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Induced variability and association of traits in the mutant lines of red rice variety MO4

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Abstract

The present investigation was carried out with 120 mutant lines of red rice variety MO4 induced by gamma rays (15, 25, 35 and 45kR) along with the two untreated checks MO4 and Jyothi. These were evaluated for induced variability and character association using Randomized complete block design during Kharif 2019 at Zonal Agricultural and Horticultural Research Station, Bhramavar. Analysis of variance exhibited highly significant differences among the mutant lines for all the characters studied. High magnitude of GCV and PCV accompanied with high heritability and genetic advance as per cent mean was observed in number of grains per panicle and number of filled grains per panicle, indicating that these traits could be used as selection indices for yield improvement. Trait association of yield contributing traits revealed significantly positive association with test weight, straw yield per plant and harvest index. Path coefficient analysis revealed harvest index, straw yield per plant, plant height, number of grains per panicle, spikelet fertility, number of tillers per plant, test weight kernel length and kernel breadth had direct positive effect on yield. Among these traits harvest index expressed both positive and high direct effects. Thus, this trait perhaps used as selection criteria in further crop improvement strategy.

Keywords: induced variability, association, PCV, GCV, path coefficient analysis, harvest index

Introduction

Rice (*Oryza sativa* L. 2n = 24) is a basic food crop and it is the most widely grown cereal crop in the world. In contempt of its position amidst the greatly placed cereals, it plays a pivotal role in feeding the millions of people worldwide, as it serves as a chief source of food. Different colors, such as purple, brown, red and white occur in the pericarp of rice. The red pigment in rice grains is due to the presence of proanthocyanidins pigment (Oki *et al.*, 2002) [15]. Proanthocyanidin pigments have shown important deterrent effects on pathogens and predators (Scalbert, 1991) [21]. It also possesses several medicinal properties which promotes blood circulation and digestion. Iron and zinc content of red rice is 2 – 3 times higher than that of white rice (Ramaiah and Rao, 1953) [18]. It also has more Vit $B_{1,}$ Vit $B_{2,}$ Vit C, N, P, K, S, Mg, Ca and edible cellulose than achromatic rice (Jing *et al*., 2000) [9]. In order to meet the demands of the growing population and to assure global food security along with nutritional value, there is a need for increasing crop yields. With the sharp increase in lifestyle-related issues and diseases, red rice again finds favours with health-conscious consumers. While the serviceability and healthy food value of red rice have increased its vogue, such that market demand for it is expected to be increased, but most of the red rice varieties suffer from low grain yield. So, there is a need for improving the red rice varieties. To initiate any crop improvement program, the presence of adequate genetic variability and its critical analysis is needed. Among the various methods of crop improvement, mutagenesis is one such powerful tool. Genetic variations are the pre-requisite for the plant breeding. Mutations are the paramount source of genetic variations. Association analysis measures the natural relationship between various plant characters and determines the components on which selection can be made for improvement. Correlation analysis has commonly used to estimate the association of different traits with grain yield or to establish the potential utility of secondary traits to improve selection efficiency. Path analysis would give a better insight into cause and effect relationship between different pairs of characters. Considering the significance of genetic variability and association of traits as the selection criteria for crop improvement strategy, the present study was conducted on mutant lines of red rice variety MO4.

Material and Methods

The experiment was conducted on mutant lines of red rice variety MO4, comprising of 120 mutant lines, thirty mutant lines from each treatment (15, 25, 35, and 45kR) and two checks (MO4 and Jyothi) during *kharif* 2019 at Zonal Agricultural and Horticultural Research Station, Bhramavar, Udupi District, Karnataka. The experiment was carried out in acidic soil pH of 5.5 which is located at the latitude 13° 25′ North and 75°45′ East longitude. The experiment was performed in a Randomized Complete Block Design (RCBD) with two replications. The seedlings were raised in wet nursery method, followed required agronomic practices and twenty-one days old seedlings from each treatment were transplanted to the well-prepared puddled field on 28th June 2019 at a spacing of 20 cm × 15 cm between row to row and plant to plant respectively. The required cultural operations and plant protection measures as per package of practice recommended were taken up to ensure uniform and healthy crop.

