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Study of coefficient of variation (GCV & PCV), heritability and genetic advance in advanced generation mutant line of rice (*Oryza sativa* L.)

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Abstract
Information of the nature and degree of variability present in the population helps in selection of base material with the desirable characters which in turn determines the success of any breeding programme. We evaluated performance, variability, heritability, genetic advance, correlation coefficient and path coefficient for 18 agromorphological characters in twenty-one rice mutant lines and their parents along with 2 checks during 2018 and 2019. High values of PCV and GCV for number of tillers and effective tillers; and low for flag leaf width, flag leaf length spikelet fertility %, days to maturity and number of sterile spikelets per panicle were recorded. High heritability along with high genetic advance as percent of mean was recorded for milled grain width, grain yield per plant, fertile spikelet/ panicle, number of tillers, number of effective tillers, paddy width, plant height, paddy length, days to maturity, days to 50% flowering, decorticated grain length and milled grain length during both the year.

Keywords: coefficient of variation, heritability and genetic, advanced generation

Introduction
Rice (*Oryza sativa* L.) cultivation is about 10,000 years old. Its adaptation to wide range of production condition and diversity in quality trait has made rice as synonym to 'food' in many parts of the world. It is an important source of dietary nutrients contributing over 21% of the total calorie intake of the world's population on daily basis (Bhattacharjee *et al.,* 2002) [3]. In the present scenario when world is facing with great challenges like growing population, shrinking resources and climate change; rice is going to play a key role to ensure global food security. This directed the research in rice breeding towards the development of high yielding fertilizer responsive and short duration crops. As a result, we have experienced a much-needed leap in the rice production contributing to the 'green revolution'. But to ensure food on the plate of every person of this world we would require to further raise our crop production to about 60%–110% by 2050 (Ray *et al.* 2013) [12]. So, increase in the production level is important but at the same time it's also important to sustain that production level.

Genetic variability undoubtedly is the backbone of every crop improvement programme. Inclusions of genetically diverse genotypes increases the probability of the programme to be successful. Landraces due to their broad genetic base are store house of great genetic variability. But in the past, we have experienced extinction of several potential landraces which is the repercussions of increased acreage under high yielding varieties. Due to the repetitive use of same parents, the modern high yield rice varieties have a narrow genetic base and adaptability. Their genetic vulnerability does not allow them to withstand the constant pressure of changing climate and biotic stress for more year. Inclusions of genetically diverse potential landraces in the breeding programme can help us to breed high yielding climate resilient varieties.

Chhattisgarh has a very diverse agro-ecosystem and a home to several locally adapted indigenous rice landraces. These landraces in many cases suffers from some serious defects like lodging, long duration, shattering, etc. Due to which they become undesirable for cultivation by the farmers. Time and again mutagenesis has been used to modify and improve the genotype of population by introducing some useful genetic variations. We have tested 22 advance generation mutants derived from three landraces of Chhattisgarh namely, Mai Dubraj, Tilkormal and Jawaphool for genetic variation in yield and related traits.

Materials and Methods

The seeds of Mai Dubraj, Tilkormal and Jawaphool were subjected to gamma irradiation with 300Gy dose at the Gamma chamber facility of Bhabha Atomic Research Centre (BARC), Trombay, Mumbai. These M_1 seeds were grown at the Research cum Instructional farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. Single panicle from each of the survived M_1 plants of three populations were harvest separately and stored. To grow M_2 population panicle to row method was used. Resulting three M_2 populations were rigorously searched for plant with reduced height, earliness, and other novel characters. All panicles from the selected putative mutants from three populations were harvested separately and stored. After a series of selection, evaluation and rejection cycle of putative mutants obtained from the irradiation of three landraces, 8 mutants of Mai Dubraj, 11 mutants of Tilkormal and 2 mutants of Jawaphool were selected from M_4 and forwarded to M_5. These mutants alongside parents and 2 checks were evaluated in replicated trail using randomized block design with 2 replications for two years i.e., year 2018 and 2019.

Recording observations

Five plants from each treatment were tagged and observed to record the data regarding 18 characters namely, days to 50 % flowering, plant height (cm), total numbers of tillers, numbers of effective tillers, flag leaf length (cm), flag leaf width (cm), panicle length (cm), number of fertile spikelet per panicle, number of sterile spikelet per panicle, spikelet fertility (%), paddy length (mm), paddy width (cm), decorticated grain length (mm), decorticated grain width (mm), milled grain length (mm), milled grain width (mm), days to maturity and grain yield per plant. The data was further analysed using combined ANOVA (Cochran and Cox, 1957) [5]; phenotypic and genotypic coefficient of variation (Burton, 1952) [4]; heritability (Hanson *et al*. 1956) [6] and genetic advance (Johanson *et al*. 1955) [7].

