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Study of Genetic Variability for Different Traits in Rice (*Oryza sativa* L.) Germplasm under Saline-Alkaline Soil

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Abstract

Rice *(Oryza sativa* L., 2n=24) is a plant belonging to the family Poaceae (Gramineae). The present investigation was carried out during *Kharif,* 2015 at Research Farm of Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad (UP.), under saline-alkaline condition ((44% ESP, 8.9 Ph, 2.45 dsm^{-1} E.C.). The characters studied were days to 50 per cent flowering, flag leaf area, plant height, panicle bearing tillers per plant, panicle length, spikelet's per panicle, spikelet fertility, test weight, grains per panicle, L/B ratio, biological yield per plant, harvest index and grain yield per plant. The expermental material will be consist of 84 genotypes along with 4 checks (Narendra User 3, CSR 10, CSR 23 and FL 478). The experimental field will be divided in to 10 blocks. In each block, 8 entries will be accommodated along with replicated 4 checks. Each entry will be planted in two rows of three meter length. The spacing between rows and within plants will be 15 cm and 15 cm. The wide range for different characters and comparison of mean of germplasm lines using least significant differences indicated existence of very high degree of variability for all the characters in the genotypes evaluated.

Keywords : *Genetic variability, germplasm, saline-alkaline soil, rice.*

Introduction

Rice is one of the three major food crops of the world and forms the staple diet of about half of the world's population. Asia is the leader in rice production accounting for about 90% of the world production. Above 75% of the world supply is consumed by people in Asian countries and thus, rice is of immense important to food security of Asia. Uttar Pradesh is an important rice growing state in the country. The area and production of rice in the state is about 5.09 million ha. and production of 15.30 million tones, with productivity of 2573 kg/ha. (1).

Genetic variation is the key factor which determines the success of every breeding program. Careful management of this variability and techniques to be employed in each case with clear understanding of the extent and nature of variability leads to crop improvement. The better chances of selecting desired types are based on the fact that how much variability present in any crop concerned. It is the raw material on which selection acts to evolve superior genotypes or varieties in plant breeding programme. The genetic variability for various characters available in the breeding populations or materials is systematically subjected to selection to change the genetic architecture of plant characters and consequently of the plant as a whole to develop improved genotypes having higher economic yield. The variability exploited in breeding programmes is derived from the naturally occurring variants and the wild relatives of crop as well as artificially developed strains and genetic stocks by human-efforts (2). The reservoir of variability for different characters of a plant species resulting from available natural or artificially synthesized variants or strains constitutes its germplasm. Thus, germplasm may include improved strains, primitive cultivars, wild relatives, absolute cultivars, special genetic stocks, seeds, pollen and vegetative parts etc.

Materials and Methods

The expermental material will be consist of 84 genotypes along with 4 checks (Narendra User 3, CSR 10, CSR 23 and FL 478). The experitmental material will be collected from the Department of Genetics & Plant Breeding, N.D. University of Agriculture and Technology, Kumarganj, Faizabad, during *Kharif* 2015. The experimental field will be divided in to 10 blocks. In each block, 8 entries will be accommodated along with replicated 4 checks. Each entry will be planted in two rows of three meter length. The spacing between rows and within plants will be 15 cm and 15 cm. The recommended cultural followed will be followed to raise a good crop. Five competitive plants from each plot were randomly selected for recording observations on all thirteen traits, except days to 50 per cent flowering and grain yield per plant, which was recorded on the plot basis. Averages of the data from the sampled plant of each plot in respect of different characters were used for various statistical analyses. The data were recorded for the following characters: Days to

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Table-1 : Analysis of variance of augmented design for 13 characters in rice genotypes.

