

## Genetic variability of panicle characters in tall indica aman rice

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### ABSTRACT

Thirty five genotypes of tall indica aman rice were evaluated for nine panicle characters under two environments to find out the extent of genetic variability present in the population. The experimental study indicated existence of considerable amount of genetic variability for all the characters studied. Genotypic and phenotypic coefficient of variation were high for unfilled florets panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, panicle number plant<sup>-1</sup>, grains panicle<sup>-1</sup>, panicle weight and 1000-grain weight. High estimates of heritability, genotypic coefficient of variation and genetic advance were observed for unfilled florets panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, panicle number plant<sup>-1</sup>, grains panicle<sup>-1</sup>, panicle weight and 1000-grain weight. These characters can be effectively improved through selection.

**Key words:** Genetic variability, tall, indica, aman rice

The inherent genetic variability, that remains unaffected by the fluctuation of environment, is very useful to a plant breeder for its exploitation in selection for superior genotypes. In this context, an attempt was made to find out the nature and magnitude of heritable and non-heritable component of variation and genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance to assess the possibility of further improvement through selection.

Thirty five genotypes of tall indica aman rice (*Oryza sativa* L.) were evaluated under two environments (shallow and semideep) during wet season 2002 at the Regional Research Station, Bidhan Chandra Krishi Viswavidyalaya, Nadia, West Bengal. The genotypes were transplanted in a randomized block design with two replications in 5 rowed plots at a spacing of 20 cm x 20 cm. Agronomical practices were followed as per the recommended package of practices. At maturity, observations were recorded on nine characters viz., panicle number plant<sup>-1</sup>, panicle length, primary branches panicle<sup>-1</sup>, secondary branches panicle<sup>-1</sup>, grains panicle<sup>-1</sup>, unfilled florets plant<sup>-1</sup>, 1000-grain weight, panicle weight and grain yield plant<sup>-1</sup> in five randomly selected plants per replication for each genotype. The pooled data under the two environments were statistically analysed.

The extent of variability present in thirty five

genotypes was measured in terms of range, mean squares (Genotype), genotypic variance ( $s^2G$ ), genotypic coefficient of variation (GCV), phenotypic variance ( $s^2P$ ), phenotypic coefficient of variation (PCV), heritability ( $h^2$ ) in broad sense and genetic advance (GA) (Table 1 and 2). All the varieties differed significantly with respect to different characters studied. The wide spectrum of variability noticed for all the characters would offer scope of selection for evolving promising types. Mani *et al.* (1997) and Barbora and Hazarika (1998) also reported wide range of variation for most of the characters studied in this crop. The estimates of genotypic and phenotypic variances were high for grains panicle<sup>-1</sup>, unfilled florets panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, secondary branches panicle<sup>-1</sup>, 1000-grain weight and panicle number plant<sup>-1</sup> and lowest for panicle weight. In this regard high genotypic and phenotypic variances have been reported for filled grain panicle<sup>-1</sup> (Roy *et al.*, 2001) and grain yield plant<sup>-1</sup> (Rao and Srivastav, 1994).

GCV, which gives a picture of extent of genetic variability, ranged from 8.00 percent (primary branches panicle<sup>-1</sup>) to 51.26 (unfilled florets panicle<sup>-1</sup>). Both GCV and PCV values were high for unfilled florets panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, panicle number plant<sup>-1</sup>, grains panicle<sup>-1</sup>, panicle weight and 1000-grain weight. So, these characters having higher range of variation have a better scope of improvement through selection.

