SHORT COMMUNICATION

ANALYSIS OF CORRELATION COEFFICIENTS FOR YIELD AND QUALITY CHARACTERS IN AROMATIC ADVANCED BREEDING LINES OF RICE (*ORYZA SATIVA* L.)

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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.) during kharif 2010 to assess the agromorphological characterization, genetic variability, association analysis and genetic divergence 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. In the present investigation Grain yield per plant was positively and significantly associated with 100-seed weight, Number of total effective tillers per plant, Filled spikelets per panicle and Total spikelets per panicle.

Keywords: Aromatic Rice, Genotypic Correlation Coefficient, Phenotypic Correlation Coefficient

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).

India is the second largest producer of rice after China has an area of over 43.77 million hectares with the production of 89.05 million tons in 2010 (Anonymous, 2011b). Rice being the main source of livelihood for more than 120-150 million rural household is the backbone of the Indian Agriculture. It occupies about 23.3 per cent of the food grain production and 55 percent of cereal production. The rice plays a very vital role in the national food security. Even then rice self-sufficiency in India is precarious. The country's population of more than a billion is growing at 1.8% per year, outpacing the 1.4% annual growth rate of rice production.

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). The prime causes of low productivity of rice in Chhattisgarh are unappropriate adoption of agronomical practices, limited irrigation (28.0 %) and lack of improved varieties suitable to different ecosystems.

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. The quality of starch gelatinization temperature and protein content mainly constitute the chemical quality of rice. The cooking qualities are indexed by alkali spreading value, cooked kernel length, and elongation ratio. Scented varieties in general are tall, photoperiod sensitive with low yield potential. Therefore, presently much emphasis is given by the researchers on the development of high yielding varieties with good grain quality and aroma.

MATERIAL AND METHODS

The present research study on "Analysis of genetic variability for yield and quality characters in aromatic advanced breeding lines of rice (*Oryza sativa* L.)" was conducted at Research Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India. Chhattisgarh state is located between 17˚ 14′ and 24˚ 45′ N latitude and 79˚16′ and 84˚15′ E longitudes whereas, Raipur lies at 21˚16′ N and 81˚36′ E with a height of 289.60 meters above the mean sea level.

The experiment was conducted during *kharif* 2010. The maximum temperature 35.7 ˚C and minimum temperatures 15 ˚C was recorded during the crop growth season. The total rainfall during crop growth season was 1104.2 mm. highest amount of rainfall during crop growth period was received in the month of July (277.8 mm). The meteorological data depict a favorable season for crop growth but due to unevenly spread of rains, adversely affected the crop.

The experimental material was consisting of ninety eight aromatic advanced breeding lines of rice along with popular standard checks *viz.,* Indira Sugandhit Dhan-1, Pusa Basmati-1, Badsha Bhog, Dubraj, Chinnor, Mahisugandha, and Kalanamak, These breeding lines were received from rice section of department of Genetics and Plant Breeding I.G.K.V Raipur (C.G.). The experiment was laid out in randomized block design with two replications. Each breeding line was grown in a plot comprising 7 rows of 5 meter long maintaining inter and intra row spacing of 20X15 cm. Transplanting of the material was done manually when the seedlings were 21 days old nursery. A fertilizer dose of 60N:40P:20K kg/ha was applied. The entire dose of phosphorus and potassium along with half dose of nitrogen was applied as basal at the time of field preparation and the remaining nitrogen dose was applied in two splits at 20 days interval on standing crop, starting from 30 days after transplanting.

Observations recorded on various agro-morphological including qualitative and quantitative characters in each plot, on five random plants. By taking the average, the mean value for the treatment was computed. The characters studied viz., Qualitative characters : Early plant vigor (EPV), Basal leaf sheath color (BLSC), Leaf blade color (LBC), Leaf blade pubescence (LBP), Ligule color (LgC), Ligule shape (LgS), Collar color (CC), Auricle color (AC), Internode color (IC), Flag leaf angle (FLA), Panicle excertion (PE), Panicle type (PT), Stigma color (SgC), Apiculous color (ApC), Awning (An), Hull color (HC), Sterile lemma color (SLmC), Seed coat color (SCC). Quantitative characters: Days to 50 per cent flowering, Plant height, Panicle length, Total number of tillers per plant, Effective tillers per plant, Total number of spikelets per panicle, Number of filled spikelets per panicle, Number of unfilled spikelets per panicle, Spikelet sterility percentage, 100-Seed weight (g), Grain yield per plant (g). Physico-chemical quality characters, Paddy length (mm), Paddy breadth (mm), Paddy length, breadth (L/B) ratio, Brown rice length (mm), Brown rice breadth (mm), Brown rice length, breadth (L/B) ratio, Kernel length (mm), Kernel breadth (mm), Kernel length, breadth (L/B) ratio, Kernel length after cooking (KLAC) (mm), Kernel breadth after cooking (KBAC) (mm), Cooked kernel L/B ratio (KLAC: KBAC), Elongation ratio (ER), Elongation index (EI), Hulling percentage, Milling percentage, Alkali spreading value (Gelatinization temperature), Aroma.

