CHARACTERIZATION OF TURKISH SESAME (*Sesamum indicum* L.) LANDRACES USING AGRONOMIC AND MORPHOLOGIC DESCRIPTORS

A.Gulhan ERCAN[1] K. Melih TAŞKIN[1] Kenan TURGUT[2] Mehmet BILGEN[2]
M. Ziya FIRAT[3]

[1]Akdeniz University, Graduate School of Natural and Applied Sciences, Department of Field Crops, Antalya-Turkey
[2]Akdeniz University, Agriculture Faculty, Department of Field Crops, Antalya-Turkey
[3]Akdeniz University, Agriculture Faculty, Department of Animal Science Biometry and Genetics Unit, Antalya-Turkey

Abstract

In this study, genetic diversity for agro-morphological traits in 52 landraces of sesame (*Sesamum indicum* L.) originated from Turkey was estimated through multivariate analysis. Populations evaluated for time to flowering, branching, capsule number per axil, carpel number per capsule, seed coat colour, capsule pubescence, capsule order, plant height to first capsule, plant height, number of seeds per capsule, number of capsules on main stem, total number of capsules per plant and 100 seed weight. This data set was reduced to 6 significant principle components (PCs) that cumulatively explained 79% of the variance. The 6 retained PC scores were used as input for hierarchical cluster analysis (Ward's minumum variance). The populations were clustered in 4 different major groups according to their similarity levels. In cluster analysis most of the populations of the South, Southeast and West regions tended to cluster as outliers outside their region of adaptation. However, the distribution of Nortwest region populations was according to their geographic origin. This study can help breeders better understand the genetic structure of Turkish sesame populations which can be used for parental selection.

Keywords: *Sesamum indicum*, multivariate analysis, agro-morphological markers, genetic diversity

Türk Susam (*Sesamum indicum* L.) Yerel Çeşitlerinin Agronomik ve Morfolojik Tanımlayıcılar Kullanılarak Karakterize Edilmeleri

Özet

Bu çalışmada, 52 adet Türk orijinli yerel susam (*Sesamum indicum* L.) çeşitlerinin genetik farklılığı, agro-morfolojik özelliklere dayanarak çok değişkenli analiz ile tahmin edilmiştir. Populasyonlar çiçeklenme zamanı, dallanma, yaprak koltuğundaki kapsül sayısı, kapsüldeki karpel sayısı, tohum kabuğu rengi, kapsül tüylülüğü, kapsül dizilişi, ilk kapsül yüksekliği, bitki boyu, kapsüldeki tohum sayısı, ana saptaki tohum sayısı, tüm bitkideki kapsül sayısı ve 100 tane ağırlığı kullanılarak değerlendirilmiştir. Bu veri seti toplam varyansın % 79 'unun açıklandığı 6 temel bileşen (PC) skoruna dönüştürülmüştür. Kalan 6 PC skoru, hierarşikıl kümeleme analizinde (Ward'sın minimum varyans metodu) veri olarak kullanılmıştır. Populasyonlar benzerlik düzeylerine göre 4 ana grupta kümelenmiştir. Kümeleme analizinde, Güney, Güneydoğu ve Batı bölgelerine ait populasyonların pekçoğu adapte oldukları bölgelerin dışında kümelenme göstermişlerdir. Bununla birlikte Kuzeybatı (Trakya) bölgesi populasyonları coğrafik orjinlerine göre bir dağılım göstermişlerdir. Bu çalışma Türk susam populasyonlarının genetik yapısı hakkında ıslahcıya bilgi vererek bitki islahında ebeveny seçiminde kullanabilmesi için yardımcı olabilir.

Anahtar kelimeler: *Sesamum indicum*, Çok Değişkenli Analiz, Agro-morfolojik Markır, Genetik Farklılık.

1. Introduction

Sesame is the most important annual oil crop in Turkey. Sesame seeds are used in the making of tahin (sesame butter) and halva, and for the preparation of rolls, crackers, cakes and pastry products in