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Classification of Wild Apricot Genotypes (*Prunus armeniaca* L.) Using Principle Component and Cluster Analysis

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Abstract

In this study, the relationships among fruit characters on 37 genotypes, previously selected from the population wild apricot of Gümüshane (Turkey) have been researched. In order to find the main variation trends between fruit and seed characters in the zerdali forms and to evaluate their correlation, data were processed according to the principal component analysis (PCA). As a result of correlation analysis, it is seen that some important relationships are found among the fruit, the seed and the fruit juice characteristics of wild apricot. The relations among fruit weight and other characteristics, except the total dry matter, have been found positive and significant. The highest relations regarding fruit weight have been observed between fruit size and flesh/seed ratio. Four groups are created according to the classification of multivariate cluster analysis; the group components consist of the following characteristics; the first component (PCA1: 33.41%); fruit thickness, fruit width, fruit weight, flesh/seed ratio and fruit length; the second component (PCA2: 20.90%); seed weight, kernel weight, seed width and seed thickness; the third component (PCA3: 13.04%); seed length, titratable acidity and pH; the fourth component (PCA4: 11.75%); soluble solids content and total dry matter. Consequently, with this study, it can be said that the knowledge that fruit weight and fruit size, seed weight and seed size, fruit acidity and pH, soluble solids content and total dry matter values can create a group, can be used; and therefore it will decrease workload and waste of time in selective breeding studies to be done on wild apricot.

Key Words: Wild apricot, *Prunus armeniaca,* classification, principal component analysis, cluster analysis

Temel Bileşen ve Kümeleme Analizi ile Zerdali (*Prunus armeniaca* L.) Genotiplerinin Sınıflandırılması

Özet

Bu çalışmada daha önceden Gümüşhane (Türkiye) ilindeki zerdali populasyonu içerisinden seçilmiş 37 genotip üzerinde önemli meyve karakterleri arasındaki ilişkiler araştırılmıştır. Genotiplerde meyve ve tohum özellikleri arasındaki temel değişimleri bulmak için veriler temel bileşen analizine (PCA) göre değerlendirilmiştir. Yapılan korelasyon analizleri sonucunda zerdalide meyve, tohum ve meyve suyu özellikleri arasında bazı önemli ilişkilerin çıktığı görülmüştür. Meyve ağırlığı ile diğer özellikler arasındaki ilişkiler, toplam kuru madde hariç, pozitif ve önemli bulunmuştur. Meyve ağırlığı ile en yüksek ilişkiler meyve boyutları ile meyve eti / çekirdek oranı arasında görülmüştür. Çok değişkenli kümeleme analizi ile sınıflandırmada oluşan dört gruptan birinci bileşende (PCA1: %33.41) meyve kalınlığı, meyve eni, meyve ağırlığı, et çekirdek oranı ve meyve boyu; ikinci bileşende (PCA2: %20.90) çekirdek ağırlığı, çekirdek içi ağırlığı, çekirdek eni ve çekirdek kalınlığı; üçüncü bileşende (PCA3: %13.04) çekirdek boyu, asitlik ve pH; dördüncü bileşende (PCA4: % 11.75) suda çözünür kuru madde miktarı ve toplam kuru madde özellikleri yer almıştır. Sonuç olarak, bu çalışma ile zerdalide yapılacak seleksiyon ıslahı çalışmalarında genel olarak meyve ağırlığı ile meyve boyutları, çekirdek ağırlığı ile çekirdek boyutları, meyve asitliği ile pH ve suda çözünür kuru madde miktarı ile toplam kuru madde değerlerinin bir grup oluşturabileceğine dair bilginin kullanılabileceği; zaman kaybını ve iş yükünü azaltabileceği söylenebilir.

Anahtar Kelimeler: Zerdali, *Prunus armeniaca*, sınıflandırma, temel bileşen analizi, kümeleme analizi

1. Introduction

Zerdali (*Prunus armeniaca* L., chulli, chulu, zardalu, hüdai) is a type of apricot. The word, zerdali, comes from Persian and means of this word is "yellow plum" (*zer: yellow, dalü: plum*) (Eyüboğlu, 1991).

While the initial ratio was 60% in terms of tree quantity and production of apricot and wild apricot population in Turkey which tended to increase until recent years, this ratio decreases to 8% at present.

