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**MORPHOLOGICAL CHARACTERISATION AND
INTERRELATIONSHIPS AMONG DESCRIPTORS
IN *Phaseolus vulgaris* ACCESSIONS**

SUMMARY

The aim of this study was the evaluation of genetic diversity in twenty common bean accessions part of the active collection of Genetic Resources Centre, Agricultural University of Tirana, by using agro morphological traits. Qualitative (19) and quantitative (11) characteristics were recorded following the IBPGR, *Phaseolus vulgaris* Descriptor list. Variation of morphological characteristics among accessions ranged from 4.40% for days to maturity (DTM) to 38.15% for pod beak length (PBL). AGB 2719 is identified as the accession with the highest values in quantitative traits like pod length (PL) and PBL, AGB 2746 in traits like DTF and DTM, AGB 2748 in traits like duration of flowering and PW, and AGB 2763 is identified with the lowest values in quantitative traits like DTF, PL, DTM, DF, PW and SW (seed width). Positive correlations are observed among descriptors, as bracteole length and size of bracteole ($r=0.76$), between DF and DTM ($r=0.74$), also for days to maturity and days to flowering (DTF) this coefficient is positive at the level $r=0.66$, pod width and seed length ($r=0.63$), for the qualitative descriptors correlation coefficient revealed that colour of wings (in terms of values) is highly correlated with colour of standard flower ($r=0.9$). The divergence between accessions was observed using hierarchical clustering dendrogram, Euclidean distance. Based on this analyse AGB 2715 and AGB 2733 are the nearest neighbour with the lowest divergence levels and AGB 2763 the farthest one.

Keywords: characterisation, descriptor, *Phaseolus vulgaris*, hierarchical clustering.

INTRODUCTION

Common bean is presumed as one of the basic component of Albanian feed, mostly in form of grain *in natura*, being considered one of the main sources proteins for people with low incomes, and also source of carbohydrate, vitamins and minerals. Nowadays it's being consumed as functional food, because of the benefits given by its fibres, with hypocholesterolic and hypoglycemic actions (Geil and Anderson, 1994).

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In our country, common bean landraces still represent important genetic resources used directly by farmers. Actually over 90% of bean cultivation area is cultivated with native bean landraces (Canko et al, 2008).

Germplasm banks are places where samples of genotypes, improved varieties, landraces, wild species and species related to a determined species of interest (generically denominated accessions) are stored under adequate conditions (Zimmerman and Teixeira, 1996). The Albanian Gene Bank (Genetic Resources Centre), part of the University of Agriculture, holds approximately 2700 accessions, *Phaseolus vulgaris* representing 7 % of total accessions.

The characterization of accessions allows quantification and structuring of the genetic variability in the germplasm which is highly important for improvement programs and for the conservation and preservation of genetic diversity. To characterize a germplasm basically means to identify and describe differences between the accessions. Besides the information on the origin of the material (passport data) differences related to the agricultural performance of the accessions are normally also considered as well as botanical differences related to normally taxon-specific descriptors (Vanderborght, 1988).

Multivariate techniques such as Euclidean distance and clustering analyses techniques such as single linkage allow the identification of duplicates. These analyses are generally carried out using agro morphological (phenotypic) data to produce dissimilarity matrixes for the accessions, which are subsequently used for cluster analyses in order to identify and group the accessions by their similarity. However, Tatieni et al (1996) argue that the phenotypic traits traditionally used for the characterization and estimation of genetic divergence may be of limited importance because they are generally influenced by the environment and the developmental stage of the plant. Singh et al (1991a) suggest that agro morphological, biochemical and molecular data should be combined for diversity studies since this combination offers complementary results.

The objectives of this study were to characterise and study diversity among twenty bean germplasm, and to evaluate the interrelations among 30 descriptors used in the characterisation process.

