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PHENOTYPIC EVALUATION OF SOME TURKISH GREEN BEAN (*PHASEOLUS VULGARIS* L.) GENOTYPES

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Abstract

This study was conducted to reveal the morphological characterization of 36 green bean genotypes collected in Turkey to find out the suitable genotypes which can be used in breeding programs. Collected plant materials were grown under Antalya ecological conditions and morphological characteristics of genotypes were evaluated in accordance with UPOV criteria. Principles Component Analysis of the data obtained from morphological characterization were conducted. The results indicated that genetic variation among some bean genotypes was not high and results revealed that first three Eigen values could be used to explain the 50% of the variation among genotypes. The genotypes far from each other with respect to dendrogram can be an important source of variance and can be used in prospective breeding programs.

Introduction

Beans play an important role in meeting the daily protein requirements and are grown in all continents, except the Antarctic. The bean spread rapidly all over the world following the discovery of its motherland America (Tunar & Kesici, 1998; Singh, 1999). According to data of 2010, world total common bean production is 19.834.297 tons (Anon., 2012).

It is a well known fact that *Phaseolus* spp., has a large genetic variation. In the Germplasm Bank of the Genetic Resources Program of the International Center for Tropical Agriculture (CIAT), the largest and most diversity bean collection in the world is preserved, with about 36,000 materials, corresponding to 44 taxa from 109 countries (Anon., 2011). The bean is grown in many developing countries to meet daily protein need and is a major consumption item in that sense. The average yield of the bean in these countries is still quite low. Reasons for low yield can be ranged from sensitivity to biotic and abiotic stress conditions to the adaptation of developing varieties being limited. The use of stored germplasm in gene banks as genetic variety sources for breeding programs will definitely affect the development of productive varieties. Similarities or differences among genotypes would help to decide on which material the breeder will use while new genetic combinations are being formed (Broughton *et al*., 2003; Hallden *et al*., 1994). In that sense, morphological characterization is commonly used in order to determine similarities or differences or two reveal genetic diversity (Jatoi & Watanabe, 2013; Shah *et al*., 2012).

In this research, some selected common bean genotypes have been examined regarding phenological and morphological characteristics according to UPOV (Anon., 1998) criteria. Defining the differences in relation to each other in genotypes taking place in present study is assumed to make it possible to obtain materials to be used in the selection of genotypes for further breeding studies as well as conservation of the genotypes.

Material and Methods

A total of 36 plants, consist of 33 common bean genotypes and 3 commercial common bean cultivars, were used as plant material in the research (Table 1). Plant materials were collected from the northern part of Turkey.

All plant materials were grown in Antalya-Turkey during two successive years for recording the morphological data. The genotypes were evaluated for 19 characters according to UPOV criteria. The criteria were; days to germination (DG), days to first flowering (DF), intensity of pod ground color (CP), median width of pod (WP), pod length (LP), pod flesh thickness (TP), pod cross section (SP), pod shape or curvature (SCP), pod pigment flecks (FP), pod prominence of grains (GP), pod shape (STP), pod stringiness (StP), beak length (LB), bracts lenght (LBr), bracts shape (SB), standard color of flower (CF), grain color (CG), grain main color (MCG), grain main secondary color (SCG). The experimental was conducted on the randomized parcel design with three replications. Each replication was consisted of 10 plants.

The spacing was 50 cm between rows and 10 cm between plants within rows. Data were collected from 10 randomly selected plant/each genotype. Statistical analyses of the data were carried out using the Anon., (1986) statistical software package.

Results and Discussion

The phenological characteristics were used for the identification of similarity and diversity between the genotypes. Mean, minimum value, maximum value and coefficient of variation of morphological characters used in the study are shown in Table 2. According to the results, DG (days to germination) and DF (days to first flowering) were varied from 5 to 14 days and 35-50 days, respectively. The average value of the DG is 8.51 days with a high variation coefficient of %18.92. As shown in correlation matrix (Table 3), there is a statistically significant correlation between DG and DF. The correlation can be associated with the earliness. According to this, Y17, Ç22' and Ç42' genotypes can be considered as early fruiting while TK1 genotype can be considered as late fruiting. Additionally, correlation matrix shows a statistically significant relationship among CG (color of grain), MCG (main color of grain) and SCG (main secondary color of grain). Similarly, a statistically significant relationship was also detected between parameters of the seed color (CG, MCG and SCG) and CF

(standard color of flower). The morphological characters were also the first markers used in linkage mapping (Kelly & Miklas, 1999).

