Indian Res. J. Genet. & Biotech. 6(4) : 595-599 (2014)

Analysis of Genetic Variability for Some Yield Related Characters Among Rice Genotypes

Mohd. Imran[1], L.K. Gangwar[2], S.A. Kerkhi[3] and Rabeena Fatma[4]

[1]Deptt.of Genetics and Plant Breeding, S.V.P.U.A. &T, Meerut, U.P.
[2]Deptt. of Genetics and Plant Breeding, M.S.K.U.A. & T, Banda, U.P.
[3]Deptt. of Genetics and Plant Breeding, CCSU, Meerut, U.P.

(Rceived : August, 2014 ; Revised : September, 2014; Accepted : October, 2014)

Abstract

Rice is one of the world's most important staple food crop and a primary source of food for more than half of the world's population due to the very good source of nutritional value; hence it is the major source of food of many developing countries. Genetic improvement totally depends upon the amount of genetic variability present in the population. In crop like rice, the genotype serves as a very useful source of base population and provides a good scope for wide variability. The present investigation was carried out to study the genetic parameters observe on different yield and yield component traits with 37 genotypes of rice in randomized complete block design with three replications during *kharif* 2011. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for number of grains per panicle (29.67 and 28.78), grain yield per plant (26.36 and 24.90), while it was moderate for harvest index (19.69 and 18.27), biological yield per plant (16.37 and 14.05), number of productive tillers per plant (15.59 and 14.73) respectively.

Key words : Genetic variability, GCV, PCV, Rice, Yield etc.

Inroduction

IRice (*Oryza sativa* L.) is an important food crop of the world and about 90 percent of the people of South-East Asian countries consume rice as staple food. According to FAO, the productivity level of rice in India is very low (about 3.21 t/ ha) as compared to the average productivity of China (6.35 t/ ha) and world (4.15 t/ h) (Anonymous, 2008). Rice is distributed globally with a high concentration in Asia (Vaughan *et al*., 2003). By increasing production and productivity of rice food demand and supply could be balanced among the increasing population of developing countries of Asia & Africa. The other countries where rice is grown are African (7.78 % of the global area), South and North American (6.4 % and 1.4 %) countries (Viraktamath, 2007).The selection of agronomically suitable diverse parents for hybridization is important for getting desired recombinants segregating generations. Hybrids showing strong heterosis are usually developed from the parental lines that are diverse in relatedness, ecotype, geographic origin etc**.** (Lin and Yaun, 1980). Genetic improvement for quantitative traits can be achieved through a clear cut understanding of the nature and variability present in the genotypes and the extent to which the desirable traits are heritable. It provides not only the basis of the selection but also some valuable information regarding the selection of variable parents for use in the hybridization

---

Corresponding author's e-mail : *imranmohd1485@gmail.com*

Published by Indian Society of Genetics, Biotechnology Research and Development, 5, E Biotech Bhawan, Nikhil Estate, Mugalia Road, Shastripuram, Sikandra, Agra 282007
Onlince management by www.isgbrd.co.in

programme. Possible selection based on phenotypic values can be predicted only in advance through knowledge of the degree of relationship between phenotypic and genotypic values in the genotypes. The estimate of the genetic variability in percent of mean provides more reliable information regarding the effectiveness of selection in improving a trait because its estimate is derived by involving phenotypic standard deviation and selection intensity. Keeping these in view, the present investigation was carried out to gather the information on genetic variability by evaluating 37 genotypes of rice.

Material and Methods

The present experiment consisted of thirty seven rice genotypes was conducted in Randomized Complete Block Design (RCBD) with three replications during *kharif* 2011, at Crop Research Centre, Department of Genetics and Plant Breeding, SardarVallabhbhai Patel University of Agriculture and Technology, Meerut. The data were recorded on the basis of five randomly selected plants per replication of each genotype for twelve quantitative traits *viz.,* plant height, number of productive tillers per plant, panicle length, number of grains per panicle, biological yield per plant, grain yield per plant, harvest index, 1000-grain weight with husk, and 1000-grain weight without husk. However, data on days to panicle emergence, days to 50 percent flowering and days to maturity characters were recorded on the plot basis. The analysis of variance was calculated as per the method suggested by Fisher (1935). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed by the method as suggested by Burton (1952).

