Genetic Parameters Studies in Aromatic Rice

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ABSTRACT

The present investigation consists of 38 rice genotypes and the experiment was conducted during Kharif-2015 in Randomized Block Design with three replications. The data were recorded for 11 quantitative characters to study genetic variability, heritability and genetic advance. On the basis of mean performance, high grain yield per plant were exhibited by the genotype Pusa-1460. Analysis of variance among 38 genotypes showed significant difference for all characters studied. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for grain yield per plant followed by biological yield per plant, panicle length, number of grain per panicle, harvest index, test weight and number of productive tillers per plant indicating that these characters could be used as selection for crop improvement. On the basis of high estimates of heritability coupled with high genetic advance was observed for plant height, number of productive tillers per plant, panicle length, biological yield per plant, harvest index, test weight and number of grains per panicle indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

Keywords: Rice, Genetic variability, Heritability and Genetic Advance.

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INTRODUCTION

Rice (Oryza sativa L.) is principal food crop of India as well as one of the pivotal staple cereal crops feeding more than one-third of the world’s population. Rice is the staple food of about 65% of Indian population. Our rice requirement by the year 2020 is estimated to be around 122 million tons as against the present production of about 100 million tons, thus leaving a gap of about 22 million tons rice. It accounts for about 43% of total food grain production and 46% of total cereal production in the country [1, 8]. Low productivity of rice in India is a major concern for food and nutritional security of more than 60% population which is dependent on rice. The slogan “Rice is life” is most appropriate for Indian as this crop plays a vital role in our national food security and a means of livelihood for millions of rural people of India. Rice occupies a pivotal place in Indian agriculture and it contributes to 15 per cent of annual GDP and provides 43 per cent calorie requirement for more than 70 per cent of Indians. The country witnessed an impressive growth in rice production due to adoption of semi dwarf varieties coupled with intensive input based management practices. In order to keep peace with growing population the estimated rice requirement by 2025 is about 130 million tones. The success of breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable Variability refers to the presence of differences among the individuals of plant population. Variation results due to difference either in genetic constitution of the individual of a plant population or in environment, they have grown. The existence of variability is essential for improvement of genetic material. Selection is also effective when there is significant amount of genetic variability among the individuals in breeding materials [18].
MATERIAL AND METHODS
The material for the present investigation consists of 38 rice genotypes were grown in Randomized block design with three replications during kharif-2015 at the Crop Research center, Chirodi of Sardar Vallabhbhai Patel University of Agriculture, Technology, Meerut Twenty five days old seedlings raised in nursery were transplanted at 20 cm x 15 cm spacing. Five representative plants for each genotype in each replication were randomly selected to record observations on days to 50% panicle emergence, days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, biological yield per plant, harvest index, test weight, number of grains per panicle and grain yield per plant. The variability was estimated as per procedure for analysis of variance suggested by Panse and Sukhatme [13]. PCV and GCV were calculated by the formula given by [5]. Heritability in broad sense (h2) was reported earlier also by Fiyaz et al. [5] and genetic advance were calculated by using the procedure given by Johnson et al. [11].

RESULTS AND DISCUSSION
Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. The analysis of variance for different characters indicated the existence of highly significant differences for all the eleven characters study at 1% level of significance suggesting each and every genotype are genetically divergent from each other and there is ample scope for selection of characters from these diverse sources for yield and its components (Table 1). These findings were in accordance with the findings of Bekele et al., [4], Sandhya et al. [16]. A wide range of variance was observed for all the eleven characters. In general the phenotypic coefficient of variance was higher than genotypic coefficient variance for all yield and its contributing characters indicate the influence of environmental factors on these traits. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) ranged between (6.097 and 6.386) to (29.062 and 29.949) for days to maturity and grain yield per plant respectively. The highest GCV and PCV was recorded for grain yield per plant (29.062 and 29.949) followed by biological yield per plant (28.647 and 29.054), panicle length (27.964 and 28.571) number of grain per panicle (26.849 and 27.034), harvest index (26.740 and 26.909), test weight (25.906 and 25.968) and number of productive tillers per plant (25.736 and 25.789). Similar results were also reported by Anjanyulu et al., [2], Idris et al. [9], Sandhya [16], Sarma et al., [17] Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV is presenting table-2 among the all traits and high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these attributes. Closely relationship between GCV and PCV was found in all the characters and PCV values were slightly greater than GCV, revealing very little influence of environment for their expression. 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 [5] 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 [11]. Heritability in broad sense includes both additive and non-additive gene effects. While, narrow sense heritability includes only additive components [11]. In the present study, heritability in broad sense was estimated. Highest heritability in broad sense (> 60%) was recorded in the case of test weight (98.900) followed by number of grains per panicle (98.600), plant height (96.000), biological yield per plant (93.300), days to 50% flowering (92.800), days to 50% panicle emergence (92.200), grain yield per plant (92.000), days to maturity (91.100), panicle length (89.700), harvest index (89.100) and number of productive tillers per plant (69.2).The high heritability denotes high proportion of genetic effects in the determination of these traits and can be adopted for improving grain yield. Studied have been reported earlier also by Fiyaz et al., [7], Dhanwani et al., [6], Sarma et al., [17] and Islam et al., [10]. Maximum genetic advance expressed as percentage of mean was revealed high (>20%) for number of grains per panicle (54.925), grain yield per plant (41.633), harvest index (38.392), plant height (26.980), number of productive tillers per plant (25.259), test weight (24.402), biological yield per plant (23.184) and panicle length (21.401). Moderate genetic advance as percentage of mean (10-20%) was observed for days to 50% panicle emergence (16.725), days to 50% flowering (15.645) and days to maturity (11.990). High heritability (h2) coupled with high genetic advance was observed for plant height, number of productive tillers per plant, panicle length, biological yield per plant, harvest index, test weight and number of grains per panicle. High heritability coupled with high genetic advance for some of these traits have also been reported earlier by Baswaraja et al., [3], Rahman et al., [14], Tiwari, [19] and Islam et al., [10]. This indicates substantial

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contribution of additive genetic variance in the expression of these traits and can be more useful in hybridization and selection for higher grain yield and these characters are largely controlled by additive gene action.

