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To Study the Genetic Variability for Different Morphological and Quality Characters

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Abstract: ***The experiment was conducted at Research Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.).To assess the genetic variability among the ninety eight aromatic advanced breeding lines of rice along with popular standard checks namely Indira Sugandhit Dhan-1, Pusa Basmati-1, Badsha bhog, Dubraj, Chinnor, Mahisugandha and Kalanamak. The mean sum of squares due to the genotypes were highly significant for all the characters studied namely, Days to 50 percent flowering, Plant height, Panicle length, Total tillers per plant, Effective tillers per plant, Filled spikelets per panicle, Unfilled spikelets per panicle, Total spikelet's per panicle, Paddy length, 100 seed weight, Grain yield per plant, Paddy breadth, Spikelet sterility percentage, Paddy L/B ratio, Hulling %, Brown Rice Length, Brown Rice breadth, Brown Rice L/B ratio, Milling %, Kernel length, Kernel breadth, Kernel L/B ratio, Elongation Index, Kernel breadth after cooking, Cooked Kernel L/B ratio, Elongation ratio and Kernel length after cooking. The high estimate of phenotypic and genotypic coefficient of variation was observed from Unfilled spikelets per panicle, Filled spikelets per panicle, Total spikelets per panicle, Spikelet sterility percentage, and Grain yield per plant and Brown rice breadth. High heritability with high genetic advance was found for number of Total spikelets per panicle and Filled spikelets per panicle.***

Keywords: phenotypic and genotypic coefficient, heritability, genetic advance

1. Introduction

Rice is the most consumed cereal grain in the world, constituting the dietary staple food for more than half of the planet's human population. In world, rice has occupied an area of 160.6 million hectares, with a total production of 459.74 million metric tons in 2010 (Anonymous, 2011a). In Asian countries, rice is the main staple crop covering about ninety per cent of rice grown in the world, with two countries, China and India, growing more than half of the total crop. Rice provides about two-third of the calorie intake for more than two billion people in Asia, and a third of the calorie intake of nearly one billion people in Africa and Latin America (Shastry *et al*., 2000).

Chhattisgarh popularly known as "Rice Bowl of India" occupies an area around 3.61 million hectares with the production of 5.22 MT (Anonymous, 2011c). Aromatic rice varieties are very much popular for their quality and aroma. Aroma quality of scented rice is major character, which increases the value of rice in the international market. In addition to long grain Basmati type which have high export potential, there are large number of indigenous short grained aromatic varieties cultivated in pockets of different states. Despite of low yield, they posses valuable genes for aroma, excellent cooking and eating quality traits and enjoy immense consumer preference in Chhattisgarh and in many other states. Grain quality in rice is a combination of many physico-chemical traits (Juliano, 1970). Physical quality is determined by the grain dimension, hulling, milling and head rice recovery.

2. Materials and Methods

The experimental material was consisting of ninety eight aromatic advanced breeding lines of rice along with popular standard checks in a randomized block design with two replications *viz.*, Indira Sugandhit Dhan-1, Pusa Basmati-1, Badsha Bhog, Dubraj, Chinnor, Mahisugandha, and Kalanamak. Each breeding line was grown in a plot comprising 7 rows of 5 meter long maintaining inter and intra row spacing of 20X15 cm.

The results of analysis of variance indicated **(table 4.1)** that the mean sum of squares due to the genotypes were highly significant for all the quantitative and quality characters studied *i.e.* days to 50 percent flowering, Plant height (cm), Panicle length (cm), Total number of tillers per plant, Effective tillers per plant, total number of spikelets per panicle, filled spikelets per panicle, Unfilled spikelets per panicle, Spikelet sterility percentage, 100- seed weight, Grain yield per plant, Paddy length (mm), Paddy breadth (mm), Paddy L/B ratio, Brown rice length (mm), Brown rice breadth (mm), Brown rice L/B ratio, Kernel length (mm), Kernel breadth (mm), kernel L/B ratio, Kernel length after cooking (mm), Kernel breadth after cooking (mm), Cooked kernel L/ B ratio, Elongation ratio, Elongation index, Hulling percentage and Milling percentage.

3. Mean and variability parameters for quantitative and quality characters

Results revealed that high degree of variability was present in the breeding lines for all the characters under study**.** The high estimate of phenotypic and genotypic coefficient of variation was observed from number of unfilled spikelets per panicle (PCV% = 42.31, GCV% = 38.37)

The number of filled spikelets per panicle, total spikelet's per panicle, spikelet sterility percentage, grain yield per plant, brown rice breadth and brown rice length/breadth ratio showed high PCV% (23.39, 22.06, 36.31, 30.65,22.50 and 26.01 respectively) in combination with high GCV% (21.52, 20.25, 33.14 25.79, 21.25 and 23.52 respectively).

