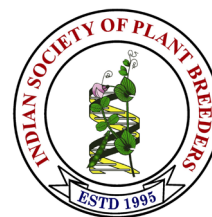


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Research Note

Genetic variability, correlation and path analysis studies for yield traits in stable mutant lines of black aromatic rice of Manipur

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Abstract

The study involved assessment of genetic variability and trait association of seed yield and its component traits in 20 EMS-derived stable mutant lines of black aromatic rice. The traits grain yield / plant, harvest index, effective tillers and biological yield/ plant recorded maximum GCV and PCV. Heritability estimates ranged from 67 percent for total number of tillers/ plant to 99 percent for days to 50 percent flowering. The trait grain yield per plant revealed high heritability (>80%) coupled with high advance in genetics (>50%). The traits fertile spikelets per panicle, effective tillers/ plant, biological yield, panicle length, and plant height were significantly and positively correlated with grain yield. The path analysis revealed maximum positive direct effects of fertile spikelets per panicle, harvest index, biological yield, grain length and effective tillers on grain yield indicating the selection of these traits for efficient crop improvement.

Keywords: Ethyl Methane Sulphonate, Black aromatic rice, variability, correlation, path analysis

Rice (*Oryza sativa* L.) is the most important cereal crop in the developing world and is the primary food source for half of the world's population. Rice, (*O. sativa* L.) (2n=24) belongs to the genus *Oryza*, family Graminae. It is a self-pollinated, annual, mainly grown under assured rainfall or irrigation. Rice is India's preeminent crop which is grown in 45.50 million ha, with a production level of 125.00 million tones, and the productivity is about 4100 kg/ha (FAO, USDA, 2022). Black rice is indigenous to Manipur, where rice is cultivated to the tune of 90% of the Gross Cropped Area of the state (Singha and Mishra, 2015) and accounts for 95% of total food grain production (Singh and Bera, 2017). Black rice is now considered as 'super food' by the researchers and scientists due its high nutritional

worth. This has attracted a lot of attention and is in high demand and therefore it is important to breed superior varieties with desirable characters.

Selection is the foremost and successful method of plant breeding and its effectiveness depends on the heritable variation present in the population. An insight into the magnitude of variability present in a crop is of utmost importance. Phenotypic variation or phenotypic variability is the observable variation present in a character of population and it includes both genotypic and environmental components. Sometimes it is difficult to assess whether the observed variation for a particular character is due to genotype or environmental factors.

Therefore, it is important to estimate the heritability component. Higher yield is the main breeding objective in all the crops, and is regarded as a complex character as it is affected by many component or contributing traits in both positive and negative directions.

Since, the indigenously available genotypes of black rice are low yielder and tall, susceptible to lodging, efforts were made to create variable mutant genotypes using chemical mutagens (EMS). The available stable mutant lines could be a base for further study for selection of promising lines. In this context, the present investigation was carried out to explicate information on variability, heritability, genetic advance, correlation and path coefficients for yield and its component traits in stable black aromatic rice mutant lines.

Experimental material comprised of 20 genotypes (19 stable mutants and the parent i.e., Poireiton), that were obtained from Genetics and Plant Breeding Department, College of Agriculture, Central Agricultural University, Imphal (**Table 1**). The present experiment was carried out during *kharif*, 2021 at GPB Experimental plot of college farm, CAU, Imphal, situated at 24.81°N latitude, 93.89°E longitude. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Twenty-five days old seedlings were transplanted adopting a spacing of 15cm x 20cm. All the suggested set of practices were followed to raise a successful crop. Observations were

recorded for 17 quantitative traits (days to 50% flowering, days to maturity, plant height (cm), number of total tillers per plant, number of effective tillers/ plant, panicle length (cm), total no. of spikelets / panicle, fertile spikelets / panicle, plant height, spikelet fertility (%), flag leaf length (cm), grain yield/ plant (gm), biological yield/ plant (gm), harvest index (%), test weight (gm), grain length (mm), grain breadth (mm) and grain length breadth ratio) on five randomly selected plants of each genotype for three replications and the data was subjected to statistical analysis. Statistical analyses of the above characters were done following the methods suggested by Rangaswamy (2010) for analysis of variance (ANOVA), Burton and Devane (1953) for genotypic and phenotypic variance, Singh and Chaudhary (1985) for correlation coefficient and Dewey and Lu (1959) for path analysis.

