I.J.S.N., VOL.6 (3) 2015: 366-371 ISSN 2229 – 6441

INTERNATIONAL JOURNAL OF SCIENCE AND NATURE

www.scienceandnature.org

STUDIES ON GENETIC VARIABILITY IN TRADITIONAL LAND RACES AND IMPROVED CULTIVARS FOR YIELD AND YIELD COMPONENTS IN RICE (*ORYZA SATIVA* L.)

[1]Savitha P. & [2]Usha kumari, R.
Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai - 625 104, Tamil Nadu, India.
Corresponding author e-mail: saviagri@gmail.com

ABSTRACT
Rice is the most stable food crop in the world, and is grown under a broad range of environmental conditions. The experimental material used were four traditional land races (Veeradangan, Kavuni, Navara and Katha nellu) and six improved high yielding varieties (IR 72, ADT 39, ADT 43, ADT 45, ASD 16 and TPS 4) and their six F_1 hybrids of Tamil Nadu raised in Randomized Block Design during Kharif 2013. The objective of this study was to evaluate the genetic variability of yield components in improved rice cultivars compared to landraces collected Tamil Nadu and Kerala. Estimates of phenotypic co-efficients of variation (PCV) were slightly higher than genotypic co-efficients of variation (GCV) for all the characters under consideration. The estimates of genotypic variances showed a considerable range of variation for most of the characters. Observation were recorded and analysed for variability parameters moderate values of PCV, GCV were observed for days to 50% flowering, plant height, number of productive tillers per plant, hundred grain weight and single plant yield indicated large extent of genetic variability for these traits in the materials studied. High heritability along with high genetic advance were observed for days to 50 % flowering, plant height, number of productive tillers per plant and hundred grain weight along with high values of the these traits indicating involvement of additive gene action for these traits and phenotypic selection based on these traits in the future generations would likely to be more effective.

KEY WORDS: Rice, Land races, Variability, Heritability, Genetic advance, Yield components

INTRODUCTION

Rice (*Oryza sativa* (L.) which belongs to the family poaceae, is the life and the prince among cereals as this unique grain helps to sustain two thirds of the world's population. Rice is the fastest growing crop and stable food in India. During the past three decades rice grain has seen a steady increase in consumption and demand. However, grain yield is a complex traits, controlled by many genes, environmentally influenced and determined by the magnitude and nature of their genetic variability in which they grow (Singh *et al.,* 2000). Rice genetic resources are widely available worldwide and largely contribute to the rich genetic diversity. Driven by natural selection of varieties distributed in diverse agro-ecoclimatic conditions coupled with continuous selection by man for his diverse in quality and aesthetic preferences, a unique rice varietal group has emerged, specialty rice all over the world (Singh *et al*., 2000). Brown rice is one of the most popular health produce due to its rich nutrients and bioactive components (Houston *et al.,*1970) that prevent a variety of diseases. Ideally, once rice is biofortified with vital nutrients, the farmer can grow indefinitely without any additional input to produce nutrient packed rice grains in a sustainable way. This is also the only feasible way of reaching the malnourished population in India. All these elements are essential for normal growth and development because, they play important role in nerve functioning, sugar metabolism, activity of numerous enzymes and in cardiac function (Milena *et al.,* 1993). In white rice varietal improvement programs, red rice varieties have proved to be useful donors for sources of nutritive, resistance and tolerance to many stress environments. In this context, breeders are now focusing on nutritional enhancement to overcome the problem of malnutrition (Nagesh *et al.,* 2012). The proper knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. The valuable information about phenotypic and genotypic interactions of various economic traits is the immense importance to a plant breeder for the selection and breeding of different genotypes with increasing yield potential. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. With view to improve the rice cultivars attempt had been made to measures of variability, heritability and genetic advance for indigenous medicinal land races and high yielding varieties of rice.

