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Division of Plant Breeding and Genetics, MRCFC, SKUAST-K, Khudwani. Jammu & Kashmir, India Studies on variability, heritability and genetic gain for quality traits in rice

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Abstract

An experiment comprising of thirty five rice (*Oryza sativa* L.) genotypes was conducted during kharif season 2015 for cooking and quality characteristics. data on fifteen cooking and quality traits were recorded and analysed for to estimate of the variability, heritability, genetic advance and genetic advance percentage of as mean. The treatment mean sum of squares due to genotypes showed significant difference in all 15 physio-chemical and cooking quality characters. The value of Phenotypic Coefficient of Variation was found higher than Genotypic Coefficient of Variation for all the traits. Gel consistency exhibited highest value of Genotypic Coefficient of Variation (22.64) and Phenotypic Coefficient of Variation (23.08) and hulling percentage exhibited lowest value (4.87) and (5.14). The highest broad sense heritability was observed for head rice recovery and amylose content (99.00) and lowest was exhibited by Kernel widening ratio (48.00). Elongation percentage exhibited the highest value of genetic advance (39.31) and lowest value was exhibited by Kernel widening ratio (45.74) and amylose content (41.73) exhibited highest of genetic advance as percentage of mean and lowest value was exhibited by Hulling percentage (9.50).

Keywords: Variability, heritability, amylose content, gel consistency and Oryza sativa

Introduction

Rice belongs to genus Oryza of family Poaceae. The genus Oryza has twenty two wild and two cultivated species viz., Oryza sativa and Oryza glaberrima. It is the most important grain crop with regard to human nutrition and caloric intake and is the staple food of over one-third of world's population (Deepti et al., 2013 and Reddy et al., 2013) ^[1, 2]. Rice is the only cereal crop which is consumed mainly after cooking whole grains, and hence, the quality considerations are more important (Hossain et al., 2009)^[7]. Physical quality traits such as size, shape, uniformity and general appearance, kernel shape and L/B ratio are important features for assessing grain quality. (Rita and Sarawgi, 2008)^[9]. Sellappan et al., 2009)^[10]. The gelatinization temperature (GT), gel consistency (GC) and amylose content (AC) are another set of traits, which are directly related to cooking and eating quality. Starch (amylose and amylopectin) and protein composition are equally important in determining the cooking quality of rice (Lisle et al., 2000; Ahmed et al., 2007) [11, 12]. A wide range of genetic variability has been reported for quality traits in the past, but still there exists untapped genetic variability in germplasm which is of paramount importance in selecting the potential parents which can be utilized in hybridization for realizing maximum Heterosis and superior recombinants with respect to quality components. Genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation are useful in predicting the amount of variability present in the available germplasm. Heritability coupled with high genetic advance helps in determining the influence of environment on the expression and reliability of characters in the genotype. The rice grain quality traits generally include milling quality, appearance, and nutritional quality viz. cooking and eating quality which are most important for the end users. Therefore, selection for improved quality of milling, cooking, eating and processing is essential to meet consumers' preference and industry standards.

Materials and Methods

The present experiment was conducted in the division of Plant Breeding and Genetics during Kharif 2014 at Mountain Research Centre for Field Crops, SKUAST-K, Khudwani, Anantnag, Kashmir (Jammu and Kashmir). The random seed samples were taken from the harvested kharif crop of 2013, replicated and analyzed for cooking quality traits *viz.*, Hulling recovery (%), Milling recovery (%), Head rice recovery (%), Kernel length before cooking (mm), Kernel length after cooking (mm), Kernel breadth before cooking (mm), Kernel breadth after cooking (mm), Kernel widening ratio,

Corresponding Author: Nusrat Jan Department of Biological Science, SHUATS, Allahabad, Uttar Pradesh, India Amylose content (%), Gel consistency (mm), Alkali digestion value, Water uptake ratio, Volume expansion ratio, Elongation ratio, Elongation (%) and Cooking time. The quality parameters were estimated by standard procedures given by respective researchers like hulling and milling, head rice recovery by Ghosh et al. (1971) [5], kernel length and breadth were calculated by dial micro meter and subsequently length/breadth ratio was calculated accordingly, alkali spreading value was measured by following the method given by Little et al. (1985), water uptake and volume expansion by Beachell and Stanel (1963), cooked kernel length was recorded using a graph paper and elongation ratio by the method adopted by Azeez and Shafi (1966) and amylose content by Juliano (1971)^[6]. The mean data of each character was subjected to statistical analysis for variance and tested the significance of each character as per the procedure of Panse and Sukhatme (1967). The variability parameters viz. range, mean genotypic coefficient of variation, phenotypic coefficient of variation per the methods given by Burton

(1952) and heritability and genetic advance as per Johnson *et al.* (1955).

