potential hidden, varied ecosystem and season is one of the reasons behind the low productivity of rice. Therefore, hybrids cater to fulfil need of developing high yielding rice varieties for varied climatic condition. Restorer would contribute in such task by maintaining the fertility in hybrids.

Genetic variability analysis significantly contribute major role in recognition of differences in genetic composition and the environment in which individual were raised. This would help in selection based on superior performance. The rice breeders exploit variability for yield improvement and remarkable restorers among them can utilized as inbred for hybrid seed production. However, studied related to it, on phenotypic and genotypic variability, heritability and genetic advance of yield and associated traits remain ignored rice genotypes to sustain yield and meet the demand of rice producers. Hence, present study on ninety restores put major concern in assessment of variability to fulfil objectives and meet the demand.

Materials and methods
Under rice improvement project, the experiment was conducted over 90 genotypes plotted in Randomized complete block design with three replications and four rows each during *kharif* season 2018 at seed breeding farm, Department of Plant breeding and Genetics, college of agriculture, Jabalpur (M.P.). From each replication randomly five representative plants were selected to mark the observations.

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Overall 29 quantitative traits were undertaken which are days to 50% flowering, days to maturity, flag leaf length, flag leaf width, total tiller per plant, productive tiller per plant, stem thickness, stem length, plant height, total number of panicle per plant, panicle length, biological yield per plant, panicle weight per plant, fertile spikelet per panicle, total spikelet per panicle, spikelet fertility percentage, spikelet density percentage, thousand seed weight, panicle index, harvest index, grain length, grain width, decorticated grain length, decorticated grain width, length/breath ratio, hulling percentage, milling percentage, head rice recovery percentage and grain yield per plant.

The analysis of variance estimated through model given by Cochran and Cox (1950) [3]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the method suggested by Burton (1952) [2]. Heritability for the present study was calculated in broad sense by adopting the formula as suggested by Hanson et al. (1956) [5]. Expected genetic advance was calculated by the method suggested by Johnson et al. (1955) [7].

Result and discussion
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 acceptable amount of variability among the genotypes. Maximum variability was observed for total number of spikelet per panicle and lowest for panicle index represented in table 1. This result was in agreement with Khan et al. (2012) [9] who observed highest genetic variability for total number of spikelet per panicle.

The range and mean of genotypes for all studied traits indicated wide ranges of variation which revealed possible amount of variability among the genotypes. The relative high mean value was reported for trait total spikelet per panicle (187.65) and fertile spikelet per panicle (149.55), the former range from 61 to 434, i.e., (373) while later ranges from 45.33 to 364.66, i.e., (319.13).The subsequent values of mean were presented in table 2.

Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were categorized as low (0-10%), moderate (10-20%) and high (>20%) as indicated by Sivasubramanian and Madhavamenon. Therefore, high GCV and PCV was recorded for the traits viz., spikelet density %

followed by total spikelet per panicle, fertile spikelet per panicle and so on, as depicted in table 2. Therefore, these characters should be considered in selection programme. Similar findings were obtained from Kiani et al. (2013) [11], Islam et al. (2016) [6], Anis et al. (2016) [1], Ranjith et al. (2018) [13] and Sarker et al. (2019) [15] for fertile spikelet per panicle; Khan et al. (2012) [9], Sumanth et al. (2017) [18] and Saha et al. (2019) [14] for total spikelet per panicle. Low value of GCV and PCV was found for traits viz., head rice recovery percentage, panicle length, panicle weight per plant followed by other consecutive values described in table 2, which was similar with the findings of Islam et al. (2016) [6]; Kiani (2013) [11] for panicle length.

Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson et al. As represented in table 2, high heritability was expressed by total spikelet per panicle, followed by fertile spikelet per panicle, spikelet fertility percentage, This findings was in consonance with Islam et al. (2016) [6] Longjam et al. (2019) [12] Dongre et al. (2014) [4], Sarker et al. (2019) [15] for fertile spikelet per panicle; Tiwari et al. (2011) [19], Dongre et al. (2014) [4], Sumantha et al. (2017) [18] for total spikelet per panicle

According to Johnson et al. (1955) [8], genetic advance as percent of mean classified as low (<10%), moderate (10-20%) and high (>20%). High genetic advance was expressed by the traits such as spikelet density percentage, total spikelet per panicle, fertile spikelet per panicle and so on in table 2. Similar findings were confirmed by Dongre et al. (2014) [4], Islam et al. (2016) [6] and Saha et al. (2019) [14] for fertile spikelet per panicle.

As per described in table 3, high heritability accompanied with high genetic advance showed by fertile spikelet per panicle followed by total spikelet per panicle, spikelet fertility percentage Similar findings were confirmed by Selvaraj et al. (2016), Islam et al. (2016) [6], Longjam et al. (2019) [12] for spikelet fertility percentage; Dongre et al. (2014) [4], Islam et al. (2016) [6] and Saha et al. (2019) [14] for fertile spikelet per panicle. High heritability accompanied with moderate genetic advance showed by head rice recovery percentage, plant height, days to maturity, and panicle weight per plant. High heritability accompanied with low genetic advance exhibited by days to fifty percent flowering, hulling percentage and milling percentage.

Table 1: ANOVA for yield and quality attributing traits in fertility restorer lines

Source of variation	d.f.	Mean sum of squares									
		DFF	DTM	FLL	FLW	TT/P	PT/P	ST	SL	PH	Pa/Pl
Replication	2	0.41	0.84	28.92	0.02	3.83	1.56	2.00	14.17	22.84	1.51
Genotype	89	69.79**	161.46**	179.06**	0.16**	12.95**	11.37**	6.81**	588.51**	617.85**	12.10**
Error	178	1.31	1.71	41.55	0.017	1.45	1.82	0.85	18.52	22.60	1.49

Source of variation	d.f.	Mean sum of squares									
		PL	BY/PL	PaWt/Pl	Fsp/Pa	Tsp./Pa	SF%	SD%	ThSWt.	PI	HI
Replication	2	1.04	99.70	0.95	1174.9	3555.10	79.59	5.86	0.27	0.02	9.81
Genotype	89	13.78**	666.49**	13.75**	10102.85**	18150.93**	333.30**	33.24**	113.12**	0.11**	389.53**
Error	178	1.64	104.24	1.64	19.56	50.55	2.01	0.25	1.08	0.02	11.48

Source of variation	d.f.	Mean sum of squares								
		GL	GW	DGL	DGW	L/B	H%	M%	HRR%	Gy/pl
Replication	2	0.14	0.23	0.05	0.05	0.04	2.10	17.35	11.71	14.33
Genotype	89	3.48**	0.59**	1.95**	0.20**	0.90**	41.46**	50.86**	98.57**	83.50**
Error	178	0.04	0.04	0.02	0.01	0.03	3.96	4.41	6.90	13.60

*Significant at 5% level, ** Significant at 1% level
Where, DFF- days to fifty percent flowering, DTM-days to maturity, FLL-flag leaf length, FLW-flag leaf width, TT/P-total tiller per plant, PT/P-productive tiller per plant, ST-stem thickness, SL-stem length, PH-plant height, Pa/Pl-Number of panicle per plant, PL- panicle length, BY/Pl-biological yield per plant, PaWt/Pl-panicle weight per plant, Fsp/pa-fertile spikelet per panicle, TSp/pa-total spikelet per panicle, SF%-spikelet fertility percentage, SD%-spikelet density percentage, ThSWt.-thousand seed weight, PI-panicle index, HI-harvest index, GL-grain length, GW-grain width, DGL-decorticated grain length, DGW-decorticated grain width, L/B-length to breath ratio, H%-hulling percentage, M%-milling percentage, HRR%- head rice recovery percentage Gy/pl- grain yoked per plant.