MATERIALS & METHODS

The experimental material consisted of four medicinal landraces *viz.,* Veeradangan, Kavuni, Kathanellu and Navara which were collected from Tamil Nadu and Navara is a medicinal landrace of Kerala these landraces are having superior nutritional grain qualities and low yielder and six improved semi-dwarf high yielding varieties *viz.,* IR 72, ADT 39, ADT 45, ASD 16 and TPS 4 of medium grain quality along with standard check ADT 43 raised in Randomized Block Design replicated thrice by adopting a spacing of 30 x 10cm at Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai during Kharif 2013. Six F_1 crosses (IR 72 x Veeradangan, ADT 39 x Kavuni, ADT 45 x Kavuni, ADT 43 x Navara, ASD 16 x Navara and TPS 4 x Katha nellu) were synthesised and crossed seeds (F_1s) were collected. The recommended package of practices was followed. Data were recorded on thirteen biometrical characters *viz.*, days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, hundred grain weight and single plant yield as per the Standard Evaluation System (SES, 1996) descriptor suggested by IRRI. The mean data for each character individually was subjected to statistical analysis. Standard statistical procedures were used for the analysis of genotypic and phenotypic coefficients of variation (Burton 1952), heritability (Lush 1940) and genetic advance.

RESULTS & DISCUSSION

Analysis of variance for biometrical characters revealed significant differences among the genotypes for characters studied indicating the existence of significant amount of variability for the characters (Table 1). The mean values indicated considerable variation for all biometrical characters (Table 2) (Fig 1). Among the parents, Kavuni (112.40 days) was the late flowering and TPS 4 (66.00 days) was the early flowering genotype. The parental genotypes, TPS 4 (66.00 days), Navara (68.20 days), Veeradangan (75.40 days), ADT 43 (75.80 days) and ASD 16 (76.40 days) showed significantly lower values than the grand mean value. Among the hybrids, ADT 39 x Kavuni (109.68 days) was the late flowering and ADT 43 x Navara (69.72 days) was the early flowering. The hybrids, ADT 43 x Navara (69.72 days), ASD 16 x Navara (70.72 days) and IR 72 x Veeradangan (78.04 days) showed significantly lower values than the grand mean value. With regard to plant height among the parents, Kavuni was found to be the tallest (138.13 cm) and the TPS 4 (74.96 cm) was the shortest. The parents, TPS 4 (74.96 cm), ADT 43 (85.18 cm), IR 72 (85.65 cm), Kathanellu (87.97cm), ADT 45 (92.28 cm) and ASD 16 (94.80 cm) showed significantly lower values than the grand mean value. Maximum plant height among the F_1 hybrids was recorded by ADT 39 x Kavuni (122.95 cm) and minimum by TPS 4 x Kathanellu (85.82 cm). The two hybrids, TPS 4 x Kathanellu (85.82 cm) and ASD 16 x Navara (94.81 cm) registered significantly lower values than the grand mean value. The undesirable characters of these landraces were tall growing, late flowering and lodging type. Among the ten parents studied, Kavuni recorded the lowest number of productive tillers per plant (10.20) while Veeradangan (15.20) showed the highest number of productive tillers per plant. The female parent ADT 39 (14.60) registered significantly higher values for this trait. In F_1 hybrids it ranged from 12.20 (ADT 43 x Navara) to 16.20 (IR 72 x Veeradangan). The hybrids *viz.,* IR 72 x Veeradangan (16.20), ASD 16 x Navara (15.04), ADT 45 x Kavuni (14.36), TPS 4 x Kathanellu (14.24) and ADT 39 x Kavuni (14.12) were found to be significant. Among the male parents Kavuni (26.35 cm) had the longest panicle length and Navara (22.53 cm) had the shortest panicle length. None of the female parents showed significant values for panicle length. Among the F_1 hybrids ADT 43 x Navara (22.54 cm) had the lowest panicle length while ADT 45 x Kavuni (27.60 cm) was with highest panicle length. Among the ten parents the highest mean value for number of filled grains per panicle was observed in ADT 43 (128.40) and Veeradangan (97.01) recorded minimum number of filled grains per panicle. ADT 43 (128.40) and ADT 45 (124.70) exhibited significantly superior values for this trait. Among the hybrids, ADT 45 x Kavuni (130.67), ADT 39 x Kavuni (127.00) recorded significant values. Among the F_1 hybrids, highest number of filled grains per panicle was recorded by ADT 45 x Kavuni (130.67) and the lowest by TPS 4 x Kathanellu (109.65).