MATERIAL AND METHODS

A trial was conducted under open field conditions at the Experimental Didactics Economy of Agricultural University of Tirana (latitude 41°19'39"N, longitude 19°49'08"E; average altitude 89 m). The region receives an average annual precipitation to 1189 mm (46.8 in) with an annual average of temperatures 16°C (from 2 to 31°C). Twenty common bean gene bank accessions obtained from Genetic Resources Center, part of Agricultural University of Tirana, where object of sowing (randomized complete block design) that took place during 2010. The following qualitative and quantitative characters were observed following "Descriptors List for Bean" IPGRI (1982):

Table 1. Morphological characters used from “Descriptors List for Bean”

Characters	Abbreviations
Pod Beak Length	PBL
Pod Beak Position	PBP
Days to Flowering	DTF
Leaflet Length	LL
Colour of Standard Flower	CS
Colour of Wings	CW
Pod Colour	PCI
Pod Length	PL
Pod Cross-Section	PC/S
Pod Curvature	PC
Seed Coat Pattern	SCP
Seed Coat Darker Colour	SCDC
Seed Coat Lighter Colour	SCLC
Seed Shape	SSH
Leaf Colour of Chlorophyl	LCCH
Leaf Colour of Anthocyanin	LCA
Leaf Shape	LSH
Days to Maturity	DTM
Size of Bracteole	SB
Shape of Bracteole	SHB
Bracteole Length Relation	BLR
Bracteole Colour	BC
Wing Opening	WO
Duration of Flowering	DF
Pod Width	PW
Pod Beak Orientation	PBO
Seed Length	SL
Seed Width	SW
Seed Height	SH
100 Seed Weight	W

The qualitative characters were scored based on visual evaluation while the quantitative traits were counted, measured using metric rulers and weighed using weighing balance. Statistical analyze were conducted using program Multi Variance Statistical Program 3.1 (2000) and Excel (2007).

RESULTS AND DISCUSSION

Variation of morphological characteristics among twenty *Phaseolus vulgaris* accessions part of the Albanian Gene Bank collection ranged from 4.40% for days to maturity to 38.15% for pod beak length (Table 2). Common bean accession in our study presented a CV at a level of 10.78% for DTF trait

with a maximum of 34 days reported for three accessions (AGB 2730, AGB 2746 and AGB 2761) and a minimum of 24 days (AGB 2736 and AGB 2763). Our results are similar with those reported for the same trait from Sofi et al (2011).

Table 2. Data of quantitative descriptors characterisation in twenty *Phaseolus vulgaris* accessions.

Acc. nr. AGB	DTF	LL	PL	DT M	DF	PW	PBL	SL	SW	SH	W
2715	28	9.1	13.8	78	24	1.2	0.8	1.37	0.57	0.73	53.5
2718	32	6.9	9.6	74	22	1.4	1.3	1.36	0.45	0.78	44.1
2719	30	7.1	14	78	24	1.1	1.5	1.37	0.38	0.5	29.4
2729	32	6.8	7.6	77	26	1.2	0.6	1.24	0.44	0.64	40.8
2730	34	7.8	11.2	82	24	1.4	1	1.39	0.34	0.87	46.5
2731	28	7.7	6.6	78	22	1	0.5	1.03	0.33	0.61	26.5
2732	30	11.4	13.3	76	23	1.3	0.6	1.24	0.39	0.54	34.5
2733	28	7.4	11.5	78	24	1.4	1.4	1.32	0.54	0.83	52.6
2734	28	6.6	11.7	80	26	1.5	0.2	1.28	0.59	0.81	47.4
2736	24	8	12	74	20	1.4	1	1.27	0.53	0.59	44.2
2737	28	7.5	11.1	83	26	1.4	1	1.38	0.41	0.66	43.5
2746	34	9.2	12.2	84	24	1.3	0.7	1.26	0.35	0.78	41.1
2747	28	6.3	10.2	80	24	1.1	1.1	1.09	0.35	0.62	26.1
2748	32	8.1	7	82	26	1.5	1.1	1.57	0.33	0.82	46.1
2759	29	7.9	10.3	78	24	1	0.8	0.89	0.37	0.53	21.1
2760	26	4.3	11.6	76	22	1.2	0.7	1.35	0.42	0.81	42.1
2761	34	7.1	8.5	84	26	1	0.7	0.98	0.37	0.63	24.8
2762	33	6.8	9.3	82	23	1	0.5	0.97	0.36	0.57	20.8
2763	24	9.1	5	72	20	0.4	0.9	1.01	0.31	0.62	24.7
2764	26	8.2	10.5	76	22	1.2	1.3	1.66	0.36	0.89	53.5
Stdev	3.17	1.42	2.43	3.45	1.8	0.3	0.33	0.21	0.08	0.12	11.2
Mean	29.4	7.66	10.3	78.6	23.6	1.2	0.88	1.25	0.41	0.69	38.2
CV %	10.8	18.5	23.5	4.4	7.95	22	38.2	16.2	20.7	17.8	29.2