The reason is that high quality apricot varieties have taken the place of wild apricots. This situation can be evaluated as a positive event in modern cultivation, but in the other hand, it should be noted that loosing genetic resources is in question, too (Asma, 2011). According to year of 2011 parameters, 335 tons production carried out from 14675 fruitful apricot trees and

209 tons production carried out from 12780 fruitful wild apricot trees in Gümüşhane province (Anonymous, 2013). Although Gümüşhane does not constitute an important place in apricot production of Turkey, it presents a crucial source for the breeding of wild apricot population.

Even there are many apricot and wild apricot breeding studies; we can say that there are a lot of works to do in terms of scanning all the regions.

In selection breeding studies, even method seems easy; application is very inconvenient and requires lots of attention. In that studies, a vast number of characters according to breeding objective can be worked on; in this situation, much time and workforce can be needed. Therefore, to know some relationships between characters will decrease workload by providing working on less character. For this purpose, some studies have been conducted on both apricot and some other fruit varieties (Bostan, 1994; Bostan, 1995; Bostan et al., 1995; Oğuz et al., 1997; Bostan, 2002a; Bostan, 2002b; Bostan, et al. 2007; İslam et al., 2005; Vela et al., 2002).

Besides this, multivariate statistical analysis which has an important place at statistic science is used especially when satisfactory results cannot be obtained from univariate statistical analysis (Küçükönder et al., 2004). For this purpose, there are studies, in which different methods and varieties are used (Barracosa et al., 2007; Horvath et al., 2011; Kara et al. 2005; Küçükönder et al., 2004; Sakar et al., 2011).

In this study, the relationships between fruit characters in previously selected genotypes from wild apricot population in Gümüşhane (Turkey) have been researched. According to these relationships, cluster analysis is made and groups have been created in terms of similar characters. Thus, it was aimed to describe the characters as in brief information and interpret them.

2. Materials and Methods

This research has been carried out on selected 37 genotypes, which are from seedling wild apricot population as a result of a selection breeding study (Bostan, 2007) in Gümüşhane (40˚26'18 92"N x 39˚ 30'30 80"E, 1153 m above sea level) province and its surroundings (Turkey). Annual average rainfall is 434 mm, temperature 10˚C, summer average temperature (June, July and August) is 19˚C, winter average temperature is 0.4˚C, summer average rainfall 16.3 mm, winter average rainfall is 33.5 mm and autumn rainfall is 38.2 mm in Gümüşhane. Gümüşhane has the maximum rain in spring season (Kalay and Altun, 2002). The locations of the genotypes are demonstrated in Figure 1.

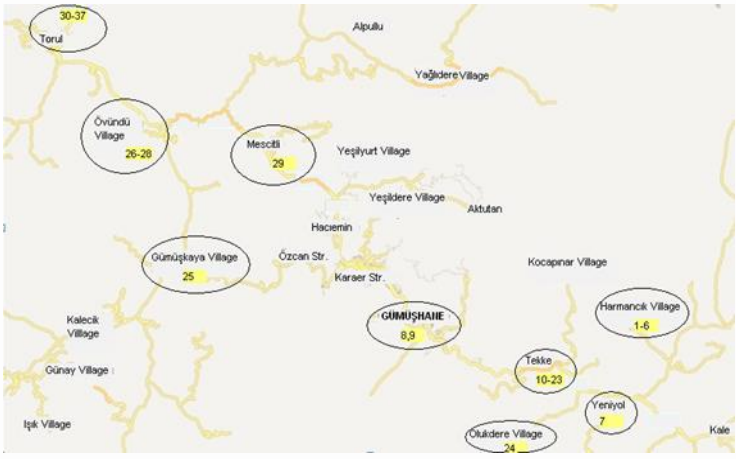

Figure 1. The locations of the genotypes in Gümüşhane province

Fruits were harvested at physiological maturity stage (ready-to-eat) on June.In the present study, The average values of fruit weight (FW, g), fruit width (FWI, mm), fruit length (FL, mm), fruit thickness (FT, mm), seed weight (SW, g), seed width (SWI, mm), seed length (SL, mm), seed thickness (ST, mm), kernel weight (KW, g), flesh/seed ratio (FSR), soluble solids content (SSC, %), titratable acidity (TA, %), pH and total dry matter (TDM, %) characteristics of two years (2003 and 2005) were used. SSC were used using a refractometer and expressed in ˚Brix at room temperature. Titratable acidity was determined in fruit juice by titrating method. TA was expressed as mill equivalents of malic acid per

100 g of fresh weight. Fruit weight, kernel weight and seed weight are mean weight of 10 fruits, kernels and seed in grams. Fruit thickness, fruit width, fruit length, seed length, seed width and seed thickness measured with caliper.