Results and Discussion

The analysis of variance for different physio-chemical and cooking quality characters (table1) showed significant difference in all 15 physio-chemical and cooking quality characters *viz.*, hulling (%), milling (%), head rice recovery, kernel length before cooking(mm), kernel length after cooking(mm), elongation ratio, elongation percentage (%), kernel breadth before cooking(mm), kernel breadth after cooking(mm), kernel widening ratio, cooking time, water uptake ratio, volume expansion ratio, gel consistency and amylose content which indicated the presence of sufficient variability among the genotypes for all these traits and suggesting ample scope for further improvement. Similar results were also reported by Bhinda *et al.*, (2017), Vanaja and Luckins (2006), Sunayana *et al.*, (2010), Kambe *et al.*, (2016) and Devi *et al.*, (2017).

Characters	Replication df =2	Treatment df = 34	Error df = 68
Hulling (%)	0.182	43.71**	1.59
Milling (%)	1.23	59.36**	0.70
Head rice recovery	0.93	158.85**	0.70
Kernel length before cooking(mm)	0.052	2.00**	0.28
Kernel length after cooking(mm)	0.057	10.67**	0.30
Elongation ratio	0.028	0.17***	0.020
Elongation (%)	283.96	1741.08**	206.73
Kernel breadth before cooking(mm)	0.014	0.64**	0.072
Kernel breadth after cooking(mm)	0.001	0.59**	0.070
Kernel widening ratio	0.002	0.064**	0.017
Cooking time	0.72	7.74**	1.09
Water uptake ratio	0.066	0.291**	0.066
Volume expansion ratio	0.11	0.64**	0.047
Gel consistency	0.30	14.81**	0.19
Amylose content %	0.10	60.54**	0.17

Where, * and ** Significant at 1% and 5% level of significance respectively.

Estimates of coefficient of variation (genotypic and phenotypic), heritability and genetic advance reflects the role of environment in the expression of phenotypic and genotypic effects. Variability can be observed through biometric parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability (broad sense h^2) and genetic advance and is of great help to breeder in evolving a selection programme for varietal improvement. The estimates of variance, coefficient of variation, heritability and genetic advance for the all physio-chemical and cooking quality characters (table 2) showed that wide range of genotypic coefficient of variation (GCV) was observed in characters and was ranged from (22.64) for the gel consistency to (4.87) for hulling percentage. High values of GCV were recorded for gel consistency (22.64) followed by amylose content (20.34), kernel length after cooking(mm) (19.35), kernel breadth before cooking(mm) (19.02) and elongation ratio (16.01), elongation percentage (16.00), water uptake ratio (12.95), head rice recovery (13.17). Whereas, low estimates of GCV were observed for volume expansion ratio (9.79), kernel widening ratio (8.60), milling (%) (6.21) and hulling (%) (4.87), indicating the existence of wide genetic base among the genotypes and possibility of genetic improvement through selection for these traits. Similar results were also observed by Babu et al., (2012)^[18] for gel consistency and kernel length, Sahu et al., (2015)^[19] for head rice recovery, Devi et al., (2016) for head rice recovery, water uptake, kernel breadth

after cooking (mm) and kernel length after cooking (mm), Dhurai *et al.*, (2014) ^[20], Bhadru *et al.*, (2012) ^[21] and Dhanwani *et al.*, (2013) ^[22] for head rice recovery, Vanaja *et* al. (2006)^[23] for amylose content, Sahu et al., (2015)^[19] for milling (%) and hulling (%), Devi et al., (2016) and Singh et al., (2006) for hulling recovery (%) and milling recovery (%). Wide range of phenotypic coefficient of variation (PCV) was observed which ranged from (23.08) for the gel consistency to (5.14) for hulling percentage. High value of phenotypic coefficient of variation was recorded for gel consistency (23.08) followed by kernel breadth before cooking(mm) (22.34), amylose content (20.43), kernel length after cooking(mm) (20.19) and elongation ratio (18) Whereas, low estimates were observed for milling (%) (6.32) and hulling (%) (5.14) indicating these traits are very much influenced by the environment. Similar results were also observed by Babu et al., (2012)^[18] for gel consistency and kernel length, Sahu et al., (2015) ^[19], Devi et al., (2016) Dhurai et al., (2014) ^[20], Bhadru *et al.*, (2012) ^[21] and Dhanwani *et al.*, (2013) ^[22], Vanaja et al. (2006) [23].

