Heritability, variability and genetic advance analysis for yield contributing characters in rice (Oryza Sativa L.)

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Abstract: Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. The estimates of heritability, coefficients of variability and genetic advance computed for 12 yield contributing traits. Genetic parameters for yield and its correspondent characters in rice were estimated from a trial with four CMS lines, fifteen testers, three checks and sixty crosses evaluated for twelve characters related to yield. In general, the magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits, indicating that the apparent variation is not only due to genotypes but, also due to the influence of environment. Therefore, caution has to be exercised in making selection for these characters on the basis of phenotypic alone as environmental variation is unpredictable in nature. High estimates of heritability and genetic advance in broad sense and narrow sense were recorded for all characters. High heritability coupled with high genetic advance in percent of mean was observed for all the traits, indicating predominance of additive gene action for these characters. Hence, simple selection based on phenotypic performance of these characters would be more effective. The estimates of additive variance (σa²) was found higher than the dominance variance (σd²) for all characters. The degree of dominance was greater than the unity for the characters.

Key Words: Heritability, Variability, Genetic advance in rice

Introduction

Genetic variability for agronomic traits is the key component of breeding programmes for broadening the gene pool of rice. Heritability (h²) of a trait is important in determining its response to selection. It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program. El-Malky et al. (2003) observed high broad sense heritability estimate of 98.89% for days to maturity, 75.20% for the number of tillers per plant, 41.74% for the number of panicles per plant, 98.97% for 1000 grain weight and 90.87% for panicle weight. Babar et al. (2007) also reported high heritability of 0.74 for panicle length, 0.75 for plant height, 0.63 for the number of panicles per plant, 0.64 for days to heading and 0.81 for grain yield. On the other hand, Kato (1997) estimated low broad sense heritability of 0.16 for the number of panicles per plant and 0.20 to 0.33 for number of spikelet per panicle.

The success of any breeding program depends on understanding the genetic nature of the character of interest, creation and prediction of genetic variability in subsequent generations and their inter relationship with other characters. Yield is a complex character and is influenced by various other characters therefore it is essential to understand the association of other characters with yield in addition to the information on genetic variability. Yield contributing traits are interrelated and highly influenced by the environments (Chandra et al., 2007; Nayak et al., 2008; Prasad et al., 2001; Eswara Reddy et al., 2013). It is essential to estimate the various types of gene action for the selection of appropriate breeding procedure to improve the quantitative and qualitative characters (Banumathy et al., 2003). Keeping in view the genetic studies in parental lines of hybrid rice were undertaken to estimate the genetic component of variance for yield and its components and to compute the heritability and genetic advance for 12 characters.

Materials and Methods

Four CMS lines having the WA cytoplasmic background viz., IR 6885A, IR 58025A, IR 6897A, and IR 79156A used as lines and fifteen promising rice varieties viz., NDR 1126, NDR 1127, IR 27723, CR 2499, Sugandha 5, NDR 3112-1, NDR 2701, NDR 2702, NDR 2704, NDR 2706, NDR 370131, NDR 370132, NDR 370133, IR 87651 and NDR 2705 were used as testers, three checks (NDR 2064, NDR 2065 and NDR 359) were the experimental materials of this study. The crosses will be made into “line x tester” mating design (Kempthorne, 1957) to produce 60 crosses. All the Eighty two genotypes were sown in randomized block design (RBD) with three replications at the Instructional farm of genetics and plant breeding, NDUAT, during 2013 kharif season. A standard spacing of 15cm x 20cm was adopted for planting. Recommended packages of practices were followed during the crop growth period. Observations were recorded for twelve
characters viz., days to 50% flowering, plant height (cm), panicle length (cm), effective tillers per plant, total no. of spikelets per panicle, total number of filled spikelets per panicle, total number of chaffy spikelets per panicle, spikelet fertility %, 100-grain weight (g), harvest index (%), length of spikelet (cm), breadth of spikelet (cm), and grain yield per plant (g) days to 50% flowering, days to maturity, plant height, Panicle bearing tillers per plant, panicle length, 1000 grain weight, Spikelets per panicle, Spikelet fertility (%), Harvest-index (%), L/B ratio, Grain yield per plant (g) and Biological yield per plant (g). Genotypic and phenotypic, Coefficient of variation, heritability and genetic advance were estimated for all twelve characters.

