

**RESEARCH ARTICLE**

# Studies on genetic variability for yield and yield traits in rice (*Oryza sativa* L.)

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## **SUMMARY**

Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. In the Asia and Pacific region, rice is the main staple food and the most important source of employment and income for rural people. Knowledge of variability and heritability of yield and its contributing traits helps in the selection of appropriate strategy for a breeding programme for evolving superior varieties. Therefore, the present investigation was conducted to assess the variability present in  $F_1$  hybrids and their parents for yield and yield contributing traits. In present study, Variance analysis for all the characters revealed significant variation among the genotypes studied, indicating the existence of sufficient amount of variability. The GCV, PCV, broad sense heritability and genetic advances as percent of mean suggested number of panicle bearing tillers per plant, spikelets fertility, plant height, panicle length, number of spikelets per panicle, test weight, and grain yield per plant were important contributing traits and selection based on these traits would be most effective.

**Key Words :** Rice, Heritability, Variability, Genetic advance

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Rice has been one of the world's most important food crops, feeding more than half of the world's population (Khush, 1997). In the Asia and Pacific region, rice is the main staple food and the most important source of employment and income for rural people (Hossain, 1998). The rice productivity has reached a plateau so it is thus imperative to find alternative means for increasing the yield potential of rice cultivars in a

sustainable manner. Of the various approaches contemplated to break the existing yield barriers in rice, hybrid rice technology offers an opportunity to boost the yield of rice under fragile conditions as hybrid rice varieties have a yield advantage of 15-20% over the conventional high yielding varieties (Virmani, 1996). Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. Knowledge of variability and heritability of yield and its contributing traits helps in the selection of appropriate strategy for a breeding programme for evolving superior varieties since these indicate the possibility and extent to which improvement is possible through selection. High

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magnitude of variability in population provides the opportunity of selection to evolve a variety having desirable characters. Johnson *et al.* (1955) pointed out that without genetic advance, the estimates of heritability would not be practical importance in selection based on phenotypic appearance. Therefore, the present investigation was conducted to assess the variability present in  $F_1$  hybrids and their parents for yield and yield contributing traits.

## MATERIAL AND METHODS

The experimental material for the present investigation comprised 24  $F_1$ s of rice, three CMS lines (*viz.*, IR 58025A, PMS 8A and PMS 10A) and 8 promising restorer lines (testers) derived by line  $\times$  tester mating design during *Kharif*, 2014. The resultant 24  $F_1$ s and 11 parents were evaluated in Randomized Block Design (RBD) with three replications during *Kharif*, 2013 at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, India. 25 days old seedlings were transplanted with one seedling per hill adopting recommended spacing of 20 x 15 cm and each entry was planted in four rows of 2.5 m length. All the recommended cultural practices and packages were applied for growing healthy and good crop. In each entry, five plants were randomly selected from each replication and following observations were recorded for Seedling growth (cm), Days to 50% flowering, Plant height (cm), Total number of tiller per plant, Panicle bearing tillers, Panicle length (cm), Spikelets per panicle, Spikelets fertility (%), 1000 grain weight (g) and Grain yield per plant (g). Co-efficient of variation was calculated by the formulae given by Burton (1952). Heritability in broad sense [ $h^2_{(b)}$ ] and genetic advance (GA) were estimated by the following formula given by Johnson *et al.* (1955).

## RESULTS AND DISCUSSION

Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. Variance analysis for all the characters revealed significant variation among the genotypes studied (Table 1 and 2), indicating the existence of sufficient amount of variability. These results were in conformity with the earlier findings of Kumar *et al.* (2006); Salgotra *et al.* (2009) and Dhanwani *et al.* (2013). The magnitude of phenotypic co-efficient of variation (PCV) in general was found higher than the genotypic co-efficient of variation

(GCV) for all the characters studied indicated the influence of environment on the manifestation of these characters (Kavitha and Reddy, 2002 and Sreeparvathy *et al.*, 2010). However, the difference between PCV and GCV was less for the traits, days to 50 per cent flowering, plant height, total spikelets per plant spikelets fertility, test weight and grain yield per plant. The similar result was observed by Dhanwani *et al.* (2013).

Among the characters, higher estimates of PCV and GCV were observed for the number of panicle bearing tillers per plant followed by grain yield per plant, test weight, number of total tillers per plant and spikelets fertility. This indicates the existence of wide genetic base among the genotypes taken for study and possibility of genetic improvement through direct selection for these traits. These results are also in conformity with the findings of Chandra *et al.* (2009); Pandey and Singh (2011); Bhadru *et al.* (2012) and Dhanwani *et al.* (2013) for grain yield per plant and number of grains per panicle. The PCV and GCV recorded moderate values for the trait seedling growth. Hence, selection for this trait may be misleading if adopted for improvement programme under integrated fertilizer management through this trait. The estimates of PCV and GCV were low for the characters days to 50% flowering, days to maturity, plant height, panicle length and total spikelets per plant. The selection for these traits would offer very little scope for genetic improvement of the genotypes under study. Similar results were also obtained by Mamta *et al.* (2007) for days to 50 per cent flowering and Das *et al.* (2005) and Kumar *et al.* (2013) for days to maturity. High co-efficient of variability indicated that there is a scope of selection and improvement of these traits. Low values indicated the need for creation of variability either by hybridization or mutation followed by selection. Similar finding were also reported by Singh *et al.* (2006) and Pandey and Anurag (2010). Environmental co-efficient of variation was highest for panicle bearing tillers followed by total tillers per plant. It was lower for total spikelets per panicle.