Five randomly selected plants from each mutant line was labelled for recording the observations on the characters *viz.*, days to fifty per cent flowering, days to maturity, plant height (cm), number of tillers per plant, number of productive tillers per plant, panicle length (cm), number of grains per panicle, number of filled grains per panicle, spikelet fertility, grain yield (g), test weight (g), straw yield per plant, harvest index, kernel length and kernel breadth. The average of observations recorded on these five plants was considered for statistical analysis. The data of mean value for all the characters were analysed for their variance following Randomized Complete Block Design outlined by Cochran and Cox (1957) [3]. The phenotypic and genotypic coefficient of variability, heritability (broad sense), genetic advance as per cent of mean, phenotypic correlation coefficient and path coefficient analysis were computed using statistical package WINDOSTAT version 9.3. The heritability and genetic advance as per cent mean were determined on the basis of criteria given by Robinson *et al.* (1949) [20] and Johnson *et al.* (1955) [10] respectively.

Table 1: Heritability was classified as suggested by Robinson *et al.* (1949) [20] depicted as follows

Classification	Heritability
Low	Less than 30%
Moderate	30-60%
High	More than 60%

Table 2: The genetic advance as per cent of mean was categorized as suggested by Johnson *et al.* (1955) [10] as

Classification	GAM
Low	0-10%
Moderate	10-20%
High	More than 20%

Result and Discussion

The analysis of variance of mutant lines and the two checks in the M_3 generation with respect to fifteen quantitative characters revealed that the mean sum of squares due to mutant genotypes were highly significant for all the characters studied indicating the presence of genetic variability among the experimental material (Table 3). PCV estimates for all the characters under study were higher than the corresponding GCV. However, for these traits the disparity between PCV and GCV was less suggesting the low environmental impact and predominance of genetic factors controlling variation in these traits. The highest phenotypic and genotypic coefficient of variation were exhibited by number of filled grains per panicle (38.78 and 36.16%) followed by number of grains per panicle (34.75 and 34.61%), number of productive tillers per plant (28.89 and 24.66%) and number of tillers per plant (23.81 and 20.09%) (Table 4). Similar findings were delineated by Durai *et al.* (2001) [4], Chakraborty and Chaturvedi (2014) [2], Ekka *et al.* (2015) [5], Sharma *et al.* (2014) [22] and Pandey *et al.* (2018) [16] for number of productive tillers per plant, number of grains per panicle and number of filled grains per panicle, Gour *et al.* (2017) [7] and Pandey *et al.* (2018) [16] for number of tillers per plant. This indicates the existence of wide genetic base among the mutant lines taken for study and possibility of genetic improvement through direct selection for these traits.

High heritability (broad sense) coupled with high genetic advance was recorded in number of tillers per plant (71.16, 34.91), number of productive tillers per plant (72.88, 43.38), number of grains per panicle (86.57, 63.86), number of filled grains per panicle (86.99, 69.49), straw yield per plant (85.20, 31.64) and harvest index (80.30, 28.10) indicating heritability for these traits is due to additive gene action and perhaps selection is effective. These results are in accordance with the findings of Gour *et al.* (2017) [7], Kranti kumar *et al.* (2015) [14] and Hasan *et al.* (2013) [8].

High GCV and PCV coupled with high heritability and high genetic advance as mean were observed for the number of tillers per plant, the number of productive tillers per plant, number grains per panicle, number of filled grains per panicle and harvest index. High GCV and PCV indicates reduced environmental impact. High heritability accompanied with high GAM specifies the predominance of additive type of gene action in controlling these traits. Thus, an evidently important contribution of additive genetic variance is involved in the expression of these traits. Hence, good response to selection can be attained in early generations in improving those traits.