In his study of Sax (1923), bean seed size and color were used as morphological markers (Andersen & Lübberstedt, 2003), and these parameters are still used for bean morphological characterization. The collection of present study included a range of different colors. Seed color parameters were quite determining in the present study, too. Zeven *et al*. (1999) reported that flowering time was positively associated with pod color intensity. But, there was no positive association between flowering time and pod color intensity in the present study (Table 3). Collection beans' locations and different environmental conditions probably contributed to the stated contrast.

Eigen values are the variances of the characters. When Eigen values are taken into consideration, first three Eigen values based on correlation matrix explained 50% of cumulative variance (Table 4). In addition, 75% of variance was explained by the help of first six Eigen values. The first, second and third eigen values explained 20, 17 and 13% of the total variation, respectively. In a research conducted by Ceolin *et al*., (2006), first eigen value explained 46% variance, and first two Eigen values explained 88.23%. Based on morphological and agronomical characters, determining the most distinct three genotypes and using the combinations of these genotypes can be suggested for further breeding programs. It is known that the cumulative variance of the first three Eigen value being lower than 50% indicated a high genetic diversity (Keleş, 2007). In the present study, the cumulative variance of the first 3 eigen values was determined as 50% indicating that genetic diversity among the genotypes was not that.

Figure 1 shows PC plots. These plots could be informative to breeders about genetic diversity and similarity among the genotypes. As shown in Table 5, TP (flesh thickness of pod), FP (pigment flecks of pod), GP (prominence of grains of pod), CG (color of grain) and SCG (secondary color of grain) were important variables composing PC1. While LP (length of pod), CF (standard color of flower), LB (length of beak) and MCG (main color of grain) were the most important characteristics for PC2, DG (days to germination), DF (days to first flowering) and LBr (length of bracts) values were found to be important for PC3. The first three PC expressed 12 traits of the morphological traits examined and that is way the first three eigen values can explain 50% of the total variation.

Table 1. The list of genotypes and standard cultivars and their origin.

Genotype	Location	Genotype	Location	Genotype	Location
1. KO	Center of Samsun	13. L	Ladik	25. Ç16'	Çarşamba
2. Ç7	Çarşamba	14. TK32	Tekkeköy	26. TK15	Tekkeköy
3. T11"''	Terme	15. TK12'	Tekkeköy	27. T6	Terme
4. Ç22	Çarşamba	16. TK12	Tekkeköy	28. TK7	Tekkeköy
5. TK47	Tekkeköy	17. T23	Terme	29. Ç31	Çarşamba
6. T26	Terme	18. TK44	Tekeköy	30. UB	SC
7. Ç14	Çarşamba	19. Ç28	Çarşamba	31. Ç22'	Çarşamba
8. TK2	Tekkeköy	20. Ç20	Çarşamba	32. X-1	Ladik
9. Ç44	Çarşamba	21. TK57	Tekkeköy	33. TK1	Tekkeköy
10. TK59	Tekkeköy	22. Ç33	Çarşamba	34. T7	Terme
11. T2	Terme	23. T9	Terme	35. Y17	SC
12. Ç24	Çarşamba	24. Ç42'	Çarşamba	36. TA	SC

*SC: Standard cultivar

Table 2. Morphological characters, mean, minimum value, maximum value and coefficient of variation in pure lines of common bean.

Morp. characters	Mean	Min-Max	CV (%)
DG	8.51 ± 0.03	5.00-14.00	18.92
DF	40.22 ± 0.07	35.00-50.00	8.04
LP	13.94 ± 0.04	3.00-20.20	14.57
WP	13.38 ± 0.03	8.89-18.16	12.11
TP	7.26 ± 0.02	3.75-10.74	11.88
LBr	5.12 ± 0.01	3.21-7.76	13.30
LB	8.67 ± 0.05	3.96-16.37	24.43

Days to germination (DG), days to first flowering (DF), intensity of ground color of pod (CP), median width of pod (WP), length of pod (LP), flesh thickness of pod (TP), cross section of pod (SP), shape or curvature of pod (SCP), pigment flecks of pod (FP), prominence of grains of pod (GP), shape of tipe of pod (STP), stringiness of pod (StP), length of beak (LB), lenght of bracts (LBr), shape of bracts (SB), standart color of flower (CF), color of grain (CG), main color of grain (MCG), main secondary color of grain (SCG)

Table 3. Correlation of the phenological and morphological characters in genotypes of common bean. ((DG), days to first flowering (DF), intensity of pod ground color (CP), median width of pod (WP), length of pod (LP), flesh thickness of pod (TP), cross section of pod (SP), pod shape or curvature (SCP), pigment flecks of pod (FP), prominence of grains of pod (GP), length of beak (LB), length of bracts (LBr), shape of bracts (SB), standard color of flower (CF), grain color (CG), grain main color (MCG), grain main secondary color (SCG)).

