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Genetic variability, heritability and genetic advance estimates of rice (*Oryza sativa* L.) strains for certain physiological traits in NEP zone under sodicity and normal soil

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Abstract

Genetic variability, heritability and genetic advance were studied in seventy four diverse rice genotypes including four checks at three different farm with Sodicity and normal levels i.e.pH-8.6 (Student instructional farm), 9.5 (Main experiment station) and 7.8 (Crop Research Station Masodha) during kharif 2020 following randomized complete block design. A collection of diverse genotypes were evaluated for certain physiological traits viz., days to 50% flowering, plant height (cm), flag leaf area (cm), biological yield per plant(g), harvest index%, chlorophyll content, leaf nitrogen, leaf temperature and grain yield per plant (g.). The analysis of variance revealed highly significant differences among all the genotypes for all the traits. The estimates of genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) indicated the presence of considerable amount variability for all the traits at three locations. In general the estimates of phenotypic coefficient of variability were higher than genotypic coefficient of variability. A high estimate of heritability was found for all parameter. The presence of high heritability coupled with high genetic advance in majority of the traits indicated the preponderance of additive gene action. So, these traits can be improved through direct selection. The moderate broad sense heritability with low genetic advance in percent of means were observed for leaf temperature indicating presence of non-additive gene action suggesting heterosis breeding may be useful for rice improvement in sodic soil. The overall result indicates the presence of enough variability for development of improved rice varieties and these traits can be used for selection further the experiment should be repeated by integrating more number of important traits in representative sodic areas of the country.

Keywords: Genotype, rice, variability, heritability, genetic advance, GCV, PCV

Introduction

Rice which is belongs to the family Poaceae (Gramineae) having the diploid chromosome $2n=24$. The cultivated rice belongs to genus *Oryza* and there are about 24 species of rice distributed in tropical, sub-tropical and warm temperate regions of the world. Out of these, most commonly cultivated species are *Oryza sativa* and *Oryza glaberrima*. The *Oryza sativa* is divided into three sub-species, namely, Indica, Japonica and Javanica. Rice is one of the cereal crops of great significance in India and primary staple food for huge population in Asia, Africa and Latin America. More than 90 per cent of the world's rice is grown and consumed in Asia, known as rice bowl of the world, where 60 per cent of the earth's people and two third of world's poor live. Rice is therefore, on the frontline in the fight against world's hunger and poverty. It's being the staple food for more than 70 per cent of our national population and source of livelihood for 120 to 150 million rural households, is backbone of the Indian Agriculture. At the time of tillering the crop requires a high temperature for growth. Temperature requirement for blooming ranges from 26.5 to 29.0°C. At the time of ripening the temperature should be between 20 to 25 °C. Its needs a hot and humid climate. Rice area with salt problem in state is estimated to be $\leq 2\%$ in land salinity areas are mainly concentrated in Raebareli, Sultanpur, Ayodhya, Azamgarh, Lucknow, Unnao and Pratapgarh district. Salinity stress is one of the major abiotic constraints which limits rice production and 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. Bacterial blight (BB) caused by the *Xanthomonas oryzae* pv. *oryzae* (Xoo) pathogen is a chief factor limiting rice