The study of correlation analysis revealed that, at the phenotypic level, grain yield had a positive and significant association with harvest index, straw yield per plant and test weight (Table 5). These results are in accordance with Ramya *et al.* (2017) [19] for straw yield per plant, Gour *et al.* (2017) [7] for harvest index and straw yield per plant, Sravan *et al.* (2012) [23], Kalyan *et al.* (2017) [11] for test weight and harvest index. Besides, it exhibited positive phenotypic association with days to fifty percent flowering, plant height, panicle length, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, spikelet fertility, and kernel length. These results align with the previous work of Allam *et al.* (2015) [1], for number of tillers per panicle, number of productive tillers per panicle and number of grains per panicle, Wattoo *et al.* (2010) [24] for spikelet fertility and panicle length. Therefore, the selection of these traits will be beneficial in the process of yield improvement program.

The phenotypic correlations of grain yield per plant with other quantitative characters were partitioned into their corresponding direct and indirect effects through path coefficient analysis. The results of path coefficient analysis revealed that the harvest index followed by straw yield per plant, plant height, number of grains per panicle, spikelet fertility, number of tillers per plant, test weight, kernel length and kernel breadth showed a direct positive effect on grain yield and also exhibited a positive correlation with grain yield at a phenotypic level (Table 6) indicating that, these traits can be considered as a selection criterion in the yield improvement program. These results were similar to the results depicted by Kole *et al.* (2008) [13], Gopikannan and Ganesh (2013) [6], Khalid *et al.* (2012) [12], and Panja *et al.* (2017) [17]. In the present study, very low residual effect of 0.0910 indicated that the traits included in this study explained high percentage of variation in the grain yield.

Table 3: Analysis of variance for yield and its components in the mutant lines of M_3 generation of red rice variety MO4

Source of variation	Df	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Number of tillers per plant	Number of productive tillers per plant	Number of grains per panicle	Number of filled grains per panicle
Replication	1	0.89	1.84	25.25	1.02	1.59	0.57	17.69	61.80
Genotype	121	53.02**	23.76**	170.43**	6.22**	21.59**	21.12**	1930.89**	1603.56**
Error	121	2.28	2.16	53.16	2.81	3.63	3.31	106.18	111.29
CD (5%)		2.99	2.91	14.43	3.32	3.77	3.60	20.40	20.91
CD (1%)		3.95	3.85	19.08	4.39	4.99	4.76	26.96	27.64
CV (%)		1.82	1.36	7.20	9.26	12.79	15.04	11.17	13.98

Source of variation	Df	Spikelet fertility (%)	Test weight (g)	Grain yield per plant (g)	Straw yield per plant (g)	Harvest index (%)	Kernel length (cm)	Kernel breadth (cm)
Replication	1	20.02	0.54	3.28	6.31	0.01	0.001	0.0004
Genotype	121	57.89**	1.60**	12.74**	54.16**	56.03**	0.006**	0.0019**
Error	121	24.03	1.17	3.57	4.34	6.10	0.003	0.0007
CD (5%)		9.70	2.15	3.74	4.20	4.99	0.11	0.05
CD (1%)		12.82	2.84	4.95	5.62	6.68	0.15	0.06
CV (%)		6.06	5.29	9.39	6.95	7.53	6.90	4.06

Table 4: Estimates of mean, range, PCV, GCV, heritability and genetic advance per cent of mean for yield and yield components traits in the mutant lines of M_3 generation of rice variety MO4

Sl no	Characters	Mean ± SE_m	Range		Coefficient of variation (%)		H^2 broad sense (%)	GAM (%)
			Minimum	Maximum	PCV	GCV		
1	Days to 50% flowering	82.74±1.06	71.75	88.35	6.35	6.08	91.73	12.01
2	Days to maturity	107.68±1.04	92.90	113.25	3.34	3.04	83.28	5.73
3	Plant height(cm)	101.16±5.15	78.60	121.65	10.45	7.56	52.45	9.29
4	Panicle length (cm)	18.09±1.18	13.10	21.00	11.74	7.21	37.75	9.13
5	Number of tillers per plant	14.91±1.34	8.50	14.91	23.81	20.09	71.16	34.91
6	Number of productive tillers per plant	12.09±1.28	5.50	21.45	28.89	24.66	72.88	43.38
7	Number of grains per panicle	92.21±7.28	50.25	167.85	34.75	34.61	86.57	63.86
8	Number of filled grains per panicle	75.51±7.43	34.25	152.45	38.78	36.16	86.99	69.49
9	Spikelet fertility (%)	80.84±3.45	66.45	92.40	7.91	5.08	41.33	6.74
10	Test weight (g)	20.52±0.76	18.4	22.50	5.75	2.25	15.38	1.82
11	Straw yield per plant(g)	36.59±1.47	30.30	44.90	18.03	16.64	85.20	31.64
12	Grain yield per plant (g)	20.13±1.33	15.25	26.40	14.18	10.63	56.17	16.41
13	Harvest index (%)	35.46±1.42	29.3	41.05	16.98	15.22	80.30	28.10
14	Kernel length(cm)	0.83±0.04	0.60	0.90	8.53	5.01	34.52	6.06
15	Kernel breadth(cm)	0.34±0.01	0.20	0.35	1.94	1.20	37.90	1.52

