GENETIC VARIABILITY AND CORRELATION STUDIES IN URDBEAN (VIGNA MUNGO L.)

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ABSTRACT

Genetic variability and correlations among 133 accessions of urdbean collected from different agro-ecological zones of Southern and Southeastern Rajasthan, India was assessed for eight quantitative traits. These accessions along with two national checks ‘KU 96-3’ and ‘RBU 38’ were evaluated in randomized block design with three replications at experimental field of Agricultural Research Station, Umedganj, Kota Rajasthan, India during kharif 2009 and 2010. Wide range of variability was observed for quantitative traits. Plant height (cm), primary branches and pods per plant showed high genetic advance and moderate heritability. Seed yield per plant showed strong positive correlation with number of pods per plant and number of branches per plant and strong negative correlation with days to fifty per cent flowering and days to maturity. Path coefficient analysis also revealed that number of pods per plant and number of branches per plant had major direct and indirect effect on yield contributing traits in urdbean.

Key words: Correlations, Path analysis, Quantitative traits, Urdbean

INTRODUCTION

Improvement of urdbean (Vigna mungo L.), being an important pulse crop of India, is an important task for pulses breeders. It is grown in various agro-ecological conditions and cropping systems with diverse agricultural practices (Gupta et al. 2001). Among pulses, it is the least researched crop and no international centre of CGIAR system has this crop on its mandate (Anonymous, 1976). Although it has been identified as a potential crop in number of countries, but no systematic research information is available on crop improvement using biometrical techniques except few reports in the recent years (Ghafoor et al. 2003). To strengthen ongoing program, study of available natural genetic variation (collection, evaluation and management) is of immense importance. The knowledge of certain genetic parameters is also essential for proper understanding and their manipulation in any crop improvement programme. Seed yield is the result of the expression and association of several plant growth components. Correlation coefficients, although useful in quantifying the size and direction of trait associations, can be misleading if the high correlation between two traits is a consequence of the indirect effect of the traits (Dewey and Lu, 1959). Path analysis partitions the genotypic correlations into direct and indirect effects of the traits and it was used by Ghafoor et al (2003); Umadevi and Ganeshan (2005); Chauhan et al (2007); Makeen et al (2009) and Isha Parveen et al (2011) to know the effect of traits on grain yield in urdbean.

Therefore, present study was planned to investigate the genetic variability, correlation coefficient and path analysis to identify the best traits to be used for future exploitation.

MATERIAL AND METHODS

The experimental material comprised of 133 diverse landraces of urdbean collected through an exploratory survey of urdbean growing areas of Southern and Southeastern Rajasthan, India during 2006-2007. The experiments was carried out during

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The variation for these traits can be exploited for yield improvement in breeding programme. On the other hand, low variation was observed for number of seeds per pod, 100 seed weight and number of branches per plant. Improvement of these traits through simple selection might be limited from germplasm used in the present study. Hence, the genes for these important traits should be explored from other sources through more collections from the area of maximum diversity or acquisition of germplasm from other sources (Ghafoor et al., 2001).

Frequency distributions for the traits were calculated to classify the cultivars into different categories (Fig.1). It is indicated that 50% accessions of the population flowered from ≥ 34.85 to 41.67 days while 48% matured in the range ≥ 70.81 to 78.59 days. Furthermore, maximum of 36% of the population were having ≥ 63.66 - 80.20 cm plant height whereas, 50% population had primary branches per plant in the range of ≥ 2.62 to 3.51.

**RESULTS AND DISCUSSION**

The genetic parameters for different quantitative characters revealed considerable variability among the existing 115 set of germplasm (Table 1). Among the eight quantitative characters, pods per plant (from 21.3 to 66.2) had maximum variation followed by plant height (from 47.1 to 113.3 cm) and seed yield per plant from 4.45 to 22.10g) showed high variation.

![Figure 1: Percent frequency distribution in each character.](image-url)
Out of 135 genotypes, 44% ranged in $\geq 32.50 - 43.71$ for pods/plant, while 50% ranged in $\geq 5.61$ to 6.55 for seeds/pod. A maximum of 44% accessions had $\geq 4.22 - 4.86$ g 100 seed weight and more than 50% accessions ranged in $\geq 4.45 - 8.87$ g seed yield per plant.

