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Estimation of genetic parameters in indigenous rice

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Abstract. Significant genetic variability was observed among 22 genotypes of indigenous rice for yield and quality contributing traits viz., number of spikelets per panicle, test weight, grain yield per hill, volume expansion ratio, head rice recovery, kernel length and length breadth ratio, indicating that there is presence of sufficient amount of variability in the study material and there is scope of selection. On the basis of mean performance of yield and yield contributing traits it was concluded that "Indrani" was the best performer for both yield and quality which was at par with the hieghest yielder genotype Jhumeri. For quality parameters Narendra-359 and Indrani were good, milling percentage of Lohandi was best followed by Bayalu & Dudagi general types. The results showed that PCV (phenotypic coefficient of variance) in general was higher than GCV (genotypic coefficient of variation) for various characters. However the difference between GCV and PCV was low for most of the characters studied. This indicates less degree of environmental influence on manifestation of these characters. High heritability coupled with high genetic advance were recorded for number of spikelets per panicle, hulling percentage, milling percent and head rice recovery indicated the major role of additive gene action in the inheritance of these character and these characters could be improved by selection in segregating generation. Thus, these characters may serve as an effective selection parameter during breeding programme for crop improvement.
Key words: rice, local land races, variability, heritability, rice quality.

Introduction. "Rice is life" was the famous theme of International Year of Rice, 2004 denoting its overwhelming importance as an item of food and commerce. Today rice is grown and harvested on every continent except Antarctica. Rice remains a staple food for the majority of the world population. More than two thirds of the world relies of the nutritional benefit of rice. Most of India's rice exports are long grain basmati and non-basmati varieties like PR-106, Kavya, Kamini, Sona mahsuri, IR-64, Sambha mahsuri and high quality basmati varieties like Bas–370, Taroari-Basmati and Pusa Basmati-1. The large spectrum genetic variability in segregating populations depends on the level of genetic diversity among genotypes offer better scope for selection. Recently, after realizing the export potentiality and also the domestic demand of basmati varieties, more attention has been given to increase the yield of basmati varieties in the country. Many local land races are still used in interiors parts of India, which are supported to be good quality but with a low productivity. Farmer interested for needs of his own family usually saw these seeds for eating purpose. Intraspecific variability of a crop evolves in relation to the peculiarities of the habitat of each and every population. The newly born state, Chhattisgarh is known as "Rice bowl of India" with an area of 3.54 million hectares under rice cultivation with production of 5.4 million ha (Directorate of Agriculture - Raipur 2005). The Chhattisgarh region and adjoining area of Orissa are considered to be the store house of vast genetic variability and very high diversity of aromatic rice cultivars due to extreme variation in the agro and eco climatic conditions, season, topography, altitude, soil and moisture stress factors coupled with variation in the cultivars heritage of the inhabitant (Richhariya 1979). The aroma and the quality are adored by the rural masses. At present many nations are facing second generation challenge of producing more rice at less cost in a deteriorating environment. These local land races are adapted to adverse conditions with least management. Efforts are to be taken with a systematic research approach to exploit the yield potential by direct and indirect selection. The large

spectrum genetic variability in segregating populations depends on the level of genetic diversity among genotypes offer better scope for selection. Estimates of GCV, PCV, heritability and genetic advance will play an important role in exploiting future research projections of rice improvement. Therefore, an attempt was made in the present studies to estimate the extent of variability, heritability, genetic advance for yield improvement in aromatic rice.

Material and Methods. The experimental material for the present study consisted of 22 indigenous rice genotypes which were evaluated in a randomized block design in three replications in 4 m^2 plot at field experimentation centre of the Department of Genetics and Plant Breeding, Allahabad Agricultural Institute - Deemed University, Allahabad during *Kharif* season (June - November), 2005. The recommended cultural practices were followed to raise the crop. The observations were recorded 10 randomly selected plants from each replication for characters *viz.,* number of panicles per hill, number of spikelets per panicle, test weight grain yield per hill, volume expansion ratio, hulling, milling, head rice recovery, kernel length, kernel breadth and length breadth ratio. The mean value were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse & Sukhatme (1967). PCV and GCV were calculated by the formula given by Burton (1952), heritability in broad sense (h^2) by Burton & De Vane (1953), and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson et al (1955).

