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AR Khaire
Regional Agriculture Research
Station, Karjat, Raigad.
Dr. Balasaheb Sawant Konkan
Krishi Vidyapeeth, Dapoli,
Maharashtra, India

RL Kunkerkar
Regional Agriculture Research
Station, Karjat, Raigad.
Dr. Balasaheb Sawant Konkan
Krishi Vidyapeeth, Dapoli,
Maharashtra, India

BS Thorat
Regional Agriculture Research
Station, Karjat, Raigad.
Dr. Balasaheb Sawant Konkan
Krishi Vidyapeeth, Dapoli,
Maharashtra, India

MP Gavai
Regional Agriculture Research
Station, Karjat, Raigad.
Dr. Balasaheb Sawant Konkan
Krishi Vidyapeeth, Dapoli,
Maharashtra, India

SG Bhave
Regional Agriculture Research
Station, Karjat, Raigad.
Dr. Balasaheb Sawant Konkan
Krishi Vidyapeeth, Dapoli,
Maharashtra, India

Correspondence

AR Khaire
Regional Agriculture Research
Station, Karjat, Raigad.
Dr. Balasaheb Sawant Konkan
Krishi Vidyapeeth, Dapoli,
Maharashtra, India

Studies on genetic variability for yield and yield contributing traits in local rice (*Oryza sativa* L.)

AR Khaire, RL Kunkerkar, BS Thorat, MP Gavai and SG Bhave

Abstract

The experiment was conducted with twenty four rice genotypes collected from local area of Maharashtra along with two check varieties in Kharif 2015-16 in randomize block design. Wide range of variability was present in the local lines of rice under study. The range of GCV and PCV was 5.76% to 24.79% and 2.62% to 24.34% respectively. The estimates of phenotypic, genotypic and environmental variances revealed that phenotypic variances were higher in magnitude over the respective genotypic variances for all the characters under study. PCV and GCV were high for number of filled spikelets per panicle and number of spikelets per panicle. The broad sense heritability ranged from 20.37% to 97.78%. High estimates of broad sense heritability was observed for number of filled spikelet per panicle, number of spikelet per panicle, days to maturity and plant height. The genetic advance and genetic advance as per cent of mean was ranged from 1.00% to 71.22% and 2.18% to 68.60% respectively. Heritability along with genetic advance is more useful for selection than the heritability alone.

Keywords: genetic variability, yield contributing, *Oryza sativa*, phenotypic variances

Introduction

Rice is staple food of more than 60% of Indian population. It accounts for about 43% of total food grain production and 46% of total cereal production in the country. Rice occupies pivotal place in Indian Agriculture. In order to meet the domestic demand of the increasing population the present day production of 107.40 million tons (Anonymous, 2015-16) [1] of milled rice has to be increased to 125 million tons by the year 2030. Since the yield of high yielding varieties (HYVs) of rice is plateauing, it is rather difficult to achieve this target with the present day inbred varieties. Therefore, to sustain the self-sufficiency in rice, additional production of 1.17 million tons is needed every year. There are a large number of indigenous rice varieties in India, which are still grown by the tribal people and small farmers of the remote areas where the modern agricultural practices, sufficient foods as well as healthcare systems are a dream. Nature has provided them some alternative ways. They have different indigenous rice varieties with its nutritional and medicinal values. The indigenous rice varieties cultivated by traditional farmers may contain a considerable genetic diversity that can serve as a source of germplasm for genetic improvements of cultivated varieties of rice. In rice varietal improvement programmes, indigenous rice varieties have proved to be useful donors for sources of resistance or tolerance to many stress environments and for imparting resistance to important pests and diseases. In general, diverse landraces traditionally cultivated by farmers around the centers of diversity and domestication of crops are as key natural resources important for maintaining the future food security in light of the changing climate. After considering this attributes, Regional Agriculture Research Station, Karjat has collected several local germplasm. These germplasm have more genetic diversity, high degree of tolerance for biotic and abiotic stresses and wide adaptability with meaningful nutritional quality.

