



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2019; SP2: 960-962

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Estimation of genetic variability parameters in rice (*Oryza sativa* L.) gene bank in NEP Zone

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Abstract

The experiment was conducted at the Research Farm of Genetics & Plant Breeding, Narendra Deva University of Agriculture & Technology, Narendra Nagar, Kumarganj, Faizabad (U. P.) during *kharif*, 2015. The experimental materials for this investigation comprised of 30 genotypes along with (two checks *viz.*, Narendra Usar 3 and IR 28) of rice were evaluated in randomized block design with three replications during *kharif*, 2015 for thirteen characters *viz.*, days to 50 % flowering, plant height (cm), flag leaf area, (cm²), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, spikelet fertility (%), biological yield per plant (g), harvest index (%), L:B ratio, 1000-grains wt. (g) and grain yield per plant (g) under salt affected soil. The present investigation was under taken with the objectives to estimate genetic variability for yield and yield contributing components. The analysis of variance revealed that the mean sum of square due to treatments were highly significant for majority of the yield and its contributing traits, indicated sufficient variation among the treatment/materials under study. In general, PCV were higher than the GCV for all characters under salt affected soil indicates influence of environment. High heritability coupled with high genetic advance were observed for spikelets per panicle, grains per panicle, biological yield per plant, L:B ratio and grain yield per plant, it indicates the presence of additive gene action. Hence, emphasis should be given to select these quantitative traits to enhance the yield potential of rice (*Oryza sativa* L.) under salt affected soil.

Keywords: Genetic variability, Heritability, Genetic advance, Rice (*Oryza sativa* L.).

Introduction

Rice, *Oryza sativa* L. (2n=24) is a cereal foodstuff which forms an important part of the diet of more than three billion people around the world. It is the principal staple food for more than half of the world's population. It is grown under diverse agro-climatic conditions and over wide geographical range (Cheng *et al.*, 2005) [4]. Drought and salinity are major constraints on crop production and food security and adversely impact the socioeconomic fabric of many developing countries. Water scarcity, declining water quality for irrigation and soil salinity are problems which are becoming more acute. It is estimated that 20% of all cultivated land and nearly half of irrigated land is affected by salt, greatly reducing the yield of crops to well below their genetic potential. There is limited evidence at present that remediation of saline soils enhance crop yield stability (Tester and Devenport, 2003) [17]. Salinity-stress effects on crop grown are manifested by impairment of photosynthetic capacity. High amounts of sodium in the soil solution impair cell metabolism and photosynthesis by imposing an osmotic stress on cell water relations and by increasing the toxicity of sodium in the cytosol. Heritability is the proportion of observed differences on a trait among individuals of a population that are due to genetic differences. Factors including genetics, environment and random chance can all contribute to the variation between individuals in their observable characteristics. Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. Therefore, present investigation was under taken with the view of to find out genetic variability in the study materials.

Materials and Methods

The experiment was conducted during *kharif*, 2015 at the Research Farm of Genetics & Plant Breeding, N.D. University of Agriculture and Technology, Kumarganj, Faizabad. The experimental materials of rice for this investigation comprised of 30 genotypes along with (two checks *viz.*, Narendra Usar 3 and IR 28) of rice were evaluated in randomized block design (Panse, V.G. and Sukhatme, P.V.; 1967) [10] with three replications with the spacing of 20 cm row to row and 15 cm plant to plant during *kharif* 2015 under salt affected soil.

Observations were recorded on randomly selected five plants from each entry in each replication. The data were recorded on days to 50 % flowering, plant height (cm), flag leaf area, (cm²), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, spikelet fertility (%), biological yield per plant (g), harvest index (%), L:B ratio, 1000-grains wt. (g) and grain yield per plant (g). Recommended cultural practices were adopted to raise good crop.

Results and Discussion

Mean sum of square due to treatments were significant for all the characters showed presence of variability in the study materials (Table 1).

The success of selection in improving plant characters depends mainly on presence of substantial genetic variability and nature of heritability and gene action. The genetic variability is the raw material of plant breeding programme on which selection acts to evolve superior genotypes. The phenotypic and genotypic coefficients of variation can be used for assessing and comparing the nature and magnitude of variability existing for different characters in the breeding materials. Heritability in broad sense quantifies the proportion of heritable genetic variance to total phenotypic variance. Estimates of heritability help in estimating expected progress through selection. The genetic advance in per cent of mean provides indication of expected selection response by taking into account the existing genetic variability and heritability of the character.

The analysis variance revealed that the treatments were highly significant for majority of the yield and its contributing traits indicating wide genetic variability among the materials under study. In general, PCV were higher than the GCV for all characters under salt affected soil indicates influence of environment. The high estimates of phenotypic and genotypic coefficient of variation (> 20%) were estimated for biological yield per plant (PCV=22.57%, GCV=22.27%) and grain yield per plant (PCV=21.45%, GCV=20.16%) but but high PCV and moderate GCV was recorded only for L:B ratio (PCV=20.30%, GCV=19.51%) indicating high opportunity of selection for these characters under salt affected soil. The moderate estimates (10-20%) of PCV and GCV were recorded for flag leaf area (PCV=11.49%, GCV=10.53%), panicle bearing tillers per plant (PCV=16.77%, GCV=12.53%), spikelets per panicle (PCV=17.25%, GCV=16.89%) and grains per panicle (PCV=17.81%, GCV=17.23%) and it was low for days to 50 % flowering (PCV=5.25%, GCV=5.15%), plant height (PCV=7.84%, GCV=7.29%), panicle length (PCV=7.52%, GCV=6.06%), spikelet fertility (PCV=6.03%, GCV=5.64%), harvest index (PCV=4.91%, GCV=2.96%) and 1000- grains weight (PCV=6.77%, GCV=5.98%) indicating little opportunity of selection for these characters under salt affected soil (Table

