



# Genetic Variation on Upland Rice (*Oryza sativa* L.) Landraces of Nagaland

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### ABSTRACT

The success of most crop improvement programs largely depends upon the genetic variability and the heritability of desirable traits. The magnitude and type of genetic variability help the breeder to determine the selection criteria and breeding schemes to be used for improvement purposes. An experiment was conducted under NU: SASRD during kharif 2015 to estimate the genetic variability, heritability and correlation coefficient in ten genotypes of upland paddy evaluated in a randomized block design with three replications. Observations were recorded for ten quantitative traits. Genetic variability analysis revealed that, the genotypic coefficient of variation was highest for grain yield per plant followed by percent sterile spikelets, panicle weight, and ear bearing tillers. Heritability values for almost all the characters were found to be high. High heritability with high genetic advance was found for plant height. Percent sterile spikelets showed high heritability with moderate value of genetic advance. Grain yield per plant showed strong significant positive genotypic association with 100 seed weight, panicle weight, ear bearing tillers and panicle length.

### 1. Introduction

Upland is an important system of rice culture and constitutes about one sixth of the world's total rice land. In Nagaland, total rice cultivation accounts to an area of 1, 83,330 hectares producing 4,05,180 tonnes of paddy (Anonymous 2014). Globally, rice is the second most important cereal crop after wheat, by meeting the dietary requirements of the people living in the tropics and sub-tropics. It is grown over an area of 158 million hectares in the world. India ranks first in area and second after China in production. West Bengal rank first in area and production contributing about 15.80% of the country's total production. (Anonymous 2014). In Nagaland, rice is the main cereal crop of the people with about 70% of the population directly or indirectly engaged in agriculture.

In Nagaland, total rice cultivation accounts to an area of 1, 83,330 hectares producing 4, 05,180 tonnes of paddy (Anonymous 2014). In Nagaland a good number of local varieties and land races are available which possess immense genetic variability, though many of them are low yielding. Yet, real success in rice breeding in Nagaland is most likely to be made up by proper utilization of promising local cultivars, which are well adapted to different agro-ecological conditions. Since the cultivated area cannot be increased, efforts are to be intensified to increase the productivity per unit area. To increase the production and productivity in these ecosystems, an alternative is to improve the existing local varieties with regard to yield potential, biotic and abiotic stress, grain quality, nutrient responsiveness, adaptability etc. through breeding programs. Therefore, present study was planned to investigate the genetic variability, heritability and correlation association between the characters to identify the best traits to be used for future exploitation.

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## 2. Material and Methods

The experimental material comprised of 10 local cultivars of rice collected from different districts of Nagaland and one from Sikkim which were evaluated during kharif 2015-16. Details of the genotypes are presented in Table 1. The experiments was carried out in randomized block design in three replications in the experimental field of Genetics and plant breeding, Nagaland University, SASRD, Medziphema. Observations were recorded for 10 quantitative characters *viz.* days to 50% flowering, days to maturity, plant height at maturity, effective tillers per plant, panicle length, panicle weight, branches per panicle, percent sterile spikelets, 100 seed weight, yield per plant. The statistical analysis of the data recorded was calculated using the formula given by Burton and De vane (1953) for phenotypic, genotypic and environmental coefficients of variation. Heritability in broad sense ( $h_{bs}^2$ ) was computed using the formula given by Allard, 1960 and phenotypic and genotypic correlation coefficients were worked out as suggested by Al-Jibouri et al. (1958).

**Table 1.** Genotype details

Sl. No	Genotype	Name	Place of collection
1	G1	SARS-1	Nagaland
2	G2	SARS-2	Nagaland
3	G3	SARS-4	Nagaland
4	G6	Khatori	Nagaland
5	G8	Chali youh	Nagaland
6	G9	Kebe be	Nagaland
7	G10	Taryu	Nagaland
8	G12	Attey	Sikkim
9	G13	Teke	Nagaland
10	G14	Datsa	Nagaland

## 3. Results and Discussion

The analysis of variance (Table 2) indicated highly significant differences among genotypes for all the characters, similar result was also reported by Patel et al. (2014). The results clearly indicated the presence of high amount of variability for yield and yield components among the genotypes studied. Therefore, there is of scope for selection for majority of the traits in the genotypes.

