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GENETIC DIVERSITY OF COMMON BEAN (*PHASEOLUS VULGARIS* L.) INTRODUCED FOR ADAPTATION IN LESOTHO

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ABSTRACT: *Common beans are introduced in Lesotho from CIAT-Malawi annually to evaluate them for adaptation and other characters of economic importance. They are not being characterized for identity, therefore the study was conducted at National University of Lesotho located in the Maseru District of Lesotho with specific objectives of (1) estimating genetic distances among the common bean genotypes using morphological features and (2) identifying morphological characteristics that contributed to discrimination of these cultivars. Randomized Complete Block Design was applied with four replications. Twenty cultivars of common beans from CIAT-Malawi were used as treatments. Data were collected using descriptor of common beans compiled by International Board of Genetic Resources Unit. Data generated were subjected to cluster analysis and principal component analysis using Genstat recover (2015). Results of cluster analysis revealed four groups, of which two consisted of five cultivars, another had four and the last one only two cultivars. Besides, there were three outliers. The results of principal component analysis showed the total variation accounted for by both principal component 1 and 2 was 35.95% with each constituting 18.62 and 17.33 %, respectively. The characters responsible for variation from the first principal component analysis were seed shape, colour of flowers, colour of wings, seed-coat pattern and pod beak orientation. The characters influencing separation along the second principal component were number of locules per pod, number of seeds per pod, leaflet length, days to flowering and pod colour. It can be deduced that the cultivars broad in to Lesotho is diverse broadening the genetic base of the existing common bean genotypes.*

Keywords: Common bean, cluster analysis, principal component analysis, Lesotho

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is a highly polymorphic species originating from two gene-pools, namely; Meso-American and Andes (Gepts *et al.*1988). Upon convergence of the two gene-pools, the third pool emerged (Gepts and Bliss, 1988). From Meso-America and Andes in the Northern America, they were disseminated through other countries to Western Europe (Logozzo, 2007) and to Africa (Asfaw *et al*. 2009; Gepts and Bliss, 1988). Dissemination of common bean

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was a result of trade and exchange of goods among different countries (Marko *et al.* 2013). During their dissemination, they evolved changing their morphological features due to adaptation to new ecological and man-made conditions (Zeven, 1997, Gepts, 1998; Marko *et al.*2013). The features included amongst others; growth habits, seed shape, seed size, seed colour, flower colour and resistance to diseases and pests. The evolutionary change in morphology resulted in a diverse species differing greatly such that the origin of some cannot be traced back by simple means (Gepts, 1998). There are millions of land-races, old and modern cultivars as well as hybrids cultivated world-wide and maintained in global gene-banks (CIAT) and collection centers at regional level (Rodino *et al.*2006). Within a species, there are number of cultivars which have been developed to suit particular purposes such as nutritional quality, maturity days, uniformity at maturity, growth habits and high yield (Simmond, 1979). Since these cultivars have unique characteristics, they can be distinguished using morphological features which have proved to be an effective tool for segregation of cultivars within the same species(Gepts, 1998).

Many cultivars of common beans are introduced annually in Lesotho from CIAT regional center in Malawi as part of collaboration between the government of Lesotho and Malawi in agricultural research. These cultivars were bred in Kenya for different purposes and distributed to Malawi where they are multiplied and distributed to different countries in the South African Development Cooperation regions (SADC). It is therefore imperative to characterize these imported cultivars using morphological features. The specific objectives of study were two-fold; (1) to estimate genetic distances among the common bean genotypes using morphological features, (2) to identify morphological characteristics that contributed to discrimination of common bean cultivars.

MATERIALS AND METHODS

Study area

The study was conducted at Roma Campus of The National University of Lesotho which is situated 34km South West of Maseru, the capital city of Lesotho. The coordinates for Roma campus are 29^0 26' 48 South latitude and 27^0 42' 29 East longitude with an altitude of 1610m above sea level.