In order to find the main variation trends between fruit and seed characters in the zerdali genotypes and to evaluate their correlation, data were processed according to principal component analysis (PCA) using SPSS for Windows (Version 15.0, SPSS Inc., 2006). Since the aim of PCA is to reveal common principles in the data. We used form means in the multivariate analysis procedures. The PCA solution was accepted when eigenvalues where greater than one (Kaiser's criterion), and it was also compatible with the Cattell's scree rule. Component scores and factor loadings were calculated after variance maximizing axes rotation (Varimax rotation) and normalization. Only factor loadings equal or greater than 0,4 were considered as defining part of a principal component. Hierarchical cluster analysis (HCA) was utilized to investigate the similarities and dissimilarities among the forms with respect to seed and fruit characters. For classification, the Ward's Minimum Variance Method was utilized. The squared Euclidean distance was used as the dissimilarity measure for Ward's method by PCA, respectively. The clusters were formed based on Sneath's index: 2/3 Dmax, where Dmax is the maximum distance (Astel et al., 2007; Tanrıverdi et al., 2010). The grouping derived from HCA was used to interpret the results of the PCA score plots. Independent two sample t test and One-way ANOVA were conducted for all the HCAs. Differences between cultivar means were tested with Tukey post hoc tests.

3. Results and Discussion

As a result of the correlation analysis, some significant correlations were determined among fruit, seed and fruit juice characteristics in wild apricot genotypes (Table 1). The correlations between fruit weight and other characteristics, except for the total dry matter, were significant and positive. The highest correlations with fruit weight were found between fruit dimensions, and flesh / seed ratio. In the other studies carried out on various fruit species, fruit weight-fruit width, fruit length and seed weight correlations were found positive in medlar (Bostan, 2002a); fruit weight-fruit width, fruit length and pH correlations were found positive, and fruit weight-titratable acidity was negative in fig (Bostan, 2002b); fruit weight-fruit size, seed weight and seed size correlations were positive in loquat (Bostan et al., 2007); correlations between nut weight with nut width, nut length, nut thickness, kernel weight, kernel width and kernel length were positive in almond (Oğuz et al., 1997); correlations between nut weight with nut size and kernel weight (İslam et al., 2005), nut weight with nut dimensions and kernel dimensions in hazelnuts were positive (Bostan,

Table 1. Pearson Correlation coefficients between morphological fruit and seed parameters

	FW												
FWI	,739**	FWI											
FL	,691**	,627**	FL										
FT	,732**	,825**	,457**	FT									
SW	,411**	,279*	,213ns	,220ns	SW								
SWI	,426**	,295*	,365**	,187ns	,742**	SWI							
SL	,440**	,126	,674**	,001ns	,434**	,534**	SL						
ST	,120ns	,051ns	-,059ns	,109ns	,571**	,429**	,024ns	ST					
KW	,376**	,332**	,173ns	,298**	,685**	,550**	,179ns	,550**	KW				
FSR	,602**	,452**	,508**	,524**	-,450**	-,210ns	,101ns	-,368**	-,252*	FSR			
SSC	-,091ns	-,056ns	-,147ns	-,045ns	,117ns	-,029ns	-,155ns	,107ns	-,068ns	-,201ns	SSC		
TA	,024ns	,151ns	-,216ns	,134ns	,209ns	,062ns	-,337**	,321**	,288*	-,155ns	-,069ns	TA	
pH	,199ns	,140ns	,307**	,164ns	,023ns	,173ns	,278*	,041ns	-,029ns	,233*	,127ns	-,139ns	pH
TDM	-,243*	-,222ns	-,225ns	-,189ns	,029ns	-,103ns	-,202ns	,087ns	-,158ns	-,248*	,759**	-,201ns	-,063ns

FW: fruit weight, FWI: fruit width, FL: fruit length, FT: fruit thickness, SW: seed weight, SWI: seed width, SL: seed length, ST: seed thickness, KW: kernel weight, FSR: flesh/seed ratio, SSC: soluble solids content, TA: titratable acidity, TDM: total dry matter.
* significant at P<0.05, ** significant at P<0.01. ns: Non-significance.

