ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND YIELD ATTRIBUTING TRAITS IN MUTANT RICE (ORYZA SATIVA L.)

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INTRODUCTION

Rice (Oryza sativa, 2n = 2x = 24, family: Gramineae) is the prime food crop of the world for more than half of the global population. India being the second largest producer of rice still lacks behind. India stands second with 108.0 MTs China occupies the first place with 144.0 MT in the world’s production table of 479.3 MT (USDA. May, 2013). The rising demand, saturation of cultivable field and low gross domestic production of rice are likely to cause a supply shortage of a crop in the near future. By the year 2025, about 785 MT of paddy which is 70 per cent more than the current production will be needed to meet the growing demand (Manomani and Khan, 2003).

The entire success of plant breeding programme of any crop largely depends on the wide range of variability present in that crop. It is the range of genetic variability in respect of important economic characters present in the population upon which is based on the effectiveness of selection. Environment has a profound influence upon the economically important characters, which are quantitatively inherited. Hence, it is difficult to decide upon whether the observed variability is heritable or due to environment and it is therefore, necessary to partition the same into its heritable and non-heritable components with suitable parameters like genetic coefficient, heritability estimates and genetic advance.

An induced mutation was used to generate genetic variability and have been successfully utilized to improve yield and yield components (Bharathi et al., 2012). This show that mutagenesis is a tool to be employed for crop improvement. In the present study, therefore, an attempt was made to partition the variance components, especially phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability ($h^2$ b.s.) and genetic advance (GA) for yield and yield components in M3 generations of rice.

MATERIALS AND METHODS

The present investigation was conducted at Agriculture Research Station (ARS) Gangavathi, Karnataka during the year 2012. With two popular varieties of rice (Oryza sativa L.) viz., BPT-5204 and RP Bio-226 were used as experimental material. Dry seeds were irradiated with 30 and 40 Kr doses of gamma ray from 60 Co source at Baba Atomic Research center (BARC), Bombay. In kharif 2011 all the harvested plant seeds from each treatment from M2 generation was sown to raise M3 generation in progeny rows in Augmented design (Federer, 1977) with 8 blocks, 2 parental checks repeated twice in each block. The observation was made in each mutant line for variants and the selected plants in M3 were recorded.

ABSTRACT

In the present study, seeds of rice variety viz., BPT-5204 and RP Bio-226 were treated with gamma irradiation (30kR and 40kR) with the objective to assess the variability in M3 generation. High GCV was found for flag leaf width (57.62), number of unproductive tillers plant-1 (26.45) and moderate for biological yield plant-1 (16.99), grain yield plant-1 (16.98). In all cases; phenotypic variances were higher than the genotypic variances. Based on high heritability coefficient ($h^2$ b.s.) coupled with high genetic advance as per cent of mean, for panicle length (87, 21.37), panicle exertion (99, 46.20), grain yield plant-1 (68, 28.92), biological yield plant-1 (64, 28.05) and test weight (61, 21.43) which indicated the predominance of additive gene action for the expression of these traits, hence are amenable for simple selection. Therefore, priority should be given to those traits which recorded higher estimates of genetic advance as per cent mean while deciding selection strategies and selection based on these characters may be useful in realizing better gain by selection.

KEY WORDS
M3 mutant Variability Heritability
The data available on individual characters was subjected to the method of analysis of variance commonly applicable to the Augmented design (Federer, 1977). Parameters estimated were the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability ($h^2$) and expected genetic advance ($GA$). All were estimated in the standard manner, expect genetic advance. The estimate of the genetic advance ($GA$, expressed as a percentage of the mean value). With assumed 1 per cent selection intensity was computed by the formula of Johnson et al. (1955):

$$GA = k \cdot \sigma_p \cdot h^2$$

Where,

$$h^2 = \text{Broad-sense heritability}$$
$$\sigma_p = \text{Phenotypic standard deviation of the mean performance of the treated population}$$
$$k = 2.64, \text{constant for 1 per cent selection intensity (i.e. the highest performing 1 % are selected)}$$

RESULTS AND DISCUSSION

The success of plant breeding programs relies heavily on the existence of genetic variability in plants for a particular trait. The analysis of variance revealed that the significant differences exist among genetic variability in plants for a particular trait. The success of plant breeding programs relies heavily on the presence of variability among the lines being evaluated and expected genetic advance. Similar result was observed by Bharathi et al. (2012). The estimation of genotypic co-efficient of variation indicates the amount of genetic variation presents for different traits while heritability gives as insight into the proportion of the variation which is inherent. However, heritability estimates, itself is an indication of the amount of genetic progress that would result from selecting the individual. Thus, the study of heritability in conjunction with genetic advance was emphasized in predicting the resultant effect for selecting the best individuals (Mehetre et al., 1996). In this investigation, high PCV and GCV were recorded (Table 2) for flag leaf width and number of unproductive tillers per plant similar results for these characters are confirmed with Basak and Gangul 1996, while moderate GCV and High PCV for Biological yield per plant and grain yield per plant was noticed similar results are confirmed with Pandey et al., 2012; Moderate GCV and PCV for Panicle length, test weight, flag leaf length, total number of tillers per plant and panicle exertion, similar results are confirmed with Gangashetty et al., 2012, Vijayalakshmi et al., 2008 and Sharma and Sharma 2007, for panicle length and Mamta singh et al., 2007 and Singh et al., 2005 for total number of tillers per plant; Low GCV and PCV was noticed for days to 50 per cent flowering, plant height, harvest index and number of spikelets per panicle similar results are confirmed with Gangashetty et al., 2012 and Pandey et al., 2012 for days to 50 per cent flowering and Mamta singh et al., 2007 and chaudhary and Motiramani 2003 for plant height, Pandey et al., 2012 for harvest index; and Rita binse et al., 2006 for number of spikelets per panicle.