Site description

Roma valley is broad, fertile and surrounded by sand stone topped cliffs to the east. The soil type consists of Berea series (Plinthaquic dystruchrepts). Top soil is a sandy loam with hue of 10 YRS, 4/3 while sub-soil is dark yellowish sandy clay loam with hue of 10yrs 4/4. The soil analysis revealed pH 3.63 with phosphorus of 0.033 and 0.000 at 0ppm, 0.197 at 1ppm, 0.223 at 2ppm, 0.329 at 3ppm and 0.525 at 4ppm determined using Bray 1.

Experimental design

The experiment was carried out using Randomized Complete Block Design with 20 treatments (bean genotypes) and four replications. The size of the field was 36 m x 17.2 m equivalent to 619.2m^2 which was divided into 4 blocks where each block had 20 plots. Each plot had 2 rows with the length of 4 m each. The inter-row and intra-row spacing were 0.9 m and 0.10 m. Bean

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seeds used in experiment were obtained from CIAT in Malawi through Department of Agricultural Research.

Agronomic practices

The land was first prepared using tractor mounted mouldboard plough, after which disc harrow was used to level the seedbed and break the clods. A compound fertilizer of 2:3:2(22)+Zn was broadcast over the field at the rate of 250 kg ha^{-1} as basal dressing. Top-dressing was not applied. Sowing of seeds was done by hand. The field was irrigated twice a week due to prolonged drought that prevailed. Weeding was done by hand-hoeing twice during the growing period of the beans to control nutsedge (*Cyprus esculentum* L.) which was very problematic. Cape Mount rifles (*Mylabris spp.*) feeding on flowers of the plants was controlled chemically by applying ripcord.

Data collection

Data were collected using Descriptors for *Phasolus vulgaris* compiled by International Board of Plant Genetic Resources Unit. The following characters were observed and measured; colour of flowers, colour of wings, cross sectiona shape, days to flowering, flower buds per inflorescence, growth type, leaflet length, node number, number of locules per pod, number of pods per plant, number of seeds per pod, pod beak orientation, pod colour, pod curvature, pod length, pod suture string, pod wall fibre, seed coat colour, seed coat pattern and seed shape.

Data analysis

Data collected were analysed using GENSTAT software package to perform both principal component analysis and cluster analysis. Cluster analysis was done according to Nei's genetic distance (1971).

RESULTS

Cluster analysis

Dendrogram generated from cluster analysis is depicted in Figure 1. Cluster analysis revealed four big groups (A, B, C and D), of which two consisted of five cultivars (B and C), one other group (A) has four cultivars and the last group (D) contained two cultivars. Besides, there were three outliers. Two big groups (B and C) were divided into sub-groups, each having two cultivars. One big group (B) consisted of cultivars; SER 45, Pink02-3-1, NUA 45, CAL 143, SER 83 and RCB 266 while the other group (C) consisted of 13607-9, VTTT 925/9-1-2, CIM NAV 02-12-1, SUGAR 131 and RCB 265. The third group (A) constituted RCB 261, MR 13905-6, RCB 233 AND SER 124. The last small group (D) had AFR 703 and VTTT 923/10-3. Outliers revealed were three, namely; PAN9249, PAN 148 and PINTO-NODAK. The sub-groups of these three large groups (A, B and C) were designated i, ii, iii, iv and v. Group A sub-group v consisted of SER 124, RCB 233 and RM 13905-6. RCB 261 was an outlier in this group (A). Group B was comprised of two sub-groups, namely; iii and iv. Sub-group iv contained SER 45, PINK 02-3-1and

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NUA 45. Group B sub-group iii consisted of CAL 143 and SER 83 with RCB 266 as an outlier. Group C was divided into two sub-groups, i and ii. Group C sub-group 1 comprised BF 13607-9 and VTT 925/9 – 1-2 while sub-group ii had CIM NAV 02-12-1 and SUGAR 131, while RCB 265 was an outlier. Among the cultivars that were grouped, the following constituted outliers: PAN 9249, PAN 148, PINTO-NODAK, RCB 266 AND RCB 261. Sub-group B (iv) and sub-group A(v) were further sub-divided into another minor subgroups, each consisting of two cultivars,