1995; Bostan and İslam, 1999); fruit weight-seed dimensions correlations were positive in carob (Barracosa et al., 2007); pod weight-pod length, pod width and pod thickness were found positive in carob (Sidina et al., 2009); pods weight-pods width positive correlated in carob (Naghmouchi et al., 2009); positive correlations were determined between fruit weight with fruit length and fruit width in strawberry tree (Yarılgaç and Bostan, 2014). Our results are generally consistent with other results.

An acceptable solution for principal component analysis was reached when four dimensions of the model were found to be significant and explained 77.13% of the total variance of the original variables set (Table 2). The first component (PCA1), accounting for 31.44% of the total variance, is dominated by fruit characters, namely FT, FWI, FW, FSR and FL. In the second component (PCA2), accounting for 20.90% of the total variance, is dominated by seed characters, SW, KW, SWI, and ST. In the third component (PCA3), accounting for 13.04% of the total variance, is dominated by fruit juice characters, SL, acid and pH. In the fourth component (PCA4), accounting for 11.75% of the total variance, is dominated by characters, SSC and TDM (Figure 2). Multivariate cluster analysis was applied to classify the Zerdali (wild apricot) based on each significant factor obtained by PCA. Four dendrograms produced by multivariate cluster analysis for these factors are shown in Figures 3, 4, 5 and 6, respectively.

Table 2. Component loadings in Principal Component Analysis (PCA)

Variables	PCA1	PCA2	PCA3	PCA4
FT (mm)	0.918			
FWI (mm)	0.892			
FW (g)	0.828			
FSR (%)	0.715			
FL (mm)	0.597			
SW (g)		0.921		
KW (g)		0.806		
SWI (mm)		0.775		
ST (mm)		0.752		
SL (mm)			0.852	
TA (%)			-0.686	
PH			0.464	
SSC (%)				0.934
TDM (%)				0.907
Variance explained by components	4.40	2.93	1.83	1.64
Percent of total variance explained	31.44	20.90	13.04	11.75
KMO		0,63		
Test of Bartlett		***		

FT: fruit thickness, FWI: fruit width, FW: fruit weight, FSR: flesh/seed ratio, FL: fruit length, SW: seed weight, KW: kernel weight, SWI: seed width, ST: seed thickness, SL: seed length, SSC: soluble solids content, TDM: total dry matter. KMO: Kaiser-Meyer-Olkin Measure of Sampling Adequacy.
*** significant at P<0.001.

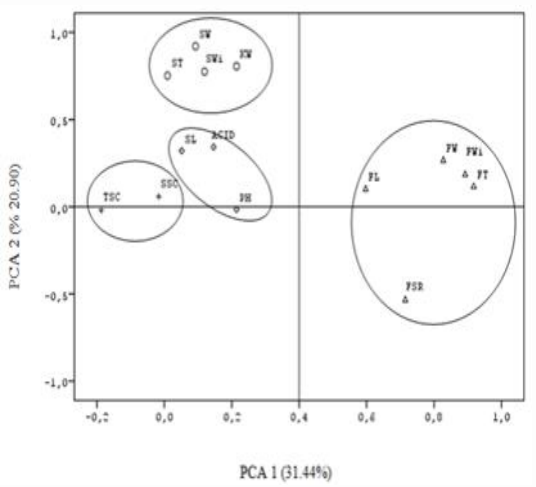

Figure 2. Patterns of four PCA components scores

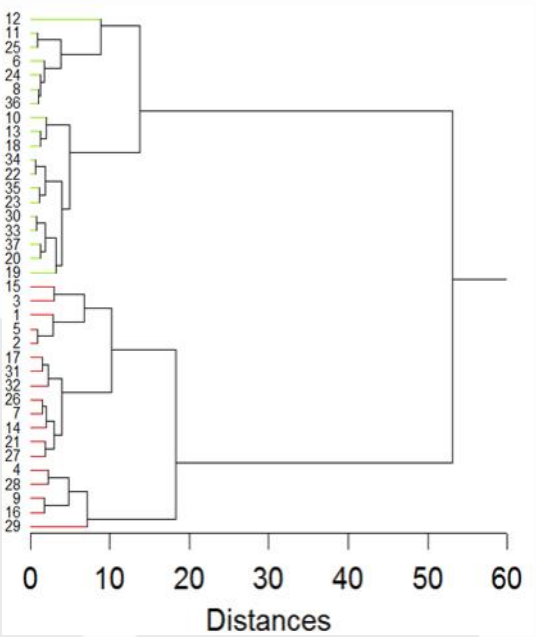

Figure 3. Dendrogram of cluster analysis for factor 1 (PCA 1) dataset (FT,FWI,FW,FSR, FL)