Materials and methods

The experiment was conducted at the Research Farm of Regional Agricultural Research Station, Karjat under Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, Maharashtra, India during *Kharif*, 2015. The experimental material for the present study consisted of twenty six genotypes of rice (*Oryza sativa* L.) which was collected from different sources, it was expected that these genotypes were phenotypically different in respect of growth habit, plant height. The present investigation was carried out by adopting Randomized Block Design with three replications. Twenty seven days old seedlings were transplanted with 20 cm distance between rows and 15 cm distance between plants within rows. All the recommended package of practices was followed along with necessary prophylactic plant protection measure raise a

good crop. Observations were recorded and the data was subjected to statistical analysis. The variability was estimated as per procedure for for analysis of variation suggested by Panse and Sukhatme (1985) [12]. PCV and GCV were calculated by the given formula by Burton and De Vane (1953) [2], broad sense heritability (h^2_b) by Lush (1949) [8] and genetic advance i.e. the expected genetics were calculated by using the procedure given by Johnson *et al.* (1955) [7].

Result and Discussion

The analysis of variance revealed that the differences among the genotypes were significant for most of the characters under study. The genotypes were thus suitable for genetical studies, as their contribution to the genotypic sum of squares was significant for most of the characters. The total variability in each of these characters could be partitioned into three components *viz.*, phenotypic, genotypic and environmental. The phenotypic variance and genotypic variance was maximum for number of spikelets per panicle, number and lowest in number of tillers per plant. Genotypic and phenotypic variances were high for number of spikelets per panicle followed by number of filled spikelets per panicle, plant height and straw yield per plant indicating wide variability for these characters. Similar result were reported Pandey and Awasthi (2002) [11].

The magnitude of PCV was highest for number of filled spikelet per panicle (24.79%) followed by number of spikelet per panicle (23.66%). The magnitude of GCV was highest for number of filled spikelet per panicle (24.34%) followed by number of spikelet per panicle (23.40%). High GCV indicated high genetic variability within the test genotype.

The phenotypic coefficient of variation was maximum for number of filled spikelet per plant (24.79%) followed by number of spikelets per panicle (23.66%), grain yield per plant (21.12%), straw yield per plant (18.23%), 1000 grain weight (15.74%), plant height (15.18%), number of tillers per plant (13.34%), harvest index (8.47%), days to 50% flowering (7.57%), panicle length (7.51%), days to maturity (6.58%) and spikelet fertility (5.76%) The genotypic coefficient of variation was maximum for number of filled spikelet per panicle (24.34%) followed by number of spikelet per panicle (23.40%), grain yield per plant (15.48%), straw yield (15.35%), plant height (14.86%), 1000 grain weight (14.56%), number of tillers per plant (9.02%), days to 50% flowering (7.34%), panicle length (5.74%), days to maturity (5.84%), harvest index (3.82%) and spikelet fertility (2.62%). The results were accordance with Chauhan and Tandon (1984) [3], Jangale *et al.* (1985) [6], Roy *et al.* (1995) [15], Deb

Choudhury and Das (1998) [4] and Naik *et al.* (2002) [19].

The broad sense heritability ranged from 20.37% to 97.78%. High estimates of broad sense heritability was observed for number of spikelet per panicle (97.78%), number of filled spikelet per panicle (96.41%), plant height (95.89%), days to 50% flowering (93.96%) while low spikelet fertility (20.68% and harvest index (20.37%). Similar results reported by Sinha and Bhattacharyya (1980) [20], Ghosh *et al.* (1981) [5], Singh and Sharma (1982) [19], Ravindranath *et al.* (1983) [13], Chauhan and Tandon (1984) [3], Sawant and Patil (1995) [18], Nath and Talukdar (1997) [10] and Naik *et al.* (2002) [9].

High genetic advance was observed for number of spikelets per panicle (71.22%), number of filled spikelets per panicle (66.14%) and plant height (42.55%). Similar results were obtained by Ghosh *et al.* (1981) [5], Singh and Sharma (1982) [19], Ravindranath *et al.* (1983) [13], Wilfred Manual and Prasad (1993) [21], Sawant and Patil (1995) [18] and Nath and Talukdar (1997) [10].

