



P-ISSN: 2349-8528

E-ISSN: 2321-4902

IJCS 2018; 6(6): 904-907

© 2018 IJCS

Received: 11-09-2018

Accepted: 15-10-2018

Himanshu Chaudhary

Research Scholar, Department of Genetics and Plant Breeding
G.B. Pant University of Agriculture and Technology,
Pantnagar, Uttarakhand, India

DC Baskheti

Professor, Department of Genetics and Plant Breeding
G.B. Pant University of Agriculture and Technology,
Pantnagar, Uttarakhand, India

Dhanraj Meena

Research Scholar, Department of Genetics and Plant Breeding
G.B. Pant University of Agriculture and Technology,
Pantnagar, Uttarakhand, India

Madhubala Kurmanchali

Research Scholar, Department of Genetics and Plant Breeding
G.B. Pant University of Agriculture and Technology,
Pantnagar, Uttarakhand, India

Correspondence

Himanshu Chaudhary

Research Scholar, Department of Genetics and Plant Breeding
G.B. Pant University of Agriculture and Technology,
Pantnagar, Uttarakhand, India

International Journal of Chemical Studies

Assessment of genetic variability parameters for yield and quality traits in aromatic rice (*Oryza sativa* L.)

Himanshu Chaudhary, DC Baskheti, Dhanraj Meena and Madhubala Kurmanchali

Abstract

A study was conducted during *kharif* 2017 to generate information on genetic variability parameters among forty four aromatic rice genotypes. These genotypes were evaluated in a Randomized Complete Block Design (RCBD) with three replications and observations were recorded on various yield and quality traits. The analysis of variance (ANOVA) showed significant differences among the genotypes for all the characters studied except grain breadth and kernel breadth, indicating that ample amount of genetic variability among the genotypes. In general, PCV were higher than the GCV for all characters indicates influence of environment. High heritability coupled with high genetic advance were observed for the characters *viz.* grain yield/plant, biological yield/plant and plant height which suggested the presence of additive gene action and thereby these traits could be considered as reliable indices for selection.

Keywords: aromatic rice, genetic variability, yield and quality

Introduction

Rice belongs to the family Graminaeae and it is recognized as “millennium crop” because it is expected to contribute towards food security in the world, as it is one of the staple cereal crop of the world and a primary source of food for about 65% of the world’s population. It is grown under diverse agro-climatic conditions and over wide geographical range (Cheng *et al.*, 2005) [3]. With an alarming raise in the population throughout the world, the demand for rice will continue to increase in near future. Therefore, rice breeders across the world aim at increasing the grain yield of rice (Song *et al.*, 2007) [18]. The efficacy of any selection programme depends upon the existence and magnitude of available genetic variability for yield and yield contributing traits in the breeding material (Pal *et al.*, 2018) [11]. A better understanding of the relationship between grain yield and its component traits becomes compulsory for making an efficient selection for the development of new varieties with improved economically important traits (Kumar *et al.*, 2014) [9]. The knowledge of heritability and genetic variability is a prerequisite for carrying out selection-based improvement. The information about genetic variability, heritability and genetic advance help in the breeding programmes by broadening the gene pool of rice and gives an indication about the efficiency of transformation of characters into future generations respectively (Selvaraj *et al.*, 2011) [16]. Heritability is a good index of the transmission of character from parents to their offspring (Falconer *et al.*, 1981) [4]. The prosperous variability of complex quantitative traits still remains un-exploited and under-exploited. Rice landraces have proven to be highly adaptive to diverse environmental conditions and are supposed to harbor a number of valuable genetic resources for crop improvement (Ganie *et al.*, 2014) [5]. In any crop species setting the breeding objective for improvement of crop yield is prime importance. Understanding of nature and magnitude of genetic variation governing the inheritance of relatively quantitative traits like yield and attributing traits are essential. Plant breeder has to analyze certain genetic variability parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance of various economic important quantitative traits to sketch future crop improvement programmes. Genetic variability plays a key role in study and identification of promising rice genotypes.