The differences between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were very low for all the traits studied except seed yield per plant followed by branches per plant and 100 seed weight indicating that these traits were less affected by environmental fluctuations. High values of GCV and PCV were observed for seed yield (38.28 and 42.05), branches per plant (24.06 and 26.21), pods per plant (23.82 and 25.92) and plant height (23.77 and 24.13) respectively, suggesting possibility of improvement in these traits through direct selection (Fig 2). Higher genetic advance coupled with high heritability was observed for plant height, seeds per pod, days to flowering and days to maturity indicating the influence of additive gene effects therefore, simple selection would be effective for improvement of these traits. These results are in agreement with earlier findings of Kanta and Verma (2003) and Malik et al (2008). Presence of high genetic advance as % of mean (71.77 %) for seed yield per plant indicated that it is governed by additive genes action and selection would be more effective in such cases as earlier reported in chickpea by Sewak et al (2012).

The genotypic correlation coefficients were marginally higher than the phenotypic correlation coefficient for most of the characters. This indicates relatively low influence of environment in modifying the total expression of the genotypes, thus altering the phenotypic expression. Plants that produce more number of pods per plant along with more number of seeds per pod are desirable. Seed yield per plant had significant positive correlation with number of pods per plant, primary branches per plant, days to 50% flowering and days to 80% maturity (Table 2). But it was non-significant between seed yield and number of seeds per pod. Similar relationships were also reported by Isha Parveen et al (2011); Makeen et al (2009); Chauhan et al (2007) and Gupta et al (2001). The number of pods per plant can be increased by increasing number of branches per plant owing to a strong significant positive correlation between them. Non-significant correlation of seed yield with plant height and 100 seed weight suggested that tall and bold seeded genotypes are not much desirable for achieving higher seed yield in black gram.

Perusal of the result obtained from path analysis revealed that number of pods per plants followed by number of primary branches per plant and number of seeds per pod exerted the high positive direct effect on seed yield (Table 3). This suggests a true relationship between these traits with seed yield per plant and direct selection for these traits would be rewarding for yield improvement. Similar findings also reported by Chauhan et al (2007) in urdbean; Makeen et al (2009) in mutant lines of urdbean; Tomar et al (2009) in chickpea and Isha Parveen et al (2011) in urdbean. Days to 50 per cent flowering, days to maturity, plant height and seed weight exerted negative direct effect on seed yield. The number of branches per plant also showed highest positive indirect effect on seed yield via number of pods per plant. The estimates of residual effect in pooled data was considerably high suggesting the inclusion of some more traits that have been left behind in the present study, for better understanding of the causal factors responsible for achieving high yield.
### TABLE 2: Estimates of genotypic (G) and phenotypic (P) correlation co-efficients among different characters in urdbean (pooled)

<table>
<thead>
<tr>
<th>Characters</th>
<th>Days to 50 % flowering</th>
<th>Days to maturity</th>
<th>Plant height (cm)</th>
<th>Branches/ plant</th>
<th>Pods/ plant</th>
<th>Seeds/ pod</th>
<th>100-seed weight (g)</th>
<th>Seed yield/ plant (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Days to 50 % flowering</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Days to 50 % flowering</td>
<td>G: 1.00</td>
<td>P: 1.00</td>
<td>G: 0.61**</td>
<td>P: 0.35**</td>
<td>G: -0.20</td>
<td>P: 0.12</td>
<td>G: 0.09</td>
<td>P: 0.12</td>
</tr>
<tr>
<td>Days to maturity</td>
<td>G: 1.00</td>
<td>P: 1.00</td>
<td>G: 0.27</td>
<td>P: 0.15</td>
<td>G: -0.27**</td>
<td>P: 0.03</td>
<td>G: -0.30</td>
<td>P: 0.03</td>
</tr>
<tr>
<td>Plant height (cm)</td>
<td>G: 1.00</td>
<td>P: 1.00</td>
<td>G: 0.26**</td>
<td>P: 0.14</td>
<td>G: -0.06</td>
<td>P: 0.11</td>
<td>G: 0.09</td>
<td>P: 0.09</td>
</tr>
<tr>
<td>Branches/ plant</td>
<td>G: 1.00</td>
<td>P: 1.00</td>
<td>G: 0.34</td>
<td>P: 0.15</td>
<td>G: -0.07</td>
<td>P: 0.09</td>
<td>G: 0.30</td>
<td>P: 0.30**</td>
</tr>
<tr>
<td>Pods/plant</td>
<td>G: 1.00</td>
<td>P: 1.00</td>
<td>G: 0.15</td>
<td>P: 0.14</td>
<td>G: -0.06</td>
<td>P: 0.11</td>
<td>G: 0.03</td>
<td>P: 0.13</td>
</tr>
<tr>
<td>Seeds/pod</td>
<td>G: 1.00</td>
<td>P: 1.00</td>
<td>G: 0.31**</td>
<td>P: 0.24**</td>
<td>G: 0.07</td>
<td>P: 0.07</td>
<td>G: 0.20</td>
<td>P: 0.20**</td>
</tr>
</tbody>
</table>

