Progressive Research – An International Journal
Vol. 4 (Special Issue) : 426-428 (2009), ISSN : 0973-6417

Society for Scientific Development in Agriculture
and Technology, Meerut (U.P.) INDIA

RICE (*ORYZA SATIVA* L.) IMPROVEMENT THROUGH VARIABILITY ANALYSIS IN ADVANCED HYBRID GENOTYPES

Shanti Bhushan* and V.N. Sahai
Rice section, Mithapur, Agricultural Research Institute (RAU, Pusa), Patna-800020
****Corresponding author** (Shanti Bhushan) **Email :** shantidixit@rediffmail.com*

ABSTRACT

In an experiment to study the variability in the twenty two rice genotypes for yield attributing traits, the analysis of variance revealed that the lines differed significantly for all the studied characters. The high phenotypic and genotypic co-efficients of variation was exhibited by plot yield. Heritability estimates were high for all the characters. Genetic advance as percent of mean (GAM) was found to be high for plot yield, number of fertile spikelet per panicle, number of panicles per square meter and plant height.

***Key words :** Genetic coefficient of variability, phenotypic coefficient of variability, heritability, genetic advance as percent of mean.*

Rice is a self-pollinated cereal crop belonging to the family *Gramineae* (synomym-Poaceae) under the order Cyperales and class Monocotyledon having chromosome number 2n=24. The genus *Oryza* includes a total of 25 recognized species out of which 23 are wild species and two, *Oryza sativa* and *Oryza glaberrima* are cultivated. Rice the most important cereal crop in the world and is cultivated under diverse agro-ecosystems in India as well as in Bihar. Hybrid rice has tremendous potential in terms of yield to feed increasing human population by adding up high to the production figure in Bihar. The presence of genetic variability in base population is an integral requirement to bring about improvement in crop plants through selection of superior types. The present study was carried out to estimate genetic variability and response to selection in 22 genotypes of rice.

MATERIALS AND METHODS

The experimental material used in the present investigation comprised of 22 genotypes of rice coded as SLHRT-1 to SLHRT-17 and Savitri, Swarna, Salivahan, KRH-2 (national check) and Rajendra Mahsuri-1 as local check. The entire lines/varieties have been taken from Shallow Lowland Hybrid Rice Trial (SLHRT), *Kharif,* 2008 under All India Co-ordinated Rice Improvement Project (AICRIP) running at Agricultural Research Institute (ARI), Patna center. The 22 genotypes were grown in Randomized Block Design with three replications during *Kharif,* 2008 at the Research Farm, ARI, Patna. Each entry was represented by six rows of 4.5 meter row length. Spacing of 15 cm between plant-to-plant within the rows and 20 cm between rows was maintained. Data were recorded on 5 randomly tagged plants per entry per replication for plant height, number of panicles per square meter, number of fertile spikelet per panicle, spikelet fertility (%), and plot yield (kg) and days to 50% flowering on plot basis. The data were analyzed statistically by analysis of variance as per randomized block design method given by Ostle (1966). The coefficients of variability i.e., genotypic (GCV) and phenotypic (PCV) coefficient of variation were calculated as per Burton and Devane (1952) and classified into three categories as suggested by Sivasubramanian and Madhavamenon (1973). Heritability in broad sense and genetic advance were calculated according to Lush (1940) and Johnson *et al.* (1955) respectively.

RESULTS AND DISCUSSION

The analysis of variance revealed that the lines differed significantly for all the six characters as shown in Table-1. The extent of variation was assessed with the help of phenotypic and genotypic variability, heritability, genetic advances (GA) and expected genetic advance as percent of mean (GAM) for all the characters which have been represented in Table-2. It is apparent from the results that coefficients of phenotypic variability were higher than their corresponding genotypic variability as obtained by Nooruddin *et.al.*, (2009), suggesting the influence of environmental component on the manifestation of these characters.. It was observed that the high phenotypic and genotypic

Table-1 : Analysis of variance (MSS) for different yield and yield attributing characters in rice.

Source of variation	d.f.	Days to 50% flowering	Plant height (cm)	No. of panicles per sq. meter	No. of fertile spikelet per panicle	Spikelet fertility (%)	Plot yield (Kg)
Replications	2	8.38	0.14	207.96	253.78	1.53	0.01
Treatments	21	205.99**	276.29**	4985.84**	1913.35**	208.63**	0.50**
Error	42	14.87	5.37	93.80	264.23	30.52	0.06

Table-2 : Estimates of variability, heritability and genetic advance for six traits in rice.