productivity worldwide because of its high epidemic potential (Sharma *et al.*, 2017). As a vascular disease that results in systemic infection, BB produces tannish grey to white lesions along leaf veins (Mew 1987, Mew *et al.*, 1993, Nino-Liu *et al.*, 2006). Most commonly, plants are affected at the maximum tillering stage. Yields are reduced by 20–30%. Infection at the tillering stage can engender total crop losses (Mew *et al.*, 1993; Busungu, 2017). Developing resistant cultivars is generally regarded as the most effective and economical means of controlling this disease (Guo *et al.*, 2005, Mew *et al.*, 1993, Khush, 2013). India's rice product is estimated at record 102.36 million tonnes in the kharif season of 2020 crop time on the reverse of appropriate thunderstorm rains and acreage, consistent with government facts. Rice product stood at 101.98 million tonnes within the kharif season of the 2019 crop time. The Union Agriculture Ministry released the first strengthen estimates of made of important kharif crops for 2020. As in line with the facts, the entire food grains affair inside the kharif season of 2020 crop time is anticipated at record 144.52 million tonnes as against 143.38 million tonnes within the former time. It is crucial to enhance rice tolerance to salinity stress to enable this stable crop to provide enough food for rice consuming communities. Although some success has been reported for enhanced salinity stress tolerance in rice, the achievement so far are quite modest. (Hoang *et al.*, 2016) [13]. The present study was undertaken to evaluate selected rice genotypes for biotic and abiotic stresses on the basis of different morphological characters, yield and yield components under field conditions.

Material and Method

Field experiments were conducted during *Kharif* season 2020 at three farms *viz*; Student Instructional Farm (pH=8.6), Main Experiment Station (pH=9.5) and Crop Research Station Masodha (pH= 7.8), Ayodhya. This research article is based on pooled data from all the environments. All the genotypes were sown in Randomized Complete Block Design with three replications plot size is 5 m length (inter-and intra-row spacing 20 cm and 15 cm, respectively). The experimental material of the study was comprised of seventy four diverse genotypes collected from different agro-climatic zones. These genotypes were procured from germplasm lines available in rice Section of the Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology Kumarganj, Ayodhya. The observations, *viz.*, days to 50% flowering, plant height (cm), flag leaf area (cm²), chlorophyll content, leaf nitrogen, leaf temperature (SPAD Value), biological yield per plant (g), harvest-index (%) and grain yield per plant (g), were recorded on the basis of five randomly selected competitive plants in each plot. The fertilizers were applied @120 kg nitrogen, 60 kg phosphorus and 60 kg potash per ha 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. The mean performance of individual genotype over two years was pooled and employed for statistical analysis. Biometrical analysis is done with Genetic variability parameter *viz.*, mean, variance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (Burton and De Vane, 1953), heritability (h²) (Hanson *et al.*, 1956) [8] and Genetic advance (GA) (Johnson *et al.*, 1955) [6] among

characters were calculated by following the standard procedures with the help of MSTATC, Statistica 2 and Genres software's.

Result and Discussion

The analysis of variance for complete randomized block design for different characters in each environment is given in Table 1, 2 highly significant differences were observed among the genotypes for nine characters in three different location mean sum of squares due to treatments were highly significant for all the characters indicating the existence of sufficient variability in the materials at both research farm of different pH level. These findings are in conformity with Panwar *et al.*, (2007) [10] and Konate *et al.*, (2016) [9]. The variability parameters obtained from the pooled data are presented in Table 2. At different environment the highest variability (genotypic and phenotypic) was exhibited in plant height (245.36 and 263.49). High variability plant height was also reported by Sumanth *et al.*, (2017) [4]. GCV and PCV more than 20% considered as high, whereas values less than 10% are considered to be low and values between 10% and 20% being considered to be moderate. According to this, most the traits have high to intermediate GCV and PCV. This indicated that these traits could be improved for breeding high yielding rice varieties through selection and hybridization. According to Johnson, Robinson and Comstock (1955) [6], broad sense heritability classified as low (60%). This shows most of the traits studied can be easily improved through selection. At three farm (Student Instructional Farm, Main Experiment Station and Crop Research Station) all traits found high heritability value (>75%). The medium heritability (>50-<75%) in panicle length, leaf temperature (61.95%) and leaf nitrogen showed the more influence of environment on this trait. Therefore, direct selection for this trait is not effective. Since heritability do not always indicate genetic gain, heritability coupled with genetic advance is more effective for selection. Genetic advance indicates the expected progress as the result of selection Pratap *et al.*, (2014) [3]. It used to estimate the type of gene action in polygenetic traits. Genetic advance as percent of mean classified as low (20%). at pH-8.6-9.5 Sodcity and 7.8 Normal level in, it ranges from 9.80 leaf nitrogen to 62.47%. At both sodicity and normal levels high heritability and high genetic advance were seen in most of the traits including grain yield (Table 2) which indicated these traits were less influenced by the environment, governed by additive gene action and can easily be selected through phenotypic selection. High heritability values indicate though the character is least influenced by environmental factors yet the selection for improvement of such characters may not be useful (Singh *et al.*, 2018) [11]. At both sodicity and normal soil days to 50% flowering has high heritability and moderate genetic advance, indicating that this character is governed by both additive and non-additive gene action. This showed there is a possibility of direct selection for this character. So, heterosis breeding could be used for such kind of traits. The genetic variation result showed that phenotypic coefficient of variation (PCV) was relatively higher than genotypic efficient of variation (GCV). This result revealed that the influence of environment on phenotypic expression of each trait (North S.2013) but the difference between genotypic and phenotypic coefficient of variation is very little for all studied trait. The broad sense heritability in the studied traits ranged from 61.40% to 978.35% (Table 2).

