Use of Linear Discriminant Function Analysis in Five Yield Sub-Characters Relationship Study in 134 Cowpea (*Vigna unguiculata* (L.) Walp) Accessions

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**Abstract**

Variations in five yield sub-characters of cowpea in 134 accessions were studied. Data were collected on number of pods per plant, pod length, pod width, peduncle length and 100-seed weight. Differences among the accessions were significant based on four of the five characters, namely pod length, pod width, peduncle length and 100-seed weight. K-means cluster analysis grouped the 134 accessions into four distinct groups. Pairwise Mahalanobis distance (D) among some of the groups was highly significant. From the study the yield sub-characters pod length, pod width, peduncle length and 100-seed weight contributed most to group separation in the cowpea accessions.

**Introduction**

Cowpea (*Vigna unguiculata* (L.) Walp) is a major crop worldwide (Singh *et al.*, 1997), and in 2005 ranked 23rd among important crop species (Bolanga & Timko, 2005). According to Aryeetey (1971) and Bennett-Lartey & Ofori (1999), the crop is one of the most important legumes in Ghana.

Despite its numerous benefits breeding of cowpea poses a lot of challenges, hence, its production is not adequate to satisfy its domestic demands (MOFA, 1991). Singh & Emechebe (1997) reported that no single variety can be suitable for all conditions even though cowpea is a single crop species. According to these authors the varietal requirements in terms of plant type, seed colour or type, maturity and use pattern are extremely diverse from region to region, making breeding programmes for the crop more complex than for other crops.

The lack of adequate research activities in a crop limits not only knowledge of the crop evolution but also the possibility of new and outstanding genetic improvement (Singh & Rachie, 1985). The evaluation of diversity existing in accessions is essential for understanding and fully utilizing its potential value (Singh *et al.*, 1997). Information on variability in crop plants is of much importance to the plant breeder since it provides him with the necessary tool to work with (Bennet-Lartey & Ofori, 1999) and the success of any breeding programme depends on the availability and use of genetic variation.

A promising method for cultivar identification and classification is offered by the numerical taxonomic approach. However, some other techniques of multivariate analysis have been applied widely to discriminate and classify cultivars and clones of several plant species. For instance, the linear discriminant function
approach is one tool that has been applied to
discriminate and classify crop germplasm
(Barone et al., 1996). It has been used to
study variation in seed morphology of 31
accessions of lima bean (Asante et al., 2006).
The paper describes the possible relationship
among five different yield sub-characters of
cowpea germplasm in Ghana. It also aims at
detecting natural grouping patterns that exist
within 134 cowpea accessions based on the
five cowpea yield sub-characters.

Materials and methods
Seeds from 134 cowpea accessions were
collected from the Plant Genetics Resources
Research Institute of the Council for
Scientific and Industrial Research at Bunso
in Ghana. The experiment was conducted at
Pokuase in the coastal savanna
agroecological zone. Each accession was
planted in a single row of 10 seeding holes
(10 plants in a row) in a block. Two seeds per
hill were planted at a spacing of 100 cm ×
100 cm. Harvested pods were sun-dried and
shelled; the seeds were also sun-dried to 10-
13 per cent moisture. Characters evaluated
were number of pods per plant, pod length
(mm), peduncle length (mm), pod width
(mm) and 100-seed weight (g). Linear
discriminant function was applied, using the
SPSS/PC+ statistical computer software.

Results and discussion
K-means non-hierarchical clustering
Table 1 presents K-means non-hierarchical
cluster of the accessions based on the means
of the five characters. Average pod width, pod
length, peduncle length, number of pods per
plant and 100-seed weight in Cluster 1 were
8.2 mm, 160.7 mm, 294 mm 22.5 and 11.5 g,
respectively. In Cluster 2, average pod width,
pod length, peduncle length, number of pods
per plant and 100-seed weight were 9.1 mm,
174 mm, 264.3 mm, 15.8 and 18.7 g,
respectively.

Accessions in Group 3 had an average pod
width of 8.4 mm, average pod length of 150.5
mm, average peduncle length of 280.8 mm,
average number of pods per plant of 19 and
average 100-seed weight of 9.1 g, seed length
of 9.1 mm, and average seed width of 7.0 mm.
Accessions in Group 4 had an average pod
width of 7 mm, average pod length of 144.8
mm, average peduncle length of 270.1 mm,
average number of pods per plant of 25.7 and
average 100-seed weight of 9.2 g.