For leaflet length (cm) trait, data recorded a mean of 7.66 cm with a variation from 4.3 cm (AGB 2760) to the higher value 11.4 cm in AGB 2732. Regarding pod length and pod beak length traits, AGB 2719 was the accession presenting the higher values 14 and 1.5 respectively. Results of our 20 accessions for PL quantitative trait (± 10.35 cm) go in accordance with those reported from other authors too (Sofi et al 2011). According to this study the evaluation of 42 *Phaseolus vulgaris* germplasm, presented an average of 12.43 cm for pod length descriptor. Similar average results for pod length are found in Stoilova et al (2005) but in our study we found higher values in coefficient of variation (CV 23.5%).

Regarding results obtained in our study for seed weight trait, we found an average of ± 38.15 g /100seed meanwhile Sofi et al (2011) reported ± 40.6 g for the same trait. The mass of hundred seeds in our study identified a variation of 29.18%, from 20.88g (AGB 2762) to 53.55g (AGB 2715). Our results are higher of those reported from Stoilova et al (2005) ($W = \pm 12.5$ g). The lowest variation among accessions was recorded for the DTM trait (4.4%) where AGB 2746

recorded the highest number of the days to maturity (84). Data recorded in our study for DTM (± 78.6) are similar with those reported from Sofi et al (2011). Also in the study of twenty Bulgaria bean landraces Stoilova et al (2005), found low coefficient variation for the same trait (CV 4.7%) with an average value of 77.9 days. Meanwhile four bean accessions among twenty studied, presented the maximum same value for DF (26) and AGB 2764 was the only one where the flowering process lasted 20 days. AGB 2763 is identified with the lowest values in most quantitative traits (6 traits) like DTF, PL, DTM, DF, PW and SW (seed width). Common bean accessions showed an average of 1.2 cm for PW trait with a variation from 0.4 cm to 1.5 cm (AGB 2748). Our results for PW are in accordance with those reported from Stoilova et al (2005) (PW ± 1 cm). Regarding seed data, AGB 2764 presented the highest value for seed length (1.66 cm) and seed height (0.89 cm).

The analysis correlation coefficient (Table 3) revealed that several descriptors are positively correlated between each other. Based on the results days to flowering is significant correlated with two traits, DTM ($r=0.67$) and duration of flowering ($r=0.57$). Positive relations are observed between pod length and pod width ($r=0.51$) and PL and seed width ($r=0.49$). Data showed that a strong correlation is recorded between DTM and DF characters ($r=0.74$). Seed length is correlated at the level of 0.64 with pod width, and less correlated with pod beak length (0.47). Seed height trait is correlated at a medium level with pod width but strongly correlated with seed length. The highest values of correlation coefficient are recorded for weight mass of 100 seeds trait which is very strongly related with seed length at the level $r=0.85$, followed by that with seed height ($r=0.78$).

Table 3. Genotypic correlation coefficient (Pearson) among eleven quantitative traits in *Phaseolus vulgaris* accessions.