Table 1: Pooled analysis of variance for nine characters of seventy four genotypes of rice over six environments

Source of variation	DF	Days to 50% flowering	Plant height(cm)	Flag leaf area (cm ²)	Biological yield/plant(g)	Harvest index (%)	Chlorophyll content	Leaf nitrogen	Leaf temperature	Grains yield per plant(g)
Replication	2	92.45	37.87	2.00	3.12	1.32	0.05	0.0250	1.66	0.22
Treatment	73	1299.98**	3669.49**	672.54**	1526.06**	288.98**	95.08**	0.0683**	34.38**	203.02**
Error	886	18.45	17.83	0.91	2.02	2.21	0.17	0.0004	1.80	0.25

Table 2: Range, grand mean, variability, heritability in broad sense and genetic advance in percent of mean for nine characters of seventy four genotypes of rice over six environments

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to 50% flowering	97.52	75.33	119.04	65.26	80.88	80.69	14.95	15.02	8.12	9.04
Plant height(cm)	98.21	64.57	135.07	245.36	263.49	93.12	31.14	30.84	15.51	16.07
Flag leaf area (cm ²)	22.14	9.98	37.35	54.78	55.70	98.35	15.12	62.47	30.58	30.84
Biological yield /plant(g)	32.69	17.31	55.01	100.72	103.12	97.68	20.43	52.88	25.97	26.28
Harvest index%	35.41	22.60	41.23	23.33	25.77	90.51	9.47	24.82	12.66	13.31
Chlorophyll content	9.54	5.40	14.57	0.01	0.01	94.70	0.17	34.22	17.07	17.54
Leaf nitrogen	0.45	0.35	0.65	3.96	6.45	61.40	3.21	9.80	6.07	7.75
Leaf temperature	31.86	28.77	36.00	2.34	3.78	61.95	2.48	11.66	7.19	9.14
Grains yield per plant	11.55	5.97	19.84	10.95	11.79	92.89	6.57	44.94	22.63	23.48

Conclusion

In the present experiment, considering the evaluation of important variability parameters i.e. Coefficient of variation, heritability and genetic advance together, it was revealed that flag leaf area, biological yield per plant and grain yield are most important characters at both Sodicy and normal levels because they have high heritability coupled with high genetic advance. This indicates involvement of additive gene in controlling gene responsible for these traits. Therefore, these characters could be improved through selection in segregating generations. The overall result showed the presence of adequate variability in the genotypes studied. This variation could be effectively manipulated using appropriate breeding techniques and program to develop improved varieties. High estimate of heritability and genetic advance were observed in most of the traits at both farm of two different Sodicy and normal soil indicating the predominance of additive gene action and the possibility of direct selection through these traits.

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