

Studies on Genetic Variability for Quantitative and Qualitative Traits in North-East Indian Rice (*Oryza sativa* L.)

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Abstract

The present investigation was carried out with twenty six rice genotypes collected from north-east states of India along with two check varieties in *Kharif* 2014 in Randomized Block Design (RBD). Wide range of variability was present in the north-east Indian lines of rice under study in konkan condition. The range of GCV and PCV was 4.57% to 37.55% and 5.85% to 50.67% respectively for quantitative traits. Whereas, the range of GCV and PCV was 18.56% to 45.70% and 20.46% to 46.98% respectively for qualitative traits. The estimates of phenotypic, genotypic and environmental variances revealed that phenotypic variances were higher in magnitude over the respective genotypic variances for all the characters under study which indicates that there is influence of genetic and environment on the expression of traits. PCV and GCV were high for straw yield per plant, grain yield per plant and amylose content (%). The broad sense heritability ranged from 19.62% to 96.47% for quantitative traits. Whereas, in case of qualitative traits, the broad sense heritability ranged from 82.32% to 99.50%. High estimates of broad sense heritability was observed for 1000 grain weight (96.47%), days to 50% flowering (95.79%), days to maturity (95.66%), plant height (92.1%), alkali spreading value (99.50%), protein content (97.30%) and amylase content (94.63%). The genetic advance and genetic advance as per cent of mean (GAM) were ranged from 1.39% to 93.89% and 7.36% to 57.32% respectively for quantitative traits. Whereas, for qualitative traits, the genetic advance and genetic advance as per cent of mean (GAM) were ranged from 2.32% to 26.13% and 34.70% to 91.58% respectively. Heritability along with genetic advance is more useful for selection than the heritability alone. High heritability along with maximum genetic advance was observed in plant height and number of spikelets per panicle used for further crop improvement.

Key words: Rice, variability, GCV, PCV, genetic advance, heritability and GAM.

Introduction

Rice is staple food of more than 60% of Indian population. It accounts for about 43% of total food grain production and 46% of total cereal production in the country. Rice occupies pivotal place in Indian Agriculture. In order to meet the domestic demand of the increasing population the present day production of 107.40 million tons (Anonymous, 2015-16) of milled rice has to be increased to 125 million tons by the year 2030. Since the yield of high yielding varieties (HYVs) of rice is plateauing, it is rather difficult to achieve this target with the present day inbred varieties. Therefore, to sustain the self-sufficiency in rice, additional production of 1.17 million tons is needed every year. There are a large number of indigenous rice varieties in India, which are still grown by the tribal people and small farmers of the remote areas where the modern agricultural practices, sufficient foods as well as healthcare systems

are a dream. Nature has provided them some alternative ways. They have different indigenous rice varieties with its nutritional and medicinal values. The north-east Indian rice germplasm cultivated by traditional farmers may contain a considerable genetic diversity that can serve as a source of germplasm for genetic improvements of cultivated varieties of rice. In rice varietal improvement programmes, north-east Indian rice varieties have proved to be useful donors for sources of resistance or tolerance to many stress environments and for imparting resistance to important pests and diseases. In general, diverse landraces traditionally cultivated by farmers around the centers of diversity and domestication of crops are considered as key natural resources important for maintaining the future food security in light of the changing climate. The development of core set is very much essential for better management of germplasm lines in crop improvement strategies. It is

helpful to precisely characterize, explore and conserve resources, monitor the genetic drift during preservation and identify gaps in genetic diversity (Frankel and Brown, 1984). After considering these attributes, Regional Agriculture Research Station, Karjat has collected several local germplasm. These germplasm have more genetic diversity, high degree of tolerance for biotic and abiotic stresses and wide adaptability with meaningful nutritional quality. North-East (NE) India, the probable origin of rice has diverse genetic resources. Many rice landraces of NE India were not yet characterized for blast resistant. (Umakant *et al.*, 2017).

Materials and methods

The experiment was conducted at the Research Farm of Regional Agricultural Research Station, Karjat under Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, Maharashtra, India during *Kharif*, 2014. The experimental material for the present study consisted of twenty six genotypes of rice (*Oryza sativa* L.) (Table 1.) which was collected from different states of North-East India, it was expected that these genotypes were phenotypically different in respect of growth habit, plant height. The present investigation was carried out by adopting Randomized Block Design with three replications. Twenty seven days old seedlings were transplanted with 20 cm distance between rows and 15 cm distance between plants

within rows. All the recommended package of practices was followed along with necessary prophylactic plant protection measures to raise a good crop. Observations were recorded and the data was subjected to statistical analysis. The variability was estimated as per procedure for analysis of variation suggested by Panse and Sukhatme (1967). PCV and GCV were calculated by the given formula by Burton and De Vane (1953), broad sense heritability (h^2b) by Lush (1949) and genetic advance i.e. the expected genetics were calculated by using the procedure given by Johnson *et al.* (1955).