Table 5: Estimates of phenotypic correlation coefficients for fifteen yield and its components characters in the mutant lines of M_3 generation of red rice variety MO4

Traits	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
X_1	1.000													
X_2	-0.0155*	1.000												
X_3	0.7580**	0.0358	1.000											
X_4	-0.0265	-0.1112	-0.0493	1.000										
X_5	0.1727**	-0.2175**	0.0001	0.0976	1.000									
X_6	0.1350*	-0.1979**	-0.0379	0.0774	0.8942**	1.000								
X_7	0.0452	-0.1072	-0.0446	0.2474**	0.1282*	0.1167	1.000							
X_8	0.0443	-0.1618**	-0.0684	0.2268**	0.1122	0.1179	0.9246**	1.000						
X_9	-0.0014	-0.1006	-0.0801	0.0782	-0.0153	0.0374	0.4200**	0.7022**	1.000					
X_{10}	0.0842	-0.0855	-0.0002	0.0687	0.1166	0.0845	0.0920	0.1112	0.1282*	1.000				
X_{11}	-0.0005	0.0212	0.0061	-0.0611	-0.0417	-0.0250	-0.0190	0.0076	0.0942	0.1154	1.000			
X_{12}	0.1013	-0.1782**	0.0109	0.0510	0.1262*	0.0942	0.1934	0.2172**	0.1728**	0.2351**	-0.2719**	1.000		
X_{13}	-0.0133	0.0176	0.1121	-0.0254	-0.1116	-0.0926	0.0440	0.0491	0.0367	-0.0644	-0.0538	0.1116	1.000	
X_{14}	0.0461	-0.0317	0.0625	0.0536	0.0740	0.0378	0.0104	0.0176	0.0127	-0.0627	0.0014	-0.0964	-0.1165	1.000
X_{15}	0.0922	-0.1492	0.0159	0.0002	0.0927	0.0749	0.1661	0.2094	0.2377	0.2988**	0.5344**	0.6630**	0.0549	-0.0778

*, ** Significance at 5% and 1% respectively,

Where,

X1-Days to fifty percent flowering (days) X2- Days to maturity (days) X3- Plant height (cm) X4 - Panicle length (cm) X5-Number of tillers per plant X6-Number of productive tillers per plant X7- Number of grains per plant X8-Number of filled grains per plant X9-spikelet fertility (%) X10-Test weight (g) X11-Straw yield per plant (g) X12-Harvest index (%) X13- kernel length (cm)

X14- kernel breadth (cm) X15- Grain yield per plant (g)

Table 6: Estimates of Phenotypic path coefficient analysis for fifteen yield and its components characters in the mutant lines of M_3 generation of red rice variety MO4

