## Study of coefficient of variation, heritability and genetic advance in hybrid rice

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## ABSTRACT

Thirty four genotypes were studied for their genotypic, phenotypic and environmental coefficient of variation during wet season 1999-2000. Results indicated that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) for all the traits. PCV was highest in grain yield (33.15%) followed by biological yield (26.67%), effective tillers/plant (25.87%) and spike lets/panicle. GCV was highest for grain yield/plant (26.19%) followed by effective tillers plant<sup>1</sup> (21.46%) and biological yield plant<sup>1</sup> (20.47%). GCV and PCV was lowest for panicle length followed by days to 50% flowering and plant height. High heritability coupled with high genetic advance was recorded for spikelets panicle<sup>-1</sup>. High heritability was observed 50% flowering, test weight and panicle length. Moderate heritability and low genetic advance was recorded for total number of tiller plant<sup>-1</sup> and effective tiller plant<sup>-1</sup>. Days to 50% flowering, plant height, seed setting percentage, grain yield and harvest index showed moderate genetic advance. Genetic advance in per cent of mean ranged from 8.39 to 40.19.

Key words: Genetic advance, heritability, hybrid rice, phenotypic coefficient of variation and genotypic coefficient of variation

Genetic enhancement is one of the important tools to improve upon the productivity. The technology to enhance genetic potential of crop species, hybrid technology has been widely acclaimed and accepted in various species. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters. The genotypic, phenotypic and environmental coefficient of variations are helpful in exposing and understanding the clear picture of existing variability in the populations.

The experimental materials comprised of population of 14  $F_1$ ,s (KMRH-2, KME+RH-3, MTUHR-2020, NDRH-2, IRI-23, PA-103, PA-111, PA-112, MPH-516, MPH-517, MPH-518, 3IR-86, AH-802 and VRH-1) their 14 F1,s and 6 standard varieties (NDR-80, NDR-118, NDR-359, Sarjoo-52, Jaya and Pant Dhan-4). 34 genotypes were planted in randomized block design with three replication during wet season 1999-2000. Thirty days old single seedling hill<sup>-1</sup> were transplanted with 20 cm plant spacing, having 4 rows of 2.5 meters long for each entry. The genotypes were studied for days to 50% flowering, plant height (cm),

total number of tillers plant<sup>-1</sup>, effective tillers plant<sup>-1</sup>, panicle length (cm), spikelets panicle<sup>-1</sup>, seed setting percentage, biological yield plant<sup>-1</sup> (g), harvest index (%) and test weight (g).

The observations were recorded on all the available plants in each population. For days to 50% flowering data were recorded on plot basis. Rest of characters, 5 randomly selected plants in  $F_1$ , at the time of maturity standard varieties and 10 random selected plant in F2 were taken for all the treatments in each replication.

Analysis of variance was calculated by the procedure suggest by Panse and Sukhatme (1967). Coefficient of variation, heritability and genetic advance were estimated by using the formula by Hanson *et al.*, (1956) and Hanson *et al.*, (1955), respectively.

The analysis of variance involving  $14 F_1$ , s their  $14 F_2$ , s and 6 standard varieties were done for eleven characters. The perusal of data (Table 1) revealed that variance due to treatment was highly significant for all the traits studied. This indicated that sufficient genetic

variation existed among the genotypes for studied traits and the estimation of different genetic parameters could be made in these materials for all eleven traits.

Phenotypic coefficient of variation (PCV) was higher than the genotypic and environmental coefficient of variation for all the characters studied. It was highest for grain yield followed by biological yield, effective tillers plant<sup>1</sup>, total number of tillers plant<sup>1</sup>, and spikelets pancile<sup>-1</sup>, while genotypic coefficient of variation (GCV) was highest for grain yield also reported by Bidhan *et al*, (2001) and Sharma and Bhuyan (2004). PCV and GCV were lowest for panicle length. Environmental coefficient of variation (ECV) was highest for grain yield plant<sup>-1</sup>. It was lowest for days to 50% flowering (Table 2). GCV was slightly lower than corresponding PCV for all the characters because of less influence of environment in the expression of these characters.

