

# VARIABILITY AND GENETIC PARAMETERS FOR GRAIN YIELD IN CMS BASED RICE HYBRID (*ORYZA SATIVA* L.)

Satyapal Singh\*, Hemant Sahu and Parmeshwar Ku. Sahu

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur-492012, Chhattisgarh (India)

Email : [spsinghkv@gmail.com](mailto:spsinghkv@gmail.com)

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**Abstract :** The present investigation was carried out during *kharif* 2012 and 2013 at Raipur to study the genetic parameters for quantitative and quality characters in eighty three genotypes in rice (*Oryza sativa* L.). Analysis of variance revealed significant differences for almost all the traits under study. The characters, viz. sterile spikelets panicle<sup>-1</sup>, fertile spikelet panicle<sup>-1</sup>, pollen fertility percent, grain yield plant<sup>-1</sup>, spikelet fertility percent, harvest index and biological yield plant<sup>-1</sup> exhibited high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Small differences between GCV and PCV were recorded for all the characters studied which indicated less influence of environment on these characters. sterile spikelet panicle<sup>-1</sup>, fertile spikelet panicle<sup>-1</sup>, pollen fertility percent, grain yield plant<sup>-1</sup>, spikelet fertility percentage, harvest index, biological yield plant, number of spikelet panicle<sup>-1</sup>, 1000 grain weight and productive tillers plant exhibited high heritability coupled with high genetic advance as per cent of mean indicating that simple selection could be effective for improving these characters.

**Keywords :** Genetic advance, GCV, Heritability, Hybrid rice, PCV

## INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops of the world meeting the dietary requirements of the people living in the tropics and sub-tropics. Quantum jump in yield improvement has achieved in rice with the development of high yielding heterotic hybrids under commercial cultivation. However, being the staple food of the population in India, improving its productivity has become a crucial importance Subbaiah *et al.*, 2011). The knowledge on the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effecting genetic improvement. It is important to evaluate the promising rice germplasm along with their hybrids for morphological characters and yield. A paradigm shift in the rice (*Oryza sativa* L.) breeding strategies from quantity centered approach to quality oriented effort was inevitable, since India has not only become self sufficient in food grain production but also is the second largest exporter of quality rice in the world (Sreedhar *et al.*, 2005). Improvement in grain quality that does not lower yield is the need of hour at present context in order to benefit all rice grower and consumers. Like grain yield, quality is not easily amenable to selection due to its complex nature. For the development of high yielding varieties with good quality the information on variability and genetic parameters of grain quality attributes and their association with each other including grain yield is necessary to formulate suitable breeding strategies for grain quality improvement. In the present investigation, an attempt has been made to elucidate information on nature and

magnitude of genetic variation observed for yield and yield components and kernel quality attributes in certain parents and rice hybrids.

## MATERIAL AND METHOD

The present experiment was conducted at Research Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh.) in *kharif* 2012 and 2013. Raipur is located at 21°16' N Latitude and 81°36' E longitude at an altitude of 289.60 meters above the mean sea level. The materials comprised of eighty three rice genotypes. The experimental material was planted in a completely randomized block design with two replications in two blocks. Each block consisted of thirty three genotypes randomized and replicated within each block. Twenty one days old seedlings were transplanted at 20 cm apart between rows and 15 cm within the row. All necessary precautions were taken to maintain uniform plant population in each treatment. All the recommended package of practices was followed along with necessary prophylactic plant protection measures to raise a good crop. Five representative plants for each genotype in each replication were randomly selected to record observations on the quantitative characters under study. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated by the formula given by Burton (1952). Heritability in broad sense ( $h^2$ ) was calculated by the formula suggested by Hanson *et al.* (1956). From the heritability estimates, the genetic advance (GA) was estimated by the formula given by Johnson *et al.* (1955).