Materials and Methods

The present experiment was conducted during *khariif*, 2017 at the Norman E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand. The experimental materials comprised of 44 genotypes grown in Randomized Complete Block Design (RCBD) with three replications possess the spacing of 30 cm row to row and 15 cm plant to plant. All recommended cultural practices were followed to raise the crop. Five plants from each genotype were taken at random from each replication for recording data on the following characters *viz.*, leaf area (cm²), plant height (cm), number of tillers/plant, panicle length (cm), biological yield/plant (g), grain yield/plant (g), harvest index, and 1000 grain weight (g). The observations on days to initiation of flowering and days to 50 per cent flowering were recorded on plot basis. Observations were also recorded to study grain quality characters *viz.*, grain length (mm), grain breadth (mm), kernel length (mm), kernel breadth (mm), L/B ratio, hulling recovery (%), milling recovery (%), head rice recovery (%), amylose content (%), gel consistency (mm) and alkali digestion value. The data were compiled by taking mean value over randomly selected plants from all the replications and subjected to the statistical analysis for randomized complete block design as per Panse and Sukhatme, 1984^[12]. Genetic parameters such as genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance were computed as per Burton and De Vane, 1953^[2] and Johnson *et al.*, 1955^[6].

Results and Discussion

Analysis of variance (ANOVA)

The analysis of variance (ANOVA) showed that mean sum of square due to treatments were significant for most of the characters indicating the presence of adequate amount of genetic variability in the study materials (Table 1) hence desirable improvement can be brought through selection for different component traits. Similar results were also reported by Singh *et al.*, (2011)^[17], Ketan *et al.*, (2014)^[7], Sameera *et al.*, (2016)^[15] and Yugandhar *et al.*, (2017)^[19].

Genotypic and phenotypic coefficients of variation (GCV and PCV), Heritability (Broad sense) h^2 and Genetic Advance (GA).

The high estimates of phenotypic and genotypic coefficient of variation (> 20%) were estimated for grain yield/plant (38.20, 38.20), biological yield/plant (34.51, 34.50), alkali digestion value (31.21, 31.21), 1000 grain weight (28.75, 28.75), number of tillers/plant (28.52, 28.16) and leaf area (23.13, 23.11) indicating high opportunity of selection for these characters. The moderate estimates (10-20%) of PCV and GCV were recorded for head rice recovery (15.83, 15.83), harvest index (15.05, 15.01) and amylose content (10.75, 10.71) and it was low for plant height (9.83, 9.82), hulling

recovery (9.48, 9.47), milling recovery (9.07, 9.06), L/B ratio (8.78, 7.99), panicle length (8.24, 8.20), kernel breadth (7.12, 6.29), gel consistency (6.51, 6.49), kernel length (6.38, 6.33), grain breadth (5.87, 5.43), days to initiation of flowering (4.76, 4.60) and grain length (4.71, 4.68) indicating little opportunity of selection for these characters (Table 2). Similar results also reported by Sameera *et al.*, (2016)^[15] and Yugandhar *et al.*, (2017)^[19]. High coefficient of variability indicated that there is a scope of selection and improvement of these traits. Low values indicated the need for creation of variability either by hybridization or mutation followed by selection. The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability.