Statistical analysis

Correlation coefficients analysis measures the mutual relationship between various characters at genotypic (g), phenotypic (p) and environmental levels with the help of following formula suggested by Miller *et al.* (1958).

Estimation of Correlation coefficients

Genotypic correlation coefficient between characters x and y

$r_{xy\ (g)} = Cov_{\ xy\ (g)} / \sqrt{(Var_{\ x\ (g)} \text{ x } Var_{y\ (g)})}$

2.1.2. Phenotypic correlation coefficient between characters x and y

$r_{\ xy\ (p)} = Cov_{\ xy\ (p)} / \sqrt{(Var_{x\ (p)} \text{ x } Var_{y\ (p)})}$

Where,

$r_{\ xy\ (g)}$ = Genotypic correlation coefficient between x and y

$r_{\ xy\ (p)}$ = Phenotypic correlation coefficient between x and y

$Cov_{\ xy\ (g)}$ = Genotypic covariance between x and y

$Cov_{\ xy\ (p)}$ = Phenotypic covariance between x and y

$Var_{\ x\ (g)}$ = Genotypic variance of x

$Var_{\ x\ (p)}$ = Phenotypic variance of x

$Var_{\ y\ (g)}$ = Genotypic variance of y

$Var_{\ y\ (p)}$ = Phenotypic variance of y

Table 1: Phenotypic (P), Genotypic (G), and Environmental (E) Correlation coefficient for quantitative traits

S.N.		DF	PH	PL	TT/P	ET/P	TS/Pa	FG/Pa	UG/Pa	SSP	SI	GY/P
		1	2	3	4	5	6	7	8	9	10	11
1	P	1.000	0.109	0.016	0.001	-0.155	0.428**	0.342**	0.382**	0.223	-0.337**	-0.051
	G	1.000	0.155	0.033	0.015	-0.203	0.466**	0.371**	0.425**	0.251	-0.418**	-0.062
	E	1.000	-0.054	-0.203	-0.137	-0.018	0.053	0.066	-0.014	-0.046	-0.081	0.012
2	P		1.000	0.374**	0.142	0.175	-0.233	-0.272*	0.017	0.176	0.048	-0.134
	G		1.000	0.429**	0.177	0.214	-0.243	-0.288**	0.031	0.208	0.035	-0.172
	E		1.000	0.108	0.035	0.108	-0.176	-0.157	-0.107	-0.069	0.146	0.051
3	P			1.000	0.086	0.179	-0.164	-0.194	0.020	0.138	-0.003	-0.020

	G			1.000	0.053	0.234	-0.220	-0.253	0.007	0.164	0.022	-0.050
	E			1.000	0.164	0.078	0.060	0.041	0.067	0.044	-0.059	0.064
4	P				1.000	0.550**	-0.074	-0.139	0.146	0.205	-0.164	-0.063
	G				1.000	0.596**	-0.127	-0.226	0.218	0.304**	-0.297	-0.230
	E				1.000	0.481**	0.081	0.110	-0.044	-0.053	0.067	0.279*
5	P					1.000	-0.079	-0.098	0.021	0.084	-0.083	0.063
	G					1.000	-0.167	-0.173	-0.047	0.061	-0.147	-0.154
	E					1.000	0.149	0.091	0.194	0.152	0.015	0.461**
6	P						1.000	0.945**	0.510**	0.080	-0.485**	0.320**
	G						1.000	0.947**	0.512**	0.082	-0.456**	0.398**
	E						1.000	0.936**	0.504**	0.074	-0.636**	0.059
7	P							1.000	0.202	0.244	0.330**	0.458**
	G							1.000	0.209	-0.238	0.261	0.557**
	E							1.000	0.167	-0.276	0.587**	0.127
8	P								1.000	0.885**	0.586**	-0.246
	G								1.000	0.885**	-0.691**	-0.279*
	E								1.000	0.885**	-0.339**	-0.146
9	P									1.000	-0.441**	-0.446**
	G									1.000	-0.594**	-0.528**
	E									1.000	-0.045	-0.189
10	P										1.000	0.486**
	G										1.000	0.521**
	E										1.000	0.418**
11	P											1.000
	G											1.000
	E											1.000

***Significant at 1% level** ****Significant at 5% level**

Note: 1. DF: Days to 50% flowering; **2. PH**: Plant Height**, 3. PL**: Panicle length; **4. TT/P:** Total tiller per plant; **5.ET/P**: Effective tiller per plant; **6. TS/Pa**: Total spikelets per panicle; 7. **FG/Pa**: Filled spikelets per panicle; **8. UG/Pa**: Unfilled spikelets per panicle; **9. SSP**: Spikelet sterility percentage; **10. SI**: 100 seed weight; **11. GY/P**: Grain yield per plant.

RESULT AND DISCUSSION

The correlation coefficients analysis is the index of association between two variables. These have been dealt in all possible combinations for important characters at phenotypic, genotypic and environmental level and are presented in table 1.

