SELECTION OF IMPORTANT YIELD COMPONENT CHARACTERS BASED ON GENETIC ANALYSIS IN CELERY (APIUM GRAVEOLENS L.)

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Abstract: Eleven genotypes (control and ten macromutants- maintained over generations through selfing) of Celery (Apium graveolens L.) are assessed based on eight phenotypic traits (plant height, number of primary branches/plant, total branches/plant, number of compound umbels/plant, number of umbels/plant, number of umbellets of first inflorescence, total seed yield and harvest index) for selection of essential trait(s) maximizing yield through efficient breeding. ANOVA depict variations among the selected traits. Phenotypic and genotypic co-variance, heritability (broad sense) and genetic gain (5% level) performed reveal three important selection indices (total branches, no. of compound umbel and total umbel per plant) in celery.

Keywords: Celery, Germplasms, Quantitative traits, Selection

INTRODUCTION

Celery (Apium graveolens L., Family – Umbelliferae; 2n=22), is an important seed spice of India, besides possessing immense therapeutic significance (Ashburn and Stats, 1999; Guerrero, 2005; Praveen, 2011; Fazal and Single, 2012). The spice is providing considerable source in National economy (Khinivasara and Bhushan, 2015) and therefore it should be under sustainable cultivation for enhancement of production in yield and value added products. Ten true breeding mutant lines are raised in celery (total plants screened - 515), which highlights breeding endeavour for improvement. Further, more knowledge of heritability (Rajput and Singh, 2003; Sabesan et al., 2009; Yadava et al., 2011) and genetic gain (Dhayal et al., 1999; Singh et al., 2003; Yadav et al., 2013; Meena et al., 2014) can also shed light on selection of essential traits under study. With the view to it, present investigation estimate genetic variability, heritability and genetic advance for eight yield and yield related traits in eleven (control and macromutants) germplasms of celery.

MATERIAL AND METHOD

In an induced mutagenesis (γ-irradiations and EMS) programme, eleven germplasms that were maintained through selfing are assessed quantitatively based on eight phenotypic traits (plant height, number of primary branches/plant, total branches/plant, number of compound umbels/plant, number of umbels/plant, number of umbellets of first inflorescence, total seed yield and harvest index). ANOVA is performed to estimate variation among the parameters; Phenotypic and genotypic co-variance, heritability (broad sense) and genetic gain (5% level) are determined for each quantitative trait in the germplasms in accordance to Burton and De Vene(1953), Hanson et al. (1956) and Johnson et al.(1955a) respectively.

RESULT AND DISCUSSION

Analysis of variance (F-test) reveal that mean sum of square due to variance is significant for all the traits (Table 1), suggesting variations among the plant types. The extent of variability measured in terms of grand mean, PCV, GCV, heritability and genetic gain as per cent of mean are given in Table 2. The estimates of genetic parameters show that the difference between genotypic (GCV) and phenotypic (PCV) co-efficient of variation is low only for plant height, indicating that this character is least affected by environment. For other traits, the differences are much inflated, thereby, depicting a positive role of environment on the expression of genotypes. Co-efficient of variability (%) both at phenotypic and genotypic level are high for total branches/plant, number of compound umbels/plant, number of umbels/plant and seed yield. High estimate of heritability is obtained for all traits excepting for no. of umbellets of first inflorescence and harvest index. Rawat et al. (2013) in their experiment with 12 quantitative characters in 13 diverse genotypes of fennel got high heritability for different traits and opined genetic influence rather than environmental influence in control of the attributes. High values of co-efficient of variation accompanied with high heritability do not mean that character...
(seed yield, no. of primary branches per plant and to an extent harvest index) will show always high genetic advance. Johnson et al. (1955a), Mishra et al. (2006), Meena et al. (2013) and many others suggested that high heritability in association with high genetic advance is more reliable for selection. In the present investigation, high heritability is coupled with high genetic gain was estimated for total branches, no. of compound umbels and total umbels per plant. These three traits also exhibit high grand mean in the population. Estimates of heritability also give some idea about the gene action involved in the various polygenetic traits (Johnson et al., 1955b). Panes (1957) reported that association of high heritability with high genetic gain is due to additive gene effect. So, it can infer that the said traits are under additive gene effects.

**Table 1.** Analysis of variance for different characters in control and mutant plant types.

<table>
<thead>
<tr>
<th>Sources</th>
<th>DF</th>
<th>Mean Sum of Squares (M.S.S) of quantitative traits (T)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>T-1</td>
</tr>
<tr>
<td>Treatments</td>
<td>10</td>
<td>1237.87**</td>
</tr>
<tr>
<td>Error</td>
<td>54</td>
<td>75.40</td>
</tr>
</tbody>
</table>

**Table 2.** Analysis of genetic parameters for different traits in 11 germplasms.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Grand mean</th>
<th>Genotypic variance</th>
<th>Environmental variance</th>
<th>Phenotypic variance</th>
<th>Co-efficient of variability (%)</th>
<th>Heritability</th>
<th>Genetic gain as % of mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plant height (cm)</td>
<td>74.62</td>
<td>211.58</td>
<td>79.13</td>
<td>290.71</td>
<td>19.49</td>
<td>22.85</td>
<td>73.0</td>
</tr>
<tr>
<td>No. of primary branches/plant</td>
<td>8.75</td>
<td>5.56</td>
<td>3.35</td>
<td>8.91</td>
<td>26.95</td>
<td>34.11</td>
<td>62.0</td>
</tr>
<tr>
<td>Total branches/plant</td>
<td>177.14</td>
<td>10888.48</td>
<td>7069.60</td>
<td>17958.08</td>
<td>58.91</td>
<td>75.65</td>
<td>61.0</td>
</tr>
<tr>
<td>No. of compound umbels/plant</td>
<td>169.55</td>
<td>10383.98</td>
<td>6883.63</td>
<td>17267.61</td>
<td>60.10</td>
<td>77.50</td>
<td>60.0</td>
</tr>
<tr>
<td>No. of umbels/plant</td>
<td>692.52</td>
<td>153165.60</td>
<td>96133.10</td>
<td>249298.70</td>
<td>56.51</td>
<td>72.10</td>
<td>61.0</td>
</tr>
<tr>
<td>No. of umbellets of first inflorescence</td>
<td>34.86</td>
<td>16.22</td>
<td>87.71</td>
<td>103.93</td>
<td>11.55</td>
<td>29.24</td>
<td>16.0</td>
</tr>
<tr>
<td>Seed yield (gm)</td>
<td>2.68</td>
<td>3.47</td>
<td>2.25</td>
<td>5.72</td>
<td>69.64</td>
<td>89.41</td>
<td>61.0</td>
</tr>
<tr>
<td>Harvest index (%)</td>
<td>18.24</td>
<td>12.50</td>
<td>19.83</td>
<td>32.33</td>
<td>19.38</td>
<td>31.17</td>
<td>39.0</td>
</tr>
</tbody>
</table>
CONCLUSION

Traits namely total branches, no. of compound umbels and total umbels per plant showing high heritability coupled with high genetic gain can be considered effective for selection and improvement in celery.

REFERENCES
