Diversity and stability analysis for yield and component traits in *Cajanus cajan* under rainfed conditions

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ABSTRACT

Twenty one genotypes of short duration pigeonpea were evaluated under rainfed condition of Manipur during *kharif* season of 2007/8, 2008/9 and 2009/10 to obtain the knowledge of genetic diversity and stability for yield and its component traits and used for identification of stable genotypes of pigeonpea. The experiment was carried out in randomized complete block design with three replications. Genetic divergence between genotypes was estimated using Mahalanobis $D^2$ method. The genotypes under study were distributed in six different clusters based on $D^2$ statistics. Highest number of genotypes were found in cluster IV (6) followed by cluster VI (5). The genotypes *viz.* GT 101 showed higher mean performance for grain yield with non-significant deviation from regression, followed by ICPL 87 and PA 134. The present study indicated that crossing between genotypes from cluster I and II could be brought a wide spectrum of genetic variability into progenies with superior combination of different traits *viz.* early maturity, short plant stature and higher grain yield.

Key words: Cluster analysis, Pigeonpea, Stability analysis.

INTRODUCTION

Pigeonpea or red gram [*Cajanus cajan* (L.) Mills] is one of the most important pulse crops for rainfed agriculture. Generally, it is grown worldwide in developing countries under tropical and subtropical climatic conditions. It occupies an area of about 4.67 million ha, out of which, 3.30 million ha is cultivated in India alone. Among Asian countries besides India, Myanmar (5, 70,000 ha), China (1,50,000 ha), and Nepal (20,988 ha) are important pigeonpea producing countries (Saxena *et al.*, 2010). In Manipur, a north eastern state of India, this crop is not grown commercially but it is mainly cultivated in the backyard of the house and generally long duration cultivars of pigeonpea are raised for green pods, consumed as vegetable. Due to long duration, crop is affected by terminal drought. Hence, productivity is very low and unstable because of its cultivation under moisture stress and low fertility conditions. Significant shift in crop productivity may be possible by breeding crop varieties for their stability for yield and its attributing characters. Genotype-environmental (GE) interaction play major role for stabilizing genotypes across the environments with high yield potential. Hence, it is essential to breed high yielding varieties, which may perform consistently well over years under different agro climatic as well as cropping systems. Development of high yielding varieties depends upon presence of genetic variability and diversity in breeding population, where selection of genetically diverse parents in hybridization programme is important to get wide array of recombinants. Keeping this in view, the present investigation was carried out to estimate the genetic divergence and stability for yield and its attributing traits in short duration pigeonpea.

MATERIALS AND METHODS

Experimental material for the present study consisting of twenty one pigeonpea genotypes were grown in randomized complete block design with 3 replications during *kharif* 2007-08, 2008-09 and 2009-10 under rainfed conditions of Manipur. The experiment was laid out at Langol Farm of ICAR Research Complex for North Eastern Hill Region, Manipur Centre, Imphal, Manipur. The research farm is located at 42.54°N to 93.5°E at altitude of 774 m. The soil of the farm was sandy loam with pH 5.5. Each plot consisted of two rows of 4 m length with spacing 60 x 20 cm. All recommended agronomic practices were followed to raise the normal crop in each year. The data were recorded on five randomly selected plants from each genotype for plant height (cm), primary branches per plant, pods per plant, pod length (cm), grains per pod, hundred seed weight (g), seed yield per plant (g), while days to 50% flowering and days to maturity were recorded on plot basis. The data were subjected...
for estimation of genetic diversity and stability parameters. Mahalanobis D² statistic was employed to measure the genetic divergence between genotypes (Mahalanobis, 1936). The genotypes were grouped into number of clusters by Tocher’s method as described by Rao (1952). Stability was analyzed using three years data according to the model given by Eberhart and Russel (1966) to determine stability regression coefficient and deviation from regression.

RESULTS AND DISCUSSION
Genetic diversity: Twenty one genotypes of short duration pigeon pea were distributed into six different clusters on the basis of D² values are presented in Table 1. The distribution of different genotypes revealed that cluster IV comprised the highest number of genotypes (6) followed by cluster VI (5). Further, cluster II and III included 3 genotypes each, while the cluster I and V contained 2 genotypes each, suggesting the impact of selection pressure in increasing the genetic divergence.