	DG	DF	CP	LP	WT	TP	LBr	SB	SCP	FP	GP	CF	SP	LB	CG	MCG	SCG
DG	1																
DF	**.73976**																
	<.0001	1															
CP	**.20876**	-.3182															
	<.0001	0.1393	1														
LP	-.00939	.08177	.07530														
	0.6628	0.0001	0.0005	1													
WT	-.01239	-.01273	-.03480	-.04449													
	0.5650'	0.5542	0.1059	0.0387	1												
TP	.00019	-.01401	**.11291**	**.14388**	-.03441												
	0.9929	0.5153	**<.0001**	**<.0001**	0.1099	1											
LBr	**.12810**	**.13317**	.01616	**.16119**	**-.24143**	.02532											
	<.0001	**<.0001**	0.4528	**<.0001**	**<.0001**	0.2395	1										
SB	-.2313	-.07901	**.24667**	**.35793**	**-.10976**	**.09749**	**.10661**										
	0.2826	0.0002	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	1									
SCP	**.16215**	.03558	-.06820	**.22944**	**.08812**	.06649	.06378	**-.33757**									
	<.0001	0.0982	0.0015	**<.0001**	**<.0001**	0.0020	0.0030	**<.0001**	1								
FP	**.09117**	.00333	-.06820	-.05260	**.24889**	-.05447	.00054	**-.19290**	**.60000**								
	<.0001	0.8771	0.0015	0.0145	**<.0001**	0.0113	0.9799	**<.0001**	**<.0001**	1							
GP	-.00622	-.08113	**.25809**	**-.47084**	**.28644**	-.05166	**-.14671**	**-.12572**	**.58867**	**.48776**							
	0.7757	0.0002	**<.0001**	**<.0001**	**<.0001**	0.0163	**<.0001**	**<.0001**	**<.0001**	**<.0001**	1						
CF	**.17166**	**.13172**	.03050	**-.26954**	-.06278	**.14512**	.02152	**-.12940**	**.26833**	**.08944**	**.20309**						
	<.0001	**<.0001**	0.1565	**<.0001**	0.0035	**<.0001**	0.3176	**<.0001**	**<.0001**	**<.0001**	**<.0001**	1					
SP	.06108	-.01113	**-.01113**	**.20324**	**-.16320**	**.18817**	**.11825**	.06100	.06325	**-.12649**	**-.26593**	0.00000					
	0.0045	0.6051	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	0.0046	0.0033	**<.0001**	**<.0001**	10.000	1				
LB	.02861	**.08947**	**-.23575**	**.26024**	-.06750	-.06822	.02181	-.03292	-.00541	.05127	**-.13877**	**.32957**	**.13367**				
	0.1837	**<.0001**	**<.0001**	**<.0001**	0.0017	0.0015	0.3111	0.1261	0.8013	0.0172	**<.0001**	**<.0001**	**<.0001**	1			
CG	**-.08926**	-.02682	**-.10783**	**-.10743**	.03105	**-.25585**	**-.12454**	**-.26687**	**.15811**	**.31623**	**.26593**	**-.14142**	**-.10000**	**.38154**			
	<.0001	0.2128	**<.0001**	**<.0001**	0.1491	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	1		
MCG	**.11264**	-.06068	-.04738	**-.34634**	.05354	**.13187**	**-.22489**	**-.17125**	.07720	**-.10808**	**.09219**	**.53857**	.00488	**-.20790**	**-.23191**		
	<.0001	0.6198	0.0277	**<.0001**	0.0128	**<.0001**	**<.0001**	**<.0001**	0.0003	**<.0001**	**<.0001**	**<.0001**	0.8206	**<.0001**	**<.0001**	1	
SCG	**-.09408**	-.03768	-.06301	-.05806	-.02247	**-.23735**	**-.13596**	**-.13049**	**.10559**	**.29038**	**.29082**	**-.20070**	**-.16696**	**.34389**	**.93913**	**-.26493**	
	<.0001	0.0800	0.0034	0.0070	0.2967	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	1