Table 1: List of genotypes included in present investigation

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	Chakhao Poireiton	14.	Busayhar
2.	Phungreila	15.	Tungou
3.	Mayul	16.	Bumanvom
4.	Mohor	17.	Chakhao Amubi
5.	Phougak Local	18.	Darachung
6.	Heimang Phou	19.	Kabok Phou
7.	Phouren Amubi	20.	Pungpat Sumei
8.	Sukha Panghi	21.	Langphou chakhao
9.	Kowavumlu Anal	22.	Taothabi
10.	Chakhao Scente	23.	Akutphou Releare
11.	Asaima	24.	Naphang
12.	Napheang	25.	Botvel
13.	Katan Chakhao	26.	Phule Samrudhi

Table 2: Analysis of variance for yield and quality contributing characters in rice

Sr. No.	Characters	Mean sum of squares		
		Replication	Treatment	Error
1.	Days to 50 per cent flowering	8.71	328.22**	4.73
2.	Days to maturity	1.88	366.93**	5.46
3.	Plant height (cm)	160.83	2133.43**	59.26
4.	Number of tillers per plant	2.49	11.54*	5.88
5.	Panicle length (cm)	2.83	22.08**	1.11
6.	Number of spikelets per panicle	342.02	7520.97**	356.99
7.	Number of filled spikelets per panicle	208.01	6153.48**	263.49
8.	Spikelet fertility (%)	31.28	57.04**	9.98
9.	1000 grain weight (g)	0.40	61.93**	0.74
10.	Grain yield per plant (g)	29.62	289.41**	112.05
11.	Straw yield per plant (g)	467.18	1056.36**	226.95
12.	Harvest index (%)	57.39	138.93**	80.20
13.	Protein content (%)	0.05	8.66*	0.08
14.	Amylose content (%)	7.47	199.28*	3.70
15.	Gel consistency (mm)	25.42	628.34*	41.98
16.	Alkali spreading value	0.02	3.82*	0.006
	D.F.	2	25	50

*Significant at 5% level of significance

Significant at 1% level of significance **Table 3: Components of variation for yield and quality attributing characters in rice



Table 3: Components of variation for yield and quality attributing characters in rice

Sr. No.	Characters	Phenotypic variance	Genotypic Variance	Environmental variance
1.	Days to 50 per cent flowering	112.56	107.83	4.73
2.	Days to maturity	125.95	120.49	5.46
3.	Plant height (cm)	750.65	691.39	59.26
4.	Number of tillers per plant	7.76	1.89	5.88
5.	Panicle length (cm)	8.10	6.99	1.11
6.	Number of spikelets per panicle	2744.99	2387.99	356.99
7.	Number of filled spikelets per panicle	2226.82	1963.33	263.49
8.	Spikelet fertility (%)	25.67	15.68	9.98
9.	1000 grain weight (g)	21.14	20.40	0.74
10.	Grain yield per plant (g)	171.17	59.12	112.05
11.	Straw yield per plant (g)	503.42	276.47	226.95
12.	Harvest index (%)	99.78	19.58	80.20
13.	Protein content (%)	2.94	2.86	0.08
14.	Amylose content (%)	68.89	65.19	3.70
15.	Gel consistency (mm)	237.44	195.45	41.98
16.	Alkali spreading value	1.28	1.27	0.006

Table 4: Estimates of genetic parameters for yield and quality attributing traits in rice

Sr. No.	Characters	PCV (%)	GCV (%)	h ² b (%)	GA	GAM (%)
1.	Days to 50 per cent flowering	10.8	10.57	95.79	20.93	21.32
2.	Days to maturity	8.78	8.59	95.66	22.11	17.30
3.	Plant height (cm)	18.28	17.54	92.1	51.98	34.69
4.	Number of tillers plant	31.11	15.34	24.32	1.39	15.51
5.	Panicle length (cm)	9.72	9.03	86.32	5.06	17.29
6.	Number of spikelets per panicle	26.56	24.77	86.99	93.89	47.60
7.	Number of filled spikelets per panicle	27.54	25.86	80.16	85.7	50.02
8.	Spikelet fertility (%)	5.85	4.57	61.1	6.37	7.36
9.	1000 grain weight (g)	16.92	16.62	96.47	9.13	33.62
10.	Grain yield per plant (g)	44.23	25.99	34.53	9.3	31.44
11.	Straw yield per plant (g)	50.67	37.55	54.91	25.38	57.32
12.	Harvest index (%)	24.32	10.77	19.62	4.03	9.81
13.	Protein content (%)	21.59	21.30	97.30	3.44	43.28
14.	Amylose content (%)	46.98	45.70	94.63	16.18	91.58
15.	Gel consistency (mm)	20.46	18.56	82.32	26.13	34.70
16.	Alkali spreading value	28.45	28.38	99.50	2.32	58.31

PCV: Phenotypic coefficient variation, GCV: Genotypic coefficient variation, h²b: Broad sense heritability, GA: Genetic advance, GAM: Genetic advance as per cent of mean.