For the hundred grain weight, among the parents ASD 16 registered the highest hundred grain weight (2.64 g) while, ADT 39 was found to be the low (1.84 g). ASD 16 (2.64 g) and Veeradangan (2.55 g) registered significantly higher values for this trait. Among the hybrids, the maximum hundred grain weight was recorded by IR 72 x Veeradangan (2.69 g) and the minimum value by ADT 39 x Kavuni (2.13 g). Among the F_1 hybrids, IR 72 x Veeradangan (2.69 g) and ASD 16 x Navara (2.49 g) showed significance over their grand mean value (2.29 g). Among the parents, Veeradangan was found to be high yielder (35.46 g) and Navara was the low yielder (25.80 g). Among the parents, none of the female parents showed significant values for single plant yield. Among the F_1 hybrids maximum single plant yield was recorded in IR 72 x Veeradangan (44.80 g) and minimum in ASD 16 x Navara (33.71 g). Among the F_1 hybrids, IR 72 x Veeradangan (44.80 g), ADT 45 x Kavuni (39.09 g) and ADT 39 x Kavuni (38.54 g) and showed significance over the grand mean value (33.33 g). Overall mean performance when compared among hybrids for important yield characters and single plant yield three hybrids *viz.,* IR 72 x Veeradangan, ADT 39 x Kavuni and ADT 45 x Kavuni were found to be the best.

The estimates of phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent of mean for the traits under study are furnished (Table 3, Fig 2). In general phenotypic co-efficients of variation were higher than the genotypic co-efficients of variation. Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing characters for enforcing selection. Nevertheless, the heritability estimates in conjunction with predicted genetic advance will be more reliable (Johnson *et al*., 1955).

TABLE 1. Analysis of variance of parents and F_1 hybrids for biometrical traits in rice

		Mean squares						
Source	df	Days to 50 % flowering	Plant height	Number of Productive tillers per plant	Panicle length	Number of filled grains per panicle	Hundred grain weight	Single plant yield
Replication	2	2.82	37.92	0.15	0.04	16.31	0.001	2.02
Genotypes	15	639.78**	764.02**	7.79**	5.44**	280.69**	0.17**	71.32**
Error	30	3.40	9.59	0.15	0.56	9.89	0.004	3.11

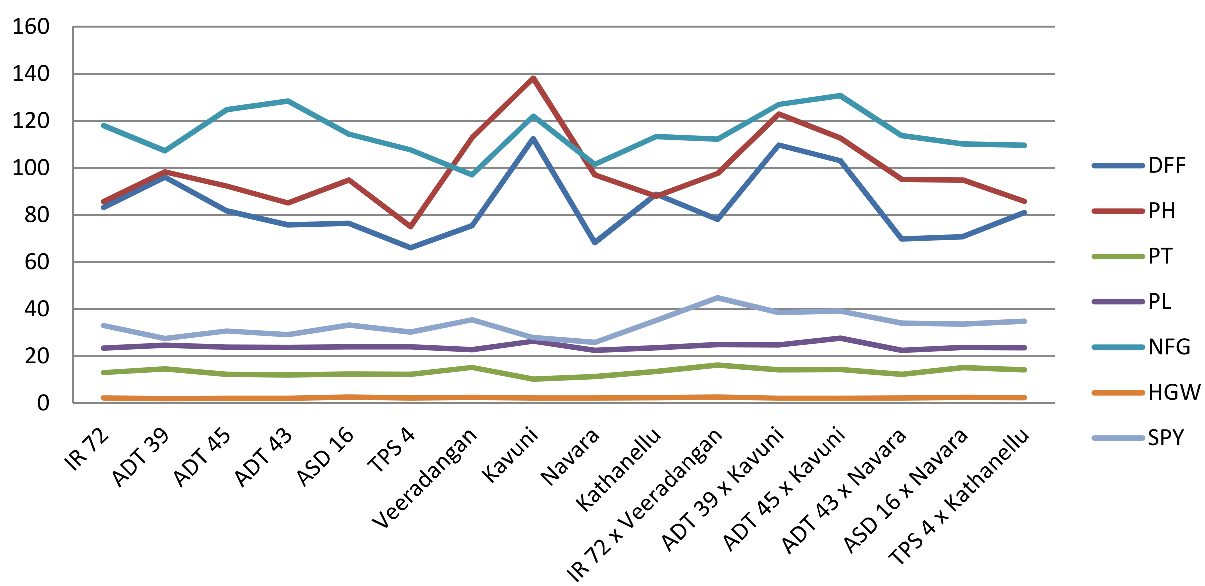
TABLE 2. Mean performance of parents and F_1 hybrids for biometrical traits in rice

