Plant Archives Volume 20 No. 1, 2020 pp. 738-740 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

VARIABILITY STUDIES AMONG RICE GENOTYPES (*ORYZA SAVITA* L.) UNDER COASTAL SALINE CONDITION

C. Praveen Sampath Kumar, Mahesh Naik, J.L. Joshi and R. Ebenezer Babu Rajan

Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar-608002 (Tamilnadu) India.

Abstract

The present investigation was carried out at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar during Samba. The study was carried out in an effort to assess the extent of genetic variability in 35 genotypes for 11 character *viz.*, days to first flowering, plant height at maturity, number of tillers per plant, number of panicles per plant, panicle length, number of grains per panicle, 1000 grain weight, grain length, grain breadth, grain L/B ratio and grain yield per plant. The characters namely, grain yield per plant, number of panicles per plant, number of tillers per plant and number of grains per panicle recorded high phenotypic and genotypic coefficient variation. High heritability along with genetic advance as percent of mean was observed for grain length and plant height at maturity followed by grain breadth, grain L/B ratio, number of grains per panicle, grain yield per plant, 1000 grain weight, number of tillers per plant, number of panicles per plant and panicle length. This may be attributed to additive gene action. Selection for these characters will play both short term and long term benefit.

Key words : Genotypes, tillers, heritability, panicles.

Introduction

Rice (*Oryza sativa* L.; 2n:2x:24) belonging to the genus *Oryza* includes 24 species, out of which 22 species are wild and only two species *viz.*, *O. sativa* and *O. glaberrima* are cultivated. The genus *Oryza* belongs to the tribe *Oryzeae* in the family Poaceae. Rice is the most important cereal crop cultivated widely in many parts of the world. South and south-east Asia form the primary centre of genetic diversity of the cultivated rice. Rice thrives over a wide range of climatic conditions extending from 45°N to 40°S and from sea level to 3000 m altitude.

Rice is central to the lives of billions of people around the world. Rice is the staple food for 2.5 billion people and growing rice is the largest single use of land for producing food, covering 9% of the earth's arable land. Rice provides 21% of global human per capita energy and 15% of per capital protein. Calories from rice are particularly important in Asia, especially among the poor, where it accounts for 50-80% of daily caloric intake. As expected, Asia accounts for over 90% of the world's production of rice, with China, India and Indonesia producing the most. Only 6-7% of the world's rice crop is traded in the world market. Thailand, Vietnam, China and the United States are the world's largest exporters. The United States produces 1.5% of the world's rice crop with Arkansas, California and Louisiana producing 80% of the U.S. rice crop. 85% of the rice that is produced in the world is used for direct human consumption. Rice can also be found in cereals, snack foods, brewed beverages, flour, oil, syrup and religious ceremonies to name a few other uses.

Breeding programmes are determined in the initial step by the variability existing in the base populations. Later, the success of the selected material depends upon the stability of the characters under selection. Thus, understanding the genetic makeup of the crop and the architecture of character set up in that crop are basic to a plant breeder. Genotypic variability is the heritable component of the apparent variability and is expressed as the heritability. Heritability is a result of additive and non-additive effects and is defined as the proportion of phenotypic variability that is due to genotype.

Hanson *et al.*, (1956) proposed heritability in broad sense as the ratio of genotypic variance of a particular character to its phenotypic variance is a function of its heritability, selection pressure and variance existing in

Table 1: Analysis of variance for eleven characters in 35 rice genotypes.

S. No	Source	df	Days to first flowering	Plant height at maturity	Number of tillers per plant	Number of panicles per plant	Panicle length	Number of grains per panicle	1000 grain weight	Grain length	Grain breadth	Grain L/B ratio	Grain yield per plant
			Mean Sum of squares										
1	Replication	2	53.2545	8.2098	1.1118	1.7049	0.4125	3.2786	0.8114	0.0000	1.1342	0.0024	8.4750
2	Genotype	34	112.2359**	361.7371**	32.4166**	26.9197**	10.1959**	2195.6423**	18.7147**	0.0265**	0.0037**	0.9412**	281.0343**
3	Error	68	31.7169	4.0729	2.3601	2.3287	1.5502	45.2736	0.6097	0.0001	0.0000	0.0140	8.1808

*Significant at 5 percent level.

the base population. Though the heritability is the relative value of the selection based on phenotypic expression of a character, the genetic advance is more useful in judging the actual value of selection as shown by Johnson *et al.,* (1955).

