Use of linear discriminant function analysis in seed morphotype relationship study in 31 Lima bean (*Phaseolus lunatus* L.) accessions in Ghana

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ABSTRACT

Variation in seed morphology of the Lima bean in 31 accessions was studied. Data were collected on 100-seed weight, seed length and seed width. The differences among the accessions were significant, based on the three seed characteristics. K-means cluster analysis grouped the 31 accessions into four distinct groups, representing four different morphotypes. Mahalanobis distances (D^2) among the groups were highly significant. The four different morphotypes were attributed to the Mesoamerican gene pool, comprising the cultigroups Sieva-Big Lima, Potato-Sieva and Potato. Sub-cultigroups of the Sieva-Big Lima and Potato cultigroups due to differences in seed weight were suggested.

RÉSUMÉ

ASANTE, I. K., ADDY, R. & CARSON, A. G.: *Application de l'analyse de fonction du discriminant linéaire dans l'étude du rapport de graine morphotype en trente accessions de haricot de lima* (Phaseolus lunatus *L.) au Ghana*. Variation en morphologie de graine du haricot de Lima en trente accessions était étudiée. Des données étaient collectées sur poids de 100 graines, longueur de graine et largeur de graine. Il y avait des différences considérables parmi les accessions basées sur les trois caractéristiques de graine. Analyse du régime par K-moyens groupait les 31 accessions en quatre groupes distincts, représentant quatre morphotypes différents. Les distances (D^2) Mahalanobis parmi les groupes étaient hautement considérables. Les quatre morphotypes différents étaient attribués au bagage héréditaire de Mesoaméricain, comprenant les groupes de cultures: Sieva-Grand Lima, Patate-Sieva et Patate. Les groupes de sous-cultures de Sieva-Grand Lima et Patate groupes de culture dû aux différences en poids de graine étaient suggérées.

Introduction

Lima bean (*Phaseolus lunatus*) is the most important food legume within the neotropical genus *Phaseolus* (Baudoin, Barthelemy & Ndungo, 1991). In Ghana, it ranks fourth in importance after cowpea, groundnut and bambara groundnut in that order (Doku, 1977). Several Lima bean varieties have great potential for contributing to the protein and calorie intake of humans and domestic animals. The main product of consumption is the dry seeds, although green and fresh pods, leaves and sprouts are sometimes used. In tropical Africa, the plant is interplanted with such crops as maize, sorghum, sweet potatoes, coffee, cotton and yams. The crop is hardy and may be advantageous in adverse conditions in which other leguminous vegetables do not grow.

Three morphotypes of Lima bean are usually recognized according to seed characteristics (Baudet, 1977; Baudoin, 1988). Debouck and co-workers showed that each different morphotype had a particular geographic distribution (Lioi, 1994). Big Lima with big flat seeds was distributed in Peru, the highlands of Colombia, Ecuador, and Bolivia; the Sieva type with medium flat seeds was distributed in Mexico, Guatemala, and Columbia at mid and low altitudes; and the Potato type with small rounded seeds was distributed in the Carribean area, coastal Colombia, and Yucatan

(Debouck, Maquet & Posso, 1989). However, recently, the intermediate forms, Potato-Sieva and Sieva-Big Lima types, have been described by Esquivel, Castineiras & Hammer (1990) among germplasm from Cuba. By using seed storage electrophoresis, two major centres of domestication of the Lima bean have been suggested and are in Middle America and the southern Andes (Debouck & Tohme, 1989; Gepts *et al.*, 1986. Debouck *et al.* (1989) and Maquet, Gutierrez & Debouck (1990) have reported that Lima beans belong to two major gene pools, Mesoamerican and Andean.

This paper describes the possible relationship among different seed morphotypes in 31 Lima germplasm in Ghana, and predicts to which of the two major gene pools they belong, by using linear discriminant function analysis.

Materials and methods

Seeds from 31 Lima bean accessions were collected from the Plant Genetic Resources Centre of the Council for Scientific and Industrial Research at Bunso in Ghana. The seeds were multiplied to provide enough for the study. They were multiplied in the University of Ghana Agriculture Farms in a randomized complete block design with three replicates. The seeds of each accession were sown at a spacing of 90 cm × 90 cm. Two seeds per hill were planted and thinned to one, 7 days after emergence. Harvested pods were sun-dried and shelled; the seeds were also sun-dried to 10-13 per cent moisture. Two hundred seeds selected randomly from each accession were used for the study. The seed characteristics determined were 100-seed weight (g), seed length (mm), and seed width (mm).

Linear discriminant function analysis was applied, using the SPSS/PC+statistical computer software.

Results and discussion

Table 1 presents a summary of seed size comparison for the 31 Lima bean accessions. The 100-seed mean weight ranged from 23.84 to 71.81 g, with a mean of 50.84 g. Seed length ranged from 0.86 to 17.7 mm, with a mean of 14.5 mm. Seed width ranged from 6.2 to 12.5 mm, with a mean of 0.985 cm. Using K-means non-hierarchical clustering, the Lima bean germplasm was grouped into four clusters based on the three seed characters (Table 2).

Average 100-seed weight, seed length and seed width for accessions in Group 1 were 67.24 g, 17.1 mm and 11.1 mm, respectively. In Group 2, average 100-seed weight was 34.25 g, average seed length was 11.5 mm, and average seed width was 8.5 mm. Accessions in Group 3 had an average 100-seed weight of 25.05 g, average seed length of 9.1 mm, and average seed width of 7.0 mm. Accessions in Group 4 had an average 100-seed weight of 58.27 g, average seed length of 16.7 mm, and average seed width of 11.1 mm.