In the present study high heritability coupled with high genetic advance was recorded for spikelets panicle<sup>-1</sup> which was reported by Sharma and Bhuyan (2004). High heritability for days to 50% flowering, plant height and seed setting percentage, test weight and panicle length was reported Kuldeep *et al.*, (2004).

Low genetic advance was recorded for total number of tiller plant<sup>-1</sup>, effective tillers plant<sup>-1</sup>, panicle length and test weight which revealed the major role of non-additive gene action in the transmission of these characters from parents of off springs. Moderate genetic advance was recorded for days 50% flowering, plant height, seed setting percentage, grain yield and harvest index.

High magnitude of variability in a population provides the opportunity of selection to evolve a variety having desirable characters. Knowledge of heritability of a character is important since it indicate the possibility and extent to which improvement is possible thorough selection (Robison *et al.*, 1949). It also indicated the relative importance of heredity and environment in the expression of characters. High heritability alone is not enough to make efficient selection in advanced generations unless accompanied by substantial amount of genetic advance. Genetic advance has added advantage over heritability as a guiding factor in a selection programme where as the important character is desired in the segregating generations. To sum up the present investigation, it could be clearly brought that

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Source of variation d.f. Days to	d.f.	Days to	Plant	Total No.	Effective	Panicle	No.of	Seed	Biological	Grain	Harvest	Test
		50%	height	of tiller <sup>-1</sup>	tillers <sup>-1</sup>	length	spikeltes <sup>-1</sup>	setting	yield <sup>-1</sup> (g)	yield <sup>-1</sup>	index (%)	weight
		flowering (cm)	(cm)			(cm)		percentage		(g)		(g)
Replication	2	18.24	$104.48^{**}$	29.00*	$34.03^{**}$	2.38*	609.89	129.81	776.28*	162.94	2.45	0.03
Treatment	33	3 186.77**	$236.91^{**}$	$40.05^{**}$	37.41**	$6.18^{**}$	6242.22**	434.02**	964.85**	350.55**	$196.66^{**}$	36.68**
Error	99	4.40	15.27	8.46	4.90	0.68	951.34	75.66	208.48	73.80	31.11	2.60

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Characters	General mean $\pm$ SE	Coeffic	Coefficient of variation (%)		Heritability	Genetic advance
		GCV	PCV	ECV	in broad sense	in percent over mean
Days to 50% flowering	99.43 <u>+</u> 1.71	7.84	8.12	2.11	93.25	15.58
Plant height (cm)	109.18 <u>+</u> 3.19	7.87	8.64	3.58	62.86	14.75
Total number of tillers plant-1	18.58 <u>+</u> 2.37	17.46	23.45	15.66	55.47	26.77
Effective tillers plant <sup>-1</sup>	15.33 <u>+</u> 1.80	21.46	25.87	14.44	67.82	36.65
Panicle length (cm)	28.37 <u>+</u> 0.67	4.79	5.59	2.91	72.84	8.39
Spiketlets panicle <sup>-1</sup>	249.25 <u>+</u> 25.18	16.84	20.91	12.37	34.95	27.66
Seed setting percentage	75.40 <u>+</u> 7.10	14.49	18.52	11.58	61.22	23.96
Grain yield plant <sup>-1</sup> (g)	36.66 <u>+</u> 7.01	26.19	35.15	23.43	55.54	40.19
Biological yield plant-1 (g)	77.56 <u>+</u> 11.78	20.47	27.67	11.78	54.74	31.19
Harvest Index (%)	47.03 <u>+</u> 4.55	15.78	19.73	11.84	6.94	25.99
Test weight (g)	23.41 <u>+</u> 1.31	14.74	16.26	6.87	82.19	27.54

Table 2. Mean, coefficient of variation, heritability (broad sense) and genetic advance for 11 characters.

the biological yield, grain yield and seed setting percentage were primarily governed by non-additive types of gene action. In the expression of characters, total number of tiller, effective tillers plant<sup>-1</sup>, spikelets panicle<sup>-1</sup>, harvest index, the additive and non-additive types of gene actions were involved.

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