	DTF	LL	PL	DTM	DF	PW	PBL	SL	SW	SH	W
DTF	1										
LL	0.03	1									
PL	-0.02	0.11	1								
DTM	0.67	-0.09	0.09	1							
DF	0.57	-0.14	0.08	0.74	1						
PW	0.25	-0.07	0.51	0.3	0.41	1					
PBL	-0.12	-0.02	0.16	-0.21	-0.17	0.11	1				
SL	-0.06	0.03	0.34	-0.04	0.11	0.64	0.47	1			
SW	-0.28	-0.12	0.49	-0.19	0.11	0.48	-0.09	0.22	1		
SH	0.07	-0.18	0.03	0.13	0.12	0.49	0.16	0.67	0.21	1	
W	-0.13	0.04	0.38	-0.06	0.11	0.71	0.26	0.85	0.57	0.78	1

Negative relations are observed among several traits as, pod beak length and days to maturity ($r= -0.21$) or between PBL and DF ($r= -0.17$). As it is seen DTM trait is negatively related with seed width ($r= -0.19$) and less with seed

weight. Negative interrelations are observed among SW and DTF, and some traits as DTM, DF, PW, PBL, SW and SH are all related negatively with LL trait.

The principal component analyzes in quantitative traits (Table 4), suggest that the first component is responsible for the largest possible variance (79.4% of total variance) in our study. Rodrigues et al (2002) showed that after discarding 25 of the 40 descriptors evaluated in 37 common bean cultivars 69% of the total variance was made up of the first four components. Chiorato et al (2005) evaluated 993 common bean accessions belonging to the IAC Germplasm Bank and found that 33% of the variation occurred in the first two components and concluded that only 18 of the 23 agro morphological descriptors were needed for evaluation of the accessions.

Table 4. Eigen values associated to the principal components, their relative and accumulated (%) variances, referring to 11 agro morphological quantitative descriptors evaluated in 20 common bean accessions of the Albanian Germplasm Bank.

Components	Eigen values	Total variance %	Accumulated variance %
1	125,2	79,43	79,43
2	20,340	12,906	92,33
3	5,127	3,253	95,58
4	3,758	2,385	97,97
5	1,862	1,181	99,15
6	1,206	0,766	99,93
7	0,103	0,065	99,98
8	0,019	0,012	99,99
9	0,009	0,006	99,99
10	0,003	0,002	100,000
11	0,001	0,000	100,000

Results in literature suggest that 10 to 20 descriptors should be considered for the characterization of common bean germplasm banks because the use of higher numbers is costly and adds little in the analysis. However it should be remembered that the most informative and variable descriptors are not always the same for all the accessions in a germplasm bank (Chiaroto et al, 2006).

Results of the hierarchical cluster analysis are presented in Figure 1. At first sight the dendrogram is formed by two major groups divided in 18 Nodes. Accession AGB 2763 is identified as the most different from all the other accessions of common bean. The dissimilarities with the other genotypes are based in the lowest values for at least 6 quantitative descriptors as DTF, PL, DTM, DF, PW and SW. The nearest neighbours clustered together with the lowest dissimilarity level (3.085) between them are AGB 2715 and AGB 2733. These two genotypes are fully similar for traits as DTF (28 days), DTM (78 days) and DF (24 days), and similar for traits like PW, SW and W. This group is joined

at the level of 3.832 of dissimilarity by AGB 2764, which is very similar with AGB 2733 for traits as PW and W.

Clustered together in one group are two other genotypes (4.85 diss.) AGB 2731 and AGB 2747 similar for traits as DTF, PW, SL, SH and SW. A little further up at the level of 5.1 of dissimilarity AGB 2730 and AGB 2748 are clustered together, similar for days to maturity (82 days), W, PW, PBL and SW. At the level of 6.11 of dissimilarity AGB 2746 is joined at this cluster, particularly for similarity with AGB 2730 in days to 50 % flowering (34 days), DF (24days), PW and SW. Accessions AGB 2734 and AGB 2737 are considered neighbours for their homogenous in descriptors as DTF (28 days), DF (26 days) and PW, but different from each other for traits as PBL, SL, SW and SH. Similarity between genotypes AGB 2761 and AGB 2762 consist mostly for PW, but analogy is observed with other descriptors too (DTF, DTM, SL and SW). AGB 2736 and AGB 2760 are near (5.53 level of dissimilarity) for DTF and PL but very different in LL, SL and SH. AGB 2759 is joined to the cluster formed by AGB 2731 and AGB 2747, further more to this group is added AGB 2719. This last accession resemble with AGB 2759 on traits as DTM (78 days), DF (24 days), PW and SW but are very different on PL, PBL and SL. The morphological analogy between AGB 2718 and AGB 2729 is observed on DTF (32 days), LL and SW. AGB 2732 part of a group of 7 accessions clustered together (7.146 diss.), differs from the others genotypes basically for the leaflet descriptor, representing the highest value.

