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STUDIES ON GENETIC VARIABILITY FOR YIELD AND QUALITY CHARACTERS IN RICE (*ORYZA SATIVA* L.) UNDER INTEGRATED FERTILIZER MANAGEMENT

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ABSTRACT

The analysis of variance revealed significant differences among the genotypes for the all the 9 quantitative and 5 quality traits in rice indicating that enough variability is present in the studied material. The magnitude of difference between PCV and GCV were relatively low for all the traits revealing little influence of the environment in the expression of these traits. The higher magnitude of PCV and GCV was recorded for number of grains per panicle (23.85%; 23.10%) and grain yield per plant (23.17%; 22.04%). All the characters showed high broad sense heritability, while high heritability coupled with high genetic advance as per cent mean was recorded for plant height (97.67%; 30.81%), number of effective tillers per plant (84.10%; 28.19%), panicle length (95.17%; 22.94%), number of grains per panicle (93.79%; 46.08%), kernel elongation ratio (95.81%; 21.88%), kernel length after cooking (99.91%; 23.77%), 1000-grain weight (89.97%;26.22%), harvest index (79.02%; 26.25%) and grain yield per plant (90.48%; 43.20%) indicates the preponderance of additive gene action and such characters could be improved through selection.

INTRODUCTION

Rice (*Oryza sativa* L.) occupies a pivotal place in the Indian agriculture. Rice is also called as the " Grain of Life", because it is not only the staple food for more than 70 percent of the Indians but also a source of livelihood for about 120-150 million rural households. At the current rate of population growth accelerating at 1.8 percent, rice requirement by the year 2020 would be around 140 million tons (Anon., 2004). As population growth continues to boost demand for rice, production growth in all the ecosystems is approaching a plateau. Therefore, efforts to enhance rice productivity with keeping grain quality must receive top priority. Increasing rice production can be achieved by application of improved agronomic techniques, developing and adopting high yielding varieties (Thakare *et al.*, 2013). Green revolution, though paved the way for a substantial increase in rice production leading to self-sufficiency and even surplus for exports, in the recent years deceleration of growth and crop yield from green revolution technologies surfaced. Among the various causes put forth for low yields in India, lack of varieties with yield stability under different climatic situations, different fertilizer managements and under different soil conditions are considered to be the foremost. This necessitated the concept of integrated fertilizer management as a modern technology, methodology and philosophy for adoption and sustainability. The complementary use of organic and biological source of plant nutrients along with chemical fertilizer is of great importance for the maintenance of soil health and productivity (Yadav and Alok Kumar, 2009), since the environmental and economic performance of sustainable farming is higher than that of conventional farming.

In this paradigm shift, farmers in India are also interested to take up integrated fertilizer management system to boost rice production and productivity to meet the production targets. However, the major constraint for the farmers is that there is no suitable variety bred for habitat specific. Conventional cultivars, bred for high yield in high-input conventional production systems, may not be well adapted to other production system (Venuprasad *et al.*, 2003; Robenzon and Rex, 2008). Grain yield is a complex character, which depends on its several components. These components are further dependent for their expression on several morphological traits, which interrelated with each other showing a complex chain of relationship and also highly influenced by the environmental conditions (Prasad *et al.*, 2001). Therefore, the parents selected for the breeding programmes aimed at increased grain yield should possess wide range of genetic variation for the characters. Besides, it could be of interest to know the magnitude of variation due to heritable component, which in turn would be a guide for selection for the improvement of a population. Therefore, an attempt has been made to find out the genetic variability for characters of economic importance and their heritability and genetic advance which would help in selection and further improvement of rice genotypes under integrated fertilizer condition.