\*Corresponding Author

## RESULT AND DISCUSSION

The analysis of variance indicated the existence of significant differences among all the genotypes for almost all the traits studied (Table 1). The variation between genotypic and phenotypic coefficient of variation was high to moderate for all characters studied except days to 50 % flowering and panicle length indication of the more influence of the environment over these two characters (Table 2). The magnitude of coefficient of variation was categorized as high (> 30%), moderate (25%) and low (< 20%). The high genotypic and phenotypic coefficient of variation was recorded for the characters, sterile spikelet panicle<sup>-1</sup> (70.18 and 72.38), fertile spikelet panicle<sup>-1</sup> (53.69 and 54.38), pollen fertility percent (45.87 and 46.54), grain yield plant<sup>-1</sup> (40.53 and 52.16), spikelet fertility percent (39.39 and 39.92), harvest index (30.51 and 32.58) and biological yield plant<sup>-1</sup> (29.41 and 31.51). The moderate genotypic and phenotypic coefficient of variation were recorded for the characters *viz.* number of spikelet panicle<sup>-1</sup> (27.77 cm and 28.94), 1000 grain weight (25.11 cm and 25.63), number of productive tillers (24.76 and 25.25) and total number of tillers (21.04 and 21.33). The low genotypic and phenotypic coefficient of variation was recorded for the characters *viz.* number of tillers (21.04 and 21.33), plant height (18.87 and 20.05), panicle length (10.10 and 11.61) and days to 50% flowering (7.17 and 7.19). The high magnitude of phenotypic coefficient of variation reveals the high genetic with environmental variability present in the material studied. The phenotypic coefficient of variation was recorded higher than genotypic coefficient of variation and was in accordance with verma *et al.* (2000). The present findings of low magnitude of GCV and PCV for days to 50% flowering are in agreement with the findings of Kaw *et al.* (1999). Similar results for high GCV and PCV in rice were also reported by Shukla *et al.* (2005) and Kumar *et al.* (2006) in grain yield plant; Panwar (2005) in spikelet fertility percent and grain yield plant<sup>-1</sup>; Das *et al.* (2005) in productive tillers plant<sup>-1</sup> and grain yield plant<sup>-1</sup>; Saleem *et al.* (2005) and Jayashudha and Sharma (2010) in spikelet fertility percent; Amudha *et al.* (2006) in productive tillers plant<sup>-1</sup> and spikelet sterility percent; and Babu *et al.* (2012) in fertile spikelet panicle<sup>-1</sup> and sterile spikelet panicle<sup>-1</sup>.

The magnitude of heritability was categorized as high (>90%), moderate (85-90%) and low (<80%). All the characters exhibited high broad sense heritability (table 2). Heritability was recorded the highest for days to 50 % flowering (99.63), plant height (98.22), fertile spikelet panicle<sup>-1</sup> (97.51), spikelet fertility percent (97.38), total numbers of tiller (97.31), pollen fertility percent (97.17), number of productive tiller (96.17), 1000 grain weight (95.99), sterile spikelet panicle<sup>-1</sup> (94.00), grain yield (92.42) and number of spikelet panicle<sup>-1</sup> (92.11)

whereas, it was found moderate for harvest index (87.71) biological yield plant<sup>-1</sup> (87.16) and low for panicle length (75.64). The high estimates of heritability for high heritability observed for grain yield plant<sup>-1</sup> is in conformity with the findings of Satyanaryana *et al.* (2005). Satyanaryana *et al.* (2005) reported high heritability estimates for spikelet sterility percent and days to 50% flowering; Patra *et al.* (2006) for plant height, panicle length and productive tillers plant; Jayashudha and Sharma (2010) for spikelet fertility percent and days to 50% flowering; Babu *et al.* (2012) for days to 50% flowering, fertile spikelet panicle<sup>-1</sup>, sterile spikelet panicle<sup>-1</sup>.