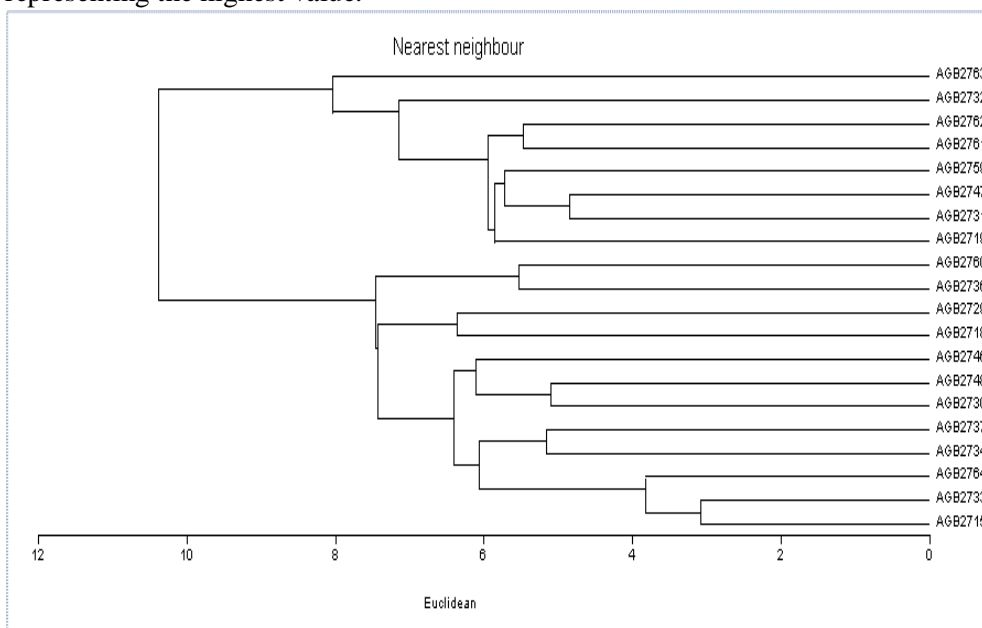


Figure 1. Single linkage dendrogram based on 11 quantitative traits for 20 common bean accessions.

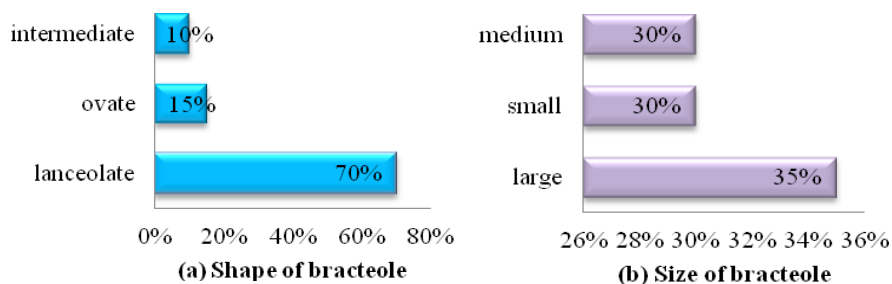


Figure 2. Size and shape of bracteole data of 20 common bean germplasm

The germplasm was also evaluated for 19 qualitative descriptors (some of them shown in table 5 in terms of Codes). Most of the accessions (55%) had white colour of standard flower, 20 % of them lilac and 10 % white with lilac edge. For the colour of wings descriptor 60 % of bean germplasm were white in colour, 20 % lilac, 10 % purple and only 5 % presented a dark lilac with purple spots colour. Variability recorded in size of bracteole and shape of bracteole descriptors is revealed in Fig.2, 95% of the plants recorded green bracteole, 25 % of them had bracteole length relation twice as long as calyx, and most of them 75% presented shorter than or equal to calyx length relation.