The genotypic and phenotypic coefficients of variation were high for yield per plant (35.20 and 35.35) and percent sterile spikelets (34.70 and 36.24). Similar results were reported by Paul et al. (2011) and. Patel et al. (2014). The high PCV and GCV values for number of yield per plant and percent spikelet sterility among the genotypes respectively suggest that there is lot of scope for selection to develop high yielding superior genotypes. Moderate values of genotypic coefficient of variation and phenotypic coefficient of variation were noticed for branches per panicle and plant height. A similar result was also reported by Pfukrei et al. (2011). Low GCV and PCV value (Table 3) were found in days to 50% flowering, days to maturity and panicle length. Aditya and Bhartiya (2013) and Fukrei et al. (2011) also reported similar result. The estimates of PCV were higher from those of GCV for all the traits indicating environment factors influencing their characters. It can be suggested that the above traits with high values may be selected for hybridization to recover superior genotype or recombinants. Besides, the values did not show much difference between GCV and PCV thereby indicating low environmental effect on these traits. The estimates of heritability alone fail to indicate the response to selection (Johnson et al. 1955). Therefore, the heritability estimates appears to be more meaningful when accompanied by estimates of genetic advance. The genetic advance as percent mean was also estimated. Heritability is usually considered to be low if it is less than 30%, moderate between (30-60%) and high if it is more than 60% (Johnson *et al.*, 1955). Heritability values for almost all the characters were found to be high and the values ranged from 68.14 to 99.19 per cent (Table 3). Grain yield recorded the highest heritability value (99.19%). Similar results were found by Tiwari (2015) followed by panicle weight (97.83%) and 100 seed weight (97.48%) also showed high heritability results. Days to 50% flowering recorded the lowest heritability value (68.14 %). High heritability coupled with high genetic advance as per cent mean was found for grain yield per plant (99.19 and 72.23), similar results of high heritability coupled with high genetic advance were reported by Singh et al. (2006) for plant height, Sravan et al. (2011). Days to 50% flowering exhibited lowest heritability. High heritability accompanied by low genetic advance was observed for plant height (94.56 and 20.54). Percent sterile spikelets exhibited high heritability with moderate genetic advance (91.67 and 68.44). High heritability and high genetic advance indicates the role of additive gene action.

**Table 2.** Mean sum square values for 10 characters of upland rice genotypes

Source	df	DTF	DTM	PH	EBT	PL	PW	B/P	SS	100gr. wt	GY/P
Replication	2	7.593	15.606	1	0.132	3.084	0.008	0.032	6.389	0.0054	1.153
Genotype	9	80.817* *	76.608* *	526.98* *	2.444* *	9.893* *	1.834* *	5.299* *	145.511* *	1.203**	42.277* *
Error	18	10.897	10.006	9.921	0.134	0.679	0.013	0.415	4.276	0.01	0.115

\*significant at 5% level of significance, \*\*significant at 1% level of significance

Information on the phenotypic and genotypic interrelationships of grain yield with its component characters and also among the component characters themselves would be useful to the breeder in developing an appropriate selection strategy. Since, yield is a complex character and influenced by number of traits and selection based on yield is usually not much effective, indirect selection on the basis of desirable component characters could be of great use. Positive and significant correlation of yield with panicle weight (0.875), 100 seed weight (0.878), effective tillers per plant (0.764) and panicle length (0.736) was observed at the genotypic level (Table 6). At the phenotypic level positive and significant correlation was observed with panicle weight (0.866), 100 seed weight (0.864), effective tillers per plant (0.689) and panicle length (0.667) (Table 5). Days to maturity had positive and significant correlation with days to flowering at both genotypic (0.988) and phenotypic level (0.985). Panicle

length showed positive and significant correlation with effective tillers per plant (0.753) at genotypic level. Panicle weight showed positive and significant correlation with panicle length and effective tillers per plant in both genotypic and phenotypic level. At genotypic level correlation with panicle length was 0.875 while in phenotypic level a value of 0.785 was seen. Effective tillers per plant at genotypic level expressed a correlation of 0.769 and 0.712 at phenotypic level. Percent sterile spikelet's showed significant negative correlation with panicle weight (-0.706) and branches per panicle (-0.578) in genotypic level while at the phenotypic level it showed negative correlation with panicle weight (-0.678). 100 seed weight showed positive and significant correlation with panicle weight (0.797), panicle length (0.659) and plant height (0.642) at the genotypic level. At the phenotypic level it showed positive and significant correlation with panicle weight (0.782), plant height (619) and panicle length (0.597).

**Table 3.** Genetic parameters for 10 upland rice genotypes

Character	Mean	Range	Gcv	Pcv	Heritability (%)	Ga As % Of Mean
DTF	110.10	103.33-118.66	4.38	5.31	68.14	7.45
DTM	140.20	133.33-148.66	3.36	4.04	68.93	5.74
PH	127.99	94-142.60	10.25	10.54	94.56	20.54
EBT	3.79	2.73-5.26	23.11	25.05	85.13	43.93
PL	25.16	22.61-29.41	6.96	7.69	81.89	12.98
PW	3.13	2.02-4.55	24.88	25.15	97.83	50.70
B/P	11.87	9.43-13.55	10.74	12.04	79.67	19.76
SS	19.77	12.48-29.87	34.70	36.24	91.67	68.44
100 SW	2.75	2.06-3.86	22.91	23.20	97.48	46.60
GY/P	10.64	6.26-17.25	35.20	35.35	99.19	72.23