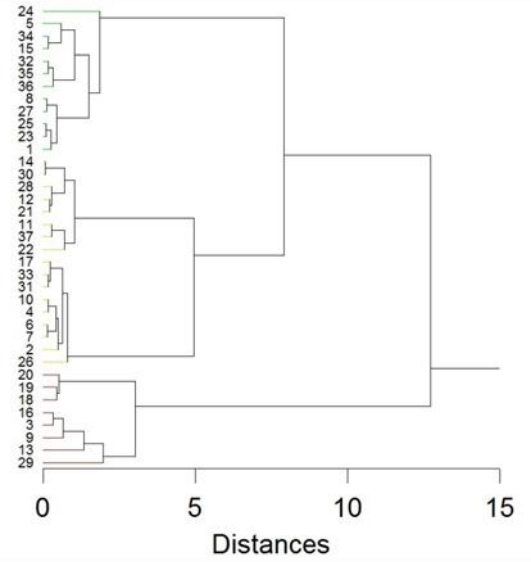

Figure 4. Dendrogram of cluster analysis for factor 2 (PCA 2) dataset (SW, SWI, ST, KW)

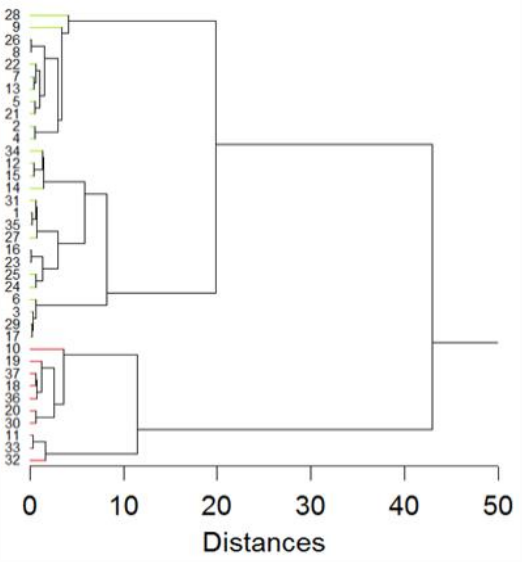

Figure 6.Dendrogram of cluster analysis for factor 4 (PCA 4) dataset (SSC)

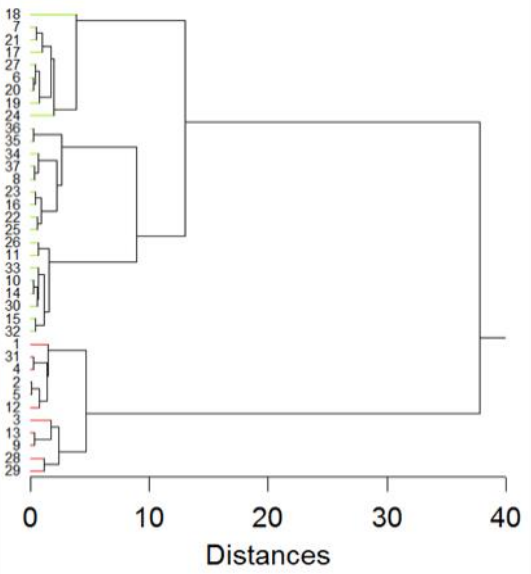

Figure 5.Dendrogram of cluster analysis for factor 3 (PCA 3) dataset (SL,TA, pH)

For factor 1, the 37 genotypes were divided into two groups by multivariate cluster analysis (Fig. 3). The average values of variables significantly related to factor 1 are presented for each group in Table 3.

Group 1 includes 19 varieties, Group 2 includes 18 varieties and Group 2 showed relatively higher FT, FWI, FW, FSR and FL than group 1.

