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Genetic variability, heritability and genetic advance estimates for different quantitative traits in Rice (*Oriza sativa* L.) under sodic soil condition

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Abstract

An investigation was carried out to assess genetic variability, heritability and genetic advance for different quantitative traits in thirty-one entries (7 female lines + 3 male lines + 21 crosses) with 2 check varieties (Narendra usar dhan-3 and CSR-43). Analysis of variance revealed that variances due to treatments, parents and crosses were highly significant for almost all the traits indicating that sufficient variability was existed in the treatments, parents and crosses. The magnitudes of phenotypic coefficient of variance (PCV) for all the characters were slightly higher than their corresponding genotypic coefficient of variance (GCV), indicated very less environmental influence on the expression of the characters. The maximum GCV was recorded for grains/panicle (189.85%), followed by biological yield/plant (66.15%), grain yield per plant (18.98%), Spikelet fertility (17.02%), days to 50% flowering (15.58%). Degree of dominance was greater than the unity for majority of the traits, indicating the presence of over dominance gene action. The higher values of broad sense heritability (>75%) were observed for majority of traits, except panicle bearing tillers plant^{-1} (53.67%) and panicle length (54.97%) which showed moderate heritability. Higher estimates of heritability in narrow sense (h^{2}ns) were reported for days to 50% flowering (34.54%) followed by Grains per panicle (25.15%) grain yield plant^{-1} (23.35%), biological yield plant^{-1} (22.44%), 1000 grain weight (14.13%) plant height (12.13%), harvest index (10.86%), spikelet fertility (10.24%). The higher values of genetic advance (GA) were recorded for grains per panicle (36.00%), followed by biological yield per plant (21.03%), grain yield per plant (11.27%), spikelet fertility (10.34%), days to 50% flowering (9.51%). The higher values of genetic advance as per cent of mean were observed for grain yield plant^{-1} (67.32%), followed by biological yield plant^{-1} (47.57%), grain panicle^{-1} (29.38%), harvest index (21.26%), panicle bearing tillers plant^{-1} (16.93%), 1000 grain weight (15.57%), spikelet fertility (12.45%), days to 50% flowering (9.76%), plant height (8.76%), panicle length (7.61%) while, it was lowest for flag leaf area (5.18%). Therefore, grains per panicle, biological yield per plant, grain yield per plant could be utilized as direct selection parameters to achieve high genetic gain under selection.

Keywords: Genetic variability, phenotypic coefficient of variance (PCV) and Genotypic coefficient of variance (GCV), Heritability, Genetic advance

Introduction

Rice (*Oryza sativa* L.) belongs to family Gramineae (Poaceae). Rice is one of the most important staple foods for developing world as well as majority of Asian countries. Rice is the major source of calories for more than half of the global population. It contains 6-12% protein, 70-80% carbohydrate, 1.2-2.0% mineral matter and significant content of fats and vitamins. Rice supplies 23% of global human/ capita energy and 16% of per capita protein requirements. The geographical distribution of rice extends from 390 N latitude (Australia) to 450 N latitude (Japan) and 500 N latitude (China).

India has the largest area 43.39 million hectare constituting 28.01% of the land under rice in the world and rank second in total production 111.50 million tonns next to china (187.490 million tonns) with an average productivity of 2804 Kg/hectare (Anonymous 2017-18) [1]. Asia has an area of only 140.036 million hectare and productivity as 5.32 tonns/ hectare (Anonymous 2017-18) [2]. More than 80% of our countrymen depend fully or partially on rice as their main were at food and staple diet. Uttar Pradesh is important rice growing state of country. The area and production of rice in this state is about 6.45 million hectare and 18.251millon tons respectively with the productivity of 4.95 tonns/ hectare (Uttar Pradesh directorate of agricultural ministry, 2017-18).

The effectiveness of selection for traits depends on the relative importance of genetic and non-genetic factors in the expression of phenotypic differences among the genotypes in a population, a concept referred to as heritability has a major impact on the method chosen for population improvement and\or selection intensity to be applied in segregating population. Single plant selection may be effective for a character with high heritability and relatively less effective for one with low heritability. The extent to which replicated testing is required for selection depends on the heritability of the character. Therefore, the present investigation was carried out to know about heritable proportion of total variability existing in the genotypes for formulation of efficient selection strategy.