The 100- seed weight, paddy length/breadth ratio, kernel rice length/breadth ratio and elongation index showed high PCV% (24.17, 21.61, 20.67 and 21.54 respectively) in combination with moderate GCV% (19.28, 19.40, 18.80 and 17.99 respectively) for this traits.

The moderate estimates of PCV% and GCV% (10-20%) were observed for days to 50 percent flowering (PCV% =11.01, GCV%=10.92), plant height (PCV% =14.22, GCV% =13.82) total number of effective tillers per plant(PCV% =18.37, GCV%=13.96), paddy length (PCV% =17.32, GCV% =16.77), brown rice length (PCV% =17.38, GCV% =16.84), kernel length (PCV% =16.96, GCV% =16.57), kernel length after cooking (PCV% =14.44, GCV% =13.91), kernel length/breadth ratio after cooking (PCV% =17.29, GCV% =15.70) and elongation ratio (PCV% =18.68, GCV% =17.73)

The number of total tillers per plant, kernel breadth and paddy breadth showed moderate PCV% (10.84, 10.57 and 13.08) in combination with low GCV % (8.62, 7.67 and 9.92).

The low estimates of PCV% and GCV% (<10%) were observed for panicle length (PCV% =9.86, GCV% =8.55), hulling percentage (PCV% =2.88, GCV% =2.30), milling percentage (PCV% =6.40, GCV% =5.01) and kernel breadth after cooking (PCV% =8.46, GCV% =6.51) **(table 4.2.)**.

The high magnitude of genotypic coefficient of variation reveals the high genetic variability present in the material studied. In the present investigation phenotypic coefficient of variation was recorded higher than genotypic coefficient of variation and was in accordance with the Sarawgi *et al.* (1994) and Ganesan *et al.* (1995). The high magnitude of genotypic coefficient of variation was noted for grain yield per plant.

Heritability and genetic advance

Heritability in broad sense (h^2bs) was highest for days to 50% flowering (98.5%) followed by kernel length (95.6%), plant height (94.6%), paddy length (93.7), brown rice length (93.9%), kernel length after cooking (92.7%) and elongation ratio (90.1%)

In addition to the above characters the other traits which exhibited high estimates of heritability where brown rice breadth (89.2%), filled spikelets per panicle (84.7%), total spikelet's per panicle (84.6%), kernel length/ breadth ratio (82.8%), kernel L/B ratio after cooking 82.4%) unfilled spikelets per panicle (82.2%), spikelet's sterility percentage (81.9 %), brown rice length/ breadth ratio (81.8%), paddy length/breadth ratio (80.5%), panicle length (75.1%), and grain yield per plant (70.8%).

The moderate value of heritability was shown by hulling percentage (69.1%), elongation index (69.8%), 100- seed weight (63.6 %), total number of tiller per plant (63.3 %), milling percentage (61.4%), kernel breadth after cooking (59.2%), effective tillers per plant(57.7 %), paddy breadth (57.6%) and kernel breadth (52.6%) **(table 4.2.)**

The high heritability observed for grain yield per plant is in conformity to the findings of Chaudhary and Motiramani (2003), Satyanaryan *et al.* (2005), Jaiswal *et al.* (2007). Similar results of high heritability for plant height was observed by Kaw *et al.* (1999), Choudhary *et al.* (2004) and Satyanaryan *et al.* (2005). The findings of high heritability estimates for days to 50% flowering which is in according with finding of Satyanaryan *et al.* (2005) and Chakraborty and Chakraborty (2010) . The high heritability for filled spikelets per panicle has been reported by Chauhan *et al.* (1993), Kaw *et al.* (1999) and Chaudhary and Motiramani (2003).

The magnitude of genetic advance as percentage of mean was categorized as high (>30%), moderate (30-10%) and low (<10%). The highest genetic advances percentage of mean was observed for total spikelet's per panicle (82.87%) followed by filled spikelets per panicle (72.82), and plant height (31.86%).

The moderate genetic advance as percentage of mean (20-30%) was recorded for days to 50% flowering (21.90%) and unfilled spikelets per panicle (26.85).

