Genetic variability and correlation analysis in F2 segregating population in brinjal (Solanum melongena L.)

INTRODUCTION

Brinjal (Solanum melongena L.) is an essential solanaceous vegetable crop in subtropical and tropical regions. Cytological studies have indicated that the basic chromosomal number is 2n = 24. Large genetic variability with respect to the size, maturity, shape of the fruit, culinary traits and spinyness exists in the original material. The low yield levels in India are due to the lack of sufficient crop genetic improvement and the development of promising genotypes. Therefore, brinjal needs constant genetic improvement. Better variability present in the initial material should be the chance for evolving desired types. A clear understanding of the variability of various quantitative characteristics of breeding materials is an asset to plant breeders for selecting superior genotypes on the basis of their phenotypic expression. Yield is a complex character influenced by various components that contributes to the genetic potential of the crop. F2 segregating populations were selfing hybrids (F1), which provided all potential variations. Therefore, assortment with fastidious...
objective (F2) segregation is extremely efficient, and inbred lines were produced by utilizing the genotypes by selfing generation after generation. Estimates of genotypic and phenotypic coefficients of variation provide an idea of the interplay of the genotype and environment that influences breeding results (Ravali et al., 2017) in brinjal. High heritability and genetic advance for specified characters denote which is governed by additive gene action and hence the successful stipulation for selection. Association studies involving yield-attributing traits and their comparative parts of fruit yield per plant are assessments in forecasting a programme on breeding. Pathway analysis accelerates the separation of the association coefficient into indirect and direct belongings on yield and other characteristics (Mahmoud et al., 2018). Path analysis is also very helpful in formulating breeding program strategies to develop superior genotypes through selection in advanced generations. Hence, the current study was implemented to analyse the concert of various agronomical traits and to measure the degree of heritability, expected genetic advance, variability, path coefficient and correlation analysis components in S. melongena.

MATERIALS AND METHODS

The experiment was conducted at the College Orchard, Department of Vegetable Crops, Horticultural College & Research Institute, Tamil Nadu Agricultural University, Coimbatore. In total, 250 F2 brinjal plants derived from the cross Sevathampatti local x Seetipulam local were evaluated for high yield and yield contributing characteristics during 2018 – 2019. The F2 progenies obtained by selfing from the F1 cross were raised. Each plant in the cross was labelled for fifteen recorded qualitative and quantitative traits, which include the number of fruits per plant, height of the plant (cm), number of branches, days to first flowering, length of the fruit (cm), weight of the fruit (g), fruit girth (cm), fruit borer infestation (%), shoot borer infestation (%) and yield (kg/plant). Singh and Chaudhary (1997) reported that the phenotypic coefficient of variation (PCV), heritability in a broad sense (h2), genotypic coefficient of variation (GCV) and genetic advance as a percentage over the mean and genetic advance (GA) were analysed. The correlation coefficient was estimated according to the formula given by Johnson et al. (1955). According to Dewey and Lu (1959), indirect and direct paths were obtained according to the method

Heritability in broad sense (h2)= \[ \frac{\sigma^2_g}{\sigma^2_p} \times 100 \] 

The range of heritability
Low<30
Moderate-30 to 60

High->60

Genetic advance (GA) \[ GA = \frac{\sigma^2_g}{\sigma^2_p} \times k \times \sqrt{\sigma^2_p} \]

Where,
\[ k = \text{Selection differential which is equal to 2.06 at 5 per cent level} \]
\[ \sigma^2_g = \text{genetic variance} \]
\[ \sigma^2_p = \text{phenotypic variance} \]

Genetic advance was expressed as per cent of mean GA as per cent of mean = Genetic advance / grand mean x 100

Genetic advance was also categorized by
Low - <10
Medium - 10 to 20
High -20

Genotypic variance (\( \sigma^2_g \)) = \( \frac{M_g - M_e}{r} \)

Phenotypic variance (\( \sigma^2_p \)) = \( \sigma^2_g + \sigma^2_e \)

Where,
\[ r = \text{Mean of replications} \]
\[ M_g = \text{Mean sum of squares for genotypes} \]
\[ M_e = \text{Mean sum of squares for error} \]
\[ \sigma^2_e = \text{Environmental variance} \]

\[ \text{PCV} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \times 100 \]

\[ \text{GCV} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100 \]

The range of following PCV & GCV values were classified as low, moderate and high.

<table>
<thead>
<tr>
<th>Range</th>
<th>Scale</th>
</tr>
</thead>
<tbody>
<tr>
<td>Less than 10%</td>
<td>Low</td>
</tr>
<tr>
<td>10 - 20%</td>
<td>Moderate</td>
</tr>
<tr>
<td>More than 20%</td>
<td>High</td>
</tr>
</tbody>
</table>

Correlation

Genotypic correlation coefficient

\[ r_{g(xy)} = \frac{\text{Cov.g(xy)}}{\sqrt{\sigma^2_g_x \times \sigma^2_g_y}} \] 

Where,
\[ r_{g(xy)} = \text{Genotypic correlation coefficient} \]
\[ \text{Cov.g(xy)} = \text{Genotypic covariance between the traits 'x' and 'y'} \]
\[ \sigma^2_g_x = \text{Genotypic variance of the trait- 'x'} \]
\[ \sigma^2_g_y = \text{Genotypic variance of the trait- 'y'} \]