The characters days to 50% flowering had a highly significant positive correlation with filled spikelets

per panicle, unfilled spikelets per panicle and total spikelets per panicle at phenotypic and genotypic level. It also showed highly significant negative correlation with 100- seed weight at phenotypic and genotypic level.
The character plant height recorded the highly significant positive correlation with panicle length at phenotypic and genotypic level. It showed highly significant negative correlation with filled spikelets per panicle at genotypic level. Filled spikelets per panicle showed significant negative correlation at phenotypic level only.
Panicle length recorded the non significant positive and negative relationship with all characters at phenotypic, genotypic and environmental levels.
Total number of tillers per plant showing the highly significant positive correlation with number of effective tillers per plant at phenotypic, genotypic and environmental level and with grain yield per plant at environmental level only. It also showed highly significant positive correlation with number of spikelets sterility percentage at genotypic level.
Number of effective tillers per plant is showing the highly significant positive association with grain yield per plant at environmental level only.
The character number of total spikelet per panicle expressed highly significant positive correlation with filled spikelets per panicle and unfilled spikelets per panicle at phenotypic, genotypic and environmental level, whereas it showed highly significant negative correlation with 100- seed weight at phenotypic, genotypic and environmental level. Grain yield per plant showed highly significant positive correlation at phenotypic and genotypic level only with this trait.
Filled spikelet per panicle is showing the highly positive correlation with Grain yield per plant at phenotypic and genotypic level. It showed highly significant positive correlation with 100- seed weight at phenotypic and environmental level only.
Unfilled spikelets per panicle showed highly significant positive association with spikelet sterility percentage at phenotypic, genotypic and environmental level, while it showed highly significant negative correlation with 100- seed weight at genotypic and environmental level. While it showed significant negative correlation with grain yield per plant at genotypic level only. The other character showing non- significant positive or negative association with this trait.
The character spikelet sterility percentage had a highly significant negative correlation with 100- seed weight and grain yield per plant at phenotypic and genotypic level only.
The character 100-seed weight showed the highly significant positive correlation with grain yield per plant at phenotypic, genotypic and environmental level.
The character grain yield per plant showing highly significant positive correlation with 100-seed weight at phenotypic, genotypic and environmental level, number of total effective tillers per plant at environmental level. On the other hand unfilled spikelet per panicle is showing significant negative correlation at genotypic level. It had shown highly significant positive correlation with filled spikelets per panicle at phenotypic and genotypic level, number of total spikelet's per panicle at phenotypic and genotypic level, while, it showed highly significant negative correlation with spikelets sterility percentage at phenotypic and genotypic level only.
In the present investigation grain yield per plant was positively and significantly associated with 100-seed weight, number of total effective tillers per plant, filled spikelets per panicle and total spikelets per panicle. The positive association of grain yield per plant with filled spikelet per panicle is in similar to the finding of Chauhan *et al.* (1993), Sarawgi *et al.* (1997), Prashanth *et al.* (1999), Singh *et al.* (2000), Shivani and Rama Reddy (2000), Surek and Beser (2003) and Sourosh *et al.* (2004), Veni and Rani (2006), Nath *et al.* (2008).
Grain yield per plant was positively and highly significant associated with total spikelets per panicle which is in conformity to the findings of, Basavaraja *et al.* (1997), Shivani and Rama Reddy (2000), Rani *et al.* (2001), and Shashidhar *et al.* (2005), Kumar (2008), Chakraborty and Chakraborty (2010). The positive association of Grain yield per plant with number of effective tillers per plant is in conformation with the findings of Sawant (1995), Sarawgi *et al.* (1997), Chaudhary and Motiramani (2003), Patil and Sarawgi (2005), Monalisa *et al.* (2006), Johnson *et al.* (2007), Kumar (2008). The positive association of Grain yield per plant with 100-seed weight is similar to finding of Yalanda and Das (1995), Sarawgi *et al.* (1997), Iftekkaruddaula *et al.* (2002), Akter *et al.* (2002), Arumugam *et al.* (2008), Nath *et al.* (2008), Subudhi and Dikshit (2009) and Chandra *et al.* (2009).

CONCLUSION

The correlation coefficients analysis is the index of association between two variables. These have been dealt in all possible combinations for important characters at different level. In the present investigation Grain yield per plant was positively and significantly associated with 100-seed weight, Number of total effective tillers per plant, Filled spikelets per panicle and Total spikelets per panicle. Based on correlation studies, it can be concluded that the selection criteria based on 100 grain weight, number of total effective tillers per plant, number of filled grains per plant and number of total spikelets per plant can provide better results for yield improvement.

Suggestions for future works

Desirable breeding lines for yield and quality characters may be used in the improvement programme to develop superior high yielding aromatic rice varieties. For hybridization programme, the better genotypes should be taken from different clusters on the basis of yield and quality characters for hybridization programme. Morphological characterization criteria may be used for marker assisted selection.

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