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Estimation of genetic parameter for yield components and quality traits in Rice (*Oryza sativa* L.)

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Abstract

The experiment was conducted to assess genetic variability, heritability and genetic advance for yield components and quality parameters among thirty aromatic rice genotypes. High PCV and GCV for Grain weight per plant, days to 50% flowering, tillers per plant, number of grains per panicle, grain weight per panicle, breadth increase ratio after cooking, kernel breadth after cooking, L:B ratio and water absorb by 10 g kernel suggested ample scope of selection for these traits. In this study, preponderance of additive genetic control was revealed as high heritability and high genetic advance were observed for grain yield along with 18 yield components and quality characters. SKG 2017-51 was exhibited high mean values for quality characters along with dwarfness, high 100 grain weight and 100 kernel weight, suggesting its use in future breeding programme as a donor. SKG 2017-84, SKG 2017-78, SKG 2017-81 and SKG 2017-85 were also identified as donor for high grain weight per plant, high hulling (%), minimum kernel breadth before cooking (fine grain) and high tillers per plant, respectively.

Keywords: Paddy, *Oryza sativa* L., Variability, yield, quality

Introduction

Rice occupies about 23.3% of gross cropped area, contributing 43% of total food grain production and 46% of the total cereal production of the country, which leads India to second position in production next to China. The genetic architecture of genotypes provides basis to formulate efficient breeding methodology. Selection based on crop yield is often a paradox in breeding programmes because yield is a complex polygenically inherited character, influenced by its component traits. Similarly, Rice quality is also a complex trait comprising many physicochemical characteristics. Consumers prefer rice based on their own concept of quality on the grain appearance, size and shape of the grain and behaviour upon cooking. Thus, grain size and shape are the first criteria for rice quality that breeders consider in developing new varieties. Preferences for grain size and shape vary with consumers as some ethnic groups prefer short bold grains, while medium and long slender grains are preferred by others. The cooking and eating qualities of rice are valuable properties, especially in Asia, where it is the most important food. However, the cooking quality preferences are known to vary with in the country, within the ethnic groups, from one country to another and within different geographical regions.

Rice improvement projects aim at the development of high yielding rice cultivars along with quality as per consumer preferences. Identification of better genotypes with desirable traits and their subsequent use in breeding programme and establishment of suitable selection criterion can helpful for successful varietal improvement programme. Therefore, development of high-yielding varieties requires through knowledge of the existing genetic variation for yield and its components. Genetic Variability facilitates genotypes with ability to adapt according to the conditions prevailing. The extent of genetic variability is considered as an important factor and a must pre-requisite for a successful hybridization programme (Nakusani *et al.* 2013) [1]. This genetic variation is the source which is exploited to improve a species and as result new efficient cultivars are achieved. In this regard, it is necessary to survey the available useful variability and nature of association among the various plant characters in the basic material.

In view of the above perspectives, the present investigation was taken up to assess genetic variability for various components of grain yield and quality to provide a basis for selection and yield improvement in basmati rice.

Materials and Methods

The experimental farm of Gurukul Narsan is situated in the foothills of Shivalik range of Himalaya and falls in the humid sub-tropical climate Zone. The experiment was laid out at Research farm of R.M.P. P.G. College, Gurukul Narsan, Haridwar (Uttarakhand) with thirty improved genotypes of aromatic rice in Randomized complete block design with three replications to assess the genetic parameters for yield components and quality traits. The plot size allotted to each genotype was 2m² and spacing was kept at 20x15 cm. The observations were recorded either plot basis or on a random sample of 10 plants from each plot for 22 quantitative characters. These characters included morphological characters viz., Days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, panicle length (cm), flag leaf length (cm), flag leaf width (cm), number of grains per panicle, grain weight per panicle (g), 100 grain weight (g) and quality parameters such as 100 kernel weight (g), hulling (%), kernel length before cooking (mm), kernel breadth before cooking (mm), kernel length after cooking (mm), kernel breadth after cooking (mm), L:B ratio, kernel elongation ratio, breath increase ratio after cooking, 100 kernel weight after cooking (g), water absorb by 10 gm kernel (ml), grain weight per plant (g).