Results and Discussion

Analysis of Variance, Range and Mean

To formulate an effective breeding programme, the genetic variability among the material is of the prime importance. For better utilization of the material, breeder should know the past history of selection, range of variability and area of adaptation. Peruse of data on analysis of variance in the present study indicated in the Table 1. A wide range of genetic variability was existed among 37 rice genotypes for yield and its component traits. The range and mean values for various traits are listed in Table 2. Days to panicle emergence ranged from 69.66 days (Rewa 862-1) to 98.33 days (CR 273-11) with grand mean value of 81.15 days. Days to 50 percent flowering ranged from 76.66 days (Govind) to 108.33 days (CR 273-11) with grand mean value of 89.48 days. Days to maturity varied from 112.00 days (Govind) to 133.00 (CHR 10) with a grand mean value of 125.10 days. Plant height ranged from 91.66 cm. (Govind) to 138.66 cm. (Rewa 862-1) with a grand mean value of 107.55 cm. Number of productive tillers per plant varied from 9.93 (CR 2928-21-5-3-1) to 17.33 (RP 5210-Bio-FBR-12-4-18) with a mean value of 13.02. Panicle length ranged from 17.43 (CR 273-11) to 25.63 (CR 646-B-12-B) with a grand mean value of 21.68. Number of grains per panicle varied from 62.66 (CR 2995-1-2-3-1-1) to 171.00 (CN 1794-2-1) with a mean value of 114.02. Wide range of variation for biological yield per plant was observed, it was noted to vary from 54.03g. (RP 5219-9-6-7-3-2-1-1) to 95.55g. (CR 646-B-12-B) with a grand mean value of 67.59g. Wide range of variation was also observed for grain yield per plant. It was noted to vary from 11.27g. (2K3-430-144-8-56-5-1-15-5-6) to 33.06g. (CR 2995-1-2-3-1-1) with a grand mean value of 18.94g. Harvest index % was ranged from 19.84 (Pusa 1121) to 41.23 (NLR 40058) with a grand mean value of 29.35. The range of variation for 1000-grain weight with husk was 15.33g. (CR 296-15-3-4-2) to 22.22g. (NDR 6206) with a grand mean value of 18.54 g. 1000-grain weight without husk was varied from 11.49g. (CR 2926-15-3-4-2) to 16.67g. (CR 2926-15-3-4-2) with a grand mean value for this character was 13.90g. Similar type of range of genetic variability was noticed for quantitative characters in rice by Kumar *et al. (*2013). Highly significant variation among the genotypes in respect to all the twelve quantitative characters was study suggested that there are enough inherent genetic variability were present among the genotypes which may be exploited further in rice improvement programme.

Table 1. Analysis of Variance for 12 Characters in Rice Genotypes

Source of variation	d.f.	Days to panicle emergence	Days to 50% flowering	Plant height (cm)	No. of productive tillers/ plant	Panicle length (cm)	No. of grains/ panicle	Days to maturity plant (g)	Biological yield/ plant (g)	Grain yield/ (%)	Harvest index husk(g)	1000- grain weight with out husk(g)	1000- grain weight with
Replication	2	8.33	32.67	2.33	0.01	1.31	0.08	18.35	28.80	1.24	0.66	0.73	1.27
Treatment	36	156.77**	179.45**	245.64**	11.48**	10.25**	3299.69**	90.50**	303.06**	69.48**	90.99**	9089**	5.56**
Error	72	37.55	30.80	51.21	0.43	0.81	67.55	21.66	32.27	2.68	4.65	0.58	0.61

** Significant at 1 % probability level

Table 2. General Mean and Range in *per se* Performance for 12 Characters in Rice Genotypes

Characters	**Genotypes**	**Minimum**	**Genotypes**	**Maximum**	**Grand Mean**
Days to panicle emergence	REWA 862-1	69.66	CR 273-11	98.33	81.15
Days to 50% flowering	Govind	76.66	CR 273-11	108.33	89.48
Plant height (cm)	Govind	91.66	REWA 862-1	138.66	107.55
No. of productive tillers/ plant	CR 2928-21-5-3-1	9.93	RP 5210-Bio-FBR1-12-4-18	17.33	13.02
Panicle length (cm)	CR 273-11	17.43	CRR 646-B-12-B	25.63	21.68
No. of grains/ panicle	CR 2995-1-2-3-1-1	62.66	CN 1794-2-1	171.00	114.02
Days to maturity	Govind	112.00	CHR 10	133.00	125.10
Biological yield/plant (g)	RP 5219-9-6-7-3-2-2-1-1	54.03	CRR 646-B-12-B	95.55	67.59
Grain yield/plant (g)	2K3-430-144-8-56-5-1-15-5-6	11.27	CR 2995-1-2-3-1-1	33.06	18.94
Harvest index (%)	PUSA 1121	19.84	NLR 40058	41.23	29.35
1000 -grain weight with husk(g)	CR 2926-15-3-4-2	15.33	NDR 6206	22.22	18.54
1000 –grain weight without husk(g)	CR 2926-15-3-4-2	11.49	NDR 6206	16.67	13.90

Table 3. Grand mean and Genotypic & Phenotypic Coefficient of Variation for 12 Characters in Rice Genotypes