Table 2: Genetic parameter of variability for yield and its components traits

Traits	Mean	Range		Coefficient of variation	h² (bs) (%)	Genetic advance	Genetic advance as % of mean	GCV%	PCV%
		MIN	MAX						
DFF	96.9	86	112.66	1.18	94.6	9.57	9.87	4.93	5.07
DTM	126.55	103	141	1.03	96.9	14.79	11.69	5.767	5.859
FLL	48.03	31	71	13.41	52.5	10.1	21.02	14.094	19.461
FLW	1.13	0.63	2.03	11.47	74.4	0.39	34.7	19.537	22.655
TT/P	8.59	3.77	14	14.01	72.5	3.43	39.96	22.782	26.75
PT/P	7.92	3.77	13.33	17.06	63.6	2.93	37.03	22.547	28.275
ST	6.72	2.78	9.61	13.74	69.9	2.42	36.1	20.96	25.064
SL	79.11	56.66	135	5.44	91.1	27.1	34.25	17.423	18.253
PH	104.17	79.89	163.22	4.56	89.8	27.49	26.39	13.522	14.272
Pa/PL	8.3	3.77	13.89	14.72	70.3	3.24	39.11	22.647	27.012
PL	25.05	20.89	31.33	5.12	71.1	3.49	13.94	8.028	9.523
BY/Pl	63.9	25.33	108.88	15.97	64.3	22.6	35.37	21.422	26.723
PaWt/Pl	25.05	20.89	31.33	5.12	71	3.48	13.91	8.015	9.514
Fsp/pl	149.55	45.33	364.66	2.95	99.4	119.08	79.62	38.765	38.878
TSp/pl	187.65	61	434	3.78	99.2	159.34	84.91	41.393	41.566
SF%	81.4	54.52	97.68	1.74	98.2	21.45	26.35	12.908	13.026
SD%	7.59	2.36	18.56	6.61	97.8	6.75	88.98	43.689	44.188
ThSWt.	23.19	5.46	37.56	4.48	97.2	12.41	53.51	26.351	26.73
PI	0.86	0.31	1.71	17.8	56.9	0.275	31.89	20.524	27.205
HI	35.64	12.13	83.09	9.5	91.6	22.138	62.1	31.494	32.898
GL	8.63	4.23	11.5	2.34	96.6	2.16	25.12	12.413	12.632
GW	2.65	2	5.5	8.08	79.9	0.78	29.64	16.103	18.018
DGL	6.77	5	9	2.3	96.4	1.62	23.95	11.846	12.068
DGW	2.16	1.7	3	5.11	83.8	0.47	21.89	11.614	12.691
L/B	3.18	2.15	5	5.97	88.9	1.04	32.86	16.922	17.946
H%	83.13	72	94.66	2.39	75.9	6.34	7.63	4.253	4.881
M%	79.61	65.66	93	2.26	77.8	7.15	8.98	4.942	5.603
HRR	57.55	42	77	4.56	81.6	10.28	17.87	9.605	10.634
Gy/Pl	21.56	9.24	39.84	17.09	63.1	7.9	36.63	22.382	28.167

Table 3: Heritability estimates with Genetic Advance

Characteristics	Traits
High heritability with high genetic advance	Fertile spikelet per panicle, total spikelet per panicle, spikelet fertility percentage, thousand seed weight, decorticated grain length, harvest index, total number of panicles per plant, decorticated grain width, L/B ratio, grain width, total tillers per plant, grain length, plant height, stem length.
High heritability with moderate genetic advance	Days to maturity, head rice recovery percentage panicle length and panicle weight per plant.
High heritability with low genetic advance	Days to fifty percent flowering, hulling percentage and milling percentage.

Conclusion
The conclusion declared significant variability and genotypes found superior on basis of mean yield was ANP 526, while quality parameters such as hulling %, milling % and head rice recovery was reported high in CBSN 168, along with it PRR 828 exhibited high mean value of total spikelet per panicle and fertile spikelet per panicle. This provides opportunity for rice breeders to utilize the superior restorers. High coefficient of variability indicates that there is a scope for selection and improvement of these traits, while low values displayed the need for creation of variability either by hybridization or mutation followed by selection. High heritability coupled with high genetic advance revealed that the traits were simply inherited in nature and controlled by few major genes or possessed additive gene effects. Hence, simple selection could be effective for improving those characters.

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