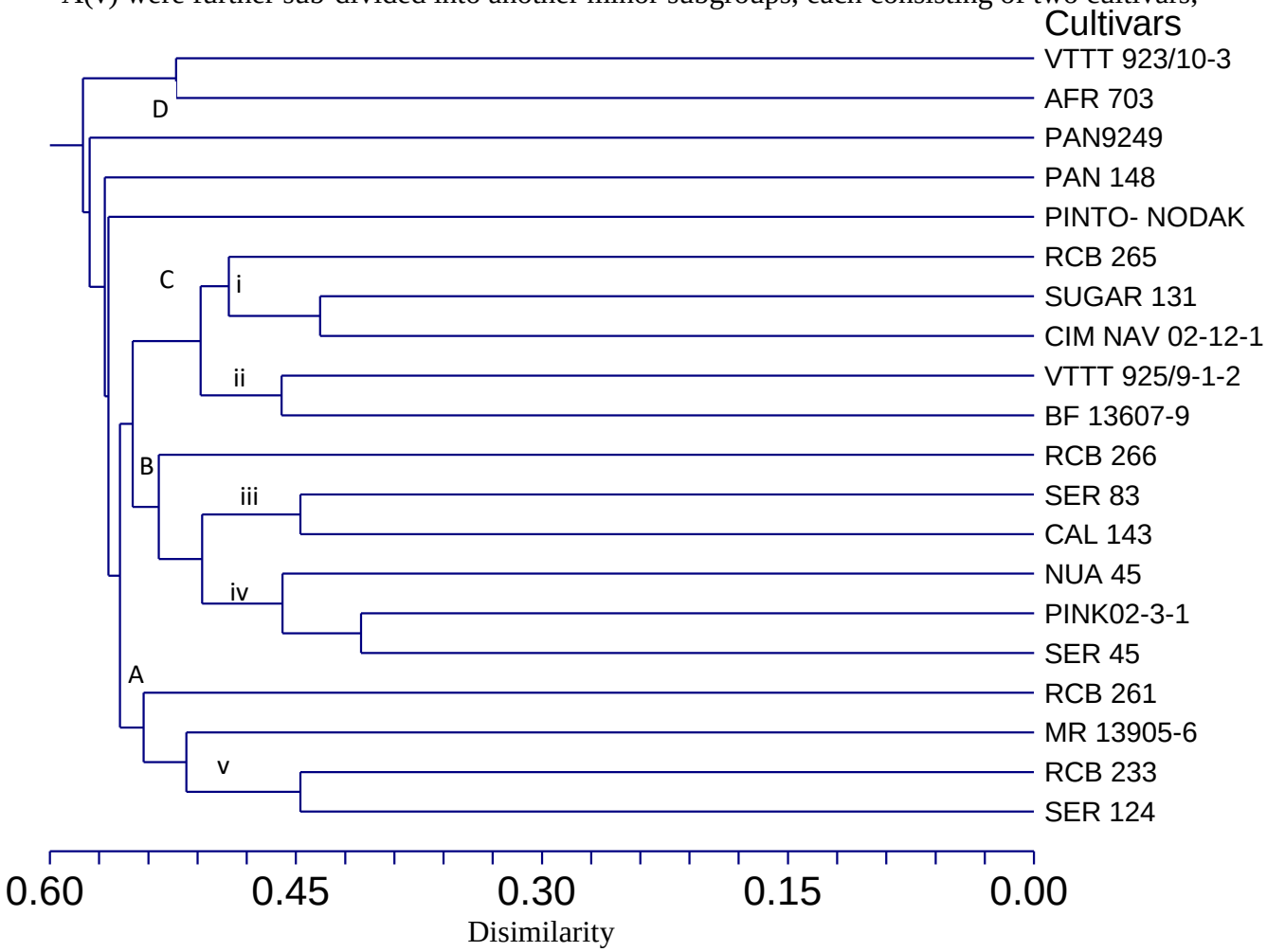

Fig. 1: Dendrogram for common bean genotypes

Principal component analysis

Principal component analysis was used to identify the characters which caused major variation among cultivars. Two principal component analyses were used to analyze the results, which constituted 35.95 % of the variation. The first one showed the variation of 18.62 % and the second one showed 17. 33 %. There were 20 characters used to distinguish the common beans varieties. The characters responsible for variation from the first principal component analysis