Genetic parameters viz., Mean, Range, Coefficients of variability (PCV and GCV) along with heritability in broad sense, genetic advance and genetic advance as percent of mean were estimated for the character studied. Analysis of variance was carried out as per methodology described by Panse and Sukhatme (1967) [10]. PCV and GCV were calculated using the formula given by Burton (1952) [2], heritability in broad sense (h^2) by Burton and De Vane (1953) [3] and genetic advance i.e. the expected genetic gain was calculated by using the procedure given by Johnson *et al.* (1955) [6]. GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (20 and above 20) according to Sivasubramanian and Menon (1973) [13]. The heritability was categorized according to Robinson *et al.* (1949) as low (0-30%), moderate (30-60%) and high (60 and above). Similarly, Genetic advance as per cent mean was categorized as low (0-10%), moderate (10-20%) and high (20 and above) as suggested by Johnson *et al.* (1955) [6].

Results and Discussion

The observations recorded on different characters and data collected was analysed through analysis of variance for yield and associated morphological and quality parameters. The results of ANOVA revealed that the mean sum of squares among the genotypes for all the characters were highly significant, which indicated that the genotypes were genetically divergent. This implicated that there is a great scope of selection of promising genotypes from the present gene pool. These findings were in accordance with the findings of Bekele *et al.* (2013) [1] and Sandhya *et al.* (2015) [12]. Information on the extent of genetic variability as well as heritability among the agronomically important traits is the requirement to design a suitable plant breeding methodology. It's very important for a plant breeder to have knowledge of genetic variability and the amount of heritable variation for important traits. Sometimes the trait of interest is influenced

by the environmental conditions prevailing, especially in case of polygenic characters so it becomes important to partition the total variability components, to have information regarding the nature and extent of actual variability present. Heritability on the other hand is a parameter widely used in establishment of breeding programs and formation of selection indices (Falconer, 1985) [4] as it gives an idea about the transmissibility of the trait of interest. As it is difficult to select suitable parents for poly genetically controlled characters, therefore, for efficient selection of superior parents there's a need of adequate genetic variation as well as considerable heritability of the trait of interest. Heritability along with genetic advance helps in assessing the amount of improvement that can be achieved through selection and gives an idea about which type of crop improvement methodology would work. Genetic advance in simple words is the expected response to selection. It gives an implication of effectiveness of selection under a particular condition for trait of interest.

Results on Mean, Range, Phenotypic (PCV) and Genotypic (GCV) coefficients of variation, broad sense heritability (h^2_b) and genetic advance as percent of mean (GAM) are presented in Table 1. However, the difference between PCV and GCV was found very low reflecting very few influences of environment in the expression of characters or lower sensitivity of genotypes to environment and greater role of genetic control governing the character is in agreement with the results explained by Karim *et al.* (2007) and Srajan *et al.* (2012) [15]. Days to flowering ranged from 72 days (Pusa Basmati-1)–135 days (SKG-2017-89) with a mean value of 92.53 days and marginally high PCV and GCV. Days to maturity ranged from 108 days (SKG-2017-53)–145 days (SKG-2017-81) with a mean value of 123.47 days and reflected moderate estimates of PCV and GCV. The Plant height ranged from 77.33cm (SKG-2017-51)–161.67cm (SKG-2017-53) with moderate PCV and GCV and mean plant height of 126.94cm. The range of number of tillers per plant varied from 4 (SKG-2017-79)–10 (SKG-2017-85) with a general mean 7.76 tillers per plant. The Phenotypic and Genotypic coefficients of variation observed to be marginally high for tillers per plant. The panicle length varied from 28.0 cm (SKG-2017-47)–56.0 cm (SKG-2017-48) with moderate PCV and GCV and a mean of 42.7cm. Flag leaf length was ranged from 26.5 cm (SKG-2017-81)–51.0cm (SKG-2017-76) with moderate PCV and GCV around a general mean of 37.3 cm. Range of flag leaf breadth was observed from 1.2 cm (SKG-2017-76)–2.1 cm (SKG-2017-36) with general mean 1.45cm and moderate PCV and GCV. Similarly, minimum flag leaf breadth was also observed for the genotype SKG-2017-77, Pusa Basmati-1 and SKG-2017-90. Number of grains per panicle exhibited wide range of variation from 85 (SKG-2017-77 and SKG-2017-82)–295 (SKG-2017-47) with high PCV and GCV and a mean value of 126 grains per panicle. The grains weight per panicle ranged from 1.72g (ADAM-CHINI)–6.47g (SKG-2017-47) and the general means of 3.18g, with high PCV and GCV. High PCV and GCV was observed for grain weight per plant, which varied from 4.43g (SKG-2017-78)–17.11g (SKG-2017-84) with the mean value of 10.59g. Moderate PCV and GCV was recorded for 100 grain weight with a range of variation from 1.26g (SKG-2017-78)–3.13g (SKG-2017-51) with a mean value of 2.36g.