The genetic advance as per cent of mean was categorized as high (>80%), moderate (50-80%) and low (<50%). The high estimate of genetic advance were exhibited as per cent of mean by the characters for sterile spikelet panicle<sup>-1</sup> (121.14), fertile spikelet panicle<sup>-1</sup> (112.11), pollen fertility percent (97.51), spikelet fertility percent (87.09), grain yield plant<sup>-1</sup> (83.33) and moderate for harvest index (61.66), biological yield plant<sup>-1</sup> (55.49), spikelet panice<sup>-1</sup> (52.89), 1000 grain weight (50.07). whereas, it was low genetic advance percent of mean for productive tiller (49.86), total number of tiller (42.34) and plant height (42.01), panicle length (17.90), days to 50% flowering (14.87) (Table 2). The high heritability along with high genetic advance were registered as percent of mean for days to 50% flowering, plant height, fertile spikelet panicle<sup>-1</sup>, spikelet fertility percent, number of total tiller plant<sup>-1</sup>, pollen fertility percent, Productive tillers plant<sup>-1</sup>, 1000 grain weight, sterile spikelet panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, total spikelet panicle<sup>-1</sup>, harvest index, biological yield plant<sup>-1</sup>, panicle length. Therefore, the improvement of these traits through selection is the most important way to achieve the genetic gain generation after generation. High heritability coupled with high genetic advance indicates the preponderance of additive gene action and such characters could be improved through selection. Similar findings were also supported by Das *et al.* (2005) for high heritability coupled with high genetic advance in grain yield plant<sup>-1</sup>, productive tillers plant, sterile spikelet panicle<sup>-1</sup> and plant height, Mall *et al.* (2005) for plant height, Saleem *et al.* (2005) for grain yield plant, Satyanarayana *et al.* (2005) for spikelet fertility percent, plant height, panicle length, Manna *et al.* (2006) for grain yield plant<sup>-1</sup>, Patra *et al.* (2006) for plant height, Jayashudha and Sharma (2010) for spikelet fertility percent and plant height; and Babu *et al.* (2012) for fertile spikelet panicle<sup>-1</sup>. In the present investigation, it was found that considerable variability was present in the experimental material under study. Therefore, it is concluded that the characters which showed high genotypic value coupled with high heritability and genetic advance should be considered for direct selection. Here sterile spikelet panicle<sup>-1</sup>, fertile spikelet panicle<sup>-1</sup>, pollen

fertility percent, grain yield plant<sup>-1</sup>, spikelet fertility percentage, harvest index, biological yield plant, number of spikelet panicle<sup>-1</sup>, 1000 grain weight and productive tillers plant among field characters

showed high GCV, PCV, heritability and genetic advance. Thus one should select these characters for direct selection.

**Table 1.** ANOVA for different quantitative and quality characters of hybrid rice

Source of variation	df	Mean sum of squares													
		1	2	3	4	5	6	7	8	9	10	11	12	13	14
Replication	1		139.56		2.43*	58.44*									
		2.40**	**	5.21**	*	*	129.93	621.71	182.37	24.57	3.57	500.96*	52.74*	6.51	4.67
Treatment	82	103.96**	984.38**	8.87**	9.52*	15.5**	9097.64**	13513.28**	7117.68*	1275.17*	1459.36*	1341.6**	302.96**	51.78*	256.57**
Error	82	0.21	9.09	0.16	0.22	2.20	363.70	172.73	211.61	16.41	20.35	92.48	11.73	1.66	16.31

\*= Significant P > 0.05, \*\*= Significant P > 0.01

- |                          |                              |                           |
|--------------------------|------------------------------|---------------------------|
| 1. Days to 50% Flowering | 6. Spikelets/Panicle         | 11. Biological Yield (g)  |
| 2. Plant height (cm)     | 7. Fertile spikelets/Panicle | 12. Grain Yield (g)       |
| 3. No. of Tillers        | 8. Sterile spikelets/panicle | 13. 1000 grain weight (g) |
| 4. Productive tillers    | 9. Spikelet Fertility (%)    | 14. Harvest index (%)     |
| 5. Panicle Length(cm)    | 10. Pollen Fertility (%)     |                           |

**Table 2.** Genotypic and phenotypic coefficient of variance (GCV and PCV), Heritability (h<sup>2</sup>) and genetic advance as percentage of mean (GA as percent of mean) for different characters.

S. N	Characters	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (%) Broad sense	Genetic advance	Genetic advance as % mean
1	Days to 50% flowering	7.17	7.19	99.63	15.07	14.87
2	Plant height (cm)	19.87	20.05	98.22	45.67	42.01
3	Tiller number (No.)	21.04	21.33	97.31	4.27	42.34
4	Productive tiller (No.)	24.76	25.25	96.17	4.40	49.86
5	Panicle length (cm)	10.1	11.61	75.64	4.60	17.90
6	Spikelet per panicle (No.)	27.77	28.94	92.11	130.86	52.89
7	Fertile Spikelet per panicle (No.)	53.69	54.38	97.51	169.16	112.11
8	Sterile spikelet per panicle (No.)	70.18	72.38	94.00	116.96	121.14
9	Spikelet fertility (%)	39.39	39.92	97.38	50.93	87.09
10	Pollen fertility (%)	45.87	46.54	97.17	54.17	97.51
11	Biological yield (gms)	29.41	31.51	87.16	48.78	55.49
12	Grain yield (gms)	40.53	52.16	92.42	23.91	83.33
13	1000 grain weight (gms)	25.11	25.63	95.99	10.12	50.07
14	Harvest index (%)	30.51	32.58	87.71	20.95	61.66

## REFERENCES

**Amudha, K., Arumugachamy, S. and Thiyyagarajan, K.** (2006). Variability in three different segregating generations in crosses involving drought tolerant genotypes. *Plant Archives* 6: 127-131.