Maximum estimates of genetic advance as per cent of mean was recorded by number of spikelet per panicle (72.83%) followed by number of filled spikelets per panicle (68.60%), plant height (44.37%), days to maturity (17.36%), straw yield per plant (15.58%) and days to 50% days to flowering (15.17%) while minimum estimates of genetic advance as per cent of mean was recorded by number of tillers per plant (2.18%), panicle length (4.11%), harvest index (5.89%), grain yield (9.20%) and spikelet fertility (10.63%).

Heritability alone don't provided clear information on the amount of genetic progress that would result from the selection without genetic advance. High heritability estimates along with high genetic advance were noticed for number of spikelet per plant, number of filled spikelet per panicle, plant height, days to 50% flowering, and days to maturity

Conclusion

It is concluded that yield is controlled by both GCV and PCV also to use appropriate selection procedure for improvement of the characters in general and yield in particular since high heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression. High heritability with low genetic advance was indicated the influence of non-additive gene action. The heritability provide the information on the magnitude of inheritance of quantitative characters, but it does not indicate the magnitude of genetic gain obtained by selection of best individual from the best population. So, heritability along with genetic advance is more useful for selection than the heritability alone.

Table 1: Analysis of variance for yield and yield contributing characters in rice

S. No.	Characters	Mean sum of squares		
		Replication	Treatment	Error
1.	Days to 50 per cent flowering	6.08**	156.35**	3.27
2.	Days to maturity	0.47	183.40**	15.04
3.	Plant height (cm)	4.26**	1354.05**	19.04
4.	Number of tillers per plant	1.22*	2.17*	0.61
5.	Panicle length (cm)	0.47	8.71**	1.67
6.	Number of spikelets per panicle	63.96**	3695.77**	27.72
7.	Number of filled spikelets per panicle	2.35**	3248.09**	39.76
8.	Spikelet fertility (%)	6.18**	37.99**	21.31
9.	1000 grain weight (g)	0.21	33.54**	1.79
10.	Grain yield per plant (g)	5.53**	41.62**	9.27
11.	Straw yield per plant (g)	50.11**	138.30**	16.67
12.	Harvest index (%)	5.35**	11.63**	6.58
	D.F.	2	25	50

Table 2: Components of variation for yield attributing characters in rice

S. No.	Characters	Phenotypic variance	Genotypic Variance	Environmental variance
1.	Days to 50 per cent flowering	54.30	51.02	3.27
2.	Days to maturity	71.08	56.03	15.04
3.	Plant height (cm)	464.04	445.00	19.04
4.	Number of tillers per plant	1.13	0.51	0.61
5.	Panicle length (cm)	4.02	2.34	1.67
6.	Number of spikelets per panicle	1250.40	1222.68	27.72
7.	Number of filled spikelets per panicle	1109.20	1069.44	39.76
8.	Spikelet fertility (%)	26.87	5.56	21.31
9.	1000 grain weight (g)	12.37	10.58	1.79
10.	Grain yield per plant (g)	20.05	10.78	9.27
11.	Straw yield per plant (g)	57.21	40.54	16.67
12.	Harvest index (%)	8.26	1.68	6.58

Table 3: Estimates of genetic parameters for yield attributing characters in rice

S. No.	Characters	PCV (%)	GCV (%)	h ² b (%)	GA	GAM (%)
1.	Days to 50 per cent flowering	7.57	7.34	93.96	14.26	15.17
2.	Days to maturity	6.58	5.84	78.82	13.69	17.36
3.	Plant height (cm)	15.18	14.86	95.89	42.55	44.37
4.	Number of tillers per plant	13.34	9.02	45.70	1.00	2.18
5.	Panicle length (cm)	7.51	5.74	58.28	2.40	4.11
6.	Number of spikelets per panicle	23.66	23.40	97.78	71.22	72.83
7.	Number of filled spikelets per panicle	24.79	24.34	96.41	66.14	68.60
8.	Spikelet fertility (%)	5.76	2.62	20.68	2.20	10.63
9.	1000 grain weight (g)	15.74	14.56	85.46	6.19	7.24
10.	Grain yield per plant (g)	21.12	15.48	53.75	4.95	9.20
11.	Straw yield per plant (g)	18.23	15.35	70.85	11.04	15.58
12.	Harvest index (%)	8.47	3.82	20.37	1.20	5.89

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