Results

The pooled data from the two years showed mean sum of square (MSS) for the treatment was highly significant ($P \leq 0.01$) for all the 18 traits indicating presence of significant genetic variability among the mutants, their parents and check varieties (Table 1a and 1b).Among all traits, days to 50% flowering and number of effective tillers showed significant altered expression in in both the season as indicated by significant MSS of year component. The non-significance of interaction between genotype and year (G x E) for the characters except number of sterile spikelets per panicle, indicates that it the differences arising between the genotypes have strong genetic basis which is also stable throughout the year. In this study we observed a wide range of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for both years. The phenotypic coefficient of variation is the total observable variation which is the result of variation arising due to genotypic differences and environmental variations (Table 2). On the other hand, genotypic coefficient of variation is attributable entirely to the genetic variations.

According to the results of 2018 PCV and GCV were high for number of tillers and effective tillers; and low for flag leaf width, flag leaf length spikelet fertility % and days to maturity. During 2019, number of sterile spikelets per panicle exhibited high PCV and GCV while panicle length, flag leaf width, spikelet fertility %, days to maturity and grain yield per plant showed low PCV and GCV. Similar result was also reported in rice by Kumar *et al*., 2018; Basavaraja *et al*., 2013; Oladosu *et al*., 2014; Kole *et al*., 2008 [9, 1, 14, 8]. Although the value of phenotypic coefficient of variation (PCV) for all character was always found to be higher than the genotypic coefficient variation (GCV) but the differences were small in magnitude. Which suggest lower influence of environment on the expression of the characters. Hence the variations have genetic base and can be further improved by selection.

Heritability estimates are very helpful in selection of superior genotypes based on their phenotypic performance. High heritability for flag leaf length, number of tillers, decorticated width, milled grain width, grain yield per plant, fertile spikelet/ panicle, effective tillers, paddy width, plant height, paddy length, days to maturity, days to 50% flowering, decorticated grain length, milled grain length indicates the high role of additive gene action in governing these traits suggesting that the phenotypic selection would be effective for improving the overall mean for these characters (Table 2) (Singh *et al.* 2018) [2]. To make selection more effective heritability should be coupled with genetic advance (Johanson *et al.*, 1955) [7]. Because heritability estimates together with the genetic advance as per of mean gives the idea about the quantum of enhancement that can be made upon phenotypic selection (Laltitha *et al.*, 2019) [10]. Estimates of heritability and genetic advance showed large variation. During 2018 the estimates of heritability (%) ranged from 18.81 % to 99.09 % while genetic advance as percent of mean ranged from 3.17 % to 47.81 %. Whereas during 2019 estimates of heritability ranged from 42.45 % to 98.82 and that of genetic advance as percent of mean ranged from 5.26 % to 35.97 %. High heritability along with high genetic advance as percent of mean was recorded for milled grain width, grain yield per plant, fertile spikelet/ panicle, number of tillers, number of effective tillers, paddy width, plant height, paddy length, days to maturity, days to 50% flowering, decorticated grain length and milled grain length during both the year. It indicates the predominance of additive gene action in governing expression of these traits. Selection for further improving these traits would be rewarding. Similar findings were reported by (Pandey *et al*., 2009; Seyoum *et al.*, 2012) [11, 13].

Table 1 (a): Combined analysis of variation for all agromorphological characters

SV	DF	DFF	PH	PL	TL	ETL	FLL	FLW	FS/P	SS/P
Replication	1									
Factor A	25	885.49**	1427.48**	14.35**	12.50**	10.75**	36.63**	0.044**	1893.71**	156.77**
Factor B	1	20.35**	0.81	2.82	6.70*	2.59*	0.65	0.01	1.99	40.61
A X B	25	3.92	8.02	1.00	0.37	0.21	0.96	0.01	52.79	76.18
Error	51	2.81	13.37	3.31	1.08	0.49	2.29	0.01	133.79	29.21**
Total	103									
CD										
Factor(A)		2.38	5.20	2.59	1.47	1.00	2.15	0.14	16.47	7.69
Factor(B)		0.66	NS	NS	0.41	0.28	NS	NS	NS	NS
(A X B)		NS	NS	NS	NS	NS	NS	NS	NS	10.88

Table 1 (b): Combined analysis of variation for all agromorphological characters

SV	DF	SFP	PDL	PDW	DGL	DGW	MGL	MGW	DTM	GY
Replication	1									
Factor A	25	51.65**	3.48**	0.23**	3.30**	0.18**	3.31**	0.16**	658.08**	21.94**
Factor B	1	12.50	0.04	0.01	0.02	0.01	0.01	0.01	2.78	2.88
A X B	25	11.93	0.01	0.01	0.01	0.01	0.01	0.01	3.89	1.43
Error	51	8.25	0.01	0.01	0.01	0.01	0.01	0.01	2.96	1.58
Total	103									
CD										
Factor(A)		4.09	0.17	0.12	0.16	0.13	0.14	0.12	2.45	1.79
Factor(B)		NS	NS	NS	NS	NS	NS	NS	NS	NS
(A X B)		NS	NS	NS	NS	NS	NS	NS	NS	NS