Test of equality

<table>
<thead>
<tr>
<th>Character</th>
<th>Cluster 1</th>
<th>Cluster 2</th>
<th>Cluster 3</th>
<th>Cluster 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pod width (mm)</td>
<td>8.2</td>
<td>9.4</td>
<td>8.4</td>
<td>7.0</td>
</tr>
<tr>
<td>Pod length (mm)</td>
<td>160.7</td>
<td>174.0</td>
<td>150.5</td>
<td>144.8</td>
</tr>
<tr>
<td>Peduncle length (mm)</td>
<td>294.6</td>
<td>264.3</td>
<td>280.8</td>
<td>270.1</td>
</tr>
<tr>
<td>No. of pods per plant</td>
<td>22.5</td>
<td>15.8</td>
<td>19.0</td>
<td>25.7</td>
</tr>
<tr>
<td>100-seed weight(g)</td>
<td>11.5</td>
<td>18.7</td>
<td>9.1</td>
<td>9.2</td>
</tr>
</tbody>
</table>
Tests of equality of the group means showed significant group mean differences for all the characters with the exception of number of pods per plant which did not show any significant difference (Table 2). The discriminant functions that differentiated among the K-means clusters were determined by stepwise procedure. All discriminatory functions were statistically significant at probabilities of 0.000 and 0.001, respectively. Cluster 1 was statistically different from Cluster 3 and Cluster 4, whilst Cluster 3 was statistically different from Cluster 4 according to the pairwise Mahalanobis distance (Table 3). Clusters 1 and 3 were the most distant. The least distant were Clusters 2 and 3.

**Classification matrix of the four groups**

Table 4 shows a classification matrix which summarizes the predictive ability of discriminatory functions. Each accession was assigned to a cluster by discriminant functions. The discriminatory function is

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**Table 2**

*Test of equality of group means*

<table>
<thead>
<tr>
<th>Character</th>
<th>Wilk’s</th>
<th>F</th>
<th>df</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pod width (mm)</td>
<td>0.583</td>
<td>27.134</td>
<td>3</td>
<td>0.000</td>
</tr>
<tr>
<td>Pod length (mm)</td>
<td>0.938</td>
<td>2.875</td>
<td>3</td>
<td>0.039</td>
</tr>
<tr>
<td>Yield per plant (g)</td>
<td>0.928</td>
<td>3.312</td>
<td>3</td>
<td>0.022</td>
</tr>
<tr>
<td>No. of pods per plant</td>
<td>0.968</td>
<td>1.444</td>
<td>3</td>
<td>0.233</td>
</tr>
<tr>
<td>100-seed weight (g)</td>
<td>0.034</td>
<td>250.021</td>
<td>3</td>
<td>0.000</td>
</tr>
</tbody>
</table>

**Table 3**

*Pairwise Mahalanobis distances (D) between four clusters of cowpea accessions*

<table>
<thead>
<tr>
<th>Cluster</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>7.228</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>1.329**</td>
<td>3.040</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>41.216*</td>
<td>21.320</td>
<td>36.770**</td>
</tr>
</tbody>
</table>

**Table 4**

*Classification matrix of four groups of cowpea accessions. (Rows being observed and columns predicted categories)*

<table>
<thead>
<tr>
<th>Group</th>
<th>Percent correct</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>Total observed</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>100.00</td>
<td>62</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>62</td>
</tr>
<tr>
<td>2</td>
<td>100.00</td>
<td>0</td>
<td>4</td>
<td>0</td>
<td>0</td>
<td>4</td>
</tr>
<tr>
<td>3</td>
<td>8.3</td>
<td>3</td>
<td>1</td>
<td>20</td>
<td>0</td>
<td>24</td>
</tr>
<tr>
<td>4</td>
<td>9.7</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>43</td>
<td>44</td>
</tr>
<tr>
<td>Total predicted</td>
<td></td>
<td>66</td>
<td>5</td>
<td>20</td>
<td>43</td>
<td>134</td>
</tr>
</tbody>
</table>
particularly informative because misclassified accessions are identified and reassigned to the appropriate group. The 62 accessions in Group 1 were correctly classified (100%). Similarly, four of the accessions in Group 2 were also correctly classified (100%). In Group 3, 20 accessions were correctly classified (8.3%), while four accessions corresponding to Group 1 (three accessions) and Group 2 (one accession), respectively, were misclassified. Forty three accessions in Group 4 were correctly classified (9.7%); one misclassified accession corresponded to Group 1.

Results from the study demonstrate that the linear discriminant function is a useful tool for screening and evaluating variation among cowpea germplasm. From the analysis it can be concluded that the 134 cowpea accessions differed in the four yield sub-characters pod length, pod width, peduncle length and 100-seed weight. The level of variation existing within the accessions can make them suitable as source materials for cowpea breeding programme.

Conclusion
The K-means non-hierarchical clustering analysis classified the 134 accessions into four groups. The test of equality of the group means showed significant group mean differences for the pod width, pod length, peduncle length, yield per plant, and the 100-seed weight, but number of pods per plant did not show any significant differences. Three out of the four clusters for the pod length, pod width, peduncle length, yield per plant and 100-seed weight revealed that only clusters 1 and 3 were not statistically significant from each other according to the pairwise Mahalanobis distance.

References