Sl No.	Characters	Estimate of genetic parameters				
		PCV (%)	GCV (%)	Heritability (%) broad sense	Genetic Advance (GA)	Genetic Advance as per cent of mean (GAM)
1.	Days to 50% flowering	7.98	7.18	81.08	14.81	13.32
2.	Plant height (cm)	11.79	11.45	94.38	19.02	22.91
3.	No. of panicles per sq. meter	12.41	12.07	94.56	80.89	24.18
4.	No. of fertile spikelet per panicle	22.09	18.16	67.54	39.69	30.77
5.	Spikelet fertility (%)	13.49	10.96	66.05	12.90	18.35
6.	Plot yield (Kg)	25.24	21.47	72.37	0.67	37.63

PCV = Phenotypic co-efficient of variability, GCV = Genotypic co-efficient of variability

co-efficients of variation was exhibited by plot yield. Moderate PCV (%) and GCV (%) was shown by plant height, number of panicles per square meter and spikelet fertility while low values of PCV (%) and GCV (%) were recorded for days to fifty percent flowering. Character as number of fertile spikelet per panicle observed high PCV (%) and moderate GCV (%). Similar results were reported by Ganesan *et al.* (1996) and Ganapathy *et al.*(2006).

Genotypic coefficient of variation measures the extent of genetic variability percent for a trait but does notsess the amount of genetic variation which is heritable. Heritability estimates were high for all the characters. It was suggested by Bidhan *et al.* (2001) that only genetic coefficients of variation and heritability are not sufficient enough for the estimation of the amount of heritable variation. The heritable variation can be determined with greater degree of accuracy if genetic advance is also studied along with heritability. In present study, high heritability (broad sense) was recorded for all the studied character, the maximum being number of panicles per square meter followed by plant height, days to fifty percent flowering, yield per plot, number of fertile spikelet per panicle and spikelet fertility. Similar finding was reported by Swamy *et al.* (2003), Ganapathy *et al.* (2006) and Nayak *et al.* (2002). Genetic advance as percent of mean (GAM) was found to be high for plot yield, number of fertile spikelet per panicle, number of panicles per square meter and plant height whereas it was moderate for days to fifty percent flowering and spikelet fertility. Similar report hav been made by Verma *et al.* (2002). High heritability coupled with high GAM indicated the predominance of additive gene action for these traits. High heritability coupled with moderate genetic advance as per cent of mean was recorded for number of productive tillers per plant and panicle length suggesting the influence of both additive and non-additive gene effects in the expression of these traits.

ACKNOWLEDGEMENT

We are thankful to Directorate of Rice Research (DRR), Hyderabad, India for providing the financial assistance and hybrid rice genotypes under All India Co-ordinated Rice Improvement Project (AICRIP) and Regional Director, ARI, Patna (Rajendra Agricultural University, Pusa, Bihar) for managing all the necessary inputs in time.

REFERENCES

1. Bidhan, Roy, M. Hossain and F. Hossain (2001). Genetic variability in yield components of rice (*Oryza sativa* L). *Environ. Ecol.*, *19(1) :* 186-189.
2. Burton, G.W. and Devane, M. (1952). Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J., 45:* 478-481.
3. Ganapathy, S., S. K. Ganesh, P. Vivekanandan, R. Chandra Babu and P. Shanmugasundaram (2006).

Genetic variability and association analysis for drought tolerance yield and its contributing traits in rice (*Oryza sativa* L.). *Second National Plant Breed. Cong*, TNAU, Coimbatore 1-3, March p. 111.

4. Ganesan, K. Manuel, W.W. Vivekanandan P. and Arumugam Pillai M. (1996). Inbreeding, variability, heritability and genetic advance in F_2 population derived from early and extra early rice cultivars. *Oryza. 33:* 163-167.
5. Johnson, H.W. Robinson, H.F. and Comstock, R.E. (1955). Genotypic and phenotypic correlation in soybean and their implications in selection. *Agron. J. 74:* 477-483.
6. Lush, J.L. (1940). Intrusive correlation and regression of off-spring on dams as method of estimating heritability of characters. *Proc. Amer. Soc. Anim. Prod. 33:* 295-302.
7. Nayak, A. R. Chaudhury, D. and Reddy, J. N. (2001). Genetic variability, heritability and genetic advance in scented rice. *Indian Agric.*, *46(112):* 45-47.
8. Nooruddin, M. Iry, N. A. Mian, M. A. K and Hasan, M. (2009). Genetic variability, correlation and path analysis in maintainer lines of rice (*Oryza sativa* L.). *Ann. Bangladesh Agric. 13(1 & 2) :* 61-67.
9. Ostle, B. (1966). Statistics in Research. Oxford and IBH. pp.363-370.
10. Sivasubramanian, S. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agric. J. 60:* 1093-1094.
11. Swamy, M. H. Rao M. R G. and Vidyachandra, B. (2003). Studies on combining ability in rice hybrids involving new CMS lines. *Karnataka J. Agric. Sci.*, *16(2) :* 228-233.
12. Verma, D.K. Thakur, R. Singh, N.K. Mishra, S.B. (2002). Heritability and genetic advance studies in F_2 population, F_3 population, parent and pooled population of intra *indica* crosses of rice grown under late sown condition. *Mysore. J. Agric. Sci.36:* 222-230.