**Table 1. Mean performances of 35 genotypes of tall indica aman rice for nine panicle characters**

Variety	Panicle number plant <sup>-1</sup>	Panicle length (cm)	Primary branches panicle <sup>-1</sup>	Secondary branches panicle <sup>-1</sup>	Grains panicle <sup>-1</sup>	Unfilled florets panicle <sup>-1</sup>	1000-grain wt. (g)	Panicle wt.(g)	Grain yield plant <sup>-1</sup> (g)
Radhunipagal	9.75	25.17	12.15	41.10	183.35	27.58	11.55	1.59	14.99
Kalonunia	7.30	25.67	10.00	32.67	131.85	26.92	17.38	1.86	11.77
Kataribhog	8.95	24.31	9.60	33.10	102.72	67.50	19.73	2.09	16.32
Andrewsali	9.95	25.48	11.05	37.85	158.93	27.05	32.15	2.82	27.18
Guarai	9.70	23.33	11.43	34.03	114.02	23.00	24.50	2.56	23.97
Sabita	7.95	23.53	11.80	36.42	120.12	32.47	25.02	2.47	18.45
Sonabarsha	12.35	28.02	11.15	32.72	151.15	28.17	24.70	2.49	29.46
Balam	11.20	23.78	10.38	26.50	85.05	38.70	23.67	1.55	15.25
Pitcher	9.55	23.74	10.85	30.50	102.62	40.90	27.40	2.64	24.27
Erosadbhog	10.70	22.09	11.90	33.30	117.53	25.88	24.60	2.51	24.91
Barojahinga	13.35	24.92	11.33	29.75	113.88	21.45	28.30	1.87	23.62
Satras	5.85	25.37	11.00	39.28	94.48	72.52	25.33	2.45	12.81
CR-260-131	7.50	22.11	10.30	32.70	102.72	12.70	28.67	2.66	18.47
CRM-30	5.90	23.28	10.90	31.88	96.40	25.73	30.15	2.61	14.30
Lilabati	8.30	23.65	11.48	34.97	107.53	63.65	26.05	2.53	20.53
Chalisa	5.80	20.46	12.18	34.88	107.60	69.40	26.60	2.64	13.88
Haldiguri	7.75	23.38	11.83	34.33	109.75	31.65	25.20	2.07	14.76
Dusali	7.65	24.75	9.88	40.42	124.20	28.40	25.40	2.80	19.99
Khayersail	6.05	20.35	11.40	36.05	122.97	26.85	30.85	3.05	17.72
Bankisali	6.75	26.17	11.30	42.97	130.90	38.45	22.88	3.22	20.62
Lunishree	5.05	21.23	10.83	29.25	86.53	49.25	27.30	2.28	10.09
Langulmutha	5.25	19.78	10.60	25.92	85.90	36.85	34.30	2.34	11.21
NC 364	5.75	21.40	9.88	31.83	146.38	46.53	26.30	2.55	13.44
Rajjhinge	8.95	22.12	10.55	32.90	132.05	34.10	22.65	2.73	23.31
Kalmisal	8.40	20.12	8.83	20.42	73.18	18.38	24.15	1.44	11.06
Brimphul	8.15	27.35	11.15	28.02	34.58	108.30	26.48	1.05	6.36
CR-260-77	14.15	21.94	9.52	20.50	82.68	22.83	26.45	1.67	22.50
Kalamkati	13.50	21.35	10.62	26.30	102.25	38.82	22.27	1.67	21.15
Neera	7.10	21.37	11.80	32.20	93.38	31.52	25.65	2.78	18.70
Suakalma	7.45	23.03	12.62	35.97	101.32	78.02	20.70	2.05	13.44
Nagra	6.65	20.89	11.23	32.70	121.12	20.95	30.33	2.93	18.46
Dinesh	8.40	23.42	11.73	34.72	105.80	40.12	30.22	2.80	22.58
Matla	8.10	26.81	12.85	37.82	125.25	66.80	27.65	3.22	24.30
Jhingesail	8.80	22.14	10.55	32.40	117.68	33.90	22.40	2.32	19.04
Samba Masuri	9.15	21.19	11.27	33.40	148.45	49.50	13.23	1.99	15.84
SE (diff)	0.20	0.26	0.18	1.00	2.38	1.18	0.14	0.04	0.57
CD (P=0.05)	0.41	0.53	0.37	2.03	4.84	2.39	0.28	0.08	1.16
C.V.	2.40	1.14	1.63	3.03	2.12	2.95	0.54	1.76	3.17

High GCV and PCV for panicle weight, grains panicle<sup>-1</sup>, panicle number plant<sup>-1</sup>, 1000-grain weight and grain yield plant<sup>-1</sup> were earlier reported by Yadav (2000).