Results and Discussion

Coefficients of variation: In general, the magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits. The high estimates of phenotypic and genotypic coefficient of variation (> 20%) were recorded for panicle bearing tillers per plant (PCV=22.40%, GCV=21.83%), spikelets fertility (PCV=22.96%, GCV=22.91%), 1000-grain weight (PCV=24.88%, GCV=24.67%), biological yield per plant (PCV=28.33%, GCV=27.79%), harvest index (PCV=23.64%, GCV=23.46%), L/B ratio (PCV=24.94%, GCV=24.77%) and grain yield per plant (PCV=28.46%, GCV=28.08%). The moderate estimates (10-20%) of PCV and GCV were recorded for days to 50% flowering (PCV=16.72%, GCV=16.62%) days to maturity (PCV=11.54%, GCV=11.47%), plant height (PCV=12.72%, GCV=12.51%), panicle length (PCV=10.98%, GCV=10.47%) and spikelet per panicle (PCV=18.64%, GCV=18.55%). have expressed low estimates (<10%) of coefficient of variation for both the parameters. Table-2

The similar results were observed for the above twelve characters are broadly in agreement with earlier reports in rice (Chaudhary et al., 2004; Babar et al., 2009; Anjaneyulu et al., 2010; Jayasudha and Sharma, 2010; Karthikeyan et al., 2010; Akhtar et al., 2011; Garg et al., 2011; Pandey, 2012; Seyoum et al., 2012; Basavaraja et al., 2013; Sathy and Jebaraj, 2013; Warkad et al., 2013).

Heritability and genetic advance: The estimates of heritability in narrow sense (h^2) have been classified by Robinson (1966) into three categories viz., high (> 30%), medium (10-30%) and low (<10%). High estimates of heritability in narrow sense were recorded for almost all characters viz., days to maturity (91.99), days to 50% flowering (99.00), plant height (97.00), panicle length (91.00), 1000-grain weight (98.00), biological yield per plant (96.00), harvest index (97.00), L/B ratio (78.43%), and grain yield per plant (77.00%).

Table-1: Analysis of variance for combining ability following line x tester mating design among 12 characters in rice