Path coefficient analysis

The direct and indirect effects were classified based on the scale

<table>
<thead>
<tr>
<th>More than 1.0</th>
<th>Very high</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.30 to 0.99</td>
<td>High</td>
</tr>
<tr>
<td>0.20 to 0.29</td>
<td>Moderate</td>
</tr>
<tr>
<td>0.10 to 0.19</td>
<td>Low</td>
</tr>
<tr>
<td>0.00 to 0.09</td>
<td>Negligible</td>
</tr>
</tbody>
</table>
RESULTS AND DISCUSSION

Variability plays an important role in crop breeding material, ensuring a better chance of producing desirable crop plants. The results of range, mean, GCV, PCV, heritability ($h^2$), GA % in the F2 population of cross Sevathampatti local x Seetipulam local are shown in Table 1. The results showed that the genotypic coefficient of variation was highest for shoot infestation (56.39%), followed by the number of branches per plant (22.73%) and plant height (20.93%), while moderate GCV was observed for the number of fruits (19.18%) and yield of individual plants (17.42%). The highest phenotypic coefficient of variation was recorded for shoot infestation (57.24%), followed by no. of branches per plant (23.42%) and yield of the individual plant (22.32%), and moderate GCV were recorded in a number of fruits (23.42%) and yield of individual plant (19.65%) and fruit infestation (10.95%). Higher GCV and PCV were recorded in a number of fruits per plant, number of fruits per plant and plant height. These findings are similar to Mili et al. (2014), who revealed that high estimates of genetic advance and heritability might be attributed to the control of additive genes, and phenotypic selection for their improvement could be achieved in brinjal by simple breeding methods.

Correlation studies achieved

The correlation between fruit yield per plant and different yield attributes is presented in Table 2. The correlation coefficient between diverse traits that yield was positive and significantly linked with no. of fruits (0.227), individual fruit weight (0.126) and no. of branches (0.105). These consequences are in agreement with the results of Ravalı et al. (2017) in brinjal and Tiwari et al. (2019) in brinjal. Plant height exhibited a significant and positive relationship with the length of the fruit (0.506) and fruit borer infestation (0.341). Tiwari et al. (2019) also obtained similar results in brinjal. First flowering had a significant and negative association with the number of branches (-0.09) and shoot infestation (-0.068). Fruit length had a significant and positive association with fruit diameter (0.46) and fruit infestation (0.265). The outcome is in accord with the findings of Tiwari et al. (2019) in brinjal. The diameter of the fruit recorded a positive correlation with individual fruit weight (0.066) and fruit infestation (0.065). The individual fruit weight was positively correlated with shoot infestation (0.069). These outcomes confirm the results of Ravalı et al. (2017) and Tiwari et al. (2019) in brinjal, which revealed the existence of sufficient

**Table 1.** Mean, range and genetic parameters in the F2 population of the brinjal hybrid Sevathampatti local x Seetipulam local

<table>
<thead>
<tr>
<th>Characters</th>
<th>Mean</th>
<th>Range</th>
<th>PCV</th>
<th>GCV</th>
<th>$h^2$</th>
<th>GA as % of mean</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Minimum</td>
<td>Maximum</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Plant height</td>
<td>88.91</td>
<td>56.17</td>
<td>146.9</td>
<td>21.10</td>
<td>20.93</td>
<td>98.36</td>
</tr>
<tr>
<td>Days to first flowering</td>
<td>48.01</td>
<td>38.00</td>
<td>56.00</td>
<td>6.93</td>
<td>4.62</td>
<td>44.48</td>
</tr>
<tr>
<td>No. of branches per plant</td>
<td>8.12</td>
<td>4.00</td>
<td>14.00</td>
<td>23.42</td>
<td>22.73</td>
<td>94.19</td>
</tr>
<tr>
<td>No. of fruits per plant</td>
<td>42.94</td>
<td>23.00</td>
<td>73.00</td>
<td>19.65</td>
<td>19.18</td>
<td>95.34</td>
</tr>
<tr>
<td>Fruit length</td>
<td>7.01</td>
<td>4.92</td>
<td>8.86</td>
<td>12.03</td>
<td>8.57</td>
<td>50.80</td>
</tr>
<tr>
<td>Fruit girth</td>
<td>12.68</td>
<td>10.10</td>
<td>15.28</td>
<td>6.55</td>
<td>3.16</td>
<td>23.19</td>
</tr>
<tr>
<td>Single fruit weight</td>
<td>50.31</td>
<td>36.00</td>
<td>59.46</td>
<td>8.02</td>
<td>5.58</td>
<td>48.40</td>
</tr>
<tr>
<td>Shoot infestation</td>
<td>14.90</td>
<td>5.94</td>
<td>52.37</td>
<td>57.24</td>
<td>56.39</td>
<td>97.06</td>
</tr>
<tr>
<td>Fruit infestation</td>
<td>20.00</td>
<td>15.93</td>
<td>25.38</td>
<td>10.95</td>
<td>9.20</td>
<td>70.57</td>
</tr>
<tr>
<td>Yield per plant</td>
<td>2.15</td>
<td>0.67</td>
<td>3.43</td>
<td>22.32</td>
<td>17.42</td>
<td>60.92</td>
</tr>
</tbody>
</table>
The authors declare that they have no conflict of interest.

REFERENCES