S. N.	Characters	Sources of variation		
		Blocks	Checks	Error
		9	3	27
1.	Days to 50% flowering	78.30**	619.89**	1.04
2.	Flag leaf area (cm^2)	8.88*	44.01**	2.48
3.	Plant height (cm)	151.29**	214.88**	1.80
4.	Panicle bearing tillers per plant	9.00**	18.59**	0.38
5.	Panicle length (cm)	3.98**	18.35**	0.68
6.	Spikelet's/panicle	900.68**	10104.87**	168.38
7.	Grains/panicle	786.66**	8946.42**	127.31
8.	Spikelet fertility	75.46*	260.99**	17.39
9.	Biological yield /plant(g)	50.00**	31.95**	2.22
10.	Harvest index (%)	4.69**	1.63	0.70
11.	Test weight(g)	4.56*	4.30	1.53
12.	L/B ratio	0.036	0.88	0.31
13.	Grain yield per plant (g)	7.52**	5.83**	0.30

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

50 per cent flowering, Flag leaf area (cm^2), Plant height (cm), Panicle bearing tillers per plant, Panicle length (cm), Spikelets per panicle, Grains per panicle, Spikelet fertility (%), Biological yield per plant (g), Harvest-index (%),Test weight (g), L/B ratio, Grain yield per plant (g). The analysis of variance for different characters in "Augmented Block Design. To obtain an estimate of experimental error variances for computing least significant differences and comparing means.

Results and Discussion

Analysis of variance : The analysis of variance revealed significant differences among the genotypes for all the thirteen characters, which validated further statistical and genetical analyses (Table-1). The assessment of existing variability in rice genotypes was done by computing means, range and least significant differences.

Genetic divergence analysis : In present study, eighty genotypes and four check varieties of rice were grouped in to ten distinct non overlapping clusters using non-hierarchical Euclidean cluster analysis (Table-2). Cluster VIII, which contained fifteen entries followed by cluster VI having fourteen genotypes, V having twelve genotypes, I and III having ten genotypes, X having eight genotypes, and VII having six genotypes, Clusters IV and IX having four genotypes . Minimum number of genotypes was presented in cluster II with one genotypes. The discrimination of lines into so many discrete clusters suggested presence of high degree of genetic diversity among the genotypes evaluated.

Mean performance of genotypes : In order to evaluate the germplasm collection, the mean performance of eighty rice genotypes and four checks for thirteen characters is presented (Table-2). Very wide range of variation in mean performance of genotypes was observed for all the characters under study. The comparison of mean performance of eighty rice genotypes for thirteen quantitative traits using least significant differences revealed existence of very high level of variability in germplasm collections.

The genotype NDRK 50047 produced highest seed yield per plant (19.29 g) and also showed high mean performance for most of yield components. NDRK 50047 was present in significant for panicle bearing tillers per plant, panicle length, spikelets per panicle, spikelet fertility, biological yield per plant, harvest index, test weight and grains per panicle while, non-significant group for days to 50% flowering. Seven genotypes viz., AT-401, IR12-T-162, NDRK5037, IR-14-T-109, NDRK5005, IR-14-T-144, and Nanabokera possessed higher grain yield per plant statistically to the highest yielding check Narendra Usar 3 constitute significant group for grain yield per plant comprising seven entries.

The second highest yielding genotype AT-401 (18.72g) was also present in significant group for grain yield per plant, grains per panicle, panicle length and biological yield per plant.

Coefficient of variation : The phenotypic and genotypic coefficients of variation were computed to assess the nature and magnitude of existing variability in the germplasm. Wide range of phenotypic and genotypic coefficient of variability was observed for all the for all the traits. The high magnitude of PCV was observed for grains/ panicle while, (<20%) magnitude of PCV was observed for spikelets per panicle and panicle bearing tillers per plant. The moderate estimate of PCV along with GCV was recorded for grain yield per plant, L/B ratio and biological yield per plant grain yield per plant, biological

Table-2 : Range, mean, C.V., heritability, genetic advance, genetic advance as % of mean and least significant differences for 13 characters of rice genotypes.