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(Table 1; Fig. 2) were seed shape (0.35241), colour of flowers (-0.35216), colour of wings (-0.35216), seed coat pattern (-0.30924) and pod beak orientation (0.29147). The characters influencing separation along the second principal component (Table 1; Fig. 2) were number of locules per pod (-0.41407), number of seeds per pod (-0.38985), leaflet length (-0.33570), days to flowering (-0.32546) and pod colour (-0.33349). Fig. 2 depicted spatial placement of cultivars on Y and X axis graph. It showed cultivar RCB 265 and NUA to be morphologically closely related. Similarly, CAL 143 and SER 83 were closely related to each other implying that they share most morphological characters. The rest of the cultivars set apart with outliers. Positioning of cultivars on the graph seemed to have no correlation with their origin as two cultivars close to each other are not from the same place.

Table 1. Loadings for Principal component 1 and Principal component 2

List of characters	Principal Component 1	Principal Component 2
Colour of flowers	-0.35216*	0.22766
Colour of wings	-0.35216*	0.2766
Cross sectional shape	-0.05742	0.10442
Days to flowering	-0.15485	0.32546*
Flower buds per inflorescence	0.00000	0.00000
Growth type	-0.24259	0.02225
Leaflet length	0.10409	-0.33570*
Node number	-0.27513	-0.27959
Number of locules per pod	-0.13679	-0.41407*
Number of pods per plant	-0.00301	-0.28362
Pod beak orientation	0.29147*	-0.07883
Pod colour	-0.03154	-0.33349*
Pod curvature	-0.01471	-0.05915
Pod length	0.26318	0.00627
Pod suture string	0.25708	0.09015
Pod wall fibre	-0.12896	0.08159
Number of seeds per pod	-0.26771	-0.38985*
Seed coat colour	0.17593	0.12177
Seed coat pattern	-0.30924*	0.15875
Seed shape	0.35241*	0.09184

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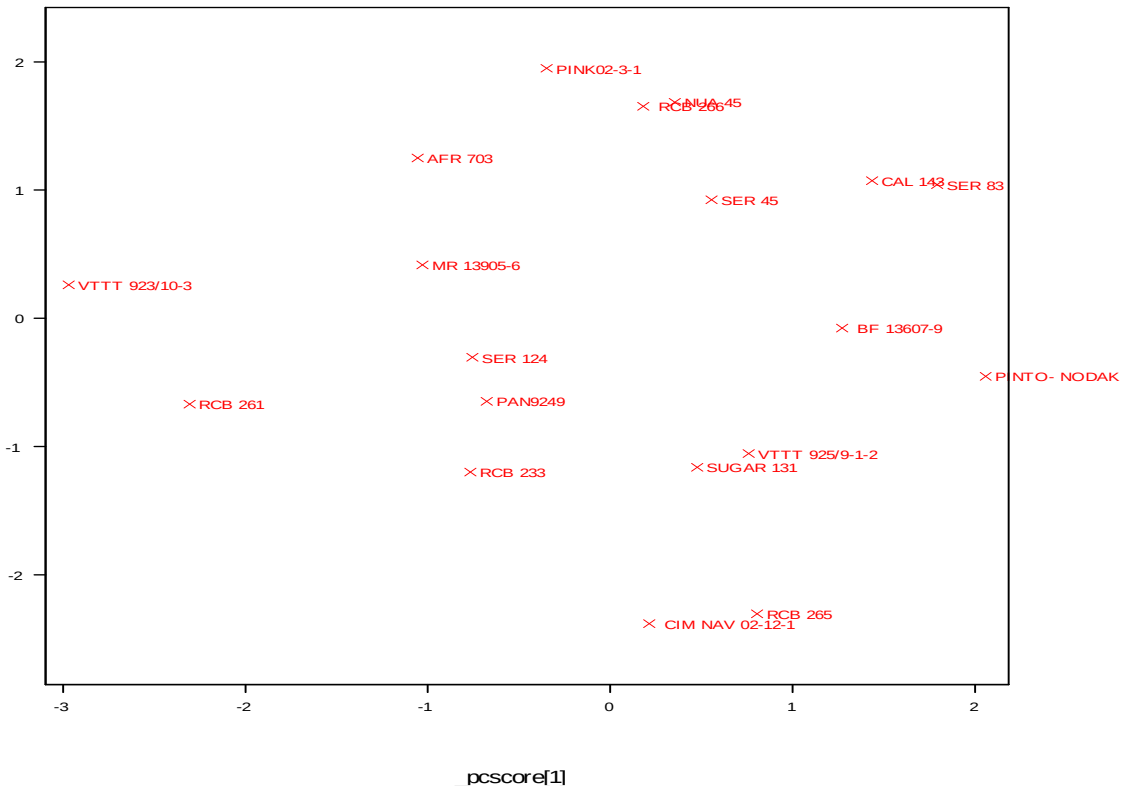