2). High coefficient of variability indicated that there is a scope of selection and improvement of these traits. Low values indicated the need for creation of variability either by hybridization or mutation followed by selection. Similar findings were also reported by Pandey *et al.* (2004) [9] and Yadav *et al.* (2002) [18]. The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability. Robinson *et al.* (1949) [12] viewed that the knowledge of heritability of a character is important to the breeder, as it indicates the possibility and extent to which improvement is possible through selection.

In the present study, high estimates of broad sense heritability (>75%) was recorded for all the characters except harvest index, which exhibited moderate estimate of heritability (50-75%). The genetic advance in per cent of mean in salt affected soil was found to be high (>20%) for spikelets per panicle, grains per panicle, biological yield per plant, L:B ratio and grain yield per plant. On the other hand, moderate genetic advance in per cent of mean (10-20%) were noted for days to 50 % flowering, plant height, flag leaf area, Panicle bearing tillers per plant, panicle length, spikelet fertility, and 1000-grain weight while low (<10%) for harvest index (Table 2). The broad sense heritability of these characters are in accordance with those of Bhattacharya (1978) [2] for grain yield per plant; Kumar and Verma (2016) [6] for days to 50% flowering, Plant height, spikelets per panicle, 1000 grain weight and grain yield per plant.

Further, results revealed that high heritability coupled with high genetic advance in per cent of mean were observed for the characters *viz.*, spikelets per panicle, grains per panicle, biological yield per plant, L:B ratio and grain yield per plant. These findings were similar to those of Mohammad and Deva, 2002 [8]; Chaudhary *et al.*, 2004 [3]; Basavaraja *et al.* 2013 [1]; and Sathya and Jebaraj, 2013 [13]. High heritability in broad sense coupled with moderate genetic advance in per cent of mean were observed for the characters *viz.*, days to 50 % flowering, plant height, flag leaf area, spikelet fertility and 1000- grain weight under salt affected soil. Similar findings were also reported by Shukla *et al.*, 2004 [14] and Mall *et al.*, 2005 [7]. High heritability coupled with high genetic advance have additive gene action and may be directly utilized for rice improvement. On the other hand the character having low heritability and high genetic advance in percent of mean and high heritability and low genetic advance in percent of mean have non-additive gene action. The high to very high estimates of direct selection parameters for above mentioned characters indicated that these would be ideal traits for improvement through selection in context of materials evaluated due to existence of high genetic variability represented by high coefficients of variation and high transmissibility denoted by high heritability for them. (Panwar *et al.*, 2007 and Yadav *et al.*, 2002) [11, 18].

Table 1: Analysis of variance for randomized block design for 13 characters in rice under salt affected soil

Characters	Sources of variation		
	Replications	Treatments	Error
D.F.	2	31	62
Days to 50% flowering	0.32	76.16**	1.02
Plant height (cm)	12.45	145.55**	7.11
Flag leaf area (cm ²)	0.57	18.72**	1.12
Panicle bearing tillers per plant	1.71	3.30**	0.69
Panicle length (cm)	0.39	6.50**	0.99
Spikelets per panicle	30.19	1336.95**	19.37

Grains per panicle	32.28	874.71**	19.46
Spikelet fertility (%)	2.08	62.31**	2.86
Biological yield per plant (g)	1.03	155.50**	1.41
Harvest-index (%)	3.47	6.58**	2.43
L:B ratio	0.04	1.27**	0.03
1000- grains weight (g)	1.23	5.82**	0.50
Grains yield per plant (g)	0.97	20.68**	0.87

*,** Significant at 5% and 1% probability levels., respectively.

Table 2: Estimates of general mean, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2_b) and genetic advance in per cent of mean for 13 characters in rice under salt affected soil

Characters	General mean ±SE	Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in per cent of mean
		PCV	GCV		
Days to 50% flowering	97.23±0.58	5.25	5.15	96.00	10.39
Plant height (cm)	93.13±1.54	7.84	7.29	87.00	13.99
Flag leaf area (cm ²)	23.00±0.61	11.49	10.53	84.00	19.89
Panicle bearing tillers per plant	7.45±0.48	16.77	12.53	56.00	19.29
Panicle length (cm)	22.36±0.57	7.52	6.06	65.00	10.06
Spikelets per panicle	124.10±2.54	17.25	16.89	96.00	34.04
Grains per panicle	97.97±2.55	17.81	17.23	94.00	34.35
Spikelet fertility (%)	78.96±0.98	6.03	5.64	87.00	10.86
Biological yield per plant (g)	32.18±0.69	22.57	22.27	97.00	45.26
Harvest-index (%)	39.74±0.90	4.91	2.96	36.00	3.67
L:B ratio	3.29±0.11	20.30	19.51	92.00	38.65
1000- grains weight (g)	22.29±0.41	6.77	5.98	78.00	10.87
Grain yield per plant(g)	12.74±0.54	21.45	20.16	88.00	39.03

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