The inter cluster distance was higher than intra cluster distance indicating that there is considerable amount of genetic diversity among genotypes studied (Table 2). Intra-cluster distance was the highest in cluster VI (17.81) as followed by cluster IV with 15.05 revealing that genotypes in this cluster was most diverged. The cluster I exhibited minimum intra cluster value of 1.51 suggesting that genotypes within this cluster exhibited close relationship. These results were similar with the earlier findings of Murthy and Dorairaj (1990) and Thombre et al., (2000). Inter cluster distances as ranged 17.93-128.60 with maximum inter cluster distance between the cluster I and II (128.60), followed by cluster II and IV (119.84). In the present study, selecting genotypes from different cluster as from cluster I and II may create the wide spectrum of variability and also provide high heterotic for yield advantage. The results are in agreement with earlier findings of Sreelakshmi et al., (2010a), Singh et al., (2010) and Patel and Acharya (2011). The average cluster mean of nine quantitative traits (Table 3) showed that the cluster I recorded the highest mean value for days to maturity (158.89), days to flowering (97.89), days to maturity (158.89) and grain yield per plant (29.86). Similarly, cluster III exhibited the maximum mean values for plant height (286.40), primary branches per plant (14.46) and pods per plant (203.16). However, cluster mean for the pod length (5.42) in cluster IV, seeds per pod (4.58) in cluster V and hundred seed weight (9.95) in cluster VI was found to be the highest only for solitary trait. Among the six clusters, cluster I and III revealed maximum mean values for three characters each in the present investigation. The genotypes from cluster I may be selected for earliness combined with high grain yield while from cluster III, selection of genotypes could be made for yield attributing traits viz., plant height, primary branches per plant and pods per plant. Thus, clustering pattern can be used for identifying the best cross combination for creating the variability with respect to different characters. Hence, for creating the wide variability and revamping the yield, the genotypes from cluster I, cluster III, cluster IV, cluster V and cluster VI may be hybridized. It was noticed that cluster II possessed the lowest mean values for days to maturity, plant height, primary branches per plant, seeds per pod, hundred seed weight and grain yield per plant, while cluster III, cluster IV and cluster VI revealed the lowest values for pod length, pods per plant and days to 50% flowering respectively. Inter crossing of genotypes among these clusters may produce variability for the respective characters (Gohil, 2006).

In the present study, the genotypes clubbed in cluster I may be intercrossed with the genotypes placed in cluster II for generating wide variability and consequently transgressive segregants may be achieved in advanced generations. Thus, superior genotypes selected on the basis of inter cluster distance and cluster means could be utilized in hybridization programme.

Stability analysis: Pooled analysis of variance for stability performance of genotypes are presented in Table 4 and revealed highly significant differences for primary branches per plant, pods per plant and grain yield per plant indicating that genotypes possessed significant variation for these traits confirming random and variable nature of environments selected, which influenced the expression of these traits. These results were contrary to the earlier findings of Sreelakshmi et al., (2010b). All the traits showed significant differences due to environment, indicating that all the years were highly variable. Component analysis of environment + (Genotype x environment) was significant for all

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Number of genotypes</th>
<th>Name of genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>2</td>
<td>AL 1491, ICPL 87</td>
</tr>
<tr>
<td>II</td>
<td>3</td>
<td>Pusa 2003-1, CORG 2001-5, GT 101</td>
</tr>
<tr>
<td>III</td>
<td>3</td>
<td>Pusa 992, H-82-1, Pant A-286</td>
</tr>
<tr>
<td>IV</td>
<td>6</td>
<td>ICPL-85010, UPAS-120, ICPL-99004, WRGE-28, Phule-T-80208-1, H-97-24</td>
</tr>
<tr>
<td>V</td>
<td>2</td>
<td>H-92-6, WRGE -31</td>
</tr>
<tr>
<td>VI</td>
<td>5</td>
<td>TT-302, Phule T-1037, ICPL 98015, ICPL 88034, PA-134</td>
</tr>
</tbody>
</table>
the traits under study. Partitioning of this variation into linear and non-linear components exhibited that mean square due to environment (linear) were highly significant for all the traits under study. This is in agreement with the findings of Sreelakshmi et al., (2010b). It suggested that environments were random and different and they reflected the expression of these traits and this variation could have arisen due to the linear response of the regression of the cultivars to the environments. The G × E (Linear) interaction revealed significant differences for pods per plant and hundred seed weight indicating that phenotypic performance of the genotypes was predictable for these characters. The non-linear component arising due to the heterogeneity measured as mean square due to pooled deviation was significant only for days to 50% flowering revealing presence of non-linear response of the genotypes to the changing environments. In traits where non-linear component was non-significant, the G × E interaction of these traits was greatly influenced by environmental factors and there exists either relationship or complex relationship between genotype and environment effect making its prediction more difficult for that trait. The same trend was also observed by Mahto et al., (2005).