Characters	Range (Min-Max)	Mean value	Coefficient of variation (%)		C.V. (%)	Heritability (h^2b) (broad sense)	Genetic advance	Genetic advance as % of mean	Range of parameters						
			PCV (%)	GCV (%)					LSD_1 5%	LSD_2 5%	LSD_3 5%	LSD_4 5%	LSD_2 5%	LSD_3 5%	LSD_4 5%
Days to 50% flowering	84.22-109.22	93.73	6.64	6.55	7.77	97	12.47	13.32	0.93	2.95	3.30	2.45	2.95	3.30	2.45
Flag leaf area (cm^2)	20.23-30.93	25.08	11.12	9.17	12.19	68	3.90	15.58	1.44	4.57	5.11	3.79	4.57	5.11	3.79
Plant height (cm)	54.32-106.29	84.94	9.66	9.53	11.33	97	16.49	19.37	1.23	3.90	4.36	3.23	3.90	4.36	3.23
Panicle bearing tillers per plant	3.82-24.03	9.87	23.77	22.94	28.44	93	4.54	45.60	0.57	1.80	2.01	1.49	1.80	2.01	1.49
Panicle length (cm)	18.61-29.92	23.47	7.33	6.43	9.49	76	2.73	11.62	0.76	2.40	2.69	1.99	2.40	2.69	1.99
Spikelet's per panicle	39.10-199.10	116.45	25.54	22.95	29.51	80	49.24	42.50	11.90	37.65	42.09	31.22	37.65	42.09	31.22
Grains/Panicle	35.82-185.07	101.81	28.42	26.16	32.93	84	50.39	49.60	10.35	32.74	36.60	27.14	32.74	36.60	27.14
Spikelet's/Fertility	70.45-97.53	86.96	6.44	4.31	6.96	44	5.18	5.95	3.82	12.10	13.53	10.03	12.10	13.53	10.03
Biological yield (g)	18.60-50.56	31.72	19.31	18.73	23.73	94	11.92	37.44	1.36	4.32	4.83	3.58	4.32	4.83	3.58
Harvest index %	36.27-44.83	40.03	4.81	4.33	5.55	81	3.22	8.04	0.77	2.43	2.72	2.02	2.43	2.72	2.02
Test weight (g)	21.85-30.53	26.17	6.29	4.14	6.98	43	1.47	5.62	1.13	3.60	4.02	2.98	3.60	4.02	2.98
L/B Ratio	2.03-83.00	2.76	18.63	-7.86	17.64	-17	-0.18	-6.83	0.51	1.62	1.81	1.34	1.62	1.81	1.34
Grain yield per plant (g)	7.16-19.29	12.68	19.70	19.23	24.02	95	4.93	38.66	0.50	1.59	1.78	1.32	1.59	1.78	1.32

Where, @ indicates negative estimates
LSD_1 = Least significant difference between two check means.
LSD_2 = Least significant difference between adjusted mean of two genotypes in same block.
LSD_3 = Least significant difference between adjusted mean of two genotypes in different block.
LSD_4 = Least significant difference between adjusted mean of genotype and check mean.
PCV = Phenotypic coefficient of variation, GVC = Genotypic coefficient of variation

and showed much differences between PCV and GCV (Table-2). This indicated greater scope of improvement through selection in the environment which showed high GCV and PCV values. Lower estimate of PCV and GCV were recorded for harvest index, test weight, plant height and days to 50% flowering. The existence of high variability for grain yield in rice has also been reported earlier by (3,4,5,6).

Conclusions

The wide range for different characters and comparison of mean of germplasm lines using least significant differences indicated existence of very high degree of variability for all the characters in the genotypes evaluated. The genotypes NDRK 50047, AT-401, IR-12-T-162, NDRK 5037 and IR-14-T-109 produced high grain yield per plant and these five lines constituted significant group for higher grain yield per plant. The above mentioned genotypes also showed high to very high mean performance for several other yield components.

The most desirable genotypes for characters other than grain yield were NDRK5037, IR6527, NDRK50064, NDR-502, NDRK5019 for early days to 50 per cent flowering; IR9897B, NDRK5024, NDRK5075, IR55179, IR72579 for grater flag leaf area; NDRK50060, IR11-T230, IR11T208, NDRK50047, IR65427 for short plant height; Narendra-2009, IR-14T104, NDRK5037, NDRK50060, NDRK50058 for highest panicle bearing tillers per plant; IR-14T104, IR-14T-144, NDRK50069, NDRK50048, NDR-502 for longer panicle length; IR11T213, IR76397, NDRK50014, IR141T26, NDRK5014 for spikelets per panicle; NDRK 50069, Narendra 2009, NDRK5032, IR65923-B-3, NDRK50063 for spikelet fertility; NDRK50070, IR14T109, IR12T162, AT401, NDRK 5001 for biological yield per plant; IR74095, NDRK 50069, NDRK-5005, IR14T107, NDRK 5037 for harvest index; NDRK50047 AT401, IR14T109, NDRK5005, NDRK5001 for test weight; jaya, IR65923, Narendra2009, NDRK5075, LD-183-B3 for L/B ratio and NDRK50014, IR11T213, NDRK5014, IR14T126 for grains per panicle.