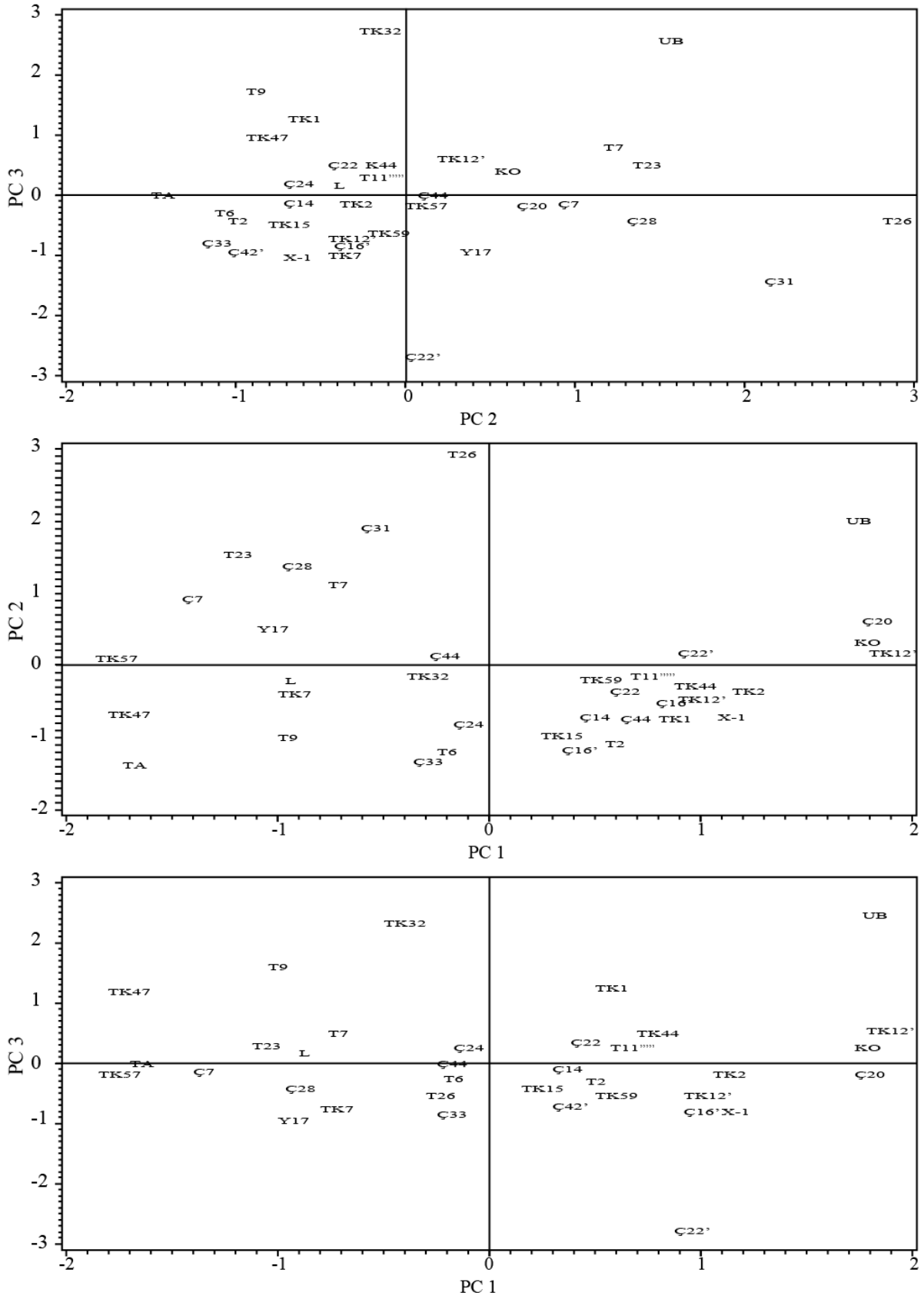

Fig. 1. PC plots.

Table 4. Percentage of variance with respect to Eigen value based on correlation matrix.

	Eigenvalue	Differences	Variance (%)	Cumulative variance (%)
1.	3.40	0.46	20	20
2.	2.95	0.64	17	37
3.	2.30	0.69	13	50
4.	1.60	0.28	9	60
5.	1.32	0.08	7	68
6.	1.23	0.21	7	75

Table 5. Results of the Principle Component Analysis of common bean genotypes.