Difference between PCV and GCV for the studied characters was very less indicating low sensitivity to environment and consequently greater role of genetic factors influencing the expression of these characters, which led to high estimates of broad sense heritability for the characters are Panicle length, days to 50 per cent flowering, plant height, biological yield per plant, grain yield per plant and number of spikelets per panicle. Almost similar results for heritability, from studies have been reported for panicle length (Seyoum et al., 2012); plant height (Hasib and Kole, 2004); days to 50 per cent flowering, test weight, harvest index and grain yield (Kole and Pandey, 2003); number of grains per panicle (Hasib and Kole, 2004) and biological yield per plant (Singh et al., 2011).

The estimates of genetic advance as percent of mean (Table 2) were high for panicle length, test weight, panicle exertion,


unproductive tillers per plant, biological yield per plant and grain yield per plant. Similar results are confirmed with panicle length (Seyoum et al., 2012); biological yield per plant (Singh et al., 2011); grain yield per plant (chaudhary and Motiramani 2003); panicle exertion (Mamta et al. 2007). Low for Days to 50 per cent flowering, number of productive tillers per plant and harvest index, similar results are confirmed with Days to 50 per cent flowering (Rita bisne et al., 2006); number of productive tillers per plant (Kuchanur et al., 2009) and harvest index (Pandey et al., 2012). High heritability accompanied by high genetic advance for Panicle length, biological yield and grain yield per plant (Alok et al., 2013) indicated the lesser influence of environment in expression of these characters the predominance of additive gene action might be involved in controlling the above traits in the M3 generation. Therefore these traits offer little scope for improvement by selection.

The overall results indicated that selection of higher panicle length, grain yield, test weight, biological yield and medium plant height with a reasonable balance for moderate grain number would particularly encourage the breeders to achieve higher grain yield. The results are in conformity with Nayak et al. (2001) for panicle length, grain yield and test weight; Hasib and Kole (2004) for plant height.

### Table 2: Estimates of range, mean and different genetic parameters for yield and yield attributing traits of mutant rice

<table>
<thead>
<tr>
<th>Characters</th>
<th>Range</th>
<th>Coefficient of variability</th>
<th>Heritability (%)</th>
<th>Expected genetic advance @ 5%</th>
<th>Genetic advance % of mean</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Min.</td>
<td>Max.</td>
<td>Phenotypic</td>
<td>Genotypic</td>
<td>broad sense</td>
</tr>
<tr>
<td>Days to 50% flowering</td>
<td>79.5</td>
<td>115.7</td>
<td>101.67</td>
<td>4.74</td>
<td>4.27</td>
</tr>
<tr>
<td>Plant height</td>
<td>61.76</td>
<td>102.7</td>
<td>77.78</td>
<td>8.27</td>
<td>7.22</td>
</tr>
<tr>
<td>Panicle length</td>
<td>16.21</td>
<td>55.21</td>
<td>20.00</td>
<td>11.90</td>
<td>11.11</td>
</tr>
<tr>
<td>Flag leaf length</td>
<td>19.65</td>
<td>32.81</td>
<td>25.04</td>
<td>13.11</td>
<td>11.62</td>
</tr>
<tr>
<td>Flag leaf width</td>
<td>1.11</td>
<td>1.86</td>
<td>1.53</td>
<td>59.04</td>
<td>57.62</td>
</tr>
<tr>
<td>Total No. of tillers plant</td>
<td>8.27</td>
<td>23.52</td>
<td>14.89</td>
<td>15.34</td>
<td>10.04</td>
</tr>
<tr>
<td>No. of productive tillers plant</td>
<td>7.38</td>
<td>19.18</td>
<td>12.56</td>
<td>15.32</td>
<td>7.37</td>
</tr>
<tr>
<td>No. of unproductive tillers plant</td>
<td>0</td>
<td>6.82</td>
<td>2.09</td>
<td>48.79</td>
<td>26.45</td>
</tr>
<tr>
<td>Panicle exertion</td>
<td>0</td>
<td>6.77</td>
<td>1.47</td>
<td>19.52</td>
<td>19.52</td>
</tr>
<tr>
<td>Biological yield plant</td>
<td>16.13</td>
<td>74.95</td>
<td>35.14</td>
<td>21.24</td>
<td>16.99</td>
</tr>
<tr>
<td>Grain yield plant</td>
<td>9.35</td>
<td>39.20</td>
<td>17.53</td>
<td>20.54</td>
<td>16.98</td>
</tr>
<tr>
<td>Harvest index</td>
<td>41.92</td>
<td>64.65</td>
<td>50.23</td>
<td>7.76</td>
<td>3.97</td>
</tr>
<tr>
<td>No. of Spikelet panicle</td>
<td>73.20</td>
<td>302.60</td>
<td>124.02</td>
<td>8.84</td>
<td>7.76</td>
</tr>
</tbody>
</table>