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>Days to 50% flowering</th>
<th>Days to maturity</th>
<th>Plant height (cm)</th>
<th>Panicle bearing tillers/plant</th>
<th>Panicle length (cm)</th>
<th>Spikelets per panicle</th>
<th>Spikelet fertility (%)</th>
<th>1000-grain wt. (g)</th>
<th>Biological yield per plant (g)</th>
<th>Harvest index (%)</th>
<th>L/B ratio</th>
<th>Grain yield/plant (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replicates</td>
<td>2</td>
<td>11.36**</td>
<td>7.40**</td>
<td>42.79**</td>
<td>0.20</td>
<td>0.22</td>
<td>16.57</td>
<td>5.93**</td>
<td>0.16</td>
<td>21.65</td>
<td>0.01</td>
<td>0.24</td>
<td></td>
</tr>
<tr>
<td>Crosses</td>
<td>59</td>
<td>304.78**</td>
<td>234.91**</td>
<td>170.82**</td>
<td>12.51**</td>
<td>17.22**</td>
<td>3211.58**</td>
<td>12.18**</td>
<td>14.92**</td>
<td>661.07**</td>
<td>22.91**</td>
<td>0.26</td>
<td></td>
</tr>
<tr>
<td>Line Effect</td>
<td>3</td>
<td>47.11</td>
<td>12.60</td>
<td>7.95</td>
<td>5.37</td>
<td>1.18</td>
<td>3343.23</td>
<td>6.74</td>
<td>3.49</td>
<td>88.98</td>
<td>3.43</td>
<td>0.30</td>
<td>15.30</td>
</tr>
<tr>
<td>Tester Effect</td>
<td>14</td>
<td>1133.83**</td>
<td>960.63**</td>
<td>617.79**</td>
<td>41.91**</td>
<td>60.30**</td>
<td>6273.34**</td>
<td>25.90**</td>
<td>37.42**</td>
<td>661.07**</td>
<td>48.26**</td>
<td>0.35</td>
<td>101.57**</td>
</tr>
<tr>
<td>Line x Tester Eff.</td>
<td>42</td>
<td>46.83**</td>
<td>8.88**</td>
<td>33.46**</td>
<td>3.23**</td>
<td>4.00**</td>
<td>2181.59**</td>
<td>7.99**</td>
<td>7.75**</td>
<td>75.14**</td>
<td>4.62**</td>
<td>0.23</td>
<td>14.31**</td>
</tr>
<tr>
<td>Variance GCA(σ^2)</td>
<td>19.07**</td>
<td>16.72**</td>
<td>9.80**</td>
<td>0.71**</td>
<td>0.93**</td>
<td>92.16**</td>
<td>0.29**</td>
<td>0.44**</td>
<td>10.52**</td>
<td>0.74**</td>
<td>0.00**</td>
<td>1.54**</td>
<td></td>
</tr>
<tr>
<td>Variance SCA(σ^2)</td>
<td>15.06**</td>
<td>2.38**</td>
<td>9.50**</td>
<td>0.89**</td>
<td>1.09**</td>
<td>724.18**</td>
<td>2.11**</td>
<td>2.40**</td>
<td>22.26**</td>
<td>1.12**</td>
<td>0.07**</td>
<td>4.45**</td>
<td></td>
</tr>
<tr>
<td>Degree of dominance</td>
<td>0.62</td>
<td>0.26</td>
<td>0.69</td>
<td>0.79</td>
<td>0.76</td>
<td>1.98</td>
<td>1.9</td>
<td>1.64</td>
<td>1.02</td>
<td>0.86</td>
<td>3.43</td>
<td>1.19</td>
<td></td>
</tr>
<tr>
<td>Predictability ratio</td>
<td>0.71</td>
<td>0.62</td>
<td>0.67</td>
<td>0.61</td>
<td>0.63</td>
<td>0.2</td>
<td>0.21</td>
<td>0.26</td>
<td>0.48</td>
<td>0.5</td>
<td>0</td>
<td>0.4</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>118</td>
<td>1.25</td>
<td>1.4</td>
<td>2.27</td>
<td>0.55</td>
<td>0.71</td>
<td>1.12</td>
<td>1.27</td>
<td>0.61</td>
<td>8.23</td>
<td>1.46</td>
<td>0.01</td>
<td>1.01</td>
</tr>
<tr>
<td>Total</td>
<td>179</td>
<td>101.41</td>
<td>78.43</td>
<td>59.28</td>
<td>4.49</td>
<td>6.15</td>
<td>1066.09</td>
<td>4.91</td>
<td>5.21</td>
<td>76.49</td>
<td>5.9</td>
<td>0.09</td>
<td>12.23</td>
</tr>
</tbody>
</table>

*, ** Significant at 5% and 1% probability levels, respectively; Predictability ratio (2s^2/2s^2 + g^2 + s^2)

Table-2: Estimates of Phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability and genetic advance in percent of mean among 12 characters in rice

<table>
<thead>
<tr>
<th>Character</th>
<th>Coefficient of variation (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Genotypic (GCV)</td>
</tr>
<tr>
<td>Days to 50% flowering</td>
<td>16.62</td>
</tr>
<tr>
<td>Days to maturity</td>
<td>11.47</td>
</tr>
<tr>
<td>Plant height (cm)</td>
<td>12.51</td>
</tr>
<tr>
<td>Panicle length (cm)</td>
<td>10.47</td>
</tr>
<tr>
<td>Spikelets per panicle</td>
<td>18.55</td>
</tr>
<tr>
<td>Spikelet fertility (%)</td>
<td>22.91</td>
</tr>
<tr>
<td>1000-grain weight (g)</td>
<td>24.67</td>
</tr>
<tr>
<td>Biological yield/plant (g)</td>
<td>27.79</td>
</tr>
<tr>
<td>Harvest-index (%)</td>
<td>23.46</td>
</tr>
<tr>
<td>L/B ratio</td>
<td>24.77</td>
</tr>
<tr>
<td>Grain yield per plant (g)</td>
<td>28.08</td>
</tr>
</tbody>
</table>