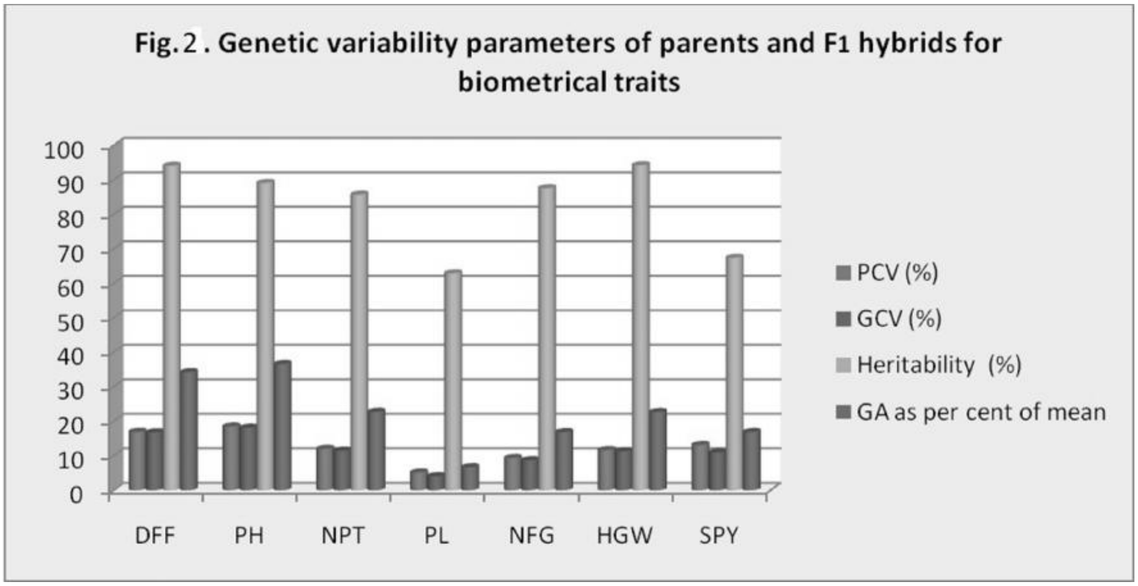
Source	Days to 50 % flowering	Plant height (cm)	Number of Productive tillers per plant	Panicle length (cm)	Number of filled grains per panicle	Hundred grain weight (g)	Single plant yield (g)
Female parents							
IR 72	83.20	85.65*	13.00	23.39	118.10	2.31	32.99
ADT 39	96.00	98.32	14.60*	24.67	107.34	1.84	27.47
ADT 45	81.80	92.28*	12.20	23.76	124.70*	1.99	30.70
ADT 43	75.80*	85.18*	12.00	23.65	128.40*	1.96	29.22
ASD 16	76.40*	94.80*	12.40	23.88	114.32	2.64*	33.29
TPS 4	66.00*	74.96*	12.20	23.94	107.64	2.33	30.16
Male parents							
Veeradangan	75.40*	112.79	15.20*	22.75	97.01	2.55*	35.46*
Kavuni	112.40	138.13	10.20	26.35*	121.98*	2.33	27.94
Navara	68.20*	97.01	11.40	22.53	101.52	2.23	25.80
Kathanellu	88.80	87.97*	13.60	23.48	113.24	2.34	35.15
F_1 hybrids							
IR 72 x Veeradangan	78.04*	97.63	16.20*	24.90	112.22	2.69*	44.80*
ADT 39 x Kavuni	109.68	122.95	14.12*	24.75	127.00*	2.13	38.54*
ADT 45 x Kavuni	103.00	112.62	14.36*	27.60*	130.67*	2.18	39.09*
ADT 43 x Navara	69.72*	95.16	12.20	22.54	113.65	2.29	34.09
ASD 16 x Navara	70.72*	94.81*	15.04*	23.61	110.21	2.49*	33.71
TPS 4 x Kathanellu	81.08	85.82*	14.24*	23.58	109.65	2.35	34.81
Grand mean	83.52	98.51	13.31	24.09	114.89	2.29	33.33
SE	1.06	1.79	0.23	0.43	1.82	0.04	1.02
CD (5 %)	3.08	5.16	0.66	1.25	5.24	0.10	2.94