MATERIALS AND METHODS

A field experiment was conducted with 32 rice (*Oryza sativa* L.) genotypes at the wetland farm of S.V Agricultural College, Tirupati which is situated at an altitude of 182.90 m above mean sea level, 13°N latitude and 79ºE longitude during *Kharif* 2009. Seeds of the 32 genotypes were sown in raised nursery bed and thirty days old seedlings of each genotype were transplanted by adopting a spacing of 20 cm between rows and 15 cm between plants within row in a randomized block design with three replications. Each genotype was grown in 3 rows with a plot size of 2.4 m^2. The crop was grown with the application of 50% organic fertilizers through FYM (which is equivalent to 60 kg N ha^{-1}) and 50% recommended dose of chemical fertilizers (which is equivalent to 60 kg N, 30 kg P_2O_5 and 30 kg K_2O per hectare in the form of urea, single super phosphate and muriate of potash (Panchali, 2009). The recommended agronomical practices and plant protection measures were followed to ensure normal crop. Five competitive plants were selected randomly from the center row of each genotype in each replication and observations were recorded for characters like, number of effective tillers per plant, plant height, panicle length, number of grains per panicle, 1000-grain weight, kernel length, kernel breadth, kernel length/breadth ratio, kernel length after cooking, kernel elongation ratio, harvest index and grain yield per plant except days to 50% flowering and days to maturity, whereas the latter two characters were recorded on plot basis. Panicle and grain characters were recorded on five panicles of selected plants, the quality characters like kernel length, kernel breadth, kernel length after cooking was measured using grain vernier (Panchali, 2009). The data recorded for all the characters whose mean values were subjected to analysis of variance to test the significance for each character as per methodology proposed by Panse and Sukhatme (1961). The genotypic and phenotypic variances as well as the genotypic (GCV) and phenotypic (PCV) coefficient of variation were calculated by the formulae given by Burton (1952). Heritability in broad sense [$h^2_{(b)}$] and genetic advance (GA) were estimated by the following formula given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. Variance analysis for all the characters revealed significant variation among the genotypes studied (Table 1), indicating the existence of sufficient amount of variability. These results were in conformity with the earlier findings of Kumar *et al.* (2006), Salgotra *et al.* (2009) and Dhanwani *et al.* (2013). The magnitude of phenotypic co-efficient of variation (PCV) in general was found higher than the genotypic co-efficient of variation (GCV) for all the characters studied indicated the influence of environment on the manifestation of these characters (Kavita and Reddy, 2002 and Sreeparvathy *et al.*, 2010). However, the difference between PCV and GCV was less for the traits, days to 50 per cent flowering, days to maturity, plant height, panicle length, number of grains per panicle, kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, kernel elongation ratio, 1000-grain weight and grain yield per plant. The similar result was observed by Dhanwani *et al.* (2013).

Among the characters, higher estimates of PCV and GCV were observed for the number of grains per panicle and yield per plant. This indicates the existence of wide genetic base among the genotypes taken for study and possibility of genetic improvement through direct selection for these traits. These results are also in conformity with the findings of Chandra *et al.* (2009), Pandey and Singh (2011), Bhadru *et al.* (2012) and Dhanwani *et al.* (2013) for grain yield per plant and number of grains per panicle. The PCV and GCV recorded moderate values for the traits, number of effective tillers per plant, plant height, panicle length, kernel length after cooking, kernel elongation ratio, 1000-grain weight and harvest index. Hence, selection for these traits may be misleading if adopted for improvement programme under integrated fertilizer management through these traits. Similar kind of findings were also observed by Raju *et al.* (2004) for number of effective

Table 1: Analysis of variance for fourteen characters in 32 rice genotypes

S.No.	Character	Mean sum of squares		
		Replications (df = 2)	Treatments (df = 31)	Error(df = 62)
1.	Days to 50% flowering	3.218	265.957**	1.146
2.	Days to maturity	1.125	326.231**	1.727
3.	Number of effective tillers per plant	2.093	649.291**	5.133
4.	Plant height (cm)	0.956	5.742**	0.340
5.	Panicle length (cm)	0.433	20.752**	0.745
6.	Number of grains per panicle	11.812	3429.436**	74.076
7.	Kernel length (mm)	0.008	0.065**	0.005
8.	Kernel breadth (mm)	0.001	0.104**	0.011
9.	Kernel L/B ratio	0.002	2.561**	0.001
10.	Kernel length after cooking (mm)	9.000	0.069**	0.005
11.	Kernel elongation ratio	2.046	28.487**	1.220
12.	1000-grain weight(g)	8.453	139.971**	11.382
13.	Harvest index (%)	0.009	0.185**	0.031
14.	Grain yield per plant (g)	1.137	34.431**	2.166

* Significant at 5% ; ** Significant at 1%

Table 2: Mean, Range, Co-efficient of variation, Heritability (broad-sense) and Genetic advance as per cent of mean for 14 characters in rice under integrated fertilizer management