Robinson *et al.* (1949)^[14] viewed that the knowledge of heritability of a character is important to the breeder, as it indicates the possibility and extent to which improvement is possible through selection. In the present study, high estimates of broad sense heritability (>60%) was recorded for all the characters. The genetic advance in per cent of mean was found to be high (>20%) for biological yield/plant, grain yield/plant and plant height. On the other hand, moderate genetic advance in per cent of mean (10-20%) were noted for head rice recovery, leaf area, hulling recovery, gel consistency, 1000 grain weight and milling recovery while low (<10%) for number of tillers/plant, days to 50% flowering, days to initiation of flowering, panicle length, amylose content, alkali digestion value, L/B ratio, harvest index and grain length (Table 2). Further, results revealed that high heritability coupled with high genetic advance in per cent of mean were observed for the characters *viz.*, grain yield/plant, biological yield/plant and plant height indicated the involvement of additive gene action. The results were found similarity with findings of Zahid *et al.*, (2006)^[20], Singh *et al.*, (2011)^[17], Ketan *et al.*, (2014)^[7], Sameera *et al.*, (2016)^[15] and Yugandhar *et al.*, (2017)^[19]. High heritability in broad sense coupled with moderate genetic advance in per cent of mean were observed for the characters *viz.*, head rice recovery, leaf area, 1000 grain weight, hulling recovery, gel consistency and milling recovery. High heritability coupled with high genetic advance has additive gene action and may be directly utilized for rice improvement. On the other hand the character having low heritability and high genetic advance in percent of mean and high heritability and low genetic advance in percent of mean have non-additive gene action. The high to very high estimates of direct selection parameters for above mentioned characters indicated that these would be ideal traits for improvement through selection in context of materials evaluated due to existence of high genetic variability represented by high coefficients of variation and high transmissibility denoted by high heritability for them. (Mall *et al.*, 2005; Panwar *et al.*, 2007; Basavaraja *et al.* 2013 and Kumar and Verma, 2016)^[10, 13, 1, 16].

Table 1: Analysis of variance for randomized complete block design for 21 characters in rice

Source of variation	Replication	Genotypes	Error
df	2	43	86
Days to initiation of flowering	1.28	56.96**	1.31
Days to 50% flowering	0.18	60.11**	1.25
Leaf area (cm ²)	0.02	189.24**	0.15
Plant height (cm)	0.09	414.50**	0.37
Number of tillers/plant	0.15	57.77**	0.46
Panicle length (cm)	0.21	20.07**	0.06
Biological yield/plant (g)	0.18	3070.76**	0.48
Grain yield/plant (g)	0.01	1001.53**	0.01

Harvest index	0.01	0.018*	0.00
Grain length (mm)	0.00	0.008*	0.00
Grain breadth (mm)	0.00	0.00	0.00
Kernel length (mm)	0.00	0.006*	0.00
Kernel breadth (mm)	0.00	0.00	0.00
L/B ratio	0.10	0.32*	0.02
1000 grain weight (g)	0.05	111.41**	0.04
Hulling recovery (%)	0.60	123.53**	0.10
Milling recovery (%)	0.05	95.60**	0.10
Head rice recovery (%)	0.01	186.96**	0.02
Amylose content (%)	0.07	16.49**	0.03
Gel consistency (mm)	0.59	124.54**	0.25
Alkali digestion value	0.01	5.63**	0.00

** Significant at 1% level, * significant at 5% level

Table 2: Estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2b) and genetic advance as per cent of mean for 21 characters in rice

Characters	Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance as per cent of mean
	PCV	GCV		
Agro-morphological traits				
Days to initiation of flowering	4.76	4.60	93.00	8.40
Days to 50% flowering	4.54	4.40	94.00	8.65
Leaf area (cm ²)	23.13	23.11	99.78	16.30
Plant height (cm)	9.83	9.82	99.75	23.65
Number of tillers/plant	28.52	28.16	97.60	8.79
Panicle length (cm)	8.24	8.20	98.99	5.18
Biological yield/plant (g)	34.51	34.50	98.51	65.29
Grain yield/plant (g)	38.20	38.20	99.99	37.03
1000 grain weight (g)	28.75	28.75	99.90	12.93
Harvest index	15.05	15.01	99.98	0.16
Quality traits				
Grain length (mm)	4.71	4.68	99.96	0.10
Grain breadth (mm)	5.87	5.43	85.00	0.02
Kernel length (mm)	6.38	6.33	98.00	0.09
Kernel breadth (mm)	7.12	6.29	78.00	0.02
L/B ratio	8.78	7.99	83.00	0.59
Hulling recovery (%)	9.48	9.47	99.73	13.82
Milling recovery (%)	9.07	9.06	99.78	11.92
Head rice recovery (%)	15.83	15.83	99.95	16.38
Amylose content (%)	10.75	10.71	99.33	4.71
Gel consistency (mm)	6.51	6.49	99.96	12.94
Alkali digestion value	31.21	31.21	99.39	2.78

Conclusion

The present study revealed the presence of wide range of genetic variability for almost all the traits under investigation. In general, PCV were higher than the GCV for all characters indicates influence of environment. High heritability coupled with high genetic advance were observed for the characters viz., grain yield/plant, biological yield/plant and plant height which suggested the presence of additive gene action and thereby these traits could be considered as reliable indices for selection.