The amount of genetic variation considered alone will not be of much use to the breeder unless supplemented with the information on heritability estimate, which gives a measure of the heritable portion of the total variation. It has been suggested by Burton and Devane (1953) that the GCV along with heritability estimate could provide a better picture of the amount of advance to be expected by phenotypic selection. Since

**Table 1 : Analysis of variance for parents and their hybrids in rice**

Source of variation	d.f.	Seedling growth	Days to 50% flowering	Plant height (cm)	No. of total tillers/ plant	Panicle bearing tillers/ plant	Panicle length (cm)	Total spikelets / panicle	Spikelet fertility %	Test weight (g)	Grain yield / plant (g)
Replications	2	7.89**	0.12	1.00	2.48	0.45	0.37	0.77	4.49	0.57	7.12**
Treatments	35	2.84**	66.65**	80.24**	33.75**	68.28**	9.04**	3.87**	652.56**	149.21**	288.55**
Error	70	124.00	1.64	4.11	0.99	0.55	1.36	15.97	2.82	0.94	1.67

**Table 2 : Mean co-efficient of variation, heritability broad sense and genetic advance for 10 characters in rice**

Sr. No.	Characters	General mean	Co-efficient of variation			Heritability in broad sense	Genetic advance	Genetic advance in per cent of mean
			GCV	PCV	ECV			
1.	Seedling growth	28.12±0.78	10.75	11.32	3.55	90.14	5.89	20.95
2.	Days to 50% flowering	102.67±0.91	4.55	4.65	0.97	95.62	9.37	9.13
3.	Plant height (cm)	84.46±1.05	6.08	6.19	1.18	96.35	10.36	12.27
4.	No. of total tillers/ plant	11.94±0.73	27.66	28.90	8.39	91.60	6.48	54.33
5.	Panicle bearing tillers/ plant	11.28±0.64	41.97	42.90	8.86	95.73	9.53	84.51
6.	Panicle length (cm)	24.77±0.67	6.60	7.74	4.03	72.82	2.87	11.61
7.	Total spikelets/ panicle	184.47±1.47	5.49	5.51	0.54	99.06	20.76	11.25
8.	Spikelet fertility %	75.81±0.96	22.00	22.04	1.31	99.64	34.25	45.17
9.	Test weight(g)	21.02±0.73	35.62	35.93	4.75	98.24	15.26	72.59
10.	Grain yield / plant (g)	26.10±0.84	37.51	37.70	3.83	98.96	19.97	76.51

genetic advance is dependent on phenotypic variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection (Johnson *et al.*, 1955). Heritability in broad sense includes both additive and non-additive gene effects (Hanson *et al.*, 1956). While, narrow sense heritability includes only additive components (Johnson *et al.*, 1955). In the present study, the heritability estimates ranged from 72.82% (panicle length) to 99.64% (spikelets fertility). High estimates of heritability were obtained by all characters, indicating the major role of additive gene action in inheritance of these traits. According to Panse (1957) if a character is governed by non-additive gene action, it may give high heritability but low genetic advance, whereas, if it is governed by additive gene action, high heritability along with high genetic advance provide good scope for further improvement. The traits number of panicle bearing tillers per plant, Test weight, yield per plant, number of total tillers per plant and spikelets fertility expressed high heritability values with high genetic advance as per cent of mean. The additive gene effects are responsible for these and selection for these traits could be beneficial. These results were in accordance with the findings of Singh *et al.* (2005) for number of effective tillers per plant; Sarkar *et al.* (2007) for panicle length and number of grains per panicle; Veerabhadhiran *et al.* (2009) for

grain yield per plant and Bhadru *et al.* (2012) for 1000-grain weight.

High estimates of heritability associated with moderate genetic advance as percentage of mean were recorded for seedling growth, total spikelets per panicle and panicle length indicating that both additive and non-additive gene effects governed these characters. Hence, simple direct selection may be effective to improve these traits. These traits could also be improved by adapting recurrent selection method. High heritability coupled with low genetic advance for days to 50 per cent flowering with present experiment suggesting greater role of non-additive gene action in their inheritance of these character. Therefore heterosis breeding could be used to improve these traits.

The overall results indicated that there is adequate genetic variability present in the material studied. The GCV, PCV, broad sense heritability and genetic advances as per cent of mean suggested number of panicle bearing tillers per plant, spikelets fertility, plant height, panicle length, number of spikelets per panicle, test weight, and grain yield per plant were important contributing traits and selection based on these traits would be most effective.

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