Our bean germplasm presented variability for pod colour, 20 % were purple stripe on green, 10 % golden or deep yellow, 20 % shine green, 55% normal green and 5 % dull green.

Table 5. Data on various qualitative morphological parameters of *Phaseolus vulgaris* accessions.

Acc. AGB	CS	CW	PCI	PCS	PC	SCDC	SCLC	LCCH	LSH	BLR	BC	WO	PBP	PBO
2715	3	3	3	1	5	3	14	3	1	7	1	7	1	5
2718	10	9	3	2	3	7	0	7	3	3	1	5	1	5
2719	3	7	10	3	7	1	0	5	1	3	1	5	2	3
2729	1	1	7	2	5	3	0	5	3	3	1	3	2	7
2730	1	1	8	1	5	8	6	7	1	7	1	5	1	7
2731	3	3	7	1	3	3	6	7	1	7	1	5	1	5
2732	4	3	10	3	3	1	0	7	3	3	1	7	2	7
2733	4	1	8	2	5	3	14	5	1	3	1	3	2	7
2734	1	1	3	1	7	3	14	5	1	3	1	5	1	5
2736	3	3	8	2	3	4	6	5	3	3	1	3	1	5
2737	0	0	9	2	5	3	14	5	1	0	0	0	1	5
2746	1	1	7	1	5	7	0	7	1	7	1	7	1	3
2747	1	1	7	1	3	8	0	7	1	3	1	3	1	5
2748	1	1	7	1	5	8	6	7	1	3	1	3	1	7
2759	1	1	7	1	3	8	0	5	1	7	1	5	1	7
2760	10	9	7	1	3	8	6	7	3	3	1	3	1	5
2761	1	1	7	1	5	8	6	7	1	3	1	5	1	7
2762	1	1	7	1	5	8	6	7	3	3	1	7	1	7
2763	1	1	7	1	5	7	0	7	3	3	1	5	2	5
2764	1	1	7	1	7	8	6	7	1	3	1	7	1	3

Low variability was recorded for PC/S trait where 65% of the accessions were very flat, 25% had pear shaped and 10 % round elliptic. Bean germplasm presented variability for seed colour darken colour trait (30 % maroon, 15% pure white, 10 % black, 40 % whitish and 5 % grey, brownish to greenish) and less variability in seed lighter colour (40 % pale-cream to buff and 40% didn't present any light colour). Regarding leaf colour of chlorophyll descriptor 60% of bean germplasm in our study was dark green, 35 % of the accessions medium green and only 5% recorded pale green. Low differences were recorded for leaf shape trait, 65% of the accessions had triangular leaf, and 35% of them rounded.

Variability is recorded in seed shape descriptor (Figure 3), where in 40% of the total accession we found only one type of shape in seeds, three different shapes are found in seeds of AGB 2734 accession (round, truncate and kidney). Most of the germoplasm tested for the seed coat pattern descriptor had homogenous seeds, constant mottled (55%), 15% of the accessions recoded seeds striped and speckled, 5% of the acc. was uniform with rhomboid spotted and 5% striped. Variability in 5% was found with constant mottled and striped seeds. This trait wasn't present in 15% of the bean germplasm.