The estimates of heritability in broad sense (h^2) was found to be highest for amylose content (99.00), head rice recovery (99.00) followed by milling percentage(97.00), gel consistency (96.00), kernel length after cooking (mm) (92.00) and hulling (%) (90.00). rest of the characters observed moderate to high heritability, which, indicated that the characters under study were less influenced by the environment in their expression. Which suggested that these traits would respond to selection owing to their high variability and transmissibility. Similar results were also observed by Devi *et al.*, (2016) Sahu *et al.*, $(2015)^{[19]}$, Babu *et al.*, $(2012)^{[18]}$, Chaudhary *et al.* $(2004)^{[25]}$, Nirmaldevi *et al.* (2015), Hussain *et al.* $(1989)^{[27]}$, and Nayak *et al.* $(2003)^{[28]}$ Sanjukta *et al.* $(2007)^{[29]}$ and Veerabadhiran *et al.* $(2009)^{[30]}$. High estimates of genetic advance was observed for elongation (39.31) followed by head rice recovery (14.86), amylose content (9.20) and milling (%) (8.95, while as, moderate estimates of genetic advance was observed by kernel length after cooking (mm) (3.67), cooking time (2.51) and kernel length before cooking (mm) (1.27). Similar results

were also observed by Abebe *et al.* (2017), Sahu *et al.*, (2015) ^[19], Babu *et al.*, (2013) ^[18] Chaudhary *et al.* (2004) ^[25] and Rathi *et al.*, (2010). Perusal of results revealed that high estimates of genetic advance as percentage of mean was observed for gel consistency (45.74) followed by amylose content (41.73), kernel length after cooking (38.22), kernel breadth before cooking (33.34), elongation ratio (27.86) and elongation percentage(27.81). While as moderate values was observed for milling (12.57), kernel widening ratio (12.22) and Hulling (9.50). Similar results were also observed by Devi *et al.*, (2016), Babu *et al.*, (2012) ^[18] and Sahu *et al.*, (2015) ^[19].

GCV	PCV	Heritability (h ² Broad Sense)	G. A.	G. A. (%)
4.87	5.14	90.00	7.31	9.50
6.21	6.32	97.00	8.95	12.57
13.17	13.25	99.00	14.86	26.95
11.07	13.57	67.00	1.27	18.62
19.35	20.19	92.00	3.67	38.22
16.01	18.96	71.00	0.39	27.86
16.00	18.96	71.00	39.31	27.81
19.02	22.34	72.00	0.76	33.34
12.82	15.19	71.00	0.73	22.28
8.60	12.45	48.00	0.18	12.22
12.00	14.67	67.00	2.51	20.22
12.95	17.82	53.00	0.41	19.37
9.79	10.89	81.00	0.83	18.13
22.64	23.08	96.00	4.46	45.74
20.34	20.43	99.00	9.20	41.73
	GCV 4.87 6.21 13.17 11.07 19.35 16.01 16.00 19.02 12.82 8.60 12.00 12.95 9.79 22.64 20.34	GCV PCV 4.87 5.14 6.21 6.32 13.17 13.25 11.07 13.57 19.35 20.19 16.01 18.96 19.02 22.34 12.82 15.19 8.60 12.45 12.00 14.67 12.95 17.82 9.79 10.89 22.64 23.08 20.34 20.43	GCVPCVHeritability (h^2 Broad Sense)4.875.1490.006.216.3297.0013.1713.2599.0011.0713.5767.0019.3520.1992.0016.0118.9671.0019.0222.3472.0012.8215.1971.008.6012.4548.0012.9517.8253.009.7910.8981.0022.6423.0896.0020.3420.4399.00	GCVPCVHeritability (h^2 Broad Sense)G. A.4.875.1490.007.316.216.3297.008.9513.1713.2599.0014.8611.0713.5767.001.2719.3520.1992.003.6716.0118.9671.000.3916.0018.9671.000.7612.8215.1971.000.738.6012.4548.000.1812.0014.6767.002.5112.9517.8253.000.419.7910.8981.000.8322.6423.0896.004.4620.3420.4399.009.20

Where, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h^2 = Broad sense heritability, G.A = genetic advance, G.A (%) mean = genetic advance as percentage of mean

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