Materials and Methods

The present investigation was carried out at the Genetics and Plant Breeding Research Farm of N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya. The crosses were made during *Kharif*, 2015 and the hybrids (F_1s) along with parental lines and check varieties were evaluated during *Kharif*, 2016. Geographically this place is located in between $26^{o}.47^{1}$ N latitude, $82^{0}.12^{1}$ longitude and at an altitude of 113 meters above mean sea level. This area falls in sub-tropical climatic zone. The climate of district Ayodhya is semi-arid with hot summer and cold winter. Seven lines (females) *viz*., NDRK- 50058, Pusa Basmati-1, NDRK-50060, NDRK-50063, IET-58, IET-51 and USAR-1 comprising genotypes / varieties of rice were crossed with three testers (males) *viz*. Jaya, CSR-10 and BPT-5204 in a line × tester mating design. A total of 21F_1s were produced during *Kharif*, 2015. The resulting set of 21F_1s along with their 10 parents and 2 check varieties (Narendra usar dhan-3 and CSR-43) were evaluated in Randomized Complete Block Design with three replications during *Kharif*, 2016. The seeds of each entry were sown on 10th July, 2016 in separate plots and 25 days (4th August 2016) old seedlings were transplanted single seedling per hill in single row plots of 3 m length with inter- and intra- row spacing of 20 cm and 15 cm, respectively. All the recommended cultural practices were followed to raise a good crop. The fertilizers were applied @ 120 kg nitrogen, 60 kg phosphorus and 60 kg potash per hectare through urea, DAP and murate of potash, respectively. The full dose of phosphorus and potash and half dose of nitrogen were applied as basal and rest of nitrogen was applied in two split doses as top dressing at tillering and panicle initiation stage of crop growth. Data on ten quantitative traits *viz*., Plant height (cm), Panicle bearing tillers per plant, Panicle length (cm), Flag leaf area, Grains per panicle, Spikelet fertility (%), 1000-grain weight (g), Biological yield per Plant (g), Harvest-index (%), Grain yield per plant (g) were recorded on plant basis while data on Days to 50 % flowering were recorded on plot basis. The mean values of recorded data were used for Analysis of variance for Randomized Complete Block Design (Panse and Sukhatme, 1967) [5], Phenotypic, genotypic, and environmental coefficients of variation for different characters (Burton and de Vane, 1953) [6], heritability in broad sense (h^2b) (Hanson *et. al*., 1956) [7], heritability in narrow sense (h^2n) (Kempthorne, 1957) [3], the expected genetic advance (Ga) (Johnson *et al*., 1955) [8].

Result and Discussion

The analysis of variance for 33 entries (7 female lines + 3 male lines + 21 crosses) was done for eleven traits *viz*., days to 50% flowering, plant height (cm), panicle bearing tillers plant^{-1}, panicle length (cm), flag leaf area (cm^2),1000 grain weight, grain panicle^{-1}, spikelet fertility (%), biological yield plant^{-1} (g), harvest index (%), and grain yield plant^{-1}(g). A perusal of Table 1 revealed that variances due to treatments, parents and crosses were highly significant for all the traits indicating sufficient variability existed in the treatments, parents and crosses.

The coefficient of variation is depicted in Table 2 Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficients of variation (GCV) for all the traits. The highest value of GCV was recorded for grains/panicle (189.85%), followed by biological yield /plant (66.15%), grain yield per plant (18.98%), Spikelet fertility (17.02%), days to 50% flowering (15.58%), panicle length (12.58%), harvest index (10.28%), 1000 grain weight (1.86%), panicle length (0.68%), flag leaf area (0.61%), but lowest for panicle bearing tillers per plant(0.39%). Highest (PCV) was recorded for grain /panicle (193.73%) followed by biological yield plant^{-1} (68.96%), grain yield plant^{-1}(19.70%), grain panicle-^{1}(18.85%), days to 50% flowering (18.70%), plant height (15.28%), harvest index (11.68%), 1000 grain weight (2.23%), flag leaf area (2.08%), panicle length (1.23%), but lowest for panicle bearing tillers plant^{-1} (0.58%).

Heritability in broad sense is presented in Table 2 The highest values of broad sense heritability (>75%) was observed for majority of traits, except panicle bearing tillers plant^{-1} (53.67%) and panicle length (54.97%) which showed moderate heritability. The highest heritability was recorded for grain/panicle (98%), grain yield plant^{-1} (96.01%), biological yield plant^{-1} (95.93%), plant height (82.33%), spikelet fertility (90.25%), 1000 grain weight (83.46%), plant height (82.33%), days to 50% flowering (83.32%), plant height (91.4%) whereas flag leaf area content showed the lowest heritability (29.36%).

The estimates of narrow sense (h^2_n) heritability are presented in Table 2 The narrow sense heritability was classified into three groups (according to Robinson, 1966) as low (< 10%), moderate (10-30%) and higher more than 30%.

