Genetic Variability in Yields and its Component Characters in Upland Rice of Nagaland

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ABCTRACT

Seventy four upland rice accessions of Nagaland (India) were evaluated for 13 quantitative traits. All the genotypes differed significantly with respect to all the quantitative characters. Maximum genotypic and phenotypic variances were observed for days to 80% flowering, days to maturity, plant height, leaf length, number of filled grains, and yield per plant. High estimates of heritability coupled with moderate or high value of genetic advance as percentage of means was observed for yield per plant, 100 seed weight, leaf length, days to 80% flowering, leaf width, number of unfilled grains, days to maturity and panicle weight.

INTRODUCTION

Upland rice is the staple food of the poorest farmers in Asia and Africa. In the North East India, the major area of upland rice is in the slash and burn system; commonly known as jhum cultivation. In this system, productivity is low and ranges from 0.8 - 1.2 t/ha (Sarma and Pattanayak 2009). The need for improving productivity by exploiting available variability in the jhum rice germplasm has been long felt. This requires systematic evaluation of the germplasm for selection of superior lines as well as to characterize the germplasm for various traits. Genetic variability studies are considered important for selection of parents for hybridization (Chaudhury and Singh 1982). Once genetic variability is ascertained, crop improvement through appropriate selection can proceed (). In rice, yield is a product of the number of panicles in a unit area, number of spikelets per panicle, spikelet fertility percentage and 1000 seed weight (De Datta 1981). It is, therefore, important to study the heritability and genetic advance under selection of the yield contributing traits so that their response to selection can be predicted (Augustina et al. 2013). Nagaland being located in a pocket of high diversity of rice germplasm and with the availability of different ecosystem for cultivation of rice, wide range of rice landraces is found in the state. The present study was made with an objective to estimate genetic variability of yield and its component characters in the jhum rice germplasm of Nagaland.

MATERIALS AND METHODS

The experiment consisted of seventy four upland rice accessions collected from all the eleven districts of Nagaland. The experiment was laid out in a Randomized Block Design with three replications keeping 20 x 15 cm spacing, and the recommended cultural practices were followed. It was conducted at the field experimentation site of State Agricultural Research Station, Yisemyong, Nagaland over a period of 3 years (2009-11). This site is located 26º40'28" N latitude and 94º59'88" E longitude at an altitude of 1, 130m MSL, with an annual rainfall of about 1,100-1,400mm. Observations were made from five randomly selected plants, and data were taken on days to 80% flowering, days to maturity, plant height, effective

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bearing tillers, leaf length, leaf width, panicle length, panicle weight, no. of primary branches, no. of filled grains, no. of unfilled grains, 100 seed weight and yield/plant. The mean data after computing for each character was subjected to the standard method of analysis of variance following Fishers (1954), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) following the formula given by Burton (1952), heritability in the broad sense as suggested by Allard (1960) and genetic advance as per cent of mean as suggested by Johnson et al. (1955).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences between the genotypes for all the traits, indicating the presence of a considerable amount of variability among the genotypes. The result of analysis of variance is presented in Table 1. Phenotypic variance was higher than the genotypic variances for all the characters thus indicating the influence of the environmental factors on these traits. The phenotypic and genotypic variations were obtained for different characters, and they are presented in Table 2. The maximum phenotypic and genotypic variation was obtained from the number of filled grains, plant height, number of unfilled grains, days to 80% flowering and days to maturity. Values of phenotypic and genotypic variance were very close for leaf width and 100 seed weight indicating the stable nature of these characters. Similar findings were reported by Fukrei et al.(2011), Yadav et al. (2010) and Singh et al. (1984).

The genotypic coefficient of variation provides a measure to compare the genetic variability present in various quantitative characters. The highest

genotypic coefficient of variation was recorded for the number of unfilled grains and yield per plant (Table 2). The characters like panicle weight, number of filled grains and 100 seed weight gave comparatively higher value for genotypic coefficient of variation. The higher values clearly indicated a high degree of variability in these quantitative characters and suggest the possibility of yield improvement through selection of these traits. Similar findings were reported by Rangare et al. (2011), Fukrei et al. (2011) and Kishor et al. (2008).

The broad sense heritability was higher for 100 seed weight, yield per plant, leaf length, days to 80% flowering, leaf width, number of unfilled grains, days to maturity and panicle weight. The results indicated that high estimates of heritability with less difference between PCV and GCV for these characters could mean that the characters are mainly controlled by the genetic factor and selection based on these characters will be rewarding. These results are in accordance with the findings of Singh et al. (1984), Rangare et al. (2012), Singh et al. (1984), Haider et al. (2012) and Kishor et al. (2009).