Heritability, variability and genetic advance analysis in rice
flowering (72.58), plant height (65.96), panicle length (61.22), panicle bearing tillers per plant (60.13), harvest-index (52.83), biological yield per plant (50.67), grain yield per plant (45.81), 1000-grain weight (35.11) and spikelets per panicle (31.65).

Moderate estimates of heritability in narrow sense were also recorded for only spikelet fertility (27.90) and L/B ratio (22.53). The high estimates of heritability and genetic advance observed for the above characters are closed in agreement with the earlier reports in rice (Suman et al., 2005; Panwar et al., 2007; Babar et al., 2009; Arvind et al., 2011; Yadavendra et al., 2011; Kiani and Nematzadeh, 2012, Singh et al., 2012).

The estimates of heritability in broad sense (h²bs) have been classified by Robinson (1966) into three categories viz., high (> 75%), medium (50-75%) and low (<50%). High estimates of heritability in broad sense were recorded for all characters viz., spikelet fertility (100.00), days to 50% flowering (99.00), days to maturity (99.00), spikelets per panicle (99.00), harvest-index (99.00), L/B ratio (99.00), 1000-grain weight (98.00), plant height (97.00), grain yield per plant (97.00), biological yield per plant (96.00), panicle bearing tillers per plant (95.00), panicle length (91.00). The high estimates of genetic advance in per cent of mean (>20%) using broad sense heritability were recorded for all the characters viz., grain yield per plant (57.07), biological yield per plant (56.14), L/B ratio (50.71), 1000-grain weight (50.39), harvest-index (47.96), spikelet fertility (47.08), panicle bearing tillers per plant (43.82), spikelets per panicle (38.04), days to 50% flowering (34.05), plant height (25.34), days to maturity (23.47) and panicle length (20.56). High heritability coupled with high genetic advance in percent of mean was observed for all the traits. The high estimates of heritability and genetic advance observed for the above characters are broadly in agreement with earlier reports in rice (Islam et al., 2004; Sharma and Sharma, 2005; Suman et al., 2005; Manna et al., 2006; Singh et al., 2007; Karad and Pol, 2008; Singh et al., 2008; Vijayalakshmi et al., 2008; Bughio et al., 2009; Raut et al., 2009; Sarangi et al., 2009; Akinwale et al., 2011; Garg et al., 2011).

Genetic components: The estimates of genetic components, additive variance and dominance variance (and) and degree of dominance are given in table-2. The estimates of additive variance (a) was found higher than the dominance variance (d) for the characters, days to 50% flowering, days to maturity, plant height, panicle bearing tillers per plant, panicle length and harvest index, on contrary, characters like spikelets per panicle, 1000-grain weight, biological yield per plant, L/B ratio and grain yield per plant, showed lower estimates of additive variance than the dominance variance.

The degree of dominance was greater than the unity for the characters spikelets per panicle, spikelet fertility, 1000-grain weight, biological yield per plant, L/B ratio and grain yield per plant, indicating the presence of over dominance gene action. The highest estimates of degree of dominance was expressed as 3.35% for L/B ratio followed by spikelets per panicle (1.98%), spikelet fertility (1.90%), 1000-grain weight (1.64%), grain yield per plant (1.20%) and biological yield per plant (1.03%). The traits viz. days to maturity (0.26), days to 50% flowering (0.62), plant height (0.69), panicle length (0.76), panicle bearing tillers per plant (0.79) and harvest index (0.86) have shown low estimate of degree of dominance (<1). (Table-2) The importance of additive as well as non-additive gene effects with predominance of non-additive gene effects in inheritance of grain yield and yield components of rice has also been reported earlier (Pradhan et al., 2007; Rashid et al., 2008; Saleem et al., 2010; Saidai et al., 2010).

References