Results and Discussion. On the basis of mean performance of yield and yield contributing traits Jhurmeri was highest yielder followed by Indrani, Sarjoo-52, Jaya and Narendra–359. For quality parameters Narendra-359 and Indrani were good. Milling percentage of Iohandi was best followed by Bayalu and Dudagi (Table 1). The analysis of variance revealed highly significant differences among the genotypes for the entire test characters, indicating the existence of high variability among the varieties. Thus there is ample scope for selection of different qualitative and quantitative characters for rice improvement. The estimates of phenotypic (Vp) and genotypic (Vg) variation were obtained for different characters and they are presented in Table 2. A wide range of phenotypic variance was observed for the characters like number of spikelets per panicle, grain yield per hill, hulling, milling and head rice recovery. Whereas lower range phenotypic variance was observed for the characters like number of panicles per hill, test weight, volume expansion ratio, kernel length, and kernel breadth and length breadth ratio. Genotypic variance is lower than the phenotypic variance for all the yield and quality character studied. Estimates of phenotypic variance revealed that number of spikelets per panicle exhibit highest phenotypic variance followed by milling percentage.

A perusal of GCV revealed that maximum value of genetic coefficient of variation (GCV) was recorded for head rice recovery (34.91) followed by breadth (30.19), grain yield per hill (29.24) and milling percentage. Head rice recovery (34.91) exhibited maximum phenotypic coefficient of variation (PCV) followed by volume expansion ratio (32.25), kernel breadth (30.19), and gain yield per hill (29.26), while low estimates were observed for test weight (15.93) and length (19.32), (29.13). These results are in confirmation to the findings of Deosarkar et al (1989) (see Table 2).

The studies on genotypic coefficient of variation and phenotypic coefficient of variation indicated that the presence of high amount of variance and role of the environment on the expression of these traits. The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters which may be due to higher degree of interaction of genotypes with the environment (Kavitha & Reddy 2002).

These values alone are not helpful in determining the heritable portion of variation (Falconer 1960). The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability (Lush 1949). In the present study high broad sense heritability was observed for traits like viz., test weight (99.25 %), grain yield per hill (97.90 %), kernel breadth (97.98 %), head rice recovery (97.98), hulling (97.88), milling (98.87 %) and length breadth ratio (96.72 %).While lowest heritability was observed in volume expansion ratio (23.82) (see Table 2).

Table 1

Mean performance of twenty two rice genotypes for their yield and grain quality characters

S.No.	Genotypes	No. of panicles per hill	No. of spikelets per panicle	Test weight (g)	Grain yield per hil (g)	Kernel length (mm)	Kernel Breadth (mm)	L/b ratio (mm)	Volume Expans-ion ratio (cm^3)	Hulling (%)	Milling (%)	HRR (%)
1	IET-15833-02	6.87	135.33	21.62	14.11	5.1	2.45	2.42	0.05	76.22	70.51	56.5
2	Sarjoo-52	10.6	139.8	19.22	29.85	5.2	2.05	2.43	0.08	80.5	71.78	46.5
3	Sonachur	8.27	129.53	17.92	14.95	4.3	2.15	2.35	0.05	41.54	33.86	23.62
4	Annada	9.6	133.27	13.22	19.84	4.3	2.65	1.93	0.05	79.54	67.17	47.5
5	Jaya	7.73	188.4	16.12	29.81	4.8	2.15	2.6	0.05	82.54	75.85	56.5
6	Narendra-359	7	177.93	20.12	29.79	5.1	5.15	2.75	0.08	81.68	71.66	61.5
7	Lohandi	7.73	153.6	22.12	27.53	4.1	2.15	2.25	0.08	85.02	83.99	66.85
8	Vishnu Bhog	5.67	130.8	14.94	20.09	3.5	2.15	1.95	0.05	41.81	31.2	18.73
9	Tulasi Muni	6.2	129.4	17.14	13.4	4.5	2.15	2.45	0.07	44.03	39.83	25.85
10	Dubraj	7.6	169.37	20.94	24.58	4.9	2.15	2.65	0.08	61.68	53.54	60.82
11	Jhumeri	8.8	188.2	24.54	37.72	3.3	2.15	1.85	0.07	74.85	58.85	39.62
12	Bhata Suarna	6.8	114.67	19.34	13.95	4.3	2.15	2.35	0.07	55.22	46.6	33.26
13	Chullai	10.93	142.8	14.94	20.52	5.1	2.15	1.63	0.05	47.47	40.6	25.06
14	Bayalu	7.27	125.07	23.64	17.85	5.1	2.15	2.33	0.05	87.21	83.36	73.32
15	HMT	8.07	127.2	22.54	24.08	3.9	2.25	2.15	0.06	84.24	71.39	54.26
16	Indrani	8	183.27	21.84	37.35	5.1	2.55	2.01	0.07	79.21	65.11	46.24
17	Bhata Sulti	10.27	146.87	17.14	28.86	3.9	2.14	2.15	0.05	51.27	33.8	22.2
18	Karhayni	9.87	111.13	21.24	23.88	4.7	1.15	2.55	0.07	67.16	55.65	31.11
19	Suarna	7.8	138.4	17.94	19.61	3.17	2.15	2.55	0.08	51.19	36.83	60.66
20	Rani Kajar	8.93	152.07	22.34	26.89	4.7	2.14	2.55	0.08	84.05	73.98	55
21	Dudagi	8.13	150.07	23.24	24.82	4.7	2.15	2.55	0.04	84.47	77.94	51.45
22	Sambha Mahsuri	10.13	146.53	21.24	29.49	5.1	2.14	2.75	0.08	78.13	71.32	53.33
	SE	**0.87**	**10.48**	**0.007**	**0.13**	**0.33**	**0.086**	**0.07**	**0.01**	**0.33**	**0.36**	**0.15**
	CV	**18.22**	**12.42**	**0.04**	**0.94**	**12.6**	**0.35**	**5.08**	**28.15**	**0.82**	**1.03**	**0.55**
	CD (5%)	**2.49**	**29.91**	**0.01**	**0.37**	**0.93**	**0.01**	**0.21**	**0.03**	**0.93**	**1.02**	**0.41**
	CD (1%)	**3.33**	**39.98**	**0.02**	**0.5**	**1.25**	**0.02**	**0.28**	**0.04**	**1.25**	**1.36**	**0.55**