The results of ANOVA (**Table 2**) revealed highly significant differences among the genotypes for all the characters studied demonstrating the presence of significant variability and intrinsic genetic variation among the experimental material. Study of coefficient of variation indicated that estimates of phenotypic coefficient of variation (PCV) are higher than the genotypic coefficient of variation (GCV), thus indicating a significant influence of the environment on the phenotypic expression of traits (**Table 3**). Similar results were earlier reported by Lalitha *et al.* (2019) and Panika *et al.* (2022). GCV and PCV values were categorized as low (less than 10%),

Table 1. List of Rice genotypes under evaluation and their source

S. No.	Genotypes	Source
1	Poireiton	CAU, Imphal.
2	CT3D1	CAU, Imphal.
3	CT3D2	CAU, Imphal.
4	CT3D3	CAU, Imphal.
5	CT3D4	CAU, Imphal.
6	CT3D5	CAU, Imphal.
7	CT3D6	CAU, Imphal.
8	CT3D7	CAU, Imphal.
9	CT3D9	CAU, Imphal.
10	CT3D11	CAU, Imphal.
11	CT3D13	CAU, Imphal.
12	CT3D14	CAU, Imphal.
13	CT3D15	CAU, Imphal.
14	CT3D16	CAU, Imphal.
15	CT3D17	CAU, Imphal.
16	CT3D18	CAU, Imphal.
17	CT3D22	CAU, Imphal.
18	CT3D23	CAU, Imphal.
19	CT3D24	CAU, Imphal.
20	CT3D25	CAU, Imphal.

Table 2. Analysis of variance for 17 different traits in 20 stable black rice mutant genotypes

S. No.	Characters	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.=19)	Error (d.f.=38)
1	Plant height	4.461	208.0**	1.562
2	Total tillers/ plant	0.881	9.200**	1.248
3	Effective tillers/ plant	0.042	8.875**	0.213
4	Panicle length	0.277	18.829**	2.192
5	Flag leaf length	2.989	16.287**	1.384
6	Total spikelets / panicle	36*	928.34**	8.59
7	Fertile spikelet / panicle	32.73*	637.14**	7.78
8	Spikelet fertility	0.025	0.161**	0.010
9	Biological yield /Plant	3.954	164.30**	1.646
10	Grain yield/plant	0.893	85.35**	2.254
11	Harvest index	1.156	197.7**	6.362
12	Days to 50% flowering	0.150	270.19**	0.413
13	Days to maturity	0.117	89.645**	0.555
14	Test weight	0.508	7.630**	0.170
15	Grain length	0.008	0.304**	0.010
16	Grain breadth	0.004	0.064**	0.002
17	Grain l/b ratio	0.002	0.149**	0.164

*, ** denotes significance at the 0.05 and 0.01 probability levels respectively.

d.f. indicates degrees of freedom.

Table 3. Estimates of Genotypic, Phenotypic coefficient of variation, Heritability and Genetic advance for 17 quantitative traits

S. No.	Character	GCV	PCV	Heritability	Genetic advance
1	DFF	9.35	9.37	0.99	19.23
2	DM	3.98	4.01	0.98	8.12
3	PH	9.49	9.6	0.97	19.34
4	TT	13.62	16.52	0.67	23.13
5	ET	17.37	18	0.93	34.53
6	FLL	7.4	8.37	0.78	13.48
7	PL	10.03	11.85	0.71	17.49
8	TSP	14.02	14.22	0.97	28.49
9	FSP	13.34	13.58	0.96	26.98
10	SF	2.40	2.61	0.84	4.54
11	GYP	27.28	28.37	0.92	54.45
12	TW	7.43	7.68	0.93	14.81
13	BYP	14.92	15.14	0.97	30.28
14	HI	20.52	21.52	0.91	40.32
15	GL	3.18	3.34	0.9	6.23
16	GB	5.07	5.31	0.91	9.99
17	GLB	6.08	7.12	0.73	10.72

