Heritability and genetic advance studies in segregating generation for yield, its components and quality traits in rice (Oryza sativa L.)

Patel HR and Patel PB

Abstract
The present study comprised of five generation viz., PI, F1, F2 and F3 of following three crosses of rice (Oryza sativa L.) were used to study heritability and genetic advance of yield, its components and qualitative traits. The present investigation was carried out at Main Rice Research Centre, Navsari Agricultural University, Navsari during kharif 2018-19. High heritability coupled with high genetic advance was estimated for productive tillers per plant in all the crosses; 100 grain weight in cross-I and cross-II; grain yield per plant in cross-II; straw yield per plant in cross-II and cross-III; L:B ratio in cross-I and amylose content in cross-III which indicated that heritability of these traits were under the control of additive gene action. For improvement of such traits, selection will be rewarding.

Keywords: Heritability, genetic advance, generation mean analysis, rice (Oryza sativa L.)

Introduction
Rice, the world’s most important cereal crop, is the primary source of food and calories for about half of the mankind (Khush, 2005) [10]. The crop is cultivated in large area but is characterized by very low productivity due to lack of high yielding varieties adapted to different seasons and agronomic conditions at different parts of country. Yield is a complex and polygenic trait which is a final product affected by the large numbers of its component traits (Renukadevi and Subbalakshmi, 2006) [14]. So, all changes in yield must be accompanied by changes in one or more of the components as have been pointed out by Grafius (1959) [8]. The eventual objective of any plant breeding programme is to develop better genotypes which are superior to their prevailing ones in one or more traits which producing the economic yield. The enrichment of mineral nutrients in rice is today’s vital need to reduce malnutrition/anaemic conditions in poor people of the world. Sufficient understanding of the inheritance of quantitative traits and information about heritability of grain yield, its components and quality traits are crucial to develop an efficient breeding approach. Assessment of heritability serves as a valuable director to the plant breeder. The heritability expresses the relative amount of heritable lot of the variation. However, the heritability assessments along with genetic advance are more useful in selecting the best population individual (Ganapati et al., 2020) [5]. The breeder is able to appreciate the proportion of variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects, that is, the heritable portion of variation in the first case, and the portion of genetic variation that is fixable in pure lines in the latter case. If heritability of a character is very high, selection for the character should be fairly easy because there would be a close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype. But for a character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects (Patel et al., 2019) [12]. Thus, assessments of heritability are suitable in predicting the transmission of characters from the parents to their offspring.

Material and Methods
The material comprising of five genetically diverse parents of rice (IET-25475, IET-25477, GNR-7, GNR-3 and GAR-13) selected on the basis of their geographic origin, variation in morphological characters and based on their mineral nutrient content. Three crosses (Cross-I: IET-25475 x IET-25477, Cross-II: GNR-7 x GNR-3 and Cross-III: GAR-13 x IET-25477) obtained by crossing of five diverse parents during summer 2018 at Main Rice Research Centre, Gujarat Agricultural University, Navsari.
Results and Discussion

Heritability is a measure of the efficiency of a selection system in separating genotypes. The quantitative traits are largely influenced by environments; therefore, those are not highly heritable. High, moderate and low heritability are not rigidly defined as it varies with character to character, but the following values are widely accepted (Robinson et al., 1949).

1. Low heritability: 0 – 30%
2. Moderate heritability: 30 – 60%
3. High heritability: > 60%

The value of expected genetic advance as percentage of mean for various characters is demarcated into three categories viz., low, moderate and high as follows (Johnson et al., 1955).

1. Low genetic advance: 0 – 10%
2. Moderate genetic advance: 10 – 20%
3. High genetic advance: > 20%

The results obtained on these aspects for different characters studied in all the crosses are presented in table 1 and table 2. High narrow sense heritability recorded for traits viz., plant height, productive tillers per plant, 100 grain weight, L:B ratio and Zn content in cross-I (IET-25475 x IET-25477); days to flowering, days to maturity, productive tillers per plant, 100 grain weight, grain yield per plant, straw yield per plant and L:B ratio in cross-II (GNR-7 x GNR-3) and days to maturity, productive tillers per plant, grains per panicle, 100 grain weight, straw yield per plant, L: B ratio, Zn content and amylose content in cross-III (GAR-13 x IET-25477).

