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ESTIMATES OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD CONTRIBUTING AND QUALITY TRAITS IN ADVANCE BREEDING LINES OF RICE (*ORYZA SATIVA* L.)

[a*]Mahendar Singh Bhinda, [b]Karnwal, M.K. and [c]Mahendra Kumar Choudhary

[a, b]Department of Genetics and Plant breeding, G. B. Pant University of Agriculture and Technology, Pantnagar-263145, U. S. Nagar, Uttarakhand
[c]Department of Genetics & Plant Breeding, S.D. Agril. University, Dantiwada-385 506 (Gujarat)
*corresponding author email: singhmahen14@gmail.com

ABSTRACT
The present investigation was carried out with objective to obtain information on genetic variability, heritability and genetic advance for Yield Contributing and Quality Traits in Advance Breeding Lines of Rice (*Oryza sativa* L.) The analysis of variance revealed significant differences among all the genotypes for all the 15 characters studied. High value of phenotypic coefficient of variability (PCV) was observed than genotypic coefficient of variability (GCV) for all the characters. Alkali spreading value exhibited highest GCV (19.44%) and PCV (21.07%) followed by filled grains per panicle (GCV 14.83% and PCV 19.90%). The highest broad sense heritability was estimated for gel-consistency (87.84%) followed by alkali spreading value (85.08%). Whereas the highest value of genetic advance was recorded for characters namely filled grains per panicle (41.01) and number of grains per panicle (38.26). High heritability coupled with high genetic advance was reported for gel-consistency, plant height, filled grains per panicle, number of grains per panicle and days to 50% flowering.

KEYWORDS: Genetic variability, GCV, PCV, Heritability, Genetic advance, Rice.

INTRODUCTION

Rice (*Oryza sativa* L.) (2n=24) belonging to family Poaceae and subfamily Orezoidea deserves a special status among cereals as world's most important wetland crop. There are two species namely, *Oryza sativa* and *O. glaberrima*, are cultivated while other twenty-two species are wild. *The Oryza sativa*; common Asian rice found in most producing countries which originated from the Eastern region of the foot hills of Himalayas. The *Oryza glaberrima*: a cultivated annual species was originated from West Africa and covering a large region extending from the central Delta of the Niger River to Senegal. About 20% of the total calorie supply worldwide comes from rice. More than 90% rice of world is produced and consumed in South and South East Asia, where approximately 60% of the population of the world is living. In India, it is staple food for more than 65 percent of the people. It provides about 29.4 per cent of total calories/capita/day in Asian countries (FAO, 2006). In India it is grown on 43.4 million hectares of land and producing approximately 106.3 million tons rice grain with an average productivity of 2.42 tons per hectare (Anonymous, 2013-14). The demand of rice is continuously increasing due to unabated growth of population. To cope up with the ever increasing population and self-sufficiency in rice production as well as for maintaining price stability there is need for new genes and improved genetic recombinants.

The world population is expected to reach eight billion by 2030 and rice production must increase by 50% in order to meet the growing demand (Khush and Brar, 2002). It is important to evaluate the promising rice germplasm along with their hybrids for morphological characters and yield. A paradigm shift in the rice (*Oryza sativa* L.) breeding strategies from quantity centered approach to quality oriented effort was inevitable, since India has not only become self sufficient in food grain production but also is the second largest exporter of quality rice in the world (Sreedhar *et al*.,2005). Improvement in grain quality that does not lower yield is the need of hour at present context in order to benefit all rice grower and consumers. Like grain yield, quality is not easily amenable to selection due to its complex nature. Lack of clear cut perception regarding the component traits of good quality rice is one of the important reasons for the tardy progress in breeding for quality rice varieties. A systematic and efficient breeding program involves the steps like creation of genetic variation, selection practices and utilization of selected genotypes to develop promising varieties and all of these steps involves biometrical and multivariate analyses (Chakravorty *et al.,* 2013).

The genetic facts are inferred from the observations on phenotypes. Since phenotype is determined by the joint effect of genotype and environment, non genetic part exerts large influence on genetic variability. The exploitable variability is therefore, required to be judged through various genetic parameters like heritability, genetic advance and others.The information on genetic variation, heritability and genetic advance help to predict the genetic gain that could be obtained in later generations. Such a study appears to be extremely necessary for planning genetic improvement

in rice. Estimation of heritability measures the flow of information for traits from parents to offspring. High heritability values indicate that the traits under study are less influenced by environment in their expression. The genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of better selection value (Akinwale *et al.*, 2011). Estimates of heritability and genetic advance will help in knowing the nature of gene action affecting the concerned trait. It also indicates the scope of genetic improvement for these traits through selection. High heritability with high genetic advance exhibited by the traits, controlled by additive gene action, (Panse *et al.,* 1957; Singh *et al.*, 2013) and can be improved through simple or progeny selection methods. Thus, selection for the traits having high heritability associated with high genetic advance leads to accumulate more additive genes. It can enhance the opportunities for further improvements of their performance. On the other hand, estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) also play vital role in selection practice for an effective rice breeding program.