Table 2

Variability parameters for different characters in twenty two rice genotypes

Characters	Mean	Range		Vg	Vp	GCV	PCV	h^2 (bs)	GA	GG
		Min.	Max.							
No. of panicles per hill	8.28	5.67	10.93	1.35	3.62	14	22.98	37.13	1.46	17.15
No. of spikelets per panicle	146.11	111.13	188.40	404.71	734.1	13.77	18.54	55.13	30.77	21.60
Test weight	19.70	13.22	24.54	9.85	9.85	15.93	15.93	99.26	6.47	32.82
Grain yield per hill	24.04	13.40	37.72	49.43	49.48	29.24	29.26	97.93	14.48	0.20
Volume Expansion ratio	4.49	3.17	5.20	0.0089	0.037	15.74	32.25	23.82	0.01	15.83
Kernel length	2.29	1.15	5.15	0.29	0.61	11.89	17.32	97.88	0.76	16.80
Kernel breadth	2.47	1.63	2.75	0.48	0.48	30.19	30.19	98.87	1.43	62.18
L/B ratio	0.06	0.04	0.08	0.47	0.48	27.62	28.08	97.98	1.38	55.95
Hulling	69.07	41.81	87.21	266.03	266.35	23.62	23.63	47.09	33.58	48.62
Milling	59.77	31.20	83.99	303.15	303.53	29.13	29.15	98.99	35.84	59.70
Head rice recovery	45.90	18.73	73.32	256.72	256.79	34.9	34.91	96.72	33.00	71.89

*h^2 (bs) = Heritability, Vg= Genotypic variance, Vp= Phenotypic variance, GCV = Genotypic coefficient of variation, PCV=Phenotypic coefficient of variance, GA = Genetic advance, GG= Genetic gain

Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. The highest genetic advance was recorded for milling percentage (35.84) followed by hulling percentage (33.58), number of spikelets per panicle (30.77) and head rice recovery (30.00). While lowest genetic advance was recorded for volume expansion ratio (0.01) followed by length (0.76) (Table 2).

A character exhibiting high heritability may not necessarily give high genetic advance; Johnson et al (1955) have showed that high heritability should be accompanied by high genetic advance to arrive at a more reliable conclusion. Therefore it should be combined with information on genetic advance. Thus a character possessing high heritability along with high genetic advance will be valuable in the selection programme. High heritability coupled with high genetic advance were recorded for number of spikelets per panicle, hulling percentage, milling percent and head rice recovery suggesting preponderance of additive gene action in the expression of these characters. Therefore, selection may be effective through these characters in segregating generation (Paramasivam et al 1996).

The characters like: number of spikelets per panicle, test weight, volume expansion ratio, kernel length, kernel breadth and L/B ratio exhibited high heritability coupled with low genetic advance suggesting preponderance on non-additive gene action in the inheritance of these traits, hence in this case selection may not be effective. Most of the above results in respect to heritability and genetic advance are in agreement with earlier reports on rice by Sawant & Patil (1995) and Sarawgi et al (2000).

It is concluded that "Indrani" is the best genotype which was the local land races, then selected and improved in Chattisgarh, both for yield and quality traits followed by Jhumeri, the highest yielder and was strong scented in aromatic character along with 46% head rice recovery. Characters like grain yield per hill, head rice recovery, kernel length and kernel breadth exhibited higher magnitude of genotypic coefficient of variation (GCV), high heritability and showed positive association with grain yield proving their potential for selection.

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