Phenotypic stability was estimated on the basis of three parameters namely; mean performance over years (x), regression coefficient (bi) and deviation from regression (S'd) as suggested by Eberhart and Russell (1966). The estimation of stability for yield and its attributing traits is depicted in Table 5. According to Eberhart and Russell (1966) a variety is likely to be stable over different environments, if a variety possesses higher mean value, unit regression coefficient (bi) with lowest deviation (non significant) from linear regression. High value of regression (bi>1) indicates that the variety is more responsive to the rich input environments, whereas low value of regression coefficient (bi<1) indicates that the variety may be suitable in poor environment. Based on stability parameters the genotypes viz., TT-302, Pusa-992, H-82-1 and GT 101 were found to be stable for days to maturity. The non-significant deviation from regression and regression coefficient (bi=1) indicates that the variety may be suitable in poor environment. Based on stability parameters the genotypes were identified as desirable and stable for days to maturity. The non-significant deviation from regression and regression coefficient (bi=1) indicates that the variety may be suitable in poor environment. Based on stability parameters the genotypes were identified as desirable and stable for days to maturity.

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Days to 50% flowering</th>
<th>Days to maturity</th>
<th>Plant height (cm)</th>
<th>Primary branches per plant</th>
<th>Pods per plant</th>
<th>Pod length (cm)</th>
<th>Seeds per pod</th>
<th>100-seed weight (g)</th>
<th>Grain yield per plant (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>97.89</td>
<td>158.89</td>
<td>281.03</td>
<td>14.25</td>
<td>184.34</td>
<td>4.44</td>
<td>4.54</td>
<td>9.29</td>
<td>29.86</td>
</tr>
<tr>
<td>II</td>
<td>81.56</td>
<td>136.19</td>
<td>174.65</td>
<td>9.23</td>
<td>93.08</td>
<td>5.27</td>
<td>4.15</td>
<td>8.83</td>
<td>27.58</td>
</tr>
<tr>
<td>III</td>
<td>94.89</td>
<td>158.00</td>
<td>286.04</td>
<td>14.46</td>
<td>203.16</td>
<td>4.41</td>
<td>4.47</td>
<td>9.75</td>
<td>28.45</td>
</tr>
<tr>
<td>IV</td>
<td>81.76</td>
<td>141.04</td>
<td>186.52</td>
<td>10.6</td>
<td>92.70</td>
<td>5.42</td>
<td>4.29</td>
<td>9.64</td>
<td>29.33</td>
</tr>
<tr>
<td>V</td>
<td>94.94</td>
<td>158.56</td>
<td>282.73</td>
<td>14.28</td>
<td>194.21</td>
<td>4.37</td>
<td>4.58</td>
<td>9.29</td>
<td>29.49</td>
</tr>
<tr>
<td>VI</td>
<td>77.07</td>
<td>140.04</td>
<td>191.06</td>
<td>10.45</td>
<td>96.48</td>
<td>5.36</td>
<td>4.28</td>
<td>9.95</td>
<td>28.46</td>
</tr>
</tbody>
</table>

**TABLE 2: Average intra (diagonal) and inter cluster distance \( (D^2 \text{ values}) \) for 21 genotypes in pigeon pea.**

<table>
<thead>
<tr>
<th>Cluster</th>
<th>I</th>
<th>II</th>
<th>III</th>
<th>IV</th>
<th>V</th>
<th>VI</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>1.51</td>
<td>7.71</td>
<td>6.64</td>
<td>15.05</td>
<td>3.80</td>
<td>17.81</td>
</tr>
<tr>
<td>II</td>
<td>7.71</td>
<td>7.71</td>
<td>6.64</td>
<td>15.05</td>
<td>3.80</td>
<td>17.81</td>
</tr>
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</tr>
</tbody>
</table>

**TABLE 3: Cluster means of for quantitative and yield component traits in pigeon pea.**

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Days to 50% flowering</th>
<th>Days to maturity</th>
<th>Plant height (cm)</th>
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<th>Pods per plant</th>
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</tr>
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<td>5.36</td>
<td>4.28</td>
<td>9.95</td>
<td>28.46</td>
</tr>
</tbody>
</table>