TABLE 3. Genetic variability parameters of parents and F_1 hybrids for biometrical traits in rice

Characters	Range		Grand Mean	Coefficient of Variation (%)		Heritability (%)	Genetic advance as % of mean
	Minimum	Maximum		Phenotypic (PCV)	Genotypic (GCV)		
Days 50 per cent flowering (days)	66.00	112.40	83.52	16.94	16.78	94.10	34.24
Plant height (cm)	74.96	138.13	98.51	18.49	18.13	89.11	36.61
No of productive tillers per plant	10.20	16.20	13.31	12.02	11.51	85.72	22.72
Panicle length (cm)	22.53	27.60	24.09	5.16	4.09	62.89	6.69
Number of filled grains per panicle	97.01	130.67	114.89	9.35	8.74	87.58	16.86
Hundred grain weight (g)	1.84	2.69	2.29	11.66	11.32	94.24	22.64
Single plant yield (g)	25.80	44.80	33.33	13.15	10.97	67.41	16.87

FIGURE 1. Mean performance of parents and F1 hybrids for biometrical traits in rice





Heritability gives the information on the magnitude of quantitative characters, while genetic advance will be helpful in calculating suitable selection procedures. Estimates of the amount of variability for different characters and their heritable components available in the population are essential for dynamic and efficient plant breeding. The values for PCV ranged from panicle length (5.16 %) to plant height (18.49 %). The moderate PCV was recorded for plant height (18.49 %), days to 50 per cent flowering (16.94 %), single plant yield (13.15 %), number of productive tillers per plant (12.02) and hundred grain weight (11.66 %). The lowest PCV was recorded for number of filled grains per panicle (9.35 %) and panicle length (5.16 %). The values of GCV ranged from panicle length (4.09 %) to plant height (18.13 %). The moderate GCV recorded for plant height (18.13 %), days to 50 per cent flowering (16.78 %), number of productive tillers per plant (11.51 %), hundred grain weight (11.32 %) and single plant yield (10. 97 %). The lowest GCV was recorded for number of filled grains per panicle (8.74 %) and panicle length (4.09 %). The genotypic and phenotypic coefficients of variation indicated the extent of variability for different traits. Those results are in conformity with those of by Chimmili (2012) and Sala (2012). Low values of phenotypic coefficient of variation and genotypic coefficient of variation indicate that the genotypes do not exhibit much variation among themselves with respect to these characters. Further low phenotypic coefficient of variation and genotypic coefficient of variation for any characters indicated less scope for selection. This was in agreement with the findings of Namita *et al.*, (2008) and Punitha *et al.*, (2011). The phenotypic and genotypic coefficients of variation indicated the extent of variability for different traits. High heritability coupled with low genetic advance, low heritability with high genetic advance or low heritability and low genetic advance offer less scope for selection, as they were more influence by environmental and accounted for non-additive gene effects. High heritability coupled with high genetic advance is indicated of greater proportion of additive genetic advance and consequently a high genetic advance is expected for selection (Singh and Rai 1981). The characters having high heritability with low genetic advance as per cent of mean appeared to be controlled by non-additive gene action and selection for such characters may not be effective (Singh and Singh 2007). The genotypes recorded high heritability values for all the characters under study. Heritability ranged from panicle length (62.89 %) to hundred grain weight (94.24 %). Genetic advance as per cent of mean ranged from panicle length (6.69 %) to plant height (36.61 %). Plant height (36.61 %) recorded the highest genetic advance followed by days to 50 per cent flowering (34.24 %), number of productive tillers per plant (22.72 %) and hundred grains weight (22.64 %). High genetic advance indicated that these characters are governed by additive genes and selection will be rewarding for improvement of study. Moderate genetic advance was recorded for single plant yield (16.87 %) and number of filled grains per panicle (16.86 %). The above findings support the results of Shet *et al.*, (2009) and Chimmili (2011).

