Original Research Article

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Genetic Variability, Heritability and Genetic Advance Studies in Rice (*Oryza sativa* L.)

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A B S T R A C T

The experimental was carried out at Indian Institute of Rice Research Farm, ICRISAT, Patencheru, Hyderabad, Telangana, India, during Rabi, 2014-2015 in order to estimate genetic variability, heritability and genetic advance in two hundred genotypes of rice. Analysis of variance revealed highly significant differences among the genotypes for all the characters indicating sufficient variability existed in the present material selected for the study. Environmental influence was very meagre on the expression of all the characters as there is a narrow difference between genotypic and phenotypic coefficients of variation. Genotypic and phenotypic coefficients of variability were high for single plant yield, number of grains per panicle, number of tillers per hill, pollen viability and spikelet fertility. The characters viz., spikelet fertility, plant height, single plant yield, number of grains per panicle, number of tillers per hill, pollen viability, number of productive tillers per hill, panicle length and 1000 grain weight exhibited high heritability estimates coupled with high genetic advance as per cent of mean which suggested that these traits were amenable for further improvement by following simple selection methods.

Keywords

Genetic Variability, Heritability, Rice

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Introduction

Rice (*Oryza sativa* L.) is the most important staple food crop for more than 60 per cent of the global population and forms the cheapest source of food energy and protein. By origin, the crop is native to South East Asia with two cultivated (*Oryza sativa* and *Oryza glaberrima*) and 22 wild species. It belongs to the genus *Oryza* and grass family *Poaceae*. The crop is cultivated under a wide range of agro-ecological situations. Although the crop is widely adoptable it is sensitive to high temperatures. Globally, it is grown in an area of 162.71 m ha with an annual production of 741.47 m t and productivity of 4556 kg ha⁻¹. It is the most important food crop of India with world ranking first in area (43.85 m

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ha) and second to China in production (FAO, 2014). In India, rice is cultivated in an area of 43.49 m ha with an annual production of 104.40 m t and average productivity of 2400 kg ha⁻¹. In Telangana, it covers an area of 1.04 m ha with a production of 3.04 m t tonnes and average productivity of 2913 kg ha⁻¹ (Indiastat, 2015-16). The slogan- “Rice is life” is due to its overwhelming importance as staple food and also a source of livelihood for about 120-150 million rural households of the country. Rice is central to the lives of billions of people around the world. With the growth of world's population towards 10 billion by 2050, the demand for rice will grow faster than for other crops. Global warming has a significant effect on rice production. Over the past 100 years, global average temperature has increased by 0.6°C and is projected to continue to rise at a rapid rate, with another 0.5–2.8°C increase predicted by the end of 21st century (Vuuren et al., 2008). Because of higher recurrence of extreme high-temperature events and a projected global average surface temperature increase of 1.5 to 4.8°C by 2100 yield decrease in the 2nd half of the century is predicted to be even stronger in the tropics than in the temperate areas (Intergovernmental Panel on Climate Change 2014). Most of the rice is currently grown in regions where current temperatures are already close to optimum for rice production. Heat waves are expected to be more intense and frequent in the future, which could jeopardize more rice areas. Therefore, any further increases in mean temperatures or of short episodes of high temperatures during sensitive stages, may be supra optimal and reduce grain yield. Though rice originated from the tropics, temperature over 35°C at flowering stage causes high pollen and spikelet sterility, leads to serious yield losses, low grain quality and low harvest index. It was suggested that spikelet fertility at high temperature can be used as a screening tool for heat tolerance during flowering stage (Prasad et al., 2006). Genetic variability is of greatest interest to the plant breeder as it plays a vital role in framing successful breeding programme. Heritability of a metric character is a parameter of particular significance to the breeder as it measures the degree of resemblance between the parents and the offsprings and its magnitude indicates the heritability with which a genotype can be identified by its phenotypic expression, while genetic advance aids in exercising the necessary selection pressure.