The 100 Kernel weight ranged from 1.10g (SKG-2017-50 and SKG-2017-78) to 2.40g (SKG-2017-51) around the mean of 1.70g with moderate PCV and GCV. Hulling (%) expanded from 57.51 (SKG-2017-87)–87.30% (SKG-2017-78) with the

mean of 72.25% along with slightly moderate PCV and GCV. Kernel length before cooking (mm) showed variation between 4.50 mm (SKG-2017-50, SKG-2017-78 and SKG-2017-87)-9.40 mm (SKG-2017-51) with a mean value of 6.78 mm and moderate PCV and GCV. Range of kernel breadth before cooking was found between 1.20 mm (SKG-2017-81)-2.40 mm (SKG-2017-36) with General mean of 1.89 mm and moderate PCV and GCV. Kernel length after cooking expanded between 5.30 mm (SKG-2017-78)-12.97 mm (SKG-2017-51) with General mean of 8.27 mm and moderate PCV and GCV. Range of kernel breadth after cooking was recorded from 2.30 mm (SKG-2017-78)-4.63 mm (SKG-2017-51) with slightly high PCV and GCV with a mean of 2.83 mm. Similarly, the genotypes SKG-2017-80, SKG-2017-85, SKG-2017-86 and SKG-2017-88 also recorded minimum kernel breadth after cooking. Range of L.B. Ratio was estimated as 1.86 (SKG-2017-87)-6.19 (SKG-2017-81) with mean of 3.70 and high PCV and GCV. Kernel Elongation Ratio varied between 1.03 (SKG-2017-84)-1.54 (SKG-2017-47) with General mean of 1.72 and slightly moderate PCV and GCV. Breadth increase ratio after cooking was found between 0.37 (SKG-2017-36)-2.32 (SKG-2017-51) with high PCV and GCV around the mean of 1.54. The 100-kernel weight after cooking was estimated between 3.40 g (SKG-2017-84 and SKG-2017-89)-6.40 g (SKG-2017-51) with general mean of 4.31 g and moderate PCV and GCV. Range of water absorption by 10 g kernel was found between 6.97 ml (SKG-2017-84)-27.60 ml (SKG-2017-49) with General mean of 15.91 ml and high PCV and GCV.

The variability among genotypes indicates ample scope for selection for different quantitative characters for rice improvement. These findings are in agreement to earlier reports by Kumar and Verma (2015)^[8], Sravan *et al.* (2016)^[15] and Srivastava *et al.* (2017)^[16] who also observed significant variability for yield and its components in rice. The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters which may be due to higher degree of interaction of genotypes with the environment.

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability (Lush, 1949)^[9]. High heritability alone is not enough to make sufficient improvement though selection in advance generation where accompanied by substantial amount of genetic advance. Heritability in broad sense for days to 50% flowering was observed high with high genetic advance as percent of mean. Days to maturity exhibited high heritability in broad sense and marginally high genetic gain. The high heritability in broad sense coupled with high genetic advance as percent of mean was observed for plant height. Broad sense heritability was found very high for number of tillers per plant with high genetic advance as percent of mean. High board sense heritability with high genetic advance as percent of mean was found for Panicle Length. Board sense heritability and genetic advance as percent of mean for Flag leaf length

was found high, while moderate board sense heritability and genetic advance as percent of mean was recorded for Flag leaf breadth. Heritability in broad sense for number of grains per panicle was observed high along with high genetic advance as percent of mean. Grain weight per Panicle exhibited high broad sense heritability and genetic advance as percent of mean. High heritability in broad sense along with very high genetic advance as percent of mean was observed for grain weight per plant. 100 grain weight also exhibited high heritability in broad sense and high genetic advance as percent of mean.