Estimates of heritability are more advantageous when expressed in terms of genetic advance. High estimates of heritability coupled with moderate or high value of genetic advance as percentage of means was observed for yield per plant, 100 seed weight, leaf length, days to 80% flowering, leaf width, number of unfilled grains, days to maturity and panicle weight. This suggested that these characters were controlled by additive gene action, which could be improved through simple selection methods. Similar high estimates of heritability and genetic advance has been reported by Kishor et al. (2008), Koli et al. (2013) and Pfukrei et al. (2011) for yield per plant, 100 seed weight and number of primary branches per plant.

Table 1 : Analysis of variance for 13 characters in Rice (*Oryza sativa* L.)

Sources of variation	Degree of freedom	Mean square												
		Days to 80% flowering	Days to maturity	Plant height	Effective bearing tillers	Leaf width	Leaf length	Panicle weight	Panicle length	No: of Primary branches	No: of filled grains	No: of unfilled grains	100 seed weight	Yield / plant
Replication	2	20.00	7.22	87.38	0.08	0.01	62.40	1.82	42.92**	6.68*	3956.09*	106.17*	0.02	7.00
Genotypes	73	457.368**	379.34**	807.01**	2.44**	0.28**	269.72**	7.17**	25.84**	18.54**	14112.62**	550.15**	1.37**	163.10**
Error	146	44.54	64.38	231.23	1.48	0.03	21.28	1.25	7.66	4.59	2671.84	72.29	0.09	12.35

**Significant at 1% level.

Table 2: Mean, range, variance, co-efficient of variation, heritability, genetic advance and genetic advance as % of mean

Characters	Mean ±S.E	Range	Variance			Co-efficient of variation			Heritability (bs) %	Genetic advance	Genetic advance as % of mean
			$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 p$	GCV	PCV	ECV			
1. Days to 80% flowering	118.36 ± 5.45	100 - 165.33	137.60	44.54	182.15	9.91	11.40	5.63	75.5	20.84	17.74
2. Days to maturity	165.18 ± 6.55	130 - 195	104.98	64.38	169.37	6.20	7.87	4.85	61.9	16.34	10.06
3. Plant height	130.03 ± 12.41	93 - 164	191.92	231.23	423.16	10.65	15.81	11.69	45.3	19.06	14.78
4. Effective bearing tillers	3.15 ± 0.99	1.33 - 7.66	0.32	1.48	1.80	17.97	42.54	38.56	17.8	0.46	15.64
5. Leaf length	55.79 ± 3.76	33.33 - 73.66	82.81	21.28	104.09	16.31	18.28	8.26	79.5	16.59	29.96
6. Leaf width	1.60 ± 0.15	0.86 - 2.20	0.08	0.03	0.11	17.79	21.35	11.81	69.4	0.48	30.53
7. Panicle length	24.57 ± 2.26	17.66 - 30.66	6.06	7.66	13.72	10.01	15.07	11.26	44.1	3.35	13.70
8. Panicle weight	3.38 ± 0.91	1.33 - 9.43	1.97	1.25	3.22	41.55	53.15	33.13	61.1	2.24	66.92
9. No: of primary branches	9.68 ± 1.75	3.66 - 17.66	4.65	4.59	9.24	22.26	31.39	22.13	50.3	3.13	32.53
10. No: of filled grains	181.69 ± 42.20	72 - 386.66	3813.59	2671.84	6485.43	33.98	44.32	28.44	58.8	96.21	53.68
11. No: of unfilled grains	22.89 ± 6.94	5 - 82	159.28	72.29	231.58	55.13	66.47	37.14	68.7	21.30	94.19
12. 100 seed weight	2.28 ± 0.25	0.93 - 4.26	0.42	0.09	0.52	28.56	31.68	13.71	81.2	1.20	53.04
13. Yield /plant	13.59 ± 2.87	2.60 - 37.90	50.25	12.35	62.60	52.15	58.21	25.85	80.2	13.0	96.25

CONCLUSION

On the basis of the results, it is concluded that rice germplasm revealed a high degree of variability. High estimates of heritability with less difference between PCV and GCV for 100 seed weight, yield per plant, leaf length, leaf width, panicle weight, days to maturity, number of filled grains, plant height and days to flowering could mean that these characters are mainly controlled by the genetic factor and selection based on these characters will be rewarding.

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