Morph. Charac.	PC1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9	PC 10
DG	-0.046	0.190	**0.529**	-0.115	-0.149	0.184	0.120	0.235	0.171	-0.078
DF	-0.064	0.055	**0.456**	-0.086	-0.329	0.172	0.390	-0.341	0.187	0.053
CP	-0.066	0.052	-0.300	0.450	-0.217	-0.146	0.371	-0.400	0.202	-0.033
LP	-0.271	**-0.317**	0.108	0.229	0.149	0.270	0.249	-0.061	-0.360	0.118
WP	0.216	0.135	-0.174	-0.056	0.058	0.679	0.019	-0.075	0.185	0.301
TP	**-0.290**	0.213	-0.015	0.262	0.428	0.012	0.230	-0.152	-0.165	-0.126
LBr	-0.214	-0.073	**0.337**	0.303	-0.300	-0.246	-0.349	0.008	-0.003	0.055
SB	-0.251	-0.132	-0.136	0.284	-0.122	0.112	0.267	0.742	0.181	-0.026
SCP	0.251	0.251	0.271	0.347	0.214	-0.025	-0.187	-0.053	-0.012	-0.272
FP	**0.318**	0.087	0.190	0.362	0.093	0.243	-0.096	0.120	-0.384	0.178
GP	**0.368**	0.244	-0.083	0.320	-0.053	-0.004	0.058	0.115	0.333	-0.238
CF	-0.015	**0.425**	0.129	-0.020	-0.020	-0.298	0.263	0.126	-0.267	0.419
SP	-0.198	-0.041	0.187	0.064	0.570	-0.137	-0.109	-0.015	0.575	0.395
LB	0.100	**-0.380**	0.256	-0.087	0.273	0.050	0.203	-0.027	0.020	-0.486
CG	**0.413**	-0.266	0.079	-0.024	0.075	-0.243	0.221	0.001	0.012	0.243
MCG	-0.021	**0.398**	-0.057	-0.331	0.205	-0.140	0.291	0.149	-0.081	-0.221
SCG	**0.391**	-0.288	0.041	0.023	0.022	-0.239	0.283	0.110	-0.008	0.155

Days to germination (DG), days to first flowering (DF), intensity of ground color of pod (CP), median width of pod (WP), length of pod (LP), flesh thickness of pod (TP), cross section of pod (SP), shape or curvature of pod (SCP), pigment flecks of pod (FP), prominence of grains of pod (GP), length of beak (LB), lenght of bracts (LBr), shape of bracts (SB), standart color of flower (CF), color of grain (CG), main color of grain (MCG), main secondary color of grain (SCG)