Estimation of co-efficient of variation helps to assess the extent of genetic variability in a population and to compare among the traits. Heritable variation could well be effectively used with greater degree of accuracy when heritability is studied in conjunction with genetic advance.

Materials and Methods

The present investigation was carried out at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. The experimental material for this genetic variability study comprised of thirty five rice genotypes collected from various places. Seeds of the thirty five rice genotypes were sown in raised nursery beds during 2015 (January-May). In each genotype, one seeding per hill was transplanted in the main field after 25 days with the spacing of 20 cm between rows and 15 cm between plants in 3m long rows. The experiment was carried out in randomized block design (RBD) with three replications. A uniform population of 10 plants in a row was maintained. Recommended agronomic practices and need based plant protection measures were adopted. The study was carried out in an effort to assess the extent of genetic variability in 35 genotypes for 11 characters *viz*., days to first flowering, plant height at maturity, number of tillers per plant, number of panicles per plant, panicle length, number of grains per panicle, 1000 grain weight, grain length, grain breadth, grain L/B ratio and grain yield per plant. Genotypic co-efficient of variation (GCV) and phenotypic (PCV) co-efficient of variation were calculated based on the formula advocated by Burton, (1952). Heritability in broad sense was calculated according to Hanson *et al*., (1956) and expressed in percentage. The GA as per cent of mean was classified according to Robinson *et al.,* (1949).

Results and Discussion

The analysis of variance revealed significant difference among the 35 genotypes for all the 11 traits indicating the existence of high genetic variability among the genotype for all the traits. The results of analysis of variance are presented in table 1. The results obtained here are in confirmation with the result reported by Nayak *et al.,* (2004); Singh *et al.,* (2005); Sabesan, (2005) and Rajasekaran, (2006).

Variability was measured by estimation of mean, coefficient of variation such as phenotypic coefficient of variation, genotypic coefficient of variation, heritability (broad sense) and genetic advance. Environment plays an important role in the expression of phenotype and genotype facts which are inferred from phenotypic observations. The estimate of PCV and GCV was studied for all eleven characters and are furnished in table 2. Heritability and genetic advance as percent of mean was studied for eleven characters and presented in table 3.

Table 2: Magnitude of variability for eleven characters in 35 rice genotypes.

S. No.	Characters	V_{ph}	V_g	Coefficient of variation	
				Phenotypic of variation	Genotypic coefficient
1	Days to first flowering	58.557	26.840	12.04	8.15
2	Plant height at maturity	123.294	119.221	13.30	13.08
3	Number of tillers per plant	12.379	10.019	22.56	20.30
4	Number of panicles per plant	10.526	8.197	25.81	22.78
5	Panicle length	4.432	2.882	9.75	7.86
6	Number of grains per panicle	762.063	716.790	21.44	20.80
7	1000 grain weight	6.645	6.035	13.89	13.23
8	Grain length	0.009	0.009	11.41	11.33
9	Grain breadth	0.001	0.001	14.20	13.94
10	Grain L / B ratio	0.323	0.309	17.00	16.63
11	Grain yield per plant	99.132	90.951	34.17	32.73

Table 3: Heritability and genetic advance as percent of mean for eleven characters in 35 rice genotypes.

S. No.	Characters	Heritability (%)	Genetic advance as percent of mean
1	Days to first flowering	45.84	11.37
2	Plant height at maturity	96.70	26.49
3	Number of tillers per plant	80.93	37.62
4	Number of panicles per plant	77.88	41.42
5	Panicle length	65.02	13.06
6	Number of grains per panicle	94.06	41.56
7	1000 grain weight	90.82	25.98
8	Grain length	98.54	23.16
9	Grain breadth	96.34	28.19
10	Grain L / B ratio	95.67	33.51
11	Grain yield per plant	91.75	64.58

The variability could be used in distinguishing different genotypes based on their morphology. In the present investigation, estimates of genetic parameters revealed that phenotypic co efficient of variability was higher than the genotypic co efficient of variability for the characters studied which indicated that they all interacted with the environments to some degree. Similar observations were made by Rajamani, (2004) and Anees salma, (2006). Moreover, the traits *viz*., grain yield per plant, number panicles per plant, number of tillers per plant and number of grains per panicle recorded high PCV and GCV while grain L/B ratio, grain breadth, 1000 grain weight, plant height at maturity, days to first flowering and grain length showed moderate PCV and GCV.