DFF- Days to 50% flowering, DTM- Days to maturity, PH- Plant height (cm), TT- Total number of tillers/ plant, ET- Effective tillers/ plant, FLL- Flag leaf length (cm), PL- Panicle length (cm), TSP- Total no. of spikelets / panicle, FSP- No. of fertile spikelets/ panicle, SF%- Spikelet fertility (%), GYP- Grain yield / plant (gm), TW- 1000 grain weight (gm), BYP- biological Yield / plant (gm), HI%- Harvest index (%), GL- Grain length (mm), Grain breadth (mm), G L/B- Grain length breadth ratio.

moderate (10%–20%), and high (more than 20%) as per Deshmukh *et al.*, 1986. High PCV and GCV were recorded for harvest index (20.52), and grain yield/ plant (27.28) indicating the presence of high variability among the experimental material used. These findings are in agreement with the results reported earlier by Devkota *et al.* (2023), Duraiswamy *et al.* (2023) for grain yield per plant and Singh *et al.* (2011), Dutta *et al.* (2013), Singh *et al.* (2021) for both the traits harvest index and grain yield per plant. Moderate values of GCV and PCV were recorded for the traits effective tillers/ plant (17.37), biological yield/ plant (14.92), total number of spikelets/ panicle (14.02), total number of tillers/ plant (13.62), fertile spikelets/ panicle (13.34) and panicle length (10.03). Similar results were reported earlier by Radhamani *et al.* (2015), Singh *et al.* (2021), Duraiswamy *et al.* (2023), Paraamanik *et al.* (2023) for effective tillers per plant, Singh *et al.* (2011) for biological yield per plant, Duraiswamy *et al.* (2023) and Umadevi *et al.* (2009) for total number of tillers per plant and panicle length. Low PCV and GCV were recorded for the traits plant height (9.49), days to 50% flowering (9.35), test weight (7.43), flag leaf length (7.4), grain length breadth ratio (6.08), grain breadth (5.07), spikelet fertility (2.40), days to maturity (3.98) and grain length which are in agreement with the results reported earlier by Singh *et al.* (2021), Lalitha *et al.* (2019) for plant height, Singh *et al.* (2011), Umadevi *et al.* (2009), Singh *et al.* (2021) for days to 50 percent flowering, Lalitha *et al.* (2019) for grain length and grain length breadth ratio, Singh *et al.* (2011), Lalitha *et al.* (2019), Devkota *et al.* (2023) for days to maturity. The high variability exhibited by the characters indicated the possibility of effective selection for the character improvement. Moderate to low variability necessitated the base population improvement.

Heritability is the measure of proportion of phenotypic variance that can be attributed to genotypic variance and is a good index of transmission of characters from parents to progeny. The heritability estimates for different characters under study was found to be high and ranged from 67% to 99% indicating the predominance of additive gene action (**Table 3**). Similar findings for additive gene action were reported by Bagudam (2018), Kole *et al.* (2020), Bhor *et al.* (2020). Genetic advance at 5% selection intensity was found to be highest for grain yield/ plant (54.45), harvest index (40.32), effective number of tillers/ plant (34.53), biological yield/ plant (30.28), total spikelets/ panicle (28.49), fertile spikelets/ panicle (26.98) and total number of tillers / plant (23.13) , similar to results contributed by Edukondalu *et al.* (2017). Moderate heritability was observed for plant height (19.34), days to 50% flowering (19.23), panicle length (17.49), test weight (14.81), flag leaf length (13.48) and grain length breadth ratio (10.72). Similar results were reported by Meena *et al.* (2019). The traits grain length (6.23), days to maturity (8.12), spikelet fertility (8.99) and grain breadth (9.99) exhibited low genetic advance, which was similar to results contributed by Dutta *et al.* (2013).