Characters	Days to panicle emergence	Days to 50% flowering	Plant height (cm)	No. of productive tillers/ plant	Panicle length (Cm)	No. of grains/ panicle	Days to maturity	Biological yield/ plant (g)	Grain yield/ plant (g)	Harvest index (%)	1000- grain weight with husk(g)	1000- grain weight with out husk(g)
Grand mean	81.15	89.48	107.55	13.02	21.68	114.02	125.10	67.59	18.94	29.35	18.54	13.90
S.E.±	3.53	3.20	4.13	0.38	0.52	4.74	2.68	3.28	0.94	1.24	0.44	0.45
C.D. 5 %	9.97	9.03	11.64	1.07	1.46	13.37	7.57	9.24	2.66	3.51	1.24	1.27
GCV (%)	7.76	7.86	7.48	14.73	8.18	28.78	3.82	14.05	24.90	18.27	9.47	9.24
PCV (%)	10.83	10.01	10.01	15.59	9.17	29.67	5.33	16.37	26.36	19.69	10.36	10.83

Genotypic and Phenotypic Coefficient of Variance

As expected, the estimates of phenotypic coefficient of variation (PCV) were found to be higher than that of genotypic coefficient of variation (GCV) showed role of environment on the expression of variability present in the material for all the traits study and listed in the Table 3. High percentage of PCV was found for number of grains per panicle (29.67) followed by grain yield per plant (26.36). While GCV was recorded for these traits was (28.78 and 24.90, respectively). Ubarhande *et al.* (2009) also observed higher estimates of PCV than the GCV for the characters studied by them in rice genotypes. Generally the assessment of genotypic and phenotypic coefficient of variation for most of the traits studied, revealed a relatively major contribution of the genotypic variation in determining the phenotypic variation. High percentage of PCV as compared to GCV for all the traits indicated that there was not much influence of environment on heritable variability present in the material for expression of the characters under study and the improvement of the genotypes might be made by considering these characters in selection breeding programme. Moderate PCV was observed for harvest index (19.69), biological yield per plant (16.37), number of productive tillers per plant (15.59). The same trend was also reported in GCV of the aforesaid traits. The above results were also in conformity by the findings observed by Subudhi and Dikshit (2009) for grains per panicle, 1000-grain weight per plant and plant height. However, maximum GCV was found for only number of grains per panicle (28.78) and moderate GCV was observed for grain yield per plant (24.90), harvest index (18.27). Low GCV was also obtained for number of productive tillers per plant (14.73), biological yield per plant (14.05) and rest of the characters showed very low GCV. Ahmed *et al.* (2007) have also reported the similar type of result in rice.

Acknowledgement

The authors are very thankful to Directorate of Rice Research Rajendranagar, Hyderabad (A.P.) to providing the genotypes for the research work.

References

1. **Ahmed M., Mustafa Yassir M.A. and Elsheikh** (2007) Variability, correlation and path coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African Crop Science* Journal, Vol.**15**, No.4, pp. 183-189.
2. **Anonymous** (2008) IRRI, World rice statistics. www.irri.org.
3. **Burton G.W.** (1952) Quantitative inheritance in grasses. Proc. 6th *Int. Grassland Conf*. **1**:227-283.
4. **Fisher R.A.** (1935) The design of experiments.Oliver and Boyd.Edinburgh Hanson, W. D., Robinson, H. F. and Comstock, R. E. 1956. Biometrical studies of yield in segregating population. *Korean Lespandeza.Agron. J*. **48**: 268-272.
5. **Kumar A., Rangare N.R., Vidyakar V.** (2013) Study of genetic variability of Indian and exotic rice germplasm in Allahabad agroclimate.*The BioscanAn International Quarterly Journal of Life Sciences*. **8** (4): 1445-1451.
6. **Lin S.C. and Yuan L.P.** (1980) Genetic divergence in plant breeding.*I Indian J. Genet*., **14**: 226-236.
7. **Subudhi H.N. and Dikshit N.** (2009) Variability and Character Association of yield components in rainfed lowland rice.*Indian J. Plant Genetic Resource*, **22** (1) 31-35.
8. **Ubarhande V.A., Prasad R., Sing R.P., Singh S.P. and Agrawal R.K.** (2009) Variability and diversity studies in rainfed rice (*Oryzasativa*L.). *Indian J. Plant Genet.Resour*: **22**(2): 134-137.
9. **Vaughan D.A., Morishim H. and Kadowaki K.** (2003) Diversity in the oryza genus.*Current opinion in Plant Molecular Biology*.6:139-146.
10. **Vikratamath B.C.** (2007) Rice Research in India Current and Future Prospects. Proceeding of 2nd Workshop Cum Training Programme on DUS Test in Rice, Directorate of Rice Research, Hyderabad, pp. 1-3.

***