Fig. 2. Principal component 1 and principal component 2 of common bean genotypes.

DISCUSSION

Cluster analysis

Cluster analysis revealed four big groups, one small group and three outliers based on morphological features which showed a high degree of similarity among 20 common cultivars (Fig. 1). This was expected because they belong to the same species and genus but there should be one or more differences which occurred naturally by evolutionary changes or manipulated genetically by man through plant breeding. Some of these cultivars were bred by CIAT in Kenya and multiplied in Malawi for distribution to other Southern African Development Cooperation countries, namely; VTTT 923/10-3, AFR 703, RCB 265, CIM NAV 02-12-1, VTTT 925/9-1-2, BF 13607-9, RCB 266, NUA 45, RCB 261, MR 13905-6 and RCB 233. It became apparent that they were bred to differ in some characters to meet particular objectives. Similarly, cultivars from South Africa were also included in this collection contributing to wider genetic base. These were PAN 9249, PAN 148, PINTO-NORDAK, SUGAR 131, CAL 143, SER 45 and SER 124. They were improved through breeding changing their features from original state. These results were consistent with the findings of Singh *et al.* (1991) who obtained two major groups and 15 sub-groups from 76 common genotypes when applying cluster analysis to determine degree of similarities. Similarly, Mavromatis *et al.* (2010) studied genetic diversity of 16 cultivars of

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common beans grown in Greece and generated dendrogram with major four groups and 9 sub-groups emanating from them.

Principal component analysis

Twenty characters used as morphological markers were adequate to discriminate twenty common bean cultivars. Different combinations of these 20 characters enabled the cultivars to be differentiated, while no single character distinguished one cultivar from the other. A combination of four or more characters, for example growth habit, seed coat pattern, seed shape, resulted in some cultivars being distinguished. The results were consistent with the findings of Figliuolo and Spagnoletti (2000) who distinguished 57 common bean cultivars and discovered that no one character can discriminate a cultivar.

Similarly, Awan *et al.* (2014) characterized thirteen cultivars of common bean grown in Pakistan and revealed distinguishing morphological characters that led to separation of cultivars. The importance of morphological markers in identifying cultivars is well documented (Stoilova *et al*., 2013; Marzooghian *et al*., 2013; Berova and Stoilova, 2009). One or two characters were able to group and sub-group cultivars but these were dependent on their discriminatory power. All characters applied in this study were found to have a perceptible influence on the segregation of cultivars, although their discriminatory power differed.

Bonnetti *et al*. (1995) and Roy (2001) reported that the cultivars which were morphologically similar had a close genetic relationship. Contrarily, Singh *et al*. (1991) argued that the morpho-agronomic characters were phenotypic traits and accessions may be similar morphologically, yet be distant genetically.

CONCLUSION

The common bean cultivars brought into Lesotho originating from South Africa and Malawi enrich the genetic resources already existing, thereby broaden base of cultivars from which farmer can choose. Breeding Programmes envisaged will benefit from the collection that is introduced. A lot of research work can be performed using this collection.

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