Heritability (h^2_{ns}) ranged from 0.07(flag leaf area) to 34.54 per cent (days to 50% flowering) low heritability was found in 0.07% (flag leaf area) the while possessed the moderate heritability grain yield plant^{-1} (23.35%), biological yield plant^{-1} (22.44%),plant height (12.13%), harvest index (10.86%), spikelet fertility (10.24%) The majority of the traits reflected high heritability.

The highest h^2_n estimates (>30%) were noted for days to 50% flowering (34.54%) Above findings also confirmed from the estimates of variance due to additive and dominance genetic components in the study.

The genetic advance (GA) in absolute terms ranged from (flag leaf area) 1.11% to 36.00% (Grain panicle^{-1}). The highest GA was recorded for grain panicle^{-1} (36.00%), followed by biological yield plant^{-1} (21.03%), grain yield plant^{-1} (11.27%), spikelet fertility (10.34%),days to 50% flowering (9.51%), plant height (8.49%), harvest index (7.94%), 1000 grain weight (3.29%), panicle length (1.61%), panicle bearing tillers plant-^{1} (1.37%), flag leaf area (1.11%).

The genetic advance (GA) in per cent of mean for 11 traits is presented in Table 4.3. The highest GA as per cent of mean was observed for grain yield plant^{-1} (67.32%), followed by biological yield plant^{-1} (47.57%), grain panicle^{-1} (29.38%), harvest index (21.26%), panicle bearing tillers plant^{-1} (16.93%), 1000 grain weight (15.57%), spikelet fertility (12.45%), days to 50% flowering (9.76%), plant height (8.76%), panicle length (7.61%), and but it was lowest for flag leaf area (5.18%).

The high estimates of direct selection parameters observed for the above traits are broadly in agreement with earlier reports of Pandey and Awasthi (2002) [4], Akhtar *et al*. (2011) [10], Seyoum *et al*. (2012) [11], Kiani (2013) [12], Dhurai *et al*. (2014) [13], Nachimuthu *et al*. (2014) [14], Rai *et al*. (2014) [15], Sindhumole *et al*. (2015) [16] and Anis *et al*. (2016) [17].

Table 1: Analysis of variance including parents and crosses for 11 traits in rice under salt affected soil

Characters	**Sources of variation**					
	Replications	**Treatments**	**Parents**	**Crosses**	**Parents vs Crosses**	**Error**
d.f.	**2**	**30**	**9**	**20**	**1**	**60**
Days to 50% flowering	**0.03**	**52.92****	124.54**	21.84**	29.96**	**3.11**
Plant height (cm)	9.74*	41.69**	87.37**	21.47**	34.95**	2.72
Panicle bearing tillers per plant	0.24	1.42**	0.81**	1.08**	13.62**	0.19
Panicle length (cm)	0.92	2.65**	2.01**	2.96**	2.11	0.54
Flag leaf area (cm^2)	1.89	2.16	5.45**	0.63	3.08	1.46
Grains per panicle	0.39	611.38**	4.77	888.777**	522.94**	4.06
Spikelet fertility (%)	3.43	54.44**	15.91**	56.10**	367.98**	1.81
1000 grain weight	0.05	5.57**	7.30**	0.75*	86.37**	0.38
Biological yield per plant (g)	0.05	202.70**	10.38**	157.87**	2830.10**	2.84
Harvest-index (%)	0.17	31.64**	4.49**	17.75**	553.79**	1.35
Grain yield per plant(g)	0.95	57.56**	1.77*	40.06**	909.86**	0.79

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

Table 2: Estimates of coefficient of variation, heritability, genetic components of variance, degree of dominance and genetic advance for 11 traits in rice under salt affected soil

Character	**Coefficient of variation (%)**		**Heritability (%)**		**Genetic advance**	**Genetic advance in % of mean**
	Genotypic	**Phenotypic**	**Broad sense**	**Narrow sense**		
Days to 50% flowering	15.58	18.70	83.32	34.54	9.51	9.76
Plant height (cm)	12.58	15.28	82.33	12.13	8.49	8.76
Panicle bearing tillers per plant	0.39	0.58	53.67	1.09	1.37	16.93
Panicle length (cm)	0.68	1.23	54.97	9.26	1.61	7.61
Flag leaf area (cm)	0.61	2.08	29.36	0.07	1.11	5.18
Grains per panicle	189.85	193.73	98.00	25.15	36.00	29.38
Spikelet fertility (%)	17.02	18.85	90.25	10.24	10.34	12.45
1000 grain weight(g)	1.86	2.23	83.46	14.13	3.29	15.57
Biological yield per plant (g)	66.15	68.96	95.93	22.44	21.03	47.58
Harvest-index (%)	10.28	11.68	87.97	10.86	7.94	21.26
Grain yield per plant(g)	18.98	19.70	96.01	23.35	11.27	67.32

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