SHORT COMMUNICATION

ANALYSIS OF HERITABILITY AND GENETIC ADVANCE 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 agronomorphological 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. High heritability with high genetic advance was found for number of Total spikelets per panicle and Filled spikelets per panicle. Grain yield per plant was positively and significantly associated with 100 seed weight, Total effective tillers per plant, Filled spikelets per panicle and Total spikelets per panicle.

Keywords: Aromatic Rice, Heritability, Genetic Advance

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 43.73 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 agromorphological 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 exertion (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**

**Range:** The lower and higher value of a character determines its range, which is expressed as follows:

Range = Highest value – Lowest value.

**Mean:** The mean is calculated by the following formula:

\[ \bar{X} = \frac{\sum X_i}{N} \]

Where,

\[ \sum X_i = \text{Summation of all the observation} \]

\[ N = \text{Total number of observation} \]

**Heritability (Broad sense):** Heritability in a broad sense was calculated by the following formula suggested by Hansan et al. (1956),

\[ h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100 \]

Where,

\[ h^2 = \text{heritability in broad sense} \]

\[ \sigma^2_g = \text{genotypic variance} \]

\[ \sigma^2_p = \text{phenotypic variance} \]

**Genetic advance:** Expected genetic advance (GA) was calculated by the method suggested by Johnson et al. (1955) as follows:

\[ GA = K \sigma_p h^2 \]

Where,

\[ K = \text{constant (standard selection differential)} \]

\[ \sigma_p = \text{phenotypic standard deviation} \]

\[ h^2 = \text{heritability.} \]

**Genetic advance as percentage of means:** Genetic advance as percentage of means was calculated by the following formula:

\[ GA \text{ as } \% \text{mean} = \frac{GA}{\bar{X}} \times 100 \]

**Table 1:** Heritability (h2) and Genetic Advance (GA) as percentage of mean, Average mean and Range for different characters.

<table>
<thead>
<tr>
<th>S.N.</th>
<th>Characters</th>
<th>Average mean</th>
<th>Range</th>
<th>h2 (bs) (%)</th>
<th>GA as % of mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Days to 50% flowering</td>
<td>98.05</td>
<td>77.5</td>
<td>122</td>
<td>98.5</td>
</tr>
<tr>
<td>2</td>
<td>Plant height (cm)</td>
<td>115.22</td>
<td>95</td>
<td>195</td>
<td>94.4</td>
</tr>
<tr>
<td>3</td>
<td>Panicle length (cm)</td>
<td>24.89</td>
<td>19.9</td>
<td>35.6</td>
<td>75.1</td>
</tr>
<tr>
<td>4</td>
<td>Total tillers per plant</td>
<td>7.93</td>
<td>5.9</td>
<td>9.6</td>
<td>63.3</td>
</tr>
<tr>
<td>5</td>
<td>Effective tillers per plant</td>
<td>6.55</td>
<td>3.1</td>
<td>8.9</td>
<td>57.7</td>
</tr>
<tr>
<td>6</td>
<td>Total number of spikelets per panicle</td>
<td>215.96</td>
<td>112.3</td>
<td>328.0</td>
<td>84.6</td>
</tr>
</tbody>
</table>
RESULT AND DISCUSSION

Heritability estimate provide the information regarding the amount of transmissible genetic variation to total variation and determine genetic improvement and response to selection. In the present investigation heritability in broad sense was calculated for all quantity and quality characters under study and is presented in table 1. Heritability in broad sense ($h^2$(bs)) 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 were 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%).

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 recorded 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 (2.24), kernel length/breadth ratio of cooked rice (0.95), elongation ratio (0.48) and elongation index (0.31).

The present findings of highest genetic advance as percent of mean for filled spikelets per panicle is similar finding to the report of Kavitha and Reddy (2002), Chandra and Pradhan (2003), Hasib (2005)
and Satyanarayan et al. (2005). For plant height high estimate of genetic advance was observed by Chaudhary et al. (2004) Bansal et al. (1999), Hasib (2005), Amudha et al. (2006), Jaiswal et al. (2007) and Subudhi and Dikshit (2009) have recorded high genetic advance for grain yield. 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.

CONCLUSION

Heritability in broad sense ($h^2$) 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.

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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