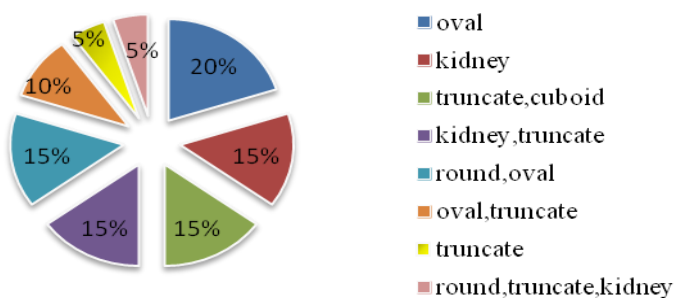


Figure 3. Data on seed shape trait among twenty bean germplasm.

Based on wing opening descriptor data, 25% of the accessions had wings widely diverging, 40% of them wings moderately diverging and 30% parallel closed wings. Evaluation done on pod beak position verified low variability on this descriptor, 75% of the bean acc. figured with marginal beak and 25 % non-marginal position of the beak. Regarding pod beak orientation 45% of bean pods were straight (curving to dorsal side), 15% upward and 40% of the pods were curving to ventral side. Only seven of bean accessions (AGB 2715 till 2719; AGB 2759; 2760; 2762 and 2763) presented Leaf Colour of Anthocyanin.

CONCLUSIONS

Among common bean genotypes object of this study, differences exist in phenotype and this suggest differences in genetic make up. AGB 2746 took more than 84 days to rich maturity. Based on the results days to 50 % flowering is significant correlated with DTM and duration of flowering. Data showed that a

strong correlation is recorded between DTM and DF descriptors ($r=0.74$). Seed length is positively correlated with pod width, and less correlated with pod beak length. Seed height trait is strongly correlated with seed length. The highest values of correlation coefficient are recorded for weight mass of 100 seeds descriptor which is very strongly related with seed length at the level $r=0.85$, followed by that with seed height ($r=0.78$). There is need for further studies to evaluate the characterised accessions over a period of two or more years in many different locations to see if similar observations will be observed.

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MORFOLOŠKA KARAKTERIZACIJA I POVEZANOST DESKRIPTORA KOD AKSEŠENA *PHASEOLUS VULGARIS*

SAŽETAK

Cilj ove studije je evaluacija genetičkog diverziteta kod dvadeset aksešena pasulja koji čine dio kolekcije Centra za genetičke resurse, na Poljoprivrednom fakultetu u Tirani, i to primjenom agro morfoloških karakteristika. Na osnovu IBPGR deskriptora za *Phaseolus vulgaris*, zabilježene su kvalitativne (19) i kvantitativne (11) karakteristike. Varijacija morfoloških karakteristika među aksešenima kretala se od 4,40% za vrijeme zriobe (DTM) do 38,15% za dužinu kljuna mahune (PBL). AGB 2719 je identifikovan kao aksešen sa najvišim vrijednostima kvantitativnih osobina kao što je dužina mahune (PL) i PBL, AGB, 2746 kod karakteristika poput DTF i DTM, AGB 2748 kod karakteristika poput trajanja cvjetanja i PW, a AGB 2763 je prepoznat kao nosilac najnižih vrijednosti kvantitativnih osobina kao što DTF, PL, DTM, DF, PW i SW (širina sjemena). Uočene su pozitivne korelacije između deskriptora, kao što su dužina i veličina bracteole ($r=0.76$), između DF i DTM ($r=0.74$). Takođe, za vrijeme zriobe i vrijeme cvjetanja (DTF), ovaj koeficijent je pozitivan na nivou $r=0.66$, širina mahune i dužina sjemena ($r=0.63$), dok je koeficijent korelacije kvalitativnih deskriptora pokazao da je boja krila (u smislu vrijednosti) povezana sa bojom standardnog cvijeta ($r=0.9$). Razlika između aksešena pručavana je primjenom dendrograma hijerarhijskog grupisanja, Euklidsko rastojanje. Na osnovu ove analize, AGB 2715 i AGB 2733 je najbliži susjed sa najnižim nivoima divergencije, dok je AGB 2763 najudaljeniji.

Ključne riječi: karakterizacija, deskriptor, *Phaseolus vulgaris*, hijerarhijsko grupisanje.