<table>
<thead>
<tr>
<th>Cross I</th>
<th>Heritability (NS %)</th>
<th>Days to flowering</th>
<th>Days to maturity</th>
<th>Plant height (cm)</th>
<th>Productive tillers per plant</th>
<th>Grains per panicle</th>
<th>100 grain weight (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>IET-25475 x IET-25477</td>
<td>25.72</td>
<td>50.13</td>
<td>136.24</td>
<td>96.50</td>
<td>-</td>
<td>121.68</td>
<td></td>
</tr>
</tbody>
</table>

Table 1: Estimates of narrow sense heritability (NS) and genetic advance for days to flowering, days to maturity, grain height, productive tillers per plant, grains per panicle and 100 grain weight in three crosses of rice
Cross-II (GNR-7 x GNR-3)

<table>
<thead>
<tr>
<th>Heritability (NS) %</th>
<th>Genetic Advance %</th>
<th>Grain yield (g)</th>
<th>Straw yield (g)</th>
<th>L: B ratio (mm)</th>
<th>Amylose content (%)</th>
<th>Zn content (ppm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>179.98</td>
<td>176.42</td>
<td>11.87</td>
<td>65.19</td>
<td>-</td>
<td>102.27</td>
<td></td>
</tr>
</tbody>
</table>

Cross-III (GAR-13 x IET-25477)

<table>
<thead>
<tr>
<th>Heritability (NS) %</th>
<th>Genetic Advance %</th>
<th>Grain yield (g)</th>
<th>Straw yield (g)</th>
<th>L: B ratio (mm)</th>
<th>Amylose content (%)</th>
<th>Zn content (ppm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>132.69</td>
<td>131.96</td>
<td>117.60</td>
<td>117.60</td>
<td>44.13</td>
<td>56.72</td>
<td></td>
</tr>
</tbody>
</table>

- indicate negative value

Table 2: Estimates of narrow sense heritability (NS) and genetic advance for grain yield per plant, straw yield per plant, L: B ratio, amylose content and Zn content in three crosses of rice

**Cross-I (IET-25475 x IET-25477)**

<table>
<thead>
<tr>
<th>Heritability (NS) %</th>
<th>Genetic Advance %</th>
<th>Grain yield (g)</th>
<th>Straw yield (g)</th>
<th>L: B ratio (mm)</th>
<th>Amylose content (%)</th>
<th>Zn content (ppm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>30.60</td>
<td>6.53</td>
<td>48.97</td>
<td>24.52</td>
<td>9.37</td>
<td>5.66</td>
<td></td>
</tr>
</tbody>
</table>

**Cross-II (GNR-7 x GNR-3)**

<table>
<thead>
<tr>
<th>Heritability (NS) %</th>
<th>Genetic Advance %</th>
<th>Grain yield (g)</th>
<th>Straw yield (g)</th>
<th>L: B ratio (mm)</th>
<th>Amylose content (%)</th>
<th>Zn content (ppm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>34.69</td>
<td>22.24</td>
<td>87.20</td>
<td>14.45</td>
<td>26.84</td>
<td>9.96</td>
<td></td>
</tr>
</tbody>
</table>

**Cross-III (GAR-13 x IET-25477)**

<table>
<thead>
<tr>
<th>Heritability (NS) %</th>
<th>Genetic Advance %</th>
<th>Grain yield (g)</th>
<th>Straw yield (g)</th>
<th>L: B ratio (mm)</th>
<th>Amylose content (%)</th>
<th>Zn content (ppm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>3.47</td>
<td>5.01</td>
<td>122.16</td>
<td>26.84</td>
<td>9.96</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Conclusion

The higher estimates of heritability indicates that these traits were comparatively less affected by environment and their phenotypes are good reflection of genotypes and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these matric traits but in case of lower heritability, pedigree, sib or progeny test can be employed for genetic improvement. The moderate to low estimates of heritability for most of the traits including yield components indicated the preponderance of non-additive variance for yield and yield attributes in the material under study.

High heritability coupled with high genetic advance indicated that heritability of these traits were under the control of additive gene action and moderate to high heritability coupled with high to moderate genetic advance indicate that heritability of these traits were due to additive gene action, suggesting that these characters can be further improved by adopting selections in succeeding generations.

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References