Result and Discussion

The analysis of variance revealed that the differences among the genotypes were significant for most of the characters under study in Konkan region. The genotypes were thus suitable for genetical studies, as their contribution to the genotypic sum of squares was significant for most of the characters. The total variability in each of these characters could be partitioned into three components *viz.*, phenotypic, genotypic and environmental. The phenotypic variance and genotypic variance was maximum for number of spikelets per panicle, lowest in number of tillers per plant. Genotypic and phenotypic variances were high for number of spikelets per panicle followed by number of filled spikelets per panicle, plant height and straw yield per plant indicating wide variability for these characters. Similar results were reported by Pandey and Awasthi (2002).

Among the quantitative traits, PCV and GCV were highest for straw yield per plant (50.67% and 37.55%), followed by grain yield per plant (44.23% and 25.99%). Among the qualitative traits PCV and GCV were highest for amylose content (46.98% and 45.70%) followed by alkali spreading value (28.45% and 28.38%) (Table 4). High GCV indicated high genetic variability within the test genotype. It indicates that there is little influence of environment on the expression of traits. Selections of such traits were used for further crop improvement.

Among the yield related traits, the phenotypic and genotypic variance values were recorded maximum for number of spikelets per plant (2744.99 and 2387.99), followed by number of filled spikelets per panicle (2226.82 and 1963.33) and plant height (750.65 and 691.39). Whereas in case of quality traits, maximum phenotypic and genotypic variance values were recorded for gel consistency (237.44% and 195.45%) followed by amylose content (68.89% and 65.19%), protein content (2.94% and 2.86%) and alkali spreading value (1.28% and) (Table 3). The results were in accordance with Chauhan and Tandon (1984), Jangale *et al.* (1985), Roy *et al.* (1995), Deb Choudhury and Das (1998) and Naik *et al.* (2002).

The estimates of broad sense heritability for both quantitative and qualitative traits ranged from 19.62% to 99.50% (Table 4). Among the quantitative traits, high estimates of broad sense heritability was observed for 1000 grain weight (96.47%), days to 50% flowering (95.79%) and days to maturity (95.66%) while low for harvest index (19.62%) and number of tillers per plant (24.32%). Whereas in quality traits, high estimates of broad sense heritability was observed for alkali spreading value

(99.50%), protein content (97.30%) and amylose content (94.63%) while low for gel consistency (82.32%) (Table 4). Similar results reported by Sinha and Bhattacharyya (1980), Ghosh *et al.* (1981), Singh and Sharma (1982), Ravindranath *et al.* (1983), Chauhan and Tandon (1984), Sawant and Patil (1995), Nath and Talukdar (1997) and Naik *et al.* (2002).

Among yield related traits, high genetic advance was observed for number of spikelets per panicle (93.89%), number of filled spikelets per panicle (85.7%) and plant height (51.58%), while low for number of tillers per plant (1.39%). In case of grain quality traits, high genetic advance was observed for gel consistency (26.13%) and amylose content (16.18%). Maximum estimates of genetic advance as per cent of mean was recorded by straw yield per plant (57.32%) followed by number of filled spikelets per panicle (50.02%) and number of spikelets per panicle (47.60%) while minimum value was recorded by spikelet fertility (7.36%) and harvest index (9.81%). Whereas in case of quality traits, maximum estimates of genetic advance as per cent of mean was recorded by amylose content (91.58%) followed by alkali spreading value (58.31%) while minimum value was recorded by gel consistency (34.70%) (Table 4). Similar results were obtained by Ghosh *et al.* (1981), Singh and Sharma (1982), Ravindranath *et al.* (1983), Wilfred Manual and Prasad (1993), Sawant and Patil (1995) and Nath and Talukdar (1997).

Heritability alone doesn't provide clear information on the amount of genetic progress that would result from the selection without genetic advance. Maximum values of broad sense heritability were observed for alkali spreading value, protein content, amylose content, 1000 grain weight, days to 50% flowering, and days to maturity, it indicates that expression of these traits were influenced by the environmental effects, the selection for improvement of such characters may not be useful. The high value of genetic advance were observed for number of spikelets per panicle, number of filled spikelets per panicle, plant height, gel consistency and straw yield per plant, it indicates that these traits were governed by additive genes and selection of these traits for further crop improvement. High heritability estimates along with high genetic advance were noticed for number of spikelets per panicle, number of filled spikelets per panicle, plant height, days to 50% flowering, and days to maturity, it indicates that these characters were governed by additive gene effects and selection of these traits is effective for further crop improvement programme.