**TABLE 4: Pooled analysis of stability for ten quantitative and yield related traits in pigeon pea.**

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>DF</th>
<th>Days to 50% flowering</th>
<th>Days to maturity</th>
<th>Plant height (cm)</th>
<th>Primary branches per plant</th>
<th>Pods per plant</th>
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<th>100-seed weight (g)</th>
<th>Grain yield per plant (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotypes</td>
<td>20</td>
<td>40.02</td>
<td>82.08</td>
<td>221.67</td>
<td>3.97**</td>
<td>741.13**</td>
<td>0.09</td>
<td>0.03</td>
<td>1.29</td>
<td>23.43**</td>
</tr>
<tr>
<td>Environments</td>
<td>2</td>
<td>1893.30**</td>
<td>3388.35**</td>
<td>73647.22**</td>
<td>171.70**</td>
<td>71574.43**</td>
<td>6.65**</td>
<td>0.50**</td>
<td>13.99**</td>
<td>6.29**</td>
</tr>
<tr>
<td>Genotype X</td>
<td>40</td>
<td>31.90</td>
<td>36.16</td>
<td>143.96</td>
<td>0.83</td>
<td>360.49**</td>
<td>0.07</td>
<td>0.02</td>
<td>0.95</td>
<td>0.46</td>
</tr>
<tr>
<td>Environment (Linear)</td>
<td>42</td>
<td>120.54**</td>
<td>195.79**</td>
<td>3644.11**</td>
<td>8.96**</td>
<td>3751.63**</td>
<td>0.38**</td>
<td>0.05**</td>
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<td>0.74*</td>
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</tr>
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<td>8.96**</td>
<td>3751.63**</td>
<td>0.38**</td>
<td>0.05**</td>
<td>1.58**</td>
<td>0.74*</td>
</tr>
<tr>
<td>Pooled error</td>
<td>126</td>
<td>16.6</td>
<td>27.17</td>
<td>136.95</td>
<td>1.18</td>
<td>286.11</td>
<td>0.07</td>
<td>0.03</td>
<td>0.54</td>
<td>10.31</td>
</tr>
</tbody>
</table>

* Significant at 5% level, ** Significant at 1% level
be adopted in poor environments, while AL-1491 exhibited low mean value for plant height with bi>1 and non significant deviation from regression. These results are in parallel with earlier findings of Reddy et al., (2011). The genotypes H-82-1 and WRGE-31 showed high mean for primary branches per plant, bi>1 and non significant deviation from regression suggesting predictable performance and stable over favorable environment. The results are corresponding to the findings of Sreelakshmi et al., (2010c). For pods per plant, five genotypes viz., Pusa 2003-1, H-97-24, Pusa 992, WRGE 31 and GT 101 registered high mean, bi>1 and non significant deviation from regression revealing their suitability in favorable environments. Kuchanur et al., (2008) reported similar results with present study. Out of 21 genotypes, 7 genotypes had higher mean values with regression coefficient (bi>1) and non-significant deviation from regression and 3 genotypes viz., H-82-1, WRGE 31 and PA 134 consisted of higher mean values with regression coefficient (bi<1) non significant deviation from regression for pod length. Four
genotypes viz., WRGE 28, Pant A 286, and ICPL 99004 were found to be stable under favorable environments (bi>1) and non significant deviation, while two genotypes H 97-24 and H 94-6 were observed to be stable in poor environments (bi<1) and non significant deviation from regression for pods per plant. For hundred seed weight, three genotypes namely, Phule-T-1037, H 94-6 and ICPL 85010 exhibited high mean (bi>1) and non significant deviation from regression whereas, Phule T-80280-1 revealed above average value, regression coefficient near to unity (bi<1) and non significant deviation from regression. The genotype GT 101 showed high mean performance for grain yield per plant, regression coefficient (bi>1) and no significant s'di values, while ICPL 87 and PA 134 registered the mean performance at par to the average value with bi>1 and non significant deviation from regression. This indicated that these genotypes were stable under favorable conditions for grain yield per plant. These findings were in agreement with Sreelakshmi et al., (2010c). These genotypes can also be utilized as parents in hybridization programme for improving the yield and wider adaptability. Ghosh (2002) also put forwarded the use of diverse genotypes for hybridization programme.

REFERENCES