**Table 4.** Mean values of 10 characters in upland rice genotypes

Genotype	Dtf	Dtm	Ph(cm)	Ebt	Pl(cm)	Pw(g)	B/P	Ss(g)	100gw(g)	Gy/P(g)
SARS-1	106.66	136.66	137.53	4.26	26.05	4.13	11.78	12.6	3.77	15.69
SARS-2	109.33	139.33	134.46	3.46	25.78	3.44	13.5	13.51	2.75	9.30
SARS-4	116.33	146.33	124.60	3.46	24.85	3.08	13.55	15.84	2.11	9.24
KHATORI	109.66	139.66	128.53	3	24.43	2.99	11.03	18.8	2.63	8.16
CHALI YOUH	110	140	131.26	4.20	24.97	3.06	13.03	28.57	2.85	13.48
KEBE BE	118.66	148.66	123.46	3.63	23.36	2.81	12.4	14.80	2.79	11.55
TARYU	108.66	138.66	142.60	5.26	29.41	4.55	12.19	12.48	3.86	17.25
ATTEY	104.33	134.33	133.76	2.80	25.07	2.11	10.65	24.22	2.15	6.53
TEKE	103.33	133.33	94	5.13	25.04	3.09	11.13	27.01	2.06	8.97
DATSA	115	145	129.66	2.73	22.61	2.027	9.43	29.87	2.51	6.26
<b>Grand mean</b>	110.10	140.20	127.99	3.79	25.16	3.13	11.87	19.77	2.75	10.64
<b>CD at 5%</b>	5.66	5.42	5.40	0.62	1.41	0.19	1.10	3.54	0.173	0.58
<b>CD at 1%</b>	7.75	7.43	7.4	0.86	1.93	0.27	1.51	4.85	0.23	0.79
<b>SE</b>	1.90	1.82	1.81	0.21	0.47	0.06	0.37	1.19	0.05	0.19

In the present study, grain yield per plant had strong positive genotypic association with 100 seed weight, panicle weight, effective tillers per plant, panicle length. Similar results of significant positive association of grain yield per plant was reported by Chaubey and Richharia (1993) for panicle length, panicle weight and test weight. Chaudhary and Motirmanii (2003) also reported strong positive genotypic association between grain yield per plant and effective tillers per plant. The correlation study shows that the characters viz. panicle weight, panicle length, effective tillers per plant and 100 seed weight contribute toward yield. Hence, selection criteria should consider these traits for the improvement of grain yield per plant in upland rice genotypes. Based on the above analysis it was seen that genotypes with good mean performance with respect to the characters mentioned, like TARYU and SARS-1 seems promising.

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**Table 5.** Phenotypic correlation ( $r_p$ ) for yield and yield contributing characters

	<b>DTF</b>	<b>DTM</b>	<b>PH</b>	<b>EBT</b>	<b>PL</b>	<b>PW</b>	<b>B/P</b>	<b>SS</b>	<b>100 SW</b>	<b>GY/P</b>
<b>DTF</b>	1	0.985**	0.083	-0.292	-0.367	-0.165	0.194	-0.135	-0.061	-0.035
<b>DTM</b>		1	0.103	-0.328	-0.379	-0.197	0.174	-0.134	-0.084	-0.057
<b>PH</b>			1	-0.243	0.371	0.28	0.148	-0.403	0.619*	0.369
<b>EBT</b>				1	0.554	0.712**	0.216	-0.181	0.45	0.689*
<b>PL</b>					1	0.785**	0.344	-0.489	0.597*	0.667*
<b>PW</b>						1	0.426	-0.678*	0.782**	0.866**
<b>B/P</b>							1	-0.495	0.146	0.414
<b>SS</b>								1	-0.53	-0.502
<b>100 SW</b>									1	0.864**
<b>GY/P</b>										1

\*significant at 5% level of significance

\*\*significant at 1% level of significance

**Table 6.** Genotypic correlation ( $r_g$ ) for yield and yield attributing characters

	<b>DTF</b>	<b>DTM</b>	<b>PH</b>	<b>EBT</b>	<b>PL</b>	<b>PW</b>	<b>B/P</b>	<b>SS</b>	<b>100 SW</b>	<b>GY/P</b>
<b>DTF</b>	1	0.988**	0.158	-0.364	-0.498	-0.209	0.278	-0.203	-0.028	-0.054
<b>DTM</b>		1	0.168	-0.396	-0.511	-0.244	0.268	-0.188	-0.049	-0.082
<b>PH</b>			1	-0.247	0.384	0.296	0.151	-0.44	0.642*	0.387
<b>EBT</b>				1	0.753**	0.769**	0.346	-0.204	0.471	0.764**
<b>PL</b>					1	0.875**	0.357	-0.536	*0.659	0.736**
<b>PW</b>						1	0.532	-0.706*	0.797**	0.875**
<b>B/P</b>							1	-0.578*	0.175	0.462
<b>SS</b>								1	-0.571	-0.529
<b>100 SW</b>									1	0.878**
<b>GY/P</b>										1

\*significant at 5% level of significance

\*\*significant at 1% level of significance