Broad sense heritability for 100 Kernel weight was recorded as high along with high genetic advance as percent of mean. Slightly high broad sense heritability but moderate genetic advance as percent of mean was observed for Hulling (%). The heritability in broad sense and genetic advance as percent of mean were found high for kernel length before cooking. Kernel breadth before cooking showed high heritability in broad sense but marginally high genetic advance as percent of mean. High heritability in broad sense along with high genetic advance as percent of mean was estimated for kernel length after cooking, kernel breadth after cooking and L.B. Ratio. Heritability in broad sense for Kernel Elongation Ratio and breadth increase ratio after cooking was also found high with high genetic advance as percent of mean. Similarly, high heritability in broad sense and genetic advance as percent of mean was observed for 100 kernel weight after cooking and water absorb by 10 g kernel.

Johnson *et al.* (1955)^[6] suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression. Based in this consideration high heritability coupled with high genetic advance as percentage of mean was registered for morphological characters such as days to 50% flowering, days to maturity, plant height, number of tillers per plant, panicle length, flag leaf length, number of grains per panicle, grain weight per panicle, 100 grain weight, grain weight per plant and quality parameters *viz.*, 100 kernel weight, kernel length before cooking, kernel breadth before cooking, kernel length after cooking, kernel breadth after cooking, L:B ratio, kernel elongation ratio, 100 kernel weight after cooking, water absorb by 10 gm kernel, suggested preponderance of additive gene action in the expression of these characters. Therefore, selection would be effective through these characters. High heritability associated with moderate genetic advance as percent of mean was observed for hulling %, which revealed the non-additive gene action in the expression of these characters, hence in this case selection may not be effective. In this study, high heritability and genetic advance were observed for grain yield along with 18 yield components and quality characters indicating presence of additive genetic control also in agreement with Bekele *et al.* (2013)^[1] and Islam *et al.* (2016)^[5] during their study in aromatic and fine rice germplasm.

Table 1: Mean, Range, Phenotypic (PCV) and Genotypic (GCV) Coefficients of Variation, heritability (h^2), genetic advance (GA) and genetic advance as percent of mean (GAM) for yield, its components and quality parameters in Rice.

Character	GM	Range	PCV	GCV	h^2	GA	GAM
Days to 50% flowering	92.53	72.00-135.33	20.42	20.38	99.61	38.77	41.90
Days to Maturity	123.47	108.00-145.33	10.21	10.16	99.12	25.74	20.85
Plant height (cm)	126.94	77.33-161.67	15.58	15.54	99.52	40.55	31.94
Number of tillers per plant	7.76	4.30-10.43	20.86	20.78	99.25	3.31	42.65
Panicle length (cm)	42.72	28.00-55.97	16.04	16.01	99.65	14.06	32.92
Flag leaf length (cm)	37.26	26.50-51.00	16.23	14.97	85.04	10.59	28.44

Flag leaf width (cm)	1.44	1.20-2.07	16.74	11.76	49.35	0.24	17.02
Number of grains per panicle	125.51	84.67-294.67	32.45	32.40	99.67	83.63	66.63
Grain weight per panicle (g)	3.18	1.72-6.47	32.09	30.05	87.67	1.84	57.95
Grain weight per plant (g)	10.59	4.43-19.27	35.82	35.22	96.67	7.55	71.33
100 grain weight (g)	2.36	1.26-3.13	15.07	17.95	98.70	0.87	36.73
100 kernel weight (g)	1.70	1.10-2.40	19.75	18.74	90.08	0.62	36.65
Hulling (%)	72.25	57.51-87.30	10.71	8.58	64.19	10.23	14.16
Kernel length before cooking (mm)	6.78	4.50-9.40	17.04	16.96	99.14	2.36	34.80
Kernel breadth before cooking (mm)	1.89	1.20-2.40	14.44	12.25	71.96	0.41	21.41
Kernel length after cooking (mm)	8.27	5.30-12.97	19.77	19.67	99.05	3.33	40.33
Kernel breadth after cooking (mm)	2.83	2.30-4.63	20.75	20.43	96.94	1.17	31.45
L.B. ratio	3.70	1.86-6.19	44.09	22.99	91.08	1.67	45.19
Kernel elongation ratios	1.22	1.03-1.54	10.86	10.45	92.52	0.25	20.70
Breath increase ratio after cooking	1.55	0.37-2.32	28.12	21.43	58.08	0.52	33.64
100 kernel weight after cooking (g)	4.31	3.40-6.30	16.13	16.01	98.56	1.41	42.74
Water absorb by 10 g kernel (ml)	15.91	6.97-27.60	34.41	32.33	88.28	9.96	62.57