Table 3. Average values of the indicators related to factor 1 (PCA 1) for the two groups computed by cluster analysis ($\bar{x} \pm s_{\bar{x}}$)

Characteristics	Group 1	Group 2	Significant
	19 varieties (n=19)	18 varieties (n=18)	
FW (g)	35.77 b ± 0.45 (SE)	42.45 a ± 0.73	***
FT (mm)	23.76 b ± 0.80	32.21 a ± 1.10	***
FWI (mm)	35.73 b ± 0.59	39.46 a ± 0.74	***
FL (mm)	8.76 b ± 0.35	12.07 a ± 0.49	***
FSR (%)	31.84 b ± 0.70	35.86 a ± 0.74	***

FW: fruit weight, FT: fruit thickness, FWI: fruit width, FL: fruit length, FSR: fruit/seed ratio. SE: Standard error
*** significant at P<0.001, according to Tukey HSD test.

Based on the second factor (PCA2) dataset (SW, SWI, ST and KW) all 37 genotypes were classified into three groups (Fig. 4). Group 1 includes 12 genotypes, Group 2 includes 17 genotypes and Group 3 includes 8 genotypes and Group 3 showed relatively higher SW, SWI, ST and KW than group 1 and 2 (Table 4).

Cluster analysis based on the third factor dataset (SL, Acid and pH) is presented in Fig. 5 Average values of related variables are listed in Table 5. Two groups were produced among the 37 genotypes. Group 1 includes 26 genotypes, and group 2 consists of eleven genotypes.

Table 4. Average values of the indicators related to factor 2 (PCA 2) for the three groups computed by cluster analysis ($\bar{x} \pm s_{\bar{x}}$)

Characteristics	Group 1	Group 2	Group 3	Significant
	12 varieties (n=12)	17 varieties (n=17)	8 varieties (n=8)	
SW (g)	3.21a ± 0.48 (SE)	2.50 b± 0.41	2.07 c ± 0.24	***
SWI (mm)	21.39 a ± 1.66	19.04 b ± 1.47	17.42 c± 1.47	***
ST (mm)	13.73 a ± 1.47	12.53 b ± 1.26	11.42 c ± 0.87	***
KW (g)	0.99 a ± 0.19	0.73 b ± 0.17	0.69 b ± 0.13	***

SW: seed weight, SWI: seed width, ST: seed thickness, KW: kernel weight, SE: Standard error
*** significant at P<0.001, according to Tukey HSD test.

Table 5. Average values of the indicators related to factor 3 (PCA 3) for the two groups computed by cluster analysis ($\bar{x} \pm s_{\bar{x}}$)

Characteristics	Group 1	Group 2	Significant
	26 varieties (n=26)	11 varieties (n=11)	
SL (mm)	23.58 b ± 0.30(SE)	29.85 a± 0.38	***
Acid	2.99 a ± 0.27	1.52 b ± 0.26	**
PH	4.88 b ± 0.13	5.42 a± 0.18	*

SL: seed length, SE: Standard error.
*** significant at P<0.001, **significant at P<0.01, *significant at P<0.05 according to Tukey HSD test.

Cluster analysis based on the third factor (PCA4) dataset (SSC and TDM) is presented in Fig. 6 Average values of related variables are listed in Table 6. Two groups were produced among the 37 genotypes. Group 1 includes 27 genotypes, and group 2 consists of ten genotypes. Group 2 SSC and TDM.

Table 6. Average values of the indicators related to factor 4 (PCA 4) for the two groups computed by cluster analysis ($\bar{x} \pm s_{\bar{x}}$)

	Group 1	Group 2	Significant
	27 varieties (n=27)	10 varieties (n=10)	
SSC (%)	15.52 b ± 0.32(SE)	20.93 a ± 0.69	***
TDM (%)	13.89 b ± 0.26	18.43 a ± 0.38	***

SSC: soluble solids content, TDM: total dry matter, SE: Standard error.
*** significant at P<0.001 according to Tukey HSD test.

Wild apricot genotypes have different characteristics because of the set in seedling and genetic absolute evolutions. Thereby, it is an expected result that different groups occur in terms of inspected characters and they show different values. In addition to this, it could be said that there can be some differences between groups because of different ecology and maintenance requirements where genotypes are and different age of trees.

With this study, it could be said that the knowledge that fruit weight and fruit size, seed weight and seed size, fruit acidity and pH, soluble solids content and total dry matter values can create a group, can be used; and therefore it will decrease workload and waste of time in selective breeding studies to be done on wild apricot.

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