Heritability is a measure of the extent of phenotypic variation caused by the action of genes. The heritability values ranged from 45.84 to 98.54 percent for days to first flowering and grain length respectively. High heritability was observed for grain length followed by plant height at maturity, grain breadth, grain L/B ratio, number of grains per panicle, grain yield per plant, 1000 grain weight, number of tillers per plant number of panicles per plant and panicle length indicating the predominance of additive gene action, while, days to first flowering had moderate heritability, enabling ease of selection. These findings are in agreement with Verma *et al*., (2002) for grain yield per plant, 1000 grain weight and number of grains per panicle; Rajamani *et al*., (2004) for number of panicles per plant and plant height at maturity, Anees salma, (2006) for grain length and grain breadth.

A perusal of genetic advance as percent of mean for all the eleven characters under study was varied between 11.37 and 64.58 percent for days to first flowering and grain yield per plant respectively. High genetic advance as percent of mean was recorded for grain yield per plant followed by number of grains per panicle, number of panicles per plant, number of tillers per plant, grain L/B rati, grain breadth, plant height at maturity, 1000 grain weight and grain length. The characters namely panicle length and days to first flowering exhibited moderate genetic advance as per as mean. Suggesting the influence of both additive and non additive gene effects in the expression of these traits.

From the foregoing discussions, high genetic variability, high heritability coupled with high genetic advance as percent of mean were observed for the traits *viz.,* grain length, plant height at maturity, grain breadth, grain L/B ratio, number of grain per panicle, grain yield per plant, 1000 grain weight, number of tillers per plant and panicle length. Selection of these characters would be fruitful for grain yield per plant in the breeding programme.

References

Anees salma, K. (2006). Studies on genetics of heterosis, inbreeding depression and variability in rice. M.Sc., (Ag.) Thesis, Annamalai Univ., Annamalainagar, India.

Burton, G.W. and E.M. Devane (1952). Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal material. *Agron. J.,* **45:** 478-481.

Hanson, C.H., H.F. Robinson and R.E. Comstock (1956). Biometrical studies of yield in segregating population of Korean lespendeza. *Agron. J.,* **48:** 267-282.

Johnson, H.W., H.F. Robinson and R.E. Comstock (1955). Genotypic and phenotypic correlation in soybean and their implications in selection. *Agron. J.,* **74:** 477-483.

Nayak, A.R., D. Chaudhury and J.N. Reddy (2004). Genetic divergence in scented rice. Oryza, **41:** 79-82.

Rajamani, S., D. Rani and D. Subramaniyam (2004). Genetic variability and character association in rice. *Andhra Agric. J.,* **51 (1&4):** 36-38.

Rajasekaran, A. (2006). Studies on genetic divergence of indica and japonica (*Oryza sativa* L.) genotypes. M.Sc., (Ag.) Thesis, Annamalai Univ., Annamalainagar.

Robinson, H.F., R.E. Comstock and P.H. Harvey (1949). Estimation of heritability and the degree of dominance in corn. *Agron. J.,* **41:** 353-359.

Sabesan, T. (2005). Studied on the genetics of quality traits in rice (*Oryza sativa* L.). Ph.D Thesis, Annamalai Univ., Annamalai nagar, India.

Singh, J., K. Day, S. Singh and J.P. Shahi (2005). Variability, heritability, genetic advance and genetic divergence in induced mutants of irrigated basmati rice (*Oryza sativa* L.). *Oryza*., **42:** 210-213.

Verma, D.K., R. Thakur, N.K. Singh and S.B. Mishra (2000). Heritability and genetic advance studies in F2 Population, F3 population, parents and pooled population of intra indica crosses of rice grown under late sown condition. *Mysore J. Agric. Sci.,* **36:** 222-230.