Table-1 Analysis of variance (ANOVA) for eleven characters of rice

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>Days to 50% panicle emergence</th>
<th>Days to 50% flowering</th>
<th>Days to maturity</th>
<th>Plant height (cm)</th>
<th>No. of productive tillers per plant</th>
<th>Panicle length (cm)</th>
<th>Panicle length</th>
<th>Biological yield per plant (g)</th>
<th>Harvest index (%)</th>
<th>Test weight (g)</th>
<th>No. of grains per panicle</th>
<th>Grain yield per plant (g)</th>
<th>Replication</th>
<th>Treatment</th>
<th>Error</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>10.798</td>
<td>6.282</td>
<td>1.719</td>
<td>32.567</td>
<td>2.888</td>
<td>0.893</td>
<td>6.620</td>
<td>1.907</td>
<td>0.023</td>
<td>5.670</td>
<td>5.670</td>
<td>246.3</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>169.210**</td>
<td>172.264**</td>
<td>161.700**</td>
<td>821.521**</td>
<td>20.619**</td>
<td>27.165**</td>
<td>1015.799**</td>
<td>157.820**</td>
<td>27.131**</td>
<td>5507.418**</td>
<td>5507.418**</td>
<td>26.909</td>
<td>11.909</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*, ** significant at 5% and 1% level, respectively

Table-2 Estimates of variability parameters for eleven characters in rice

<table>
<thead>
<tr>
<th>Character</th>
<th>Mean</th>
<th>Range</th>
<th>Coefficient of variation</th>
<th>Heritability % (broad sense)</th>
<th>Genetic advance</th>
<th>Genetic advance (% of mean)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Lowest-Highest</td>
<td>GCV (%)</td>
<td>PCV (%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Days to 50% panicle emergence</td>
<td>87.59</td>
<td>73.00-109.00</td>
<td>8.455</td>
<td>8.805</td>
<td>92.2</td>
<td>14.651</td>
</tr>
<tr>
<td>Days to 50% flowering</td>
<td>94.91</td>
<td>80.00-116.66</td>
<td>7.882</td>
<td>8.182</td>
<td>92.8</td>
<td>14.849</td>
</tr>
<tr>
<td>Days to maturity</td>
<td>118.50</td>
<td>106.66-136.66</td>
<td>6.097</td>
<td>6.386</td>
<td>91.1</td>
<td>14.209</td>
</tr>
<tr>
<td>Plant height (cm)</td>
<td>122.97</td>
<td>86.46-154.56</td>
<td>13.365</td>
<td>13.638</td>
<td>96.0</td>
<td>33.179</td>
</tr>
<tr>
<td>No. of productive tillers per plant</td>
<td>16.60</td>
<td>12.03-22.80</td>
<td>25.736</td>
<td>25.789</td>
<td>69.2</td>
<td>4.194</td>
</tr>
<tr>
<td>Panicle length (cm)</td>
<td>26.93</td>
<td>20.26-32.56</td>
<td>27.964</td>
<td>28.571</td>
<td>89.7</td>
<td>5.765</td>
</tr>
<tr>
<td>Biological yield per plant (g)</td>
<td>156.13</td>
<td>113.73-187.73</td>
<td>28.647</td>
<td>29.054</td>
<td>93.3</td>
<td>36.200</td>
</tr>
<tr>
<td>Harvest index (%)</td>
<td>36.01</td>
<td>23.90-54.06</td>
<td>26.740</td>
<td>26.909</td>
<td>89.1</td>
<td>13.827</td>
</tr>
<tr>
<td>Test weight (g)</td>
<td>25.21</td>
<td>21.00-31.00</td>
<td>25.906</td>
<td>25.968</td>
<td>98.9</td>
<td>6.152</td>
</tr>
<tr>
<td>No. of grains per panicle</td>
<td>159.21</td>
<td>72.40-241.66</td>
<td>26.849</td>
<td>27.034</td>
<td>98.6</td>
<td>87.451</td>
</tr>
<tr>
<td>Grain yield per plant (g)</td>
<td>55.85</td>
<td>33.70-78.33</td>
<td>29.062</td>
<td>29.949</td>
<td>92.0</td>
<td>23.253</td>
</tr>
</tbody>
</table>

CONCLUSION
In the present investigation which included 38 genotypes of rice was carried out in order to study the nature and amount of variability, heritability and genetic advance for 11 quantitative characters. On the basis of mean performance, high grain yield per plant were exhibited by the genotype Pusa-1460.
Analysis of variance among 38 genotypes showed significant difference for all characters studied. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for number of productive tillers per plant, panicle length, biological yield per plant, harvest index, test weight, number of grains per panicle and grain yield per plant indicating that these characters could be used as selection for crop improvement. High heritability coupled with high genetic advance as percent of mean estimated for plant height, number of productive tillers per plant, panicle length, biological yield per plant, harvest index, test weight, number of grains per panicle and grain yield per plant indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

**REFERENCE**


**Citation of this Article**