S.No.	Character	Mean	Range	Phenotypic co-efficient of variation	Genotypic co-efficient of variation	Heritability in broad sense (h^2b)	Genetic advance as % of mean
1.	Days to 50% flowering	100.75	76.67-117.67	9.38	9.33	98.83	19.10
2.	Days to maturity	127.38	102.00-145.67	8.21	8.18	99.33	16.79
3.	Plant height (cm)	96.83	77.37-130.43	15.31	15.13	97.67	30.81
4.	Number of effective tillers per plant	8.99	5.93-11.00	16.27	14.92	84.10	28.19
5.	Panicle length (cm)	22.85	17.73-26.87	11.70	11.41	95.17	22.94
6.	Number of grains per panicle	144.79	87.83-206.93	23.85	23.10	93.79	46.08
7.	Kernel length (mm)	5.73	5.06-6.11	4.38	4.32	97.39	8.78
8.	Kernel breadth (mm)	2.31	2.01-2.56	6.46	6.39	97.76	13.01
9.	Kernel L/B ratio	2.49	2.08-2.90	7.56	7.45	97.02	15.11
10.	Kernel length after cooking (mm)	8.00	5.80-9.92	11.55	11.54	99.91	23.77
11.	Kernel elongation ratio	1.39	1.01-1.67	11.09	10.85	95.81	21.88
12.	1000-grain weight (g)	22.55	16.50-27.27	14.15	13.45	89.97	26.22
13.	Harvest index (%)	45.67	24.63-55.82	16.13	14.33	79.02	26.25
14.	Grain yield per plant (g)	15.11	7.77-21.30	23.17	22.04	90.48	43.20

tillers per plant and 1000-grain weight; Kumar *et al.* (2013) for plant height; Mishra and Pravin (2004) and Singh *et al.* (2013) for panicle length and harvest index and Patil *et al.* (2003) for kernel length after cooking. The estimates of PCV and GCV were low for the characters days to 50% flowering, days to maturity, kernel length, kernel breadth and kernel L/B ratio. The selection for these traits would offer very little scope for genetic improvement of the genotypes under study. Similar results were also obtained by Singh *et al.* (2005) for kernel length, kernel breadth and kernel L/B ratio; Mamta Singh *et al.* (2007) for days to 50 per cent flowering and Das *et al.* (2005) and Kumar *et al.* (2013) for days to maturity. 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. Similar finding were also reported by Singh *et al.* (2006) and Pandey and Anurag (2010).

The amount of genetic variation considered alone will not be of much use to the breeder unless supplemented with the information on heritability estimate, which gives a measure of the heritable portion of the total variation. It has been suggested by Burton and Devane (1953) that the GCV along with heritability estimate could provide a better picture of the amount of advance to be expected by phenotypic selection. Since genetic advance is dependent on phenotypic variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection (Johnson *et al.,* 1955). Heritability in broad sense includes both additive and non-additive gene effects (Hanson *et al.,* 1956). While, narrow sense heritability includes only additive components (Johnson *et al.,* 1955). In the present study, the heritability estimates ranged from 79.02% (harvest index) to 99.91% (kernel length after cooking). High estimates of heritability were obtained by all characters, indicating the major role of additive gene action in inheritance of these traits. According to Panse (1957) if a character is governed by non-additive gene action, it may give high heritability but low genetic advance, whereas, of it is governed by additive gene action, high heritability along with high genetic advance provide good scope for further improvement. The traits number of effective tillers per plant, plant height, panicle length, number of grains per panicle, kernel elongation ratio, kernel length after cooking, 1000-grain weight, harvest index and yield per plant expressed high heritability values with high genetic advance as per cent of mean. The additive gene effects are responsible for these and selection for these traits could be beneficial. These results were in accordance with the findings of Singh *et al.* (2005) for number of effective tillers per plant; Chaturvedi *et al.* (2011) and Singh *et al.* (2013) for plant height; Nayudu *et al.* (2007) for panicle length and number of grains per panicle; Chikkalingaiah *et al.* (1999) for kernel elongation ratio; Veerabadhiran *et al.* (2009) for kernel length after cooking and grain yield per plant and Bhadru *et al.* (2012) for 1000-grain weight and harvest index.

High estimates of heritability associated with moderate genetic advance as percentage of mean were recorded for days to 50 per cent flowering, days to maturity, kernel breadth and kernel L/B ratio indicating that both additive and non-additive gene effects governed these characters. Hence, simple direct selection may be effective to improve these traits. These traits could also be improved by adapting recurrent selection method. These results were in consonance with the findings of Mamta Singh *et al.* (2007) for days to 50 per cent flowering; Das *et al.* (2005) for days to maturity; Sarawgi *et al.* (2000) for kernel breadth and kernel L/B ratio. Sarkar *et al.* (2007) and Raju *et al.* (2004) recorded high heritability coupled with low genetic advance for kernel length which is in conformity with present experiment suggesting greater role of non-additive gene action in their inheritance of these character. Therefore heterosis breeding could be used to improve these traits.

The overall results indicated that there is adequate genetic variability present in the material studied. The GCV, PCV, broad sense heritability and genetic advances as percent of mean suggested number of effective tillers per plant, plant height, panicle length, number of grains per panicle, kernel elongation ratio, kernel length after cooking, 1000-grain weight, harvest index and grain yield per plant were important contributing traits and selection based on these traits would be most effective.

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