The low magnitude of genetic advance (<20%) was recorded for panicle length (3.80%), total number of tillers per plant(1.12%), effective tillers per plant(1.43), spikelet sterility percentage (10.64%), 100- seed weight (0.57%) and grain yield per plant (11.28), paddy length (2.82), paddy breadth (0.31), paddy L/B ratio (1.55), hulling percentage (3.12), brown rice length (2.14) , brown rice breadth (0.73), brown rice length/breadth ratio (1.64), milling percentage (5.12), kernel length (1.82), kernel breadth (0.19), kernel L/B ratio (1.17), kernel length after cooking (2.05), kernel breadth after cooking (0.24), kernel length/breadth ratio of cooked rice (0.95), elongation ratio (0.48) and elongation index (0.31) **(table 4.2.)**

The present findings of highest genetic advance as percent of mean for filled spikelets per panicle. For plant height high estimate of genetic advance was observed

High magnitude of genetic advance indicates that the characters are governed by additive genes and selection will be rewarded. Moderate genetic advance indicate the existence of additive as well as non additive gene action for these traits. The low genetic advance indicated that characters are governed by non additive genes and heterosis breeding may be exploited for the traits.

Table 4.1: Analysis of variance for different quantitative and qualitative characters

S. N.	Characters	Mean sum of square		
		Replication (df=1)	Treatment (df=97)	Error (df=97)
1	Days to 50% flowering	8.625**	231.235**	1.730
2	Plant height (cm)	15.250	521.917**	15.046
3	Panicle length (cm)	0.781	10.560**	1.504
4	Total tillers per plant	1.787**	1.207**	0.271
5	Effective tillers per plant	7.287**	2.286**	0.612
6	Total number of spikelets per panicle	18.000	4175.072**	348.773
7	Filled spikelets per panicle	4.000	3219.81**	267.628
8	Unfilled spikelets per panicle	4.281	457.746**	44.599
9	Spikelet sterility percentage	0.890	72.371**	7.718

10	100 seed weight (g)	0.004	0.304**	0.067
11	Grain yield per plant (g)	11.210	102.083**	17.443
12	Paddy length (mm)	0.166	4.140**	0.135
13	Paddy breadth (mm)	9.429**	0.104**	0.028
14	Paddy L/B ratio	0.516**	1.597**	0.172
15	Brown Rice Length(mm)	0.793**	2.363**	0.074
16	Brown Rice breadth(mm)	3.830**	0.300**	0.017
17	Brown Rice L/B ratio	14.544**	1.724**	0.172
18	Kernel length (mm)	2.913**	1.666**	0.037
19	Kernel breadth (mm)	1.014**	0.047**	0.014
20	Kernel L/B ratio	0.960**	0.858**	0.080
21	Kernel length after cooking (mm)	1.439**	2.217**	0.083
22	Kernel breadth after cooking(mm)	2.583**	0.060**	0.015
23	Cooked Kernel L/B ratio	2.900**	0.572**	0.055
24	Elongation ratio	0.066**	0.127**	0.006
25	Elongation Index	0.061**	0.078**	0.014
26	Hulling %	2.250	8.123**	1.484
27	Milling %	13.00*	26.456**	6.332

Note -: **Significant at 1% * Significant at 5%

Table 4.2: Genotypic and phenotypic coefficient of variance (GCV and PCV), heritability, (h2) and genetic advance (GA) as percentage of mean average and range for different characters