Traits	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
X_1	-0.0026	0.0004	-0.0020	0.0001	-0.0005	-0.0004	-0.0001	-0.0001	0.0000	-0.0002	0.0000	-0.0003	0.0000	-0.0001
X_2	0.0014	-0.0089	-0.0003	0.0010	0.0019	0.0018	0.0010	0.0014	0.0009	0.0008	-0.0002	0.0016	-0.0002	0.0003
X_3	0.0035	0.0002	0.0046	-0.0002	0.0000	-0.0002	-0.0002	-0.0003	-0.0004	0.0000	0.0000	0.0001	0.0005	0.0003
X_4	0.0000	0.0002	0.0001	-0.0016	-0.0002	-0.0001	-0.0004	-0.0004	-0.0001	-0.0001	0.0001	-0.0001	0.0000	-0.0001
X_5	0.0040	-0.0051	0.0000	0.0023	0.0233	0.0208	0.0030	0.0026	-0.0004	0.0027	-0.0010	0.0029	-0.0026	0.0017
X_6	-0.0013	0.0020	0.0004	-0.0008	-0.0089	-0.0100	-0.0012	-0.0012	-0.0004	-0.0008	0.0002	-0.0003	0.0009	-0.0004
X_7	0.0019	-0.0046	-0.0019	0.0106	0.0055	0.0050	0.0429	0.0397	0.0180	0.0039	-0.0008	0.0083	0.0019	0.0004
X_8	-0.0022	0.0080	0.0034	-0.0111	-0.0055	-0.0058	-0.0454	-0.0491	-0.0345	-0.0055	-0.0004	-0.0107	-0.0024	-0.0009
X_9	0.0000	-0.0033	-0.0026	0.0025	-0.0005	0.0012	0.0136	0.0227	0.0324	0.0042	0.0030	0.0056	0.0012	0.0004
X_{10}	0.0002	-0.0002	0.0000	0.0001	0.0002	0.0002	0.0002	0.0002	0.0003	0.0020	0.0002	0.0005	-0.0001	-0.0001
X_{11}	-0.0004	0.0163	0.0047	-0.0469	-0.0321	-0.0192	-0.0146	0.0059	0.0723	0.0887	0.7683	-0.2089	-0.0413	0.0011
X_{12}	0.0877	-0.1541	0.0097	0.0441	0.1092	0.0815	0.1673	0.1879	0.1495	0.2034	-0.2352	0.8652	0.0966	-0.0834
X_{13}	0.0000	0.0000	0.0001	0.0000	-0.0001	-0.0001	0.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.0007	-0.0001
X_{14}	0.0001	-0.0001	0.0002	0.0002	0.0002	0.0001	0.0000	0.0001	0.0000	-0.0002	0.0000	-0.0003	-0.0004	0.0030
X_{15}	0.0922	-0.1492	0.0159	0.0002	0.0927	0.0749	0.1661	0.2094	0.2377	0.2988	0.5344	0.6630	0.0549	-0.0778
r value	-0.0002	0.0013	0.0001	0.0000	0.0022	-0.0007	0.0071	-0.0103	0.0077	0.0006	0.4106	0.5736	0.0000	-0.0002

Residual effect: 0.0910,
where,
X1-Days to fifty percent flowering (days) X2- Days to maturity (days) X3- Plant height (cm) X4 - Panicle length (cm) X5-Number of tillers per plant X6-Number of productive tillers per plant X7- Number of grains per plant X8-Number of filled grains per plant X9-spikelet fertility (%) X10-Test weight (g) X11-Straw yield per plant (g) X12-Harvest index (%) X13- kernel length (cm) X14- kernel breadth (cm) X15- Grain yield per plant (g)

Conclusion

The analysis of variance resulted in significant changes for all the traits studied, indicating the presence of genetic variability among the experimental material. The traits like number of grains per panicle, number of filled grains per panicle exhibited high genetic parameters of GCV, PCV and moderate magnitude of PCV and GCV was seen in straw yield per plant, grain yield per plant and harvest index. Besides, these had high heritability accompanied by high genetic advance as mean. All these specifies the reduced effect of external environment on these traits and simple selection can improve these traits. The trait grain yield per plant had significant positive correlation with test weight, straw yield per plant and harvest index, indicating that these trait improvements can enhance the grain yield per plant. Very low residual effect of 0.0910 depicted that the traits included in the study explained high percentage of variation in grain yield. Plant height, number of tillers per plant, number of grains per panicle, spikelet fertility, test weight, straw yield per plant, harvest index, kernel length and kernel breadth had positive and direct effect on grain yield at phenotypic level. Hence, selection of these traits would be more rewarding for yield improvement strategy.

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