With the help of GCV alone, it is not possible to determine the amount of variation that is heritable. Heritable variation can be found out with greater degree

of accuracy when heritability is studied in conjunction with genetic advance. The heritability estimates were high for all the characters suggesting that the environmental effects constitute a minor portion of total phenotypic variation and hence direct selection for this character will be effective. Expected genetic advance and its estimate as percentage of mean for various

**Table 2. Variability and genetic parameters for different panicle characters in tall indica aman rice**

Characters	Mean	Range	Mean squares (genotype)	Phenotypic variance	Genotypic variance	G.C.V.	P.C.V.	h <sup>2</sup>	G.A.	G.A. as % of mean
Panicle number plant <sup>-1</sup>	8.49	4.80-14.30	10.91**	5.48	5.44	27.46	27.57	0.992	4.78	56.30
Panicle length (cm)	23.25	19.66-28.32	9.19**	4.63	4.56	9.18	9.25	0.985	4.37	18.80
Primary branches panicle <sup>-1</sup>	11.03	8.60-12.95	1.59**	0.81	0.78	8.00	8.17	0.960	1.78	16.14
Secondary branches panicle <sup>-1</sup>	32.85	20.00-43.90	50.60**	25.80	24.81	15.16	15.46	0.962	10.06	30.62
Grains panicle <sup>-1</sup>	112.41	33.00-185.45	1471.49**	738.58	732.92	24.08	24.18	0.992	55.36	49.25
Unfilled florets panicle <sup>-1</sup>	40.14	11.45-109.05	848.15**	424.78	423.38	51.26	51.35	0.997	42.32	105.43
1000 - grains wt. (g)	25.25	11.45-34.35	44.55**	22.29	22.27	18.76	18.77	0.999	9.72	38.65
Panicle wt. (g)	2.35	1.00-3.33	0.55**	0.27	0.27	22.29	22.36	0.994	1.08	45.96
Grain yield plant <sup>-1</sup>	18.14	6.14-30.17	57.12**	28.77	28.44	29.41	29.58	0.989	10.92	60.20

\* Significant at 5% level, \*\* Significant at 1% level

characters revealed that unfilled florets panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, panicle number plant<sup>-1</sup>, grains panicle<sup>-1</sup>, panicle weight and 1000-grain weight had high genetic advance. Though characters such as primary branches panicle<sup>-1</sup>, panicle length and secondary branches panicle<sup>-1</sup> had high heritability values, their GCV were comparatively less resulting in less genetic advance. It confirms the findings of Burton (1952) that GCV together with heritability estimate would give a better picture of genetic advance to be expected from selection. Swarup and Changale (1962) also pointed out that high heritability was not always accompanied by high genetic advance. If heritability was mainly owing to non-additive gene action, the expected genetic advance could be expected. It is clear from Table 2 that the characters like unfilled florets panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, panicle number plant<sup>-1</sup>, grains panicle<sup>-1</sup>, panicle weight and 1000-grain weight possessing high GCV, heritability and genetic advance could be effectively used in selection (Johnson *et al.*, 1955). High heritability coupled with high genetic advance for grains panicle<sup>-1</sup>, panicle length and grain yield plant<sup>-1</sup> was earlier reported by Paramasivam and Rangaswamy (1988); for grains panicle<sup>-1</sup>, 1000-grain weight, panicle length and grain yield plant<sup>-1</sup> by Sawant *et al.* (1995); for number of chaffy or unfilled florets panicle<sup>-1</sup>, grains panicle<sup>-1</sup>, 1000-grain weight and secondary branches panicle<sup>-1</sup> by Barbora and Hazarika (1998); for grain yield plant<sup>-1</sup> by Balan *et al.* (2000) and for number of grains panicle<sup>-1</sup> and grain yield plant<sup>-1</sup> by Roy *et al.*

(2001). High heritability and moderate genetic advance observed in case of secondary branches panicle<sup>-1</sup> indicating predominance of additive gene action. High heritability and low genetic advance observed in other characters namely primary branches panicle<sup>-1</sup> and panicle length indicated that expression of these characters was governed by non-additive gene action.

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