Estimates of heritability along with genetic advance will make the selection more effective by indicating the quantum of genetic enhancement made due to phenotypic selection (Johnson *et al.*, 1955). The trait grain yield was found to be exhibiting high heritability (> 80%) coupled with high genetic advance (> 50%) and the results are in accordance with the findings of Bhargavi *et al.* (2021), Dutta *et al.* (2013). The traits harvest index, Effective tillers per plant, biological yield per plant, Total spikelets / panicle and Fertile spikelets / panicle were found to exhibit high heritability (above 80%) and moderate genetic advance (above 25%) which are in agreement with the results of Edukondalu *et al.* (2017), Singh *et al.* (2011), Dutta *et al.* (2013). Thus, the trait grain yield per plant with high heritability and high genetic advance controlled by additive gene action could be improved through simple selection methods whereas the traits with high heritability and low genetic advance indicating the presence of non-additive gene action could be improved by intermating superior genotypes of segregating population.

In plant breeding, correlation coefficient analysis measures the relationship between various plant characters and determines the component characters on the basis of which selection can be practiced for genetic improvement in yield. The traits fertile spikelets/ panicle, effective tillers / plant, biological yield / plant, panicle length and plant height showed positive and highly significant correlation with grain yield per plant both at genotypic and phenotypic levels (**Table 4**). Similar results were reported by Rahman *et al.* (2014) and Akinwale *et al.* (2011) for the traits fertile spikelets/ panicle and effective tillers / plant. Kole *et al.* (2020) showed similar results for harvest index, effective tillers / plant and biological yield/ plant. The trait days to maturity showed significantly negative correlation with grain yield / plant indicating that the early maturing genotypes result in higher grain yields. This kind of negative association may be due to linkage or pleiotropy. Similar result for this negative association of days to maturity was reported earlier by Osundare *et al.* (2017). The traits fertile spikelets / panicle, panicle length, effective tillers/ plant, plant height and biological yield/ plant showed positive correlation with grain yield per plant and these traits are positively interrelated among themselves signifying their importance in crop improvement.

The true contribution of character towards the yield or a dependent character cannot be provided by simple correlation because the extent of change in one variable due to change in another variable cannot be determined. So, through path coefficient analysis the genotypic and phenotypic correlations are partitioned into direct and indirect effects which allows for better interpretation of cause-and-effect relationship. The results of path analysis (**Table 5**) revealed that maximum positive direct effects on grain yield / plant was observed from fertile spikelets per panicle (0.7049), followed by Harvest index

Table 4. Genotypic (lower diagonal) and phenotypic correlation coefficient between grain yield per plant and its 16 component traits

	PH	NT	ET	FL	PL	TS	FS	SF	BY	TW	HI	LB	GL	GB	DFF	DM	GY
PH	1**	-0.357**	0.017	0.239	0.49**	0.422**	0.442**	0.026	-0.046	-0.452	0.456**	-0.317	-0.501**	0.076	-0.202	-0.303*	0.328*
NT	-0.441**	1	0.454**	-0.316*	-0.37**	-0.126	-0.103	0.033	0.555**	-0.029	-0.15	0.229	0.084	-0.18	0.208	-0.019	0.193
ET	0.012	0.54*	1	-0.294*	0.05	0.395**	0.348**	-0.181	0.78**	-0.239	0.418**	0.226	-0.055	-0.254*	0.032	-0.273*	0.771**
FL	0.288	-0.49*	-0.297	1	0.488**	0.337**	0.351**	-0.003	-0.102	-0.114	0.09	-0.027	0.045	0.457	0.2432	-0.118	0.012
PL	0.568**	-0.56*	-0.004	0.683**	1	0.472**	0.467**	-0.051	-0.089	-0.086	0.428**	-0.171	0.034	0.216	-0.2	-0.103	0.273*
TS	0.43	-0.15	0.416	0.369	0.554*	1	0.929**	-0.309**	0.356**	-0.175	0.785**	0.039	0.031	-0.024	-0.021	-0.68**	0.7.9**
FS	0.451*	-0.13	0.368	0.389	0.57**	0.939	1	0.061	0.33**	-0.173	0.768**	-0.089	-0.022	0.107	0.013	-0.589**	0.769**
SF	0.025	0.002	-0.205	-0.005	-0.008	-0.315	0.026	1	-0.133	0.01.8	-0.139	-0.326*	-0.133	0.348**	0.047	0.321*	-0.163
BY	-0.044	0.666**	0.806**	-0.093	-0.123	0.386	0.356	-0.164	1	-0.294*	0.107	0.291*	-0.032	-0.347**	0.449**	-0.291*	0.652**
TW	-0.462*	-0.348	-0.244	-0.207	-0.108	-0.189	-0.186	0.026	-0.306	1	-0.12	-0.173	0.376**	0.561**	-0.262*	0.232	-0.265*
HI	0.486*	-0.178	0.423	0.109	0.513*	0.838**	0.818**	-0.173	0.109	-0.136	1	-0.057	-0.058	0.067	-0.313*	-0.478**	0.82**
LB	-0.368	0.278	0.267	-0.025	-0.202	0.043	-0.109	-0.416	0.368	-0.191	-0.073	1	0.543**	-0.761**	0.407**	-0.083	0.088
GL	-0.526*	0.137	-0.062	0.065	0.062	0.032	-0.014	-0.102	-0.031	0.382	-0.054	0.576**	1	-0.042	0.159	0.045	-0.091
GB	0.075	-0.213	-0.258	0.027	0.239	-0.017	0.129	0.417	-0.369	0.574**	0.07	-0.851**	-0.677	1	-0.475**	0.098	-0.119
DFF	-0.204	0.249	0.035	0.276	-0.221	-0.019	0.014	0.049	0.458*	-0.267	-0.331	0.463*	0.167	-0.494*	1	0.074	-0.004
DM	-0.306	-0.0194	-0.2786	-0.1424	-0.1184	-0.6954	-0.597**	0.36	-0.3	0.235	-0.507*	-0.107	0.039	0.096	0.075	1	-0.518**
GY	0.3495	0.245	0.799**	0.0278	0.3144	0.847	0.82**	-0.207	0.668**	-0.287	0.809**	0.116	-0.09	-0.133	-0.004	-0.546*	1