The yield is a complex character which is controlled by association of number of components most of which are under polygenic control. Thus the identification of important components and information about their association with yield and other traits are very useful for developing efficient breeding strategy for evolving high yielding varieties. Thus, the yield component breeding to increase grain yield would be most effective.

Improvement in grain quality that does not lower yield is the need of hour at present context in order to benefit all rice growers and consumers. Breeding rice varieties with preferred grain quality features has become second most important objective next to yield. Rice quality comes from a polygenic group of traits that are affected by environmental factors, crop management and the resulting interactions among these. As unattractive grain characters and unsatisfactory cooking quality hampers the acceptance and spread of the modern high yielding varieties, quality improvement needs special emphasis since last decades. Like grain yield, quality is not easily amenable to selection due to its complex nature. Lack of clear cut perception regarding the component traits of good quality rice is one of the important reasons for tardy progress in breeding for quality rice varieties. With increase in yield, there is also a need to look into the quality aspects to have a better consumer acceptance, which determine the profit margin of rice growers which in turn dictates the export quality and foreign exchange in India. Grain quality characteristics are very important in rice breeding as it is predominantly consumed as a whole grain.

Thus, knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative character like yield, its components and quality traits is essential for effecting genetic improvement. A critical analysis of the genetic variability is a prerequisite for initiating any crop improvement programme and for adopting of appropriate selection techniques.

MATERIALS & METHODS

The present investigation "Estimates of Genetic Variability, Heritability and Genetic Advance For Yield Contributing and Quality Traits in Advance Breeding Lines of Rice (*Oryza sativa* L.)'' was carried out during *kharif* season 2014 at the N. E. Borlaug, Crop Research Centre (CRC) of G. B. Pant University of Agriculture and Technology, Pantnagar. A series of quality test also conducted in Rice Breeding Laboratory of Department of Genetics and Plant Breeding, College of Agriculture. The Experimental material for the present investigation comprised of 42 genotypes including three prominent checks. Each genotype Considered as one treatment, the experimental material was planted in Randomized Complete Block Design with three replications in main plots in the month of June, 2014. Each plot had 5m x 1.6m (8m^2) area and 45 cm. apart. Twenty seven days old seedlings raised in nursery were transplanted at spacing of 20 cm. x 15 cm. The recommended package of agronomic practice was followed to raise a healthy crop. The observations were recorded on five randomly selected competitive plants from each plot in all replications for plant height, panicle length, number of panicles per plant, number of grains per panicle, filled grains per panicle, whereas, on the whole plot basis the observations were recorded for days to 50 per cent flowering, days to maturity and yield per plot, and on the composite sample basis 1000 grain weight.

The mean data after computing for each character was subjected to standard method of analysis of variance following genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Heritability in board sense (h2), genetic advance as percent of mean were estimated by the formula as suggested.

RESULTS & DISCUSSION
Analysis of variance

Analysis of variance revealed that, the mean square among the genotypes for all the fifteen characters namely, day to 50% flowering, plant height (cm), panicle length (cm), number of panicles per plant, number of grains per panicle, filled grains per panicle, grain length (mm), grain breadth (mm), L/B ratio, 1000 grain weight (gm), alkali spreading value, amylose content, gel-consistency, days to maturity and yield per plot (kg) were found significant. These results indicated the presence of sufficient variability among the genotypes for all the characters studied, providing greater scope for further improvement (Table 1).

Coefficient of variability

The estimated values of phenotypic coefficient of variation (PCV) were greater than genotypic coefficient of variation (GCV) for all the characters studied (Table 2), indicating the influence of environmental factors on the expression of these traits studied which are in agreement with the findings of Paikhomba *et al.* (2014).

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TABLE 1: Analysis of variance for grain yield and other characters in advance breeding lines of rice

Sl. No.	Characters	Replication (df = 2)	Treatment (df = 41)	Error (df = 82)
1.	Days to 50% flowering	4.068	120.952***	15.137
2.	Plant height(cm)	927.317	335.557***	18.865
3.	Panicle length(cm)	57.705	27.524**	5.984
4.	Number of panicles per plant	11.664	6.849**	1.757
5.	Number of grains per panicle	837.607	2802.947**	711.676
6.	Filled grains per panicle	417.151	2.712.743**	571.435
7.	Grain length(mm)	1.322	0.639**	0.040
8.	Grain breadth(mm)	0.677	0.123**	0.022
9.	L/B ratio	0.722	0.516**	0.032
10.	1000 grain weight(gm)	52.039	13.582**	4.086
11.	Alkali Spreading Value	5.979	3.346**	0.185
12.	Amylose Content	14.842	2.003**	0.967
13.	Gel-consistency	275.024	263.862***	11.634
14.	Days to maturity	99.460	126.670**	29.021
15.	Grain yield per plot(kg)	0.203	0.492**	0.051

* and ** = Significant at 5% and 1% level, respectively

TABLE 2: Range, General Mean (GM), Standard error mean (SEm) and Variability parameters in advance breeding lines of rice