Conclusion

The present study concluded that high PCV and GCV for Grain weight per plant, days to 50% flowering, tillers per plant, number of grains per panicle, grain weight per panicle, breadth increase ratio after cooking, kernel breadth after cooking, L:B ratio and water absorb by 10 g kernel suggested ample scope of selection for these traits on one hand and high heritability coupled with high genetic advance as percent of mean for all these characters indicated the effectiveness of selection for desired improvement in these traits on the other. These findings infer that these characters could be improved through mass selection and progeny selection. SKG 2017-51 was found superior germplasm line recording high mean values for quality characters like kernel length before cooking, kernel length after cooking, kernel breadth after cooking, breadth increase ratio after cooking, 100 kernel weight after cooking, along with dwarfness, high 100 grain weight and 100 kernel weight, suggesting its use in future breeding programme as a donor for these traits. SKG 2017-84, SKG 2017-78, SKG 2017-81 and SKG 2017-85 were also identified as donor for high grain weight per plant, high hulling (%), minimum kernel breadth before cooking (fine grain) and high tillers per plant, respectively.

References

1. Bekele BD, Rakh S, Naveen GK, Kundur PJ, Shashidhar HE. Estimation of genetic variability and correlation studies for grain zinc concentrations and yield related traits in selected rice (*Oryza sativa* L.) genotypes. Asian Journal of Biological Sciences. 2013; 4(3):391-397.
2. Burton GW. Quantitative inheritance in grasses. Proc. 6th Interaction. Grassland Cong. J. 1952; 1:227-283.
3. Burton GW, De Vane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy J. 1953; 45:478-481.
4. Falconer DS. Introduction to Quantitative Genetics. ELBS, Longman, 1985.
5. Islam MZ, Khalequzzaman M, Bashar MK, Ivy NA, Haque MM, Mian MAK. Variability assessment of aromatic and fine rice germplasm in Bangladesh based on quantitative traits. The Scientific World Journal, vol. 2016, Article ID 2796720, 14 pages, 2016.
6. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955; 47(7):314-318.
7. Karim D, Sarkar U, Siddique MNA, Khaleque Miah MA, Hasnat MZ. Variability and Genetic Parameter Analysis in Aromatic rice. Int. J Sustain. Crop Prod. 2007; 2(5):15-18.
8. Kumar A, Verma OP. Correlation and path coefficient analysis in certain quantitative traits in rice (*Oryza sativa* L.) under saline-alkaline condition. Res. Envi. Life Sci. 2015; 8(3):443-446.
9. Lush JL. Heritability of quantitative characters in farm animals. Hereditas, suppl, 1949, 356-375.
10. Panse VG, Sukhatme PV. Statistical methods of agricultural workers. 2nd edition, pp:381, I.C.A.R. Publ. New Delhi, 1967.
11. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and degree of dominance in corn. Agron. J. 1949; 41:353-359.
12. Sandhya, Alok K, Rngare NR, Vidyakar V. Study of genetic variability of Indian and exotic rice germplasm in Allahabad agroclimate. The Bioscan. 2015; 8(4):1345-1350.
13. Sivasubramanian S, Madhava Menon P. Genotypic and phenotypic variability in rice, Madras Agric. J. 1973; 60:1093-1096.
14. Sravan T, Rangare N, Suresh B, Kumar S. Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). Journal of Rice Research. 2012; 5:24-29.
15. Sravan T, Jaiswal HK, Waza SA, Kumari P. Analysis of Variability and Character Association in Indigenous Aromatic Rice (*Oryza sativa* L.) Electronic Journal of Plant Breeding. 2016; 7(1):159-164.
16. Srivastava N, Babu GS, Singh ON, Verma RL, Pathak SK. Appraisal of genetic variability and character association studies in some exotic upland rice germplasm. Plant Archives. 2017; 17(2):1581-1586.