Tests of equality of the group means showed significant group mean differences (Table 3). The discriminant functions that differentiated among the K-mean clusters were determined by stepwise procedure. All discriminatory functions were statistically significant at probabilities of 0.000 and 0.001, respectively. Latent roots indicated that the first two functions accounted for 100 per cent of total variance (Table 4). The four clusters were statistically different from each other to the Mahalanobis distance (Table 5). Clusters 1 and 3 were the most distant. The most similar were Clusters 2 and 3.

Table 6 presents a classification matrix which summarizes the predictive ability of discriminatory functions when classifying the different groups of germplasm. Each accession was assigned to a cluster by discriminant functions. The discriminatory function is particularly informative because misclassified accessions are identified and reassigned to the appropriate group. The nine accessions in Group 1 were correctly classified (81.8 %); the two misclassified accessions corresponded to Group 4. The 83.3 per cent of the entries in Group 2 were correctly classified; one misclassified accession corresponded to

TABLE 1

Quantitative Characters of Seeds of 31 Lima Bean Accessions

Accession	100-seed weight (g)	Seed width (mm)	Seed length (mm)
99/001	63.50	11.6	17.5
99/002	41.12	9.6	14.0
99/003	23.84	6.2	8.6
99/004	38.96	9.5	13.0
99/005	61.25	11.2	16.9
99/006	65.53	12.5	18.8
99/007	27.39	7.0	9.8
99/008	32.37	8.9	10.8
82/293	70.36	12.1	17.7
82/292	25.06	7.4	9.0
99/009	29.45	7.4	9.7
99/010	67.72	9.5	15.3
99/011	62.94	10.8	16.7
/99/012	60.47	11.5	17.0
82/414	69.66	12.6	17.2
82/125	66.97	7.6	16.4
87/160	59.33	11.7	17.4
87/134	32.10	8.1	10.0
82/166	70.19	11.5	17.7
87/118	67.53	11.7	17.4
99/013	31.53	7.4	11.3
82/482	59.77	10.7	16.4
82/493	63.40	11.1	16.8
82/469	23.90	7.3	9.0
82/489	54.84	10.7	15.7
99/014	55.83	10.8	16.2
99/015	71.81	11.6	17.0
99/017	57.81	11.5	17.3
99/018	61.83	10.9	17.0
82/496	54.01	11.5	16.58
82/505	57.51	10.7	16.6
CV (%)	35.82	24.34	53.50
SED	2.935	0.340	0.590

Group 3. Four of the accessions in Group 3 were correctly classified (100 %); similarly, 10 of the accessions in Group 4 were correctly classified (100 %).

Seed weight, seed length and seed width were used to distinguish among different morphotypes in *Phaseolus lunatus* (Esquivel *et al*., 1990). The 100-seed weight, seed length, and seed width for the morphotypes Big Lima, Sieva, Potato, Potato-Sieva and Sieva-Big Lima were 100-110 g, 25 mm, 14 mm; 30-45.3 g, 12 mm, seed width; 34.5 g, 9 mm, 8 mm; 36.3 g, 11 mm, 8 mm; and 77.5 g, 17 mm, 11 mm; respectively (Lioi, 1994; Esquival *et al*., 1990).

The four clusters in this study represent four distinct morphotypes. Accessions of Cluster1 belong to Sieva-Big Lima cultigroup in seed length and seed width characteristics, and accessions of Cluster 2 belong to Potato-Sieva cultigroup. Accessions of Cluster 3 belong to the Potato cultigroup strictly in seed length and seed width. Accessions of Cluster 4 resemble Sieva-Big Lima cultivar in seed length and seed width. They resemble the cluster accessions in seed length and seed width; however, they differ in 100-seed weight. These two groups might have diverged from each other in seed weight differences. The study hypothesizes that sub-cultigroups evolved from the Sieva-Big Lima and Potato cultigroups in seed weight differences during Lima bean domestication. Generally, the experimental finding rules out Big Lima in the accessions used for the study. According to Lioi (1994), the Big Lima cultigroup is of Andean gene pool, while all other cultigroups belong to the Mesoamerican gene pool. Therefore, the 31 Lima

TABLE 2

Comparison Profile of the Four Groups of Phaseolus lunatus *Accessions Classified by K-means Clustering (Figures are Means for the Accessions in Each Cluster)*

Character	Cluster			
	1	2	3	4
100-seed weight (g)	67.24	34.25	25.05	58.27
Seed length (mm)	17.1	11.50	9.10	16.7
Seed width (mm)	11.1	8.50	7.0	11.1

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TABLE 3

Test of Equality of Group Means

Character	Wilk's 8	F	df	P
100-seed weight (g)	0.035	250.021	3	0.000
Seed length (mm)	0.080	102.972	3	0.000
Seed width (mm)	0.269	24.454	3	0.000

TABLE 4

Discriminant Functions that Distinguish Between Clusters of Phaseolus lunatus *Accessions*

Function	Latent root	Variance function	% cumulative	Wilk's 8	Π	df	P
1	27.863	98.0	98.0	0.022	103.156	6	0.000
2	0.581	2.0	100.0	0.633	12.367	2	0.002

TABLE 5

Pairwise Mahalanobis Distances (D^2) Between Four Clusters of Phaseolus lunatus *Germplasm*

Cluster	1	2	3
1			
2	32.988**		
3	42.199**	9.212*	
4	8.972*	24.017**	33.229**

TABLE 6

Classification Matrix of Four Groups of Phaseolus *Germplasm (Rows Being Observed and Columns Predicted Categories)*

Group	% correct	1	2	3	4	Total observed
1	81.8	9	0	0	2	11
2	83.3	0	5	1	0	6
3	100.0	0	0	4	0	4
4	100.0	0	0	0	10	10
Total no. predicted		9	5	5	12	31

bean cultivars can be attributed to the Mesoamerican gene pool.

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