**Materials and Methods**

The experimental material comprised of two hundred germplasm of rice (Oryza sativa L.) grown in Augmented RBD at IIRR Farm, ICRISAT, Patencheru, Hyderabad, Telangana, India, during Rabi 2014-2015. The recommended agronomic and plant protection measures were followed in order to raise a normal crop. Observations on eleven different quantitative characters viz., days to 50% flowering, days to maturity, plant height, panicle length, number of tillers per hill, number of productive tillers per hill, number of grains per panicle, spikelet fertility, 1000 grain weight, pollen viability and single plant yield were recorded on five randomly selected competitive plants for each genotype except for days to 50% flowering, and days to maturity where data is recorded on plot basis during various phenophases of the crop. Mean values from the five randomly selected plants for each genotype were averaged and expressed as the mean of the respective character and considered for statistical analysis. Analysis of variance was computed based on Randomized Block Design for each of the character separately as per standard statistical procedure given by (Panse and Sukhatme, 1978). Heritability (h²) in the broad sense was calculated according to the formula given by (Allard, 1960) for all characters. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed.
Results and Discussion

Analysis of variance for the experiment involving a set of 200 germplasm lines of rice for eleven characters viz., days to 50% flowering, days to maturity, plant height, panicle length, number of tillers per hill, number of productive tillers per hill, number of grains per panicle, spikelet fertility, 1000 grain weight, pollen viability and single plant yield revealed highly significant differences among the genotypes for all the characters indicating sufficient variability existed in the present material selected for the study and indicating the scope for selection of suitable initial breeding material for crop improvement.

The results pertaining to genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability ($h^2_{bs}$) and genetic advance as percent of mean (GAM) for all the eleven characters are furnished in Table 1 and Figure 1. It is apparent from the Table 1 that there is almost perfect relation between PCV and GCV of each character. This could be seen from the highest magnitude of both PCV (39.43%) and GCV (39.15%) for single plant yield, number of grains per panicle (31.85-31.44%), number of tillers per hill (23.99-23.43%), pollen viability (22.63-21.98%) and spikelet fertility (20.50-20.44%) suggesting that these characters were under the influence of genetic control. So the characters can be relied upon and simple selection can be practiced for further improvement. The characters number of productive tillers per hill (19.10-18.39%), plant height (16.56-16.47%), 1000 grain weight (16.41-14.93%) and panicle length (11.80-11.02%) were recorded for moderate magnitudes of both PCV and GCV, respectively. The traits days to flowering (6.32-6.16%) and days to maturity (4.56-1.75%) showed lower magnitudes of both PCV and GCV, respectively. Similar results were reported by Harsh et al., (2015) and Umarani et al., (2017) for single plant yield; Ketan and Sarkar (2014), Khare et al., (2014) and Tiwari (2017) for number of grains per panicle; Kumar et al., (2013) and Ketan and Sarkar (2014) for spikelet fertility; Padmaja et al., (2008) for number of tillers per hill; Konate et al., (2016), Kumar and Verma (2016), Rohit et al., (2017) and Rashid et al., (2107) for number of productive tillers per hill; Khare et al., (2014) for plant height, panicle length and 1000 grain weight; Bhati et al., (2015) and Rohit et al., (2017) for days to 50% flowering and days to maturity.

The phenotypic coefficient of variation was higher than genotypic coefficient of variation (GCV) for all the characters under study but the GCV was greater than the variation produced by the environment for all the characters. The results are in agreement with the findings of Bai et al., (1992). The difference between the estimates of PCV and GCV were low for days to 50% flowering, days to maturity, plant height, panicle length, number of tillers per hill, number of productive tillers per hill, number of grains per panicle, spikelet fertility, pollen viability and single plant yield showing thereby lesser role played by the environment in the expression of these characters. The difference between the estimates of PCV and GCV was high for 1000 grain weight, indicating the significant role played by the environment in the expression of this character.

Heritability estimates revealed the heritable portion of variability present in different characters. The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a
given situation (Li and Yang, 1985). All the characters recorded high estimates of heritability. Broad sense heritability estimates ranged from 82.82 percent (1000 grain weight) to 99.43 percent (spikelet fertility). The characters like plant height (98.98%), single plant yield (98.60%), number of grains per panicle(97.42%), number of tillers per hill(95.34%), days to 50% flowering (94.89%), pollen viability (94.38%), number of productive tillers per hill(92.71%), panicle length (87.19) and days to maturity (87.14%) exhibited high heritability. The results are in consonance with the reports given by Tiwari et al., (2015), Rashid et al., (2017) and Rohit et al., (2017) for days to 50% flowering, days to maturity, plant height, 1000 grain weight and single plant yield; Kumar et al., (2013), Harsh et al., (2015) and Prasad et al., (2017) for panicle length, number of tillers per hill and number of productive tillers per hill; Ketan and Sarkar (2014), SubrataChakraborty and Chaturvedi (2014), Tiwari (2017) and Umarani et al., (2017) for spikelet fertility.