* , ** denotes significance at the 0.05 and 0.01 probability levels respectively.

PH- Plant height (cm), NT- Number of tillers/ plant, ET- Effective tillers/ plant, FL- Flag leaf length (cm), PL- Panicle length (cm), TS- Total no. of spikelets, FS- No. of fertile spikelets, SF%- Spikelet fertility (%), BY- biological Yield / plant (gm), TW- 1000 grain weight (gm), , HI%- Harvest index (%), LB- Grain length breadth ratio, GL- Grain length (mm), Grain breadth (mm), G DFF- Days to 50% flowering, DM- Days to maturity, GY- Grain yield (gm).

Table 5. Genotypic path coefficient matrix of grain yield with different characters

	PH	NT	ET	FL	PL	TS	FS	SF	BY	TW	HI	LB	GL	GB	DFF	DM
PH	0.058	-0.03	0.001	0.017	0.033	0.025	0.026	0.002	-0.00	-0.03	0.028	-0.02	-0.03	0.004	-0.01	-0.02
NT	0.027	-0.06	-0.03	0.031	0.035	0.009	0.008	-0.00	-0.04	0.002	0.011	-0.02	-0.01	0.013	-0.02	0.001
ET	0.001	0.051	0.095	-0.03	-0.00	0.039	0.035	-0.02	0.076	-0.02	0.040	0.025	-0.01	-0.02	0.003	-0.03
FL	0.017	-0.03	-0.02	0.060	0.041	0.022	0.023	-0.00	-0.01	-0.01	0.006	-0.00	0.003	0.002	0.016	-0.00
PL	-0.08	0.082	0.001	-0.10	-0.15	-0.08	-0.08	0.001	0.018	0.016	-0.07	0.029	-0.01	-0.03	0.033	0.017
TS	-0.26	0.089	-0.26	-0.23	-0.34	-0.61	-0.57	0.194	-0.24	0.116	-0.52	-0.03	-0.02	0.010	0.012	0.427
FS	0.318	-0.09	0.259	0.273	0.401	0.662	0.704	0.01	0.251	-0.13	0.576	-0.08	-0.01	0.091	0.009	-0.42
SF	-0.01	-0.00	0.050	0.001	0.002	0.077	-0.01	-0.24	0.040	-0.01	0.042	0.101	0.025	-0.10	-0.01	-0.08
BY	-0.02	0.368	0.446	-0.05	-0.07	0.213	0.197	-0.09	0.553	-0.16	0.060	0.203	-0.02	-0.20	0.253	-0.16
TW	0.037	0.002	0.020	0.017	0.008	0.015	0.015	-0.00	0.025	-0.08	0.011	0.015	-0.03	-0.04	0.022	-0.02
HI	0.308	-0.11	0.268	0.069	0.325	0.532	0.519	-0.11	0.069	-0.08	0.634	-0.05	-0.03	0.044	-0.21	-0.32
LB	-0.05	0.039	0.037	-0.00	-0.03	0.006	-0.02	-0.05	0.052	-0.03	-0.01	0.141	0.081	-0.12	0.065	-0.02
GL	0.006	-0.00	0.001	-0.00	-0.00	-0.00	0.000	0.001	0.000	-0.00	0.001	-0.01	-0.01	0.00	-0.00	-0.00
GB	0.014	-0.04	-0.05	0.005	0.044	-0.00	0.024	0.077	-0.07	0.106	0.013	-0.16	-0.01	0.184	-0.09	0.018
DFF	0.017	-0.02	-0.00	-0.02	0.018	0.002	-0.00	-0.00	-0.04	0.022	0.027	-0.04	-0.01	0.041	-0.08	-0.01
DM	-0.03	-0.00	-0.02	-0.01	-0.01	-0.06	-0.05	0.029	-0.02	0.019	-0.04	-0.01	0.003	0.008	0.01	0.082
GY	0.349	0.245	0.799	0.278	0.314	0.847	0.820	-0.21	0.668	-0.29	0.809	0.116	-0.09	-0.13	-0.00	-0.55