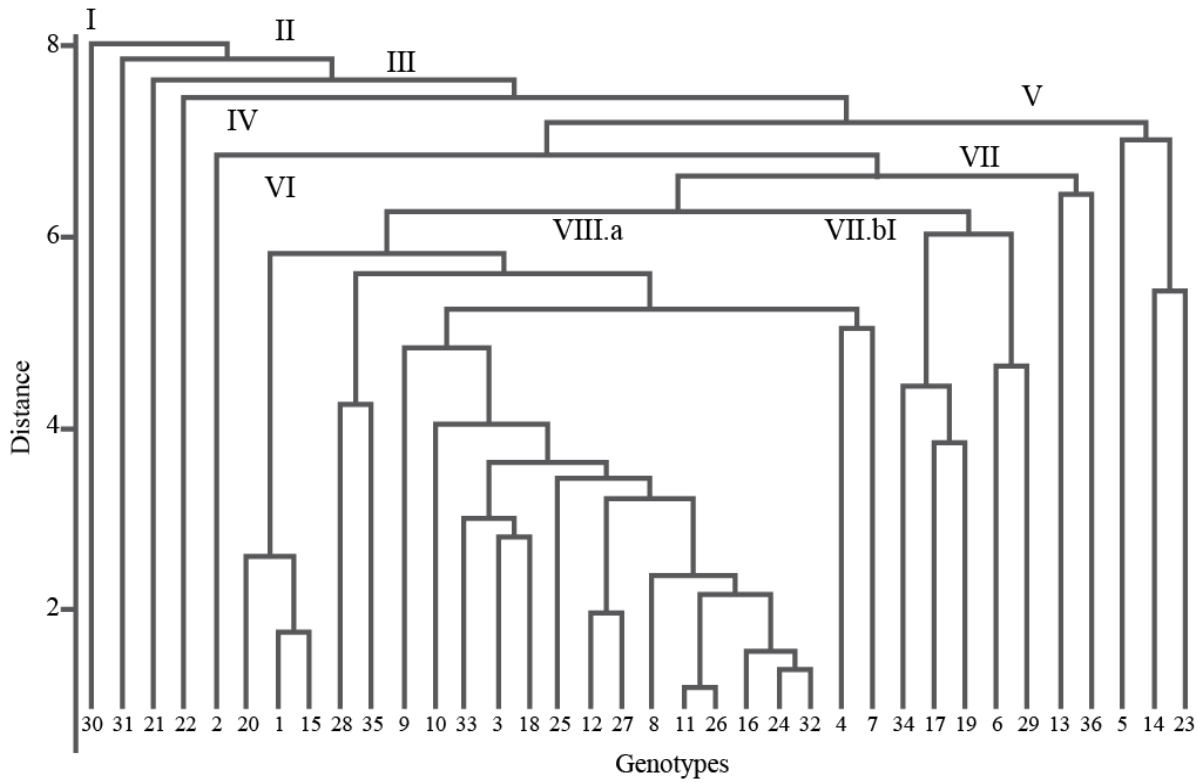

Fig. 2. Dendrogram of obtained by cluster analysis indicating the similarities rate of worked on common bean genotypes.

To understand better the diversity of genotypes, the data obtained were analyzed by cluster analysis. Cluster analysis based on morphological and physiological characters grouped genotypes into 8 main branches (Fig. 2). The dendrogram indicated that Ç22", UB, TK57and Ç33 were different from the others and each other. TK47, TK32 and T9 genotypes formed a group but these genotypes were not genetically very close. Besides, Ç7 line can be considered as an independent group. L and TA lines took place as a different group on the dendrogram. Finally, the largest group was formed from Ç20, KO, TK12', TK7, Y17, Ç44, TK59, TK1, TK44, T11"", Ç16', Ç24, T6, TK2, T2, TK15, TK12, Ç42', X-1, Ç22, Ç14, T7, T23, Ç28, T26 and Ç3. The largest group divided into 2 subgroups in itself. The first subgroup included 21 genotypes (Ç20, KO, TK12', TK7, Ç44, TK59, TK1, T11"", TK44, Ç16', Ç24, T6, TK2, T2, TK15, TK12, Ç42', X-1, Ç22, Ç14 and Y17). The second subgroup was formed by the other genotypes (T7, T23, Ç28, T26, Ç31). T2 and TK15, Ç42' and X-1, KO and TK12', lastly Ç24 and T6 were found as the most genetically closest lines. Flores *et al*. (2003) reported regional differences among 112 common bean accessions they studied. They obtained higher variation in west side than east side of northern Spain where the common bean accessions were collected. According to results of the present study, genotypes with genetic affinity were detected in Terme, Tekkeköy and Çarşamba. But Ladik showed regional variation by separate clustering in dendrogram and was associated with Tamara cultivar.

Madakbaş *et al*., (2007) examined morphological and physiological traits of green beans grown in central blacksea region. In their study, the following common bean genotypes, TK15, TK7, TK57, T26, Ç31, T7, KO, TK1, T23 and Ç28, which were also used in the present study in Antalya, were determinated as promising genotypes for further breeding researches. Escribano *et al*. (1997) investigated morphological and physiological characters of 59 common bean populations and 5 commercial cultivars in 3 different environments. At the end of the research, environment x genotype interaction was found to be important in terms of fresh pod and dry seed traits. Similarly, the some genotypes grown both in Antalya and Samsun showed different physiological responses to environmental conditions. For example, KO and TK1 genotypes had different germination days in Samsun and Antalya which can be explained by environment x genotype interaction and this point should be taken into consideration in future studies.

Conclusion

According to results of the study, genetic diversity among genotypes was not high. Green bean is a self-pollinated plant and many farmers use their own seed resources for production. It is most likely that seeds used by the farmers may be mixed with each other over the time and using the same seeds every year may create a genetic bottle-neck. If the genotypes far away from each other are taken into consideration (such as Ç22' and T2 or Ç22' and TK15) with respect to dendrogram, these genotypes can be an important source of variance to be used in future breeding programs.

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