**Babu, V.R., Shreya, K., Dangi, K.S., Usharani, G. and Nagesh, P.** (2012). Genetic Variability Studies for Qualitative and Quantitative traits in popular Rice (*Oryza sativa* L.) hybrids of India. *International Journal of Scientific and Research Publications* 2:2250-3153.

**Burton, G.W. and Devane, E.H.** (1952). Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal* 45: 478-481.

**Das, R., Borbora, T.K., Sarma, M.K. and Sarma, N.K.** (2005). Genotypic variability for grain yield and flood tolerance in semi deep water rice (*Oryza sativa* L.) of Assam. *Oryza* 42: 313-314.

**Hanson, W.D., Robinson, H.F. and Comstock, R.E.** (1956). Biometrical studies of yield in segregating population Korean *Lespedeza*. *Agronomy Journal* 48: 268-272.

- Jayashudha, S. and Sharma, D.** (2010). Identification of maintainers and restorers for CMS lines of rice under shallow low lands. *Electronic Journal of Plant Breeding* 1: 311-314.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E.** (1955). Estimation of genetic and environmental variability in soybean. *Agronomy Journal* 47: 314-318.
- Kaw, R.N., Aquino, R.C., Mom, H.P., Yae, J.D. and Haq, N.** (1999). Variability and inter relations in rice under cold stress environments. *Oryza* 36: 1-4.
- Kumar, S., Gautam, A.S. and Chandel, S.** (2006). Estimates of genetic parameters for quality traits in rice (*Oryza sativa* L.) in midhills of Himachal Pradesh. *Crop Research Hisar* 32: 206-208.
- Mall, A.K., Babu, J.D.P. and Babu, G.S.** (2005). Estimation of genetic variability in rice. *Journal of Maharashtra Agriculture University* 30: 166-168.
- Manna, M., Ali, M.N. and Sasmal, B.G.** (2006). Variability, correlation and path coefficient analysis in some important traits of lowland rice. *Crop Research Hisar* 31: 153-156.
- Panwar, L.L.** (2005). Line X tester analysis of combining ability in rice. *Indian Journal of Genetics* 65: 51-52.
- Patra, B.C., Pradhan, K.C., Nayak, S.K. and Patnaik, S.S.C.** (2006). Genetic variability in long-awned rice genotypes. *Environment and Ecology* 24(Special 1): 27-31.
- Saleem, M.Y., Atta, B.M. and Cheema, A.A.** (2005). An attempt to establish selection criteria for segregating generations in rice (*Oryza sativa* L.). *Bioscience Research* 2: 111-117.
- Satyanarayana, P.V., Srinivas, T., Reddy, P.R., Madhavilatha, L. and Suneetha, Y.** (2005). Studies on variability, correlation and path coefficient analysis for restorer lines in rice (*Oryza sativa* L.). *Research on Crops* 6: 80-84.
- Shukla, V., Singh, S., Singh, S.K. and Singh, H.** (2005). Estimation of genetic variability, heritability and genetic advance in "New Plant Type" Tropical Japonica rice under upland environment. *Agricultural Science Digest* 25: 207-209.
- Sreedhar, S., Vanisree, S., Kulakarni, N. and Ganesh, M.** (2005). Gene effects for certain physical quality traits and grain yield in rice. *Madras Agricultural Journal* 92: 183-187.
- Subbaiah, P.V., Sekhar, M.R., Reddy, K.H.P. and Reddy, N.P.E.** (2011). Variability and genetic parameters for grain yield and its components and kernel quality attributes in CMS based rice hybrids (*Oryza sativa* L.). *International Journal of Applied Biology and Pharmaceutical Technology* 2: 603-609.
- Verma, O.P., Singh U.S., Dwivedi, J.L. and Singh, P.P.** (2000). Genetic variability, heritability and genetic advance for quantitative traits in rice. *Oryza* 37: 38-40.