PH- Plant height (cm), NT- Number of tillers/ plant, ET- Effective tillers/ plant, FL- Flag leaf length (cm), PL- Panicle length (cm), TS- Total no. of spikelets, FS- No. of fertile spikelets, SF%- Spikelet fertility (%), BY- biological Yield / plant (gm), TW- 1000 grain weight (gm), HI%- Harvest index (%), LB- Grain length breadth ratio, GL- Grain length (mm), Grain breadth (mm), G DFF- Days to 50% flowering, DM- Days to maturity, GY- Grain yield (gm).

(0.6348), Biological yield / plant (0.5533), Grain breadth (0.1848), Days to maturity (0.0817), flag leaf length (0.0602) and plant height (0.0549). These results are in conformity with the findings of Ekka et al. (2011), Shinde et al. (2015), Roy et al. (2020). The direct effect of the traits grain length (-0.0107), number of tillers (-0.0632), days for 50% flowering (-0.0832), Test weight (-0.0821) and panicle length (-0.1476) on grain yield/ plant were noticed to be negative both at genotypic and phenotypic levels. Negative direct effect of panicle length on grain yield / plant could be due to negative indirect effect of this character via plant height, flag leaf length, total spikelets, fertile spikelets, harvest index, grain length and grain breadth. Similarly negative direct effect of grain length could be due to negative indirect effects through number of total tillers per plant, flag leaf length, panicle length, total spikelets / panicle, test weight, grain length breadth ratio, and days to 50% flowering. The present results were in accordance with the findings reported by Roy et al. (2020) for grain length, Gupta et al. (2020) and Gayathri et al. (2018) for days to 50% flowering, Kole et al. (2020) and Parimala et al. (2020) for panicle length, Maurya et al. (2018) for test weight. Though the direct effect of total number of spikelets/ panicle (-0.6149) was found to be negative, its correlation (0.847) with the grain yield was high in positive direction compared to rest of the traits indicating the indirect positive contribution via the traits harvest index (0.532) and biological yield per plant (0.2136).

In conclusion, high genetic variability was found among the studied rice genotypes for grain yield per plant and harvest index. The trait grain yield per plant showed high heritability and high genetic advance. The correlation and path analysis studies together revealed that the traits fertile spikelets / panicle, harvest index, biological yield / plant, plant height, grain breadth and days to maturity are important components for increasing grain yield. Hence, these traits could be given due importance for enhancing grain yield in rice.

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