S.N.	Characters	Average mean	Range		GCV (%)	PCV (%)	h2 (bs) (%)	GA as % of mean
			Min	**Max**				
1	Days to 50% flowering	98.05	77.5	122	10.92	11.01	98.5	21.90
2	Plant height (cm)	115.22	95	195	13.82	14.22	94.4	31.86
3	Panicle length (cm)	24.89	19.9	35.6	8.55	9.86	75.1	3.80
4	Total tillers per plant	7.93	5.9	9.6	8.62	10.84	63.3	1.12
5	Effective tillers per plant	6.55	3.1	8.9	13.96	18.37	57.7	1.43
6	Total number of spikelets per panicle	215.96	112.3	328.0	20.25	22.02	84.6	82.87
7	Filled spikelets per panicle	178.49	99.9	290.7	21.52	23.39	84.7	72.82
8	Unfilled spikelets per panicle	37.46	9.5	78.30	38.37	42.31	82.2	26.85
9	Spikelet sterility percentage	17.22	6.47	35.0	33.14	36.61	81.9	10.64
10	100 seed weight (g)	1.78	1.00	3.00	19.28	24.17	63.6	0.57
11	Grain yield per plant (g)	25.22	10.90	45.42	25.79	30.65	70.8	11.28
12	Paddy length(mm)	8.44	5.75	10.4	16.77	17.32	93.7	2.82
13	Paddy breadth(mm)	1.97	1.20	2.50	9.92	13.08	57.6	0.31
14	Paddy L/B ratio	4.35	2.66	6.61	19.40	21.61	80.5	1.56
15	Brown Rice Length (mm)	6.35	4.25	8.45	16.84	17.38	93.9	2.14
16	Brown Rice breadth (mm)	1.77	1.35	2.95	21.25	22.50	89.2	0.73
17	Brown Rice L/B ratio	3.74	2.10	5.89	23.52	26.01	81.8	1.64
18	Kernel length (mm)	5.44	3.50	7.15	16.57	16.96	95.6	1.82
19	Kernel breadth (cm)	1.66	1.35	1.95	7.67	10.57	52.6	0.19
20	Kernel L/B ratio	3.31	1.88	4.93	18.80	20.67	82.8	1.17
21	Kernel length after cooking (mm)	7.42	5.55	9.70	13.91	14.44	92.7	2.05
22	Kernel breadth after cooking (mm)	2.31	1.65	2.70	6.51	8.46	59.2	0.24
23	Cooked Kernel L/B ratio	3.23	2.21	4.60	15.70	17.29	82.4	0.95
24	Elongation ratio	1.38	0.87	1.95	17.73	18.68	90.1	0.48
25	Elongation Index	0.99	0.50	1.62	17.99	21.54	69.8	0.31
26	Hulling %	76.18	71.55	80.55	2.30	2.88	69.1	3.12
27	Milling %	63.31	54.75	70.40	5.01	6.40	61.4	5.12

Note: GCV: Genotypic coefficient of variation; **PCV**: Phenotypic coefficient of variation;
h^2 (bs): Heritability in broad sense; **GA**: Genetic advance.

4. Summary, Conclusions

The 98 genotypes along with seven popular standard checks were characterization on the basis of 18 qualitative characters and given in appendix III. The genotypes also classified for aroma, 89 genotypes grouped into mild scented and nine genotypes into highly scented.

Analysis of variance indicated that the mean sum of squares due to the genotypes were highly significant for all the characters studied namely, Days to 50 percent flowering, Plant height , Panicle length, Total tillers per plant, Effective tillers per plant, Filled spikelets per panicle, Unfilled spikelets per panicle, Total spikelet's per panicle, Paddy length, 100 seed weight, Grain yield per plant, Paddy breadth, Spikelet sterility percentage, Paddy L/B ratio, Hulling %, Brown Rice Length, Brown Rice breadth, Brown Rice L/B ratio, Milling %, Kernel Length, Kernel breadth, Kernel L/B ratio, Elongation Index, Kernel breadth after cooking, Cooked Kernel L/B ratio, Elongation ratio and Kernel length after cooking.

The coefficient of variation is an important tool for obtaining comparison of the variability present among different characters. The number of Filled spikelets per panicle, Unfilled spikelets per panicle, Total spikelet's per panicle, Spikelet sterility percentage, Grain yield per plant, Brown rice width and Brown rice length/breadth ratio showed high PCV % in combination with high GCV %. The moderate estimates of PCV and GCV were observed for Days to 50 percent flowering, Plant height, Total number of effective tillers per plant, Paddy length, Brown rice length, Kernel length, Kernel length after cooking, Kernel length/breadth ratio after cooking and Elongation ratio.

Heritability in broad sense (h^2_{bs}) was highest for days to 50% flowering followed by Kernel length, Plant height, Paddy length, Brown rice length, Kernel length after cooking and Elongation ratio. The highest genetic advances percentage of mean was observed for total spikelets per panicle followed by Filled spikelets per panicle, and Plant height.

5. Conclusion

Beside the biometrical studied all the 98 genotypes have been characterized for 18 morphological traits and for aroma. Based on leaf aroma test 9 genotypes had strongly scented, and 89 had mild scent. A wide range of variation was observed for most of the characters in the genotypes studied; indicating that selection based on these characters is expected to be effectives. High magnitude of genetic advance indicates that the characters are governed by additive genes and selection will be rewarded. Moderate genetic advance indicate the existence of additive as well as non additive gene action for these traits. The low genetic advance indicated that characters are governed by non additive genes and heterosis breeding may be exploited for the traits.

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