Traditional rice varieties, or landraces, have a high level of genetic heterogeneity compared to modern improved rice cultivars. This genetic variability is very important for the sustainability of small farmers, because despite the low yield capacity, these varieties present high yield stability (Oka, 1991). The genetic improvement in traditional land races of rice is possible through selection exercised for those characters which showed high values of phenotypic coefficient of variation and genotypic coefficient of variation, heritability and genetic advance. This will provide an opportunity to select better recombinants for variability for these characters in the future generations. However, characters predominantly controlled by additive gene action would be conventional breeding methods. This will also help modern breeding programs to plan crosses to incorporate this variability into the genetic background of elite traditional rice landraces, which in turn will generate new nutritional and medicinal properties rich improved rice cultivars.

REFERENCES

Burton, G.W. (1952) Quantitative inheritance in grasses. Proceedings of 6th International Grassland Congress 1: 277 - 283.

Chimmili, S.R. (2012) Genetic analysis for nutritive traits using medicinal land races of rice (*Oryza sativa* L.). M.Sc. (Ag.) Thesis (Unpubl.), TNAU, Coimbatore.

Houston, D.F. & Kohler, G.O. (1970) Background and present situation in: Nutritional properties of rice. National Academy of Sciences: Washington.

Johnson, H.W., Robinson, H.F. & Comstock, R.E. (1955) Estimates of genetic and environmental variability in soybean. Agron J., 47: 314-318.

Mandi, D. & Kenjeri Piri, A.P. (1993) Intake of some minerals in healthy adult volunteers. *Inter.* J. of Food Sciences and Nutrition. 60: 77-87.

Lush, J.L. (1940) Intra - sire correlation and regression of offspring on dams as a method of estimating heritability of characters. Proceedings of American Social Animal produces, 33: 293-301.

Nagesh Ravindrababu, V., Usharani, G. & Dayakar Reddy, T. (2012) Grain iron and zinc association studies in (*Oryza sativa* L.) F_1 progenies. Archives of Applied Science Research 4(1): 696-702.

Namita Singh, K.P., Raju, D.V.S., Prasad, K.V., Mishra and Bharadwaj, C. (2008) Studies on genetic variability, heritability and genetic advance in Franch marigold (*Tagetes patula*) genotypes. J. Ornamental Hort., 9: 30-4.

Punetha, P., Rao, V.K. & Sharma, S.K. (2011) Evaluation of different chrysanthemum (*Chrysanthemum montrifolium*) genotypes under mid hill conditions of Gartwal Himalaya. Indian J. Agric. Sci., 81: 830.

Sala, M. (2012) Rice breeding for biofortification with high iron and zinc content in segregating population. M.Sc. (Ag.) Thesis (Unpubl.), TNAU, Madurai.

Shet, R.M., Gireesh, C., Jagadeesha, N., Lokesh, G.Y. and Jayarame Gowda (2009) Genetic variability in segregating generation of interspecific hybrids of finger millet (*Eleusine coracana* (L.) Gaertn.). Environ. Ecol., 27(3): 1013-1016.

Singh, A.K. & Singh, N. (2007) Studies on genetic variability and heritability in balsam (*Impaties balsamina*). *J*. of Ornamental Horticulture 10: 128-30.

Singh, R.P. & Rai, J.N. (1981) Note on the heritability and genetic advance in chilli (*Capsicum annum* L.). Progressive Horticulture 13(1): 89-92.

Singh, R.K., Gautam, P.L., Saxena, S. & Singh, S. (2000) Scented rice germplasm: conservation, evaluation and utilization. Oxford and IBH pubishing, New Delhi, pp: 107-133.

Standard Evaluation System (1996) IRRI (International Rice Research Institute).

Oka, H.I. (1991) Genetic diversity of wild and cultivated rice. In: Khush G.S and Toenniessen G.H (eds) Rice Biotechnology. IRRI, Los Baños, pp 55-81.