All the characters recorded high estimates of heritability indicating that they were least influenced by the environmental effects, however selection for improvement of such characters may not be useful, because broad sense heritability is based on total genetic variance which includes additive, dominant and epistatic variances. Thus, the heritability values along with estimates of genetic advance would be more reliable than heritability alone (Johnson et al., 1967). The genetic advance expressed as percent of mean values ranged from 8.77 percent (days to maturity) to 80.10 percent (single plant yield). The character single plant yield (80.10%) recorded for highest magnitude of genetic advance as percent of mean followed by number of grains per panicle (63.93%), number of tillers per hill (47.12%), pollen viability (44.00%), spikelet fertility (41.98%), number of productive tillers per hill (36.49%), plant height (33.77%), 1000 grain weight (28.00%) and panicle length (21.20%). The character days to 50% flowering (12.37%) showed moderate magnitude of genetic advance as percent of mean. The trait days to maturity (8.77%) recorded the lowest magnitude of genetic advance as percent of mean.

Maximum amount of genetic advance was found for single plant yield followed by number of grains per panicle, number of tillers per hill, pollen viability, spikelet fertility, number of productive tillers per hill, plant height, 1000 grain weight and panicle length. Similar results for high genetic advance were reported by Gokulakrishnan et al., (2014), Kishore et al., (2015), Rohit et al., (2017) and Prasad et al., (2017) for single plant yield; Rakesh Kumar et al., (2013) and Khare et al., (2014) for plant height, number of productive tillers per hill and panicle length; Sharma and GK Koutu (2013) for number of tillers per hill; Padmaja et al., (2008) and Binse et al., (2009) for number of grains per panicle and spikelet fertility; Nandan and Sweta Singh (2010), Fiyaz et al., (2011) and Kumar and Verma (2016) for 1000 grain weight.

All the characters recorded high estimates of heritability indicating that they were least influenced by the environmental effects, however selection for improvement of such characters may not be useful, because broad sense heritability is based on total genetic variance which includes additive, dominant and epistatic variances. Thus, the heritability values along with estimates of genetic advance would be more useful on correlating selection criteria than heritability alone (Johnson et al., 1967).

High heritability with moderate genetic advance was recorded for days to 50% flowering. These traits appear to be under the control of both additive and non additive gene actions.
### Table 1: Estimation of genetic parameters for eleven characters in rice (*Oryza sativa* L.)