References

- Basavaraja T, Asif M, Mallikarjun SK, Gangaprasad S. Variability, heritability and genetic advance for yield and yield attributing characters in different local rice (*Oryza sativa* L.) cultivars. Asian J of Bio. Sci. 2013; 8(1): 60-62.
- Burton GW, De Vane EW. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953; 45:478-481.
- Cheng SH, Cao LY, Zhan XD. Techniques for hybrid rice seed production. Jindun Publishing House, Beijing, 2005.
- Falconer DS. Introduction to Quantitative Genetics, 2nd ed. Longman, New York, 1981.
- Ganie SA, Karmakar J, Roychowdhury R, Mondal TK, Dey N. Assessment of genetic diversity in salt-tolerant rice and its wild relatives for ten SSR loci and one allele mining primer of salT gene located on 1st chromosome, Plant Systematics and Evolution, 2014. (DOI 10.1007/s00606-014-0999-7, Published online).
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron. 1955; 47:314-318.
- Ketan R, Sarkar G. Studies on variability, heritability and genetic advance in some indigenous Aman rice (*Oryza sativa* L.) Journal of Crop and Weed. 2014; 10(2):308-315.
- Kumar A, Verma OP. Genetic variability, heritability and genetic advance studies in rice (*Oryza sativa* L.) under sodic soil. Res. Environ and Life Sci. 2016; 9(2):149-151.
- Kumar V, Koshta N, Sohgaure N, Koutu GK. J Agric. Technol. 2014; 1(1):43-51.
- Mall AK, Babu JDP, Babu GS. Estimation of genetic variability in rice. J Maharashtra Agric. Univ. 2005; 30(2):166-168.

11. Pal D, Verma SK, Panwar RK, Arora A, Gaur AK. Correlation and Path Analysis Studies in Advance Lines of Pigeonpea [*Cajanus cajan* (L.) Millspaugh] under Different Environments. *Int. J Curr. Microbiol. App. Sci.* 2018; 7(4):378-389.
12. Panse VG, Sukhatme PV. *Statistical Methods for Agricultural Workers*, 3rd Edition, Indian Council of Agricultural Research, New Delhi, 1984, 343.
13. Panwar A, Dhaka RPS, Vinod K. Path analysis of grain yield in rice (*Oryza sativa* L.). *Advances in Plant Sci.* 2007; 20(1):27-28.
14. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and degree of dominance in corn. *Agro. J.* 1949; 41:353-359.
15. Sameera SK, Srinivas T, Rajesh AP, Jayalakshmi V, Nirmala PJ. Variability for yield and yield components in rice. *Bangladesh J Agril. Res.* 2016; 41(2):259-271.
16. Selvaraj CI, Nagarajan P, Thiyagarajan K, Bharathi M, Rabindran R. *African J Biotech.* 2011; 10(17):3322-3334.
17. Singh SK, Singh CM, Lal GM. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Research in Plant Biology.* 2011; 1(4):73-76.
18. Song XJ, Huang W, Shim ZM, Lin H. *Nat Genet.* 2007; 3(9):623-630.
19. Yugandhar PR, Dahat DV, Barahte KK, Suneetha K. Study on variability, heritability and genetic advance for agro-morphological and grain quality parameters in restorer lines of rice (*Oryza sativa* L.). *Int. J Pure App. Biosci.* 2017; 5(4):1202-1206.
20. Zahid MA, Akhter M, Sabar M, Manzoor Z, Awan T. Correlation and path analysis studies of yield and economic traits in Basmati rice (*Oryza sativa* L.). *Asian J Plant Sci.* 2006; 5(4):643-645.