*, **: Significant at P= 0.05 & 0.01, respectively

### TABLE 3: Direct and indirect effect of component characters on seed yield in urdbean at genotypic level over two year

<table>
<thead>
<tr>
<th>Characters</th>
<th>Days to 50 % flowering</th>
<th>Days to maturity</th>
<th>Plant height</th>
<th>Primary branches/ plant</th>
<th>Pods/ plant</th>
<th>Seeds/ pod</th>
<th>100-seed weight</th>
<th>Correlation with seed yield</th>
</tr>
</thead>
<tbody>
<tr>
<td>Days to 50 % flowering</td>
<td>-0.10</td>
<td>-0.01</td>
<td>-0.05</td>
<td>0.02</td>
<td>-0.09</td>
<td>0.02</td>
<td>-0.00</td>
<td>-0.22*</td>
</tr>
<tr>
<td>Days to maturity</td>
<td>-0.07</td>
<td>-0.02</td>
<td>-0.04</td>
<td>-0.00</td>
<td>-0.13</td>
<td>0.01</td>
<td>0.01</td>
<td>-0.24**</td>
</tr>
<tr>
<td>Plant height</td>
<td>-0.04</td>
<td>-0.01</td>
<td>-0.13</td>
<td>0.03</td>
<td>-0.03</td>
<td>0.02</td>
<td>-0.00</td>
<td>-0.16</td>
</tr>
<tr>
<td>Primary branches/ plant</td>
<td>-0.01</td>
<td>0.00</td>
<td>-0.02</td>
<td>0.20</td>
<td>0.15</td>
<td>-0.01</td>
<td>-0.01</td>
<td>0.30**</td>
</tr>
<tr>
<td>Pods/ plant</td>
<td>0.02</td>
<td>0.01</td>
<td>0.01</td>
<td>0.07</td>
<td>0.44</td>
<td>0.00</td>
<td>-0.00</td>
<td>0.54**</td>
</tr>
<tr>
<td>Seeds/pod</td>
<td>-0.01</td>
<td>-0.00</td>
<td>-0.01</td>
<td>-0.01</td>
<td>0.00</td>
<td>0.17</td>
<td>0.01</td>
<td>0.14</td>
</tr>
<tr>
<td>100-seed weight</td>
<td>-0.00</td>
<td>0.00</td>
<td>-0.00</td>
<td>0.02</td>
<td>0.01</td>
<td>-0.02</td>
<td>-0.09</td>
<td>-0.08</td>
</tr>
</tbody>
</table>

Residual effect = 0.7906  
Diagonal values are direct effects

Seed yield is highly complex trait, thus indirect selection based on major component traits may increase the efficiency of breeder. In the present study, number of primary branches per plant and number of pods per plant having high genetic advance coupled with moderate to high heritability also had high positive correlation with seed yield due to their highest positive direct as well as indirect effect on seed yield. Therefore, direct as well as indirect selection based on these traits would be fruitful to develop high yielding varieties after further evaluation and some accessions may be used as parents in the crossing programme to create better recombinants.

### REFERENCES