<table>
<thead>
<tr>
<th>S.No.</th>
<th>Characters</th>
<th>PCV (%)</th>
<th>GCV (%)</th>
<th>ECV (%)</th>
<th>Heritability ($h^2_{bs}$) (%)</th>
<th>Genetic Advance (1%)</th>
<th>Genetic Advance as percent of Mean (1%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Days to 50% flowering</td>
<td>6.32</td>
<td>6.16</td>
<td>1.43</td>
<td>94.89</td>
<td>12.81</td>
<td>12.37</td>
</tr>
<tr>
<td>2.</td>
<td>Days to maturity</td>
<td>4.88</td>
<td>4.56</td>
<td>1.75</td>
<td>87.14</td>
<td>11.72</td>
<td>8.77</td>
</tr>
<tr>
<td>3.</td>
<td>Plant height (cm)</td>
<td>16.56</td>
<td>16.47</td>
<td>1.67</td>
<td>98.98</td>
<td>31.56</td>
<td>33.77</td>
</tr>
<tr>
<td>4.</td>
<td>Panicle length (cm)</td>
<td>11.80</td>
<td>11.02</td>
<td>4.22</td>
<td>87.19</td>
<td>4.72</td>
<td>21.20</td>
</tr>
<tr>
<td>5.</td>
<td>Number of tillers per hill</td>
<td>23.99</td>
<td>23.43</td>
<td>5.18</td>
<td>95.34</td>
<td>7.70</td>
<td>47.12</td>
</tr>
<tr>
<td>6.</td>
<td>Number of productive tillers per hill</td>
<td>19.10</td>
<td>18.39</td>
<td>5.15</td>
<td>92.71</td>
<td>4.48</td>
<td>36.49</td>
</tr>
<tr>
<td>7.</td>
<td>Number of grains per panicle</td>
<td>31.85</td>
<td>31.44</td>
<td>5.11</td>
<td>97.42</td>
<td>65.02</td>
<td>63.93</td>
</tr>
<tr>
<td>8.</td>
<td>Spikelet fertility (%)</td>
<td>20.50</td>
<td>20.44</td>
<td>1.55</td>
<td>99.43</td>
<td>31.82</td>
<td>41.98</td>
</tr>
<tr>
<td>9.</td>
<td>1000-grain weight (g)</td>
<td>16.41</td>
<td>14.93</td>
<td>6.80</td>
<td>82.82</td>
<td>5.56</td>
<td>28.00</td>
</tr>
<tr>
<td>10.</td>
<td>Pollen viability (%)</td>
<td>22.63</td>
<td>21.98</td>
<td>5.36</td>
<td>94.38</td>
<td>32.19</td>
<td>44.00</td>
</tr>
<tr>
<td>11.</td>
<td>Single plant yield (g)</td>
<td>39.43</td>
<td>39.15</td>
<td>4.66</td>
<td>98.60</td>
<td>16.01</td>
<td>80.10</td>
</tr>
</tbody>
</table>

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation and GAM = Genetic Advance as percent of mean at 5% level.
Fig.1 Graph showing distribution of genetic parameters for yield and yield components in rice
The present finding is in consonance with the findings of Padmaja et al., (2008), Kumar et al., (2013), Gokulakrishnan et al., (2014), Ketan and Sarkar (2014), Khare et al., (2014), Subrata Chakraborty and Chaturvedi (2014), Tiwari et al., (2015) and Konate et al., (2016). High heritability with low genetic advance was recorded for days to maturity, indicating non additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than genotype and hence, selection for such traits may not be rewarding. Similar results were reported by Bhati et al., (2015). In the present investigation, high heritability coupled with high genetic advance was observed for spikelet fertility, plant height, single plant yield, number of grains per panicle, number of tillers per hill, pollen viability, number of productive tillers per hill, panicle length and 1000 grain weight. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by pedigree method of breeding. Similar results for high heritability coupled with high genetic advance for various traits were earlier reported by Gokulakrishnan et al., (2014), Ketan and Sarkar (2014), Chakraborty and Chaturvedi (2014), Harsh et al., (2015), Bhati et al., (2015), Tiwari et al., (2015), Bhinda et al., (2017) and Rashid et al., (2017) for plant height and number of grains per panicle; Nayak et al., (2002), Sabesan et al., (2009), and Khare et al., (2014) for panicle length; Sharma and GK Koutu (2013) and Prasad et al., (2017) for number of tillers per hill and number of productive tillers per hill; Padmaja et al., (2008), Bisne et al., (2009) and Kumar et al., (2013) for spikelet fertility; Bharadwajetal. (2007), Nandan and Sweta Singh (2010), Fiyazetal. (2011),Khare et al., (2014), Srihima et al., (2015), Kumar and Verma (2016) for 1000 grain weight; Nayudu et al., (2007), Anbanandanetal. (2009), Garg et al., (2010), Kishore et al., (2015) and Rohit et al., (2017) for single plant yield.

In conclusion, high estimates of PCV and GCV were recorded for single plant yield, number of grains per panicle, number of tillers per hill, pollen viability and spikelet fertility which provides considerable variability and offers scope for genetic improvement through selection. Further high heritability coupled with high genetic advance were observed for spikelet fertility, plant height, single plant yield, number of grains per panicle, number of tillers per hill, pollen viability, number of productive tillers per hill, panicle length and 1000 grain weight indicates the role of additive gene action in controlling the traits, hence pedigree method of breeding will be a rewarding one to improve the traits under investigation.

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