Table 2: Estimation of mean, GCV, PCV, heritability and genetic advance as percent of mean

	Mean		h^2		GCV		PCV		Genetic Advance		Genetic Advance % means	
	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018	2017	2018
DFF	104.42 ± 2.07	103.54 ± 2.04	98.79	98.68	14.38	14.21	14.46	14.31	30.73	30.11	29.43	29.09
PH	116.98 ± 2.56	117.14 ± 2.69	95.93	96.58	15.60	16.45	15.92	16.74	36.81	39.01	31.47	33.30
PL	22.71 ± 0.33	23.04 ± 0.32	36.08	42.45	6.35	6.54	10.52	10.03	1.78	2.02	7.82	8.77
TL	8.33 ± 0.28	8.83 ± 0.25	75.05	65.55	21.34	16.72	24.63	20.65	3.17	2.46	38.08	27.89
ETL	6.94 ± 0.26	7.25 ± 0.22	86.33	78.42	24.98	19.342	26.88	21.84	3.32	2.56	47.81	35.28
FLL	28.78 ± 0.46	28.62 ± 0.43	71.12	86.03	9.81	10.20	11.63	10.99	4.90	5.58	17.04	19.48
FLW	1.48 ± 0.02	1.48 ± 0.02	18.81	61.73	3.55	7.25	8.19	9.22	0.05	0.17	3.17	11.73
FS/P	162.56 ± 3.11	162.86 ± 3.35	85.05	67.35	12.86	12.29	13.94	14.98	39.71	33.85	24.42	20.79
SS/P	31.94 ± 1.02	30.69 ± 1.32	66.76	56.52	19.03	23.23	23.29	30.89	10.23	11.04	32.03	35.97
SFP	83.39 ± 0.59	84.09 ± 0.64	72.78	46.56	4.43	3.74	5.19	5.49	6.49	4.43	7.78	5.26
PDL	8.38 ± 0.13	8.34 ± 0.13	98.11	98.59	11.18	11.05	11.29	11.13	1.91	1.89	22.81	22.60
PDW	2.14 ± 0.03	2.14 ± 0.03	90.25	87.38	10.95	10.83	11.53	11.59	0.46	0.45	21.43	20.86
DGL	6.28 ± 0.13	6.25 ± 0.13	98.8	98.57	14.41	14.56	14.50	14.67	1.85	1.86	29.51	29.79
DGW	1.83 ± 0.03	1.82 ± 0.03	80.08	85.35	10.44	12.03	11.67	13.02	0.35	0.42	19.25	22.90
MGL	6.04 ± 0.12	6.02 ± 0.13	99.09	98.82	14.945	15.20	15.02	15.29	1.85	1.87	30.65	31.13
MGW	1.60 ± 0.03	1.59 ± 0.03	83.13	84.76	12.04	12.52	13.21	13.60	0.36	0.38	22.61	23.74
DTM	134.27 ± 1.80	133.94 ± 1.75	98.16	98.29	9.677	9.42	9.77	9.50	26.52	25.77	19.75	19.24
GY	23.07 ± 0.37	23.40 ± 0.33	84.69	67.31	10.84	8.46	11.78	10.31	4.74	3.35	20.55	14.30

DFF= Days to 50% flowering, PH= Plant height, PL= Panicle length, T= Tillers, ET= Effective tillers, FLL= Flag leaf length, FLW= Flag leaf width, FS/P= Fertile spikelets per panicle, SS/P= Sterile spikelets per panicle, SF= Spikelet fertility %, PD L= Paddy length, PD W= Paddy width, DGL= Decorticated grain length, DGW= Decorticated grain width, MGL= Milled grain length, MGW= Milled grain width, DTM= Days to maturity, Cr GY= Correlation coefficient of gain yield per plant, h2=broad sense heritability, GCV=genotypic coefficient of variation, PCV= Phenotypic coefficient of variation,

Conclusion

Genetic variation plays an important role in the development of better varieties to increase and sustain the crop production. Improvement of landraces through mutation breeding can help us to attain this objective. 21 mutants line developed from three landraces along with 2 checks were evaluated to determine genetic diversity for 18 characters which includes yield and other related traits. Results showed presence of large genetic variation for all the characters. However, days to 50% flowering, plant height, days to maturity, fertile spikelet per panicle and paddy length, decorticated grain length and milled grain length showed high heritability along with high genetic advance as percent of meanwhile 50% flowering, plant height, days to maturity displayed the negative correlation with grain yield and rest all showed a positive effect on the grain yield. The overall result suggests that the selection of lower plant height early flowering and maturity along with long grain length and high fertile spikelet per panicle would help in improving the grain yield among the genotypes under study.

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