Conclusion

It is concluded that yield is controlled by both GCV and PCV also to use appropriate selection procedure for improvement of the characters in general and yield in particular since high heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression. High heritability with low genetic advance was indicated the influence of non-additive gene action. The heritability provide the information on the magnitude of inheritance of quantitative characters, but it does not indicate the magnitude of genetic gain obtained by selection of best individual from the best population. So, heritability along with genetic advance is more useful for selection than the heritability alone.

References

- Anonymous, 2015-16. Directorate of Economics and Statistics. Ministry of Agriculture, Government of India, New Delhi.
- Bangale Umakanth, Balija Vishalakshi, P. Sathish Kumar, S. J. S. Rama Devi, Vijay Pal Bhadana, P. Senguttuvel, Sudhir Kumar, Susheel Kumar Sharma, Pawan Kumar Sharma, M. S. Prasad, and Maganti S. Madhav, 2017. Diverse Rice Landraces of North-East India Enables the Identification of Novel Genetic Resources for *Magnaporthe* Resistance *frontier Plant Sci.* **8** pp:1500.
- Burton GW and De Vane EH. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy. Journal.* **45** pp: 478-481.
- Chauhan VS and Tandon JP. 1984. Genetic variability and character association in hill rices. *Oryza.* **21** : 138-142.
- Deb Choudhury PK and Das PK. 1998. Genetic variability, correlation and path coefficient analysis in deep-water rice. *Annals of. agricultural. Research.* **19** (2) PP: 120
- Frankel O. H., Brown A. H. D. (1984). Plant genetic resources today: a critical appraisal, in *Crop Genetic Resources: Conservation and Evaluation*, eds Holden J. H. W., Williams J. T., editors. (London: George Allen and Unwin Ltd.), pp: 249–257.
- Ghosh AK, Bhattacharya PK and Asthana AN. 1981. Genetic variability in indigenous rice varieties of Meghalaya. *Indian Journal of agricultural. Sciences.* **51** (5) pp: 281-283.
- Jangale, R.D.; Sangave, R.A.; Ugale, S.D. and Dumbre, A.D.1985. Studies on variability, heritability and genetic advance for some quantitative characters in upland paddy. *J. Maharashtra agric. Univ.*, **10** (1) pp: 69-70.
- Johnson, H.W.; Robinson, H.F. and Comstock, R.E.1955. Estimates of genetic and environmental variability in soybean. *Agron. J.* **47** (7) pp: 314-318.
- Lush, J.C. 1949. Intra sire correlation and regression of offspring on dams and method of estimating heritability of character. *Proc. Amer Soc.* **32** : 293-301.
- Naik, A.R.; Chaudhary, D. and Reddy, J.N. 2002. Genetic variability, heritability and genetic advance in scented rice. *The Andhra Agric.* **49** (1&2) pp: 143-145.
- Nath, N. and Talukdar, P. 1997. Genetic variability and correlation studies in segregating populations of indigenous scented x high yielding non-scented crosses of rice. *Oryza.* **34** (2) pp: 91-93.
- Pandey, V.K. and Awasthi, L.P. 2002. Studies on genetic variability for yield contributing traits in aromatic rice. *Crop Res.*, **23** (2) : 214-218.
- Panase, V.G. and P.V. Sukhatme 1967. Statistical methods for agricultural workers. ICAR, New Delhi. pp. 381.
- Ravindranath, B.A., Peraiah, B., Ramayya, N., Sreerama Reddy, D. Subramanyam and K.R.K. Murthy 1983. Studies on genetic variability, heritability and genetic advances for yield and its components in rice. *Andhra Agric. J.* **30** (1) pp: 26-28.
- Roy, A.; Panwar, D. V .S. and Sarma, R.N. 1995. Genetic variability and causal relationship in rice. *Madras Agric. J.* **84** (4) pp: 251-255.
- Sawant, D.S. and Patil, S.C. 1995. Genetic variability and heritability in rice. *Ann. Agric. Res.*, **16** (1) pp: 59-61.
- Singh, T.B. and A.C. Sharma 1982. Note on the genetic analysis of yield component characteres in 'Noirangphov x Jaya' Rice. *Indian J. Agric. Sci.* **82**(4) pp: 243-244.
- Sinha, T.S. and Bhattacharya, R.K. 1980. Note on genetic variability in Sundarban rice varieties under saline soil. *Indian J. agric. Sci.* **50** (9) pp: 719-721.
- Wilfred Manual, W. and Prasad, M.N. 1993. Genetic variability in medium duration rice. *Oryza.* **30** pp: 355-356.