These superior lines identified for grain yield and other characters may be use as donor parents in hybridization program me for improving the characters for which they showed high mean performance.

The grain yield per plant exhibited a very strong positive association with biological yield per

Table-3 : Most desirable rice genotypes identified for 13 characters.

S. N.	Characters	Genotypes
1.	Days to 50% flowering	NDRK5037, IR-6527, NDRK50064, NDR-502, NDRK5019
2.	Flag leaf area (cm^2)	IR9897-B, IR9897-B, NDRK-5024, NDRK-5075, IR55179
3.	Plant height (cm)	IR65427, NDRK-50070, IR11T-208, IR11T-230, NDRK50060
4.	Panicle bearing tillers per plant	Narendra 2009, IR 14T-104, NDRK 5037, NDRK 50060, IR-86376,
5.	Panicle length (cm)	IR14T 104, IR14T144, NDRK50069, NDRK 50048, NDR-502
6.	Spikelet's per panicle	NDRK50014, IR11T213, NDRK5014, NDRK5032, IR141T26
7.	Grains per panicle	NDRK50014, IR11T213, NDRK5014, NDRK5032, IR14T126
8.	Spikelet fertility (%)	NDRK50069, Narendra2009, NDRK5032, IR-65923-B-3, NDRK 50063
9.	Biological yield (g)	NDRK50047, IR14T109, IR12T162, AT401, NDRK5001
10.	Harvest index %	NDRK-50069, IR-74095, NDRK-5005, IR14T107, NDRK 5037
11.	Test weight (g)	NDRK50047, AT401, IR14T109, NDRK5005, IR-9749-2B-29
12.	L/B ratio	Jaya, IR 65923-B-3, Narendra 2009, NDRK 5075, LD 183-B-3
13.	Grain yield per plant (g)	NDRK 50070, AT401, IR-12T162, NDRK5037, IR-14T109

Table-4 : Clustering pattern of 84 rice genotypes including checks on the basis of non-hierarchical Euclidean cluster analysis of 13 characters.

Cluster No.	Number of genotypes	Genotypes
I	10	IR-8-117232, NDRK-50046, IR12T 147, NDRK50070, IR86376, LD183-3, NDRK 5072, NDRK 50058, IR55179, IR8673
II	1	Narendra 2009
III	10	NDRK-5024, NDRK5049, CSR10(c) ,NDRK 5095, IR-65427, IR13T148, NDRK 5001, IR11T 183, NDRK5037, IR11T230
IV	4	IR-9418, IR65423, IR11T 208, NDRK 50060,
V	12	IR14T-107, NDRK50069, IR57499-2B-29, NDRK-66, NDRK5005, IR74095, NDRK-50048, Nanabokera, Narendra usar-3 (c) IR14 T128, IR14T144, NDRK 510
VI	14	NDRK-50063, IR14T117, IR-870-B-B-2, IR-76397, NDRK-50014, IR11T-197, IR12T 2010, NDRK-5014, IR14T120, FL478(c), NDRK50051, NDRK-50051, NDRK-5032, IR11T 213, IR14T 126
VII	6	IR14T 109, IR12T-162, IR11T-189, IR65923-B-3, NDRK 50047, AT401
VIII	15	IR14T-121, NDRK50059, IR14T113, IR14T105, NDRK50064, CSR23(c) IR13T147, IR8418, NDRK5019, IR12T 193, NDR-502, IR14T102, IR12T195, IR13T-144, NDRK50053,
IX	4	Jaya, IR86341-2B, IR77664, IR12T266,
X	8	CSR-36, IR9897-B, IR72579, IR11-T171, Kalanamak, IR11T-205, IR14T104, NDRK-5075

plant, test weight, grains per panicle, spikelet per panicle and spikelet fertility.

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