Character	Range	GM	SEm±	PCV(%)	GCV(%)	h^2 (%)	G_A	G_A As % of mean
Day To 50% Flowering	78.33 - 110.00	100.770	2.246	7.046	5.894	69.972	10.234	10.156
Plant Height(cm)	67.00 – 132.00	89.541	2.507	12.458	11.475	84.839	19.495	21.772
Panicle length (cm)	21.77 – 33.43	28.774	1.412	12.610	9.312	54.542	4.076	14.167
No. of panicles per plant	8.20 - 15.67	12.516	0.765	14.849	10.409	49.139	1.881	15.031
No. of grains per panicle	140.00 – 274.00	206.286	15.402	18.195	12.799	49.483	18.259	18.547
Filled grains per panicle	125.00 – 246.67	180.111	13.801	19.904	14.833	55.537	41.015	22.272
Grain length (mm)	4.80 – 6.93	5.967	0.115	8.197	7.489	83.478	0.841	14.096
Grain width (mm)	1.63 – 2.50	1.930	0.086	12.228	9.508	60.452	0.294	15.228
L/B ratio	1.92 - 3.79	3.140	0.103	13.994	12.790	83.531	0.756	24.080
1000 grain weight(gm)	21.76 - 30.40	26.135	1.167	10.303	6.808	43.655	2.422	9.266
Alkali spreading value	3.50 - 6.83	5.281	0.248	21.071	19.437	85.087	1.951	36.934
Amylose content	19.21 - 22.44	20.940	0.568	5.470	2.807	26.335	0.621	2.967
Gel-consistency	52.67 - 85.33	71.262	1.969	13.728	12.867	87.845	17.704	24.843
Days to Maturity	112.00 - 144.67	133.706	3.111	5.869	4.267	52.865	8.545	6.391
Grain Yield per plot(kg)	2.44 - 4.32	3.480	0.130	12.775	11.021	74.430	0.682	19.588

Whereas, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h^2 = Heritability, G_A = Genetic advance and
G_A (%) = Genetic advance as % of mean.

The character alkali spreading value exhibited highest phenotypic coefficient of variation (21.07) followed by number of filled grains per panicle (19.90), number of grains per panicle (18.19), and number of panicles per plant (14.85), indicating that these characters are much influence by the environment. Whereas, low phenotypic coefficient of variation value estimate for amylose content (5.47), days to maturity (5.87), days to 50% flowering (7.05) and kernel length (8.19).

The character alkali spreading value exhibited highest genotypic coefficient of variation (19.44) followed by number of filled grains per panicle (14.83), gel-consistency (12.87), number of grains per panicle (12.79), L/B ratio (12.79), plant height (11.48) and grain yield per plot (11.02). The small value of GCV was estimated for amylose content (2.81), days to maturity (4.27) and days to 50 % flowering (5.89). Similar findings of PCV and GCV have been reported to days to 50% flowering, amylose contents and grain yield per plant by Vivek *et al.* (2004), Mall *et al.* (2005) and Kumar *et al.* (2007).

Heritability

The heritability refers to as an index of transmissibility, to measure the genetic relationship between the parents and their offspring. Heritability indicates as to how much emphasis should be placed in for selection of a particular trait. The estimate of heritability and expected genetic advance are presented in Table 2.

Highest estimated heritability (broad sense) values was observed for gel consistency (87.84) followed by alkali spreading value (85.09), plant height (84.84), L/B ratio (83.53), grain length (83.48), yield per plot (74.43), days to 50% flowering(69.97). Moderate estimate of heritability was observed for grain breadth (60.45) followed by filled grain per panicle (55.54), panicle length (54.54), days to maturity (52.86), number of grains per panicle (49.48), number of panicles per plant (49.14) and 1000 grain weight (43.65). The lowest estimate of heritability was recorded for amylose content (26.34).

Genetic advance

The estimates of genetic advance as per cent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. Genetic advance denotes the improvement in the genotypic value of the new population over the original population. The genetic advance indicates the expected genetic progress for a particular trait under a selection cycle and measures the extent of its stability under selection pressure.

The genetic advance was highest for number of filled grains per panicle (41.01) followed by number of grains per panicle (38.26), plant height (19.49), gel consistency (17.70), days to 50% flowering (10.23) and days to maturity (8.54). Low genetic advance was expressed in grain breadth (0.29) followed by amylose content (0.62), grain yield per plot (0.68), L/B ratio (0.76), and grain length (0.84) (Table 2). Both heritability estimates and genetic advance were observed higher for gel consistency, plant height, days to 50% flowering, filled grains per panicle and number of grains per panicle. Based on these results, it is suggested that the high heritability is most likely due to additive gene effects and selection may be effective. The results are in accordance with reports of Mall *et al.* (2005), Dhanwani *et al.* (2013) and Yadav (2000).

Number of panicles per plant and amylose content showed low heritability as well as low genetic advance , it indicated that these characters are highly influenced by environmental factors. Therefore selection would be ineffective. In the present investigation, grain yield per plot, kernel length, L/B ratio and alkali spreading values exhibited high heritability but low genetic advance which indicated that these traits are governed by non-additive gene action and phenotypic selection may not be rewarding. It also indicates greater role of non-additive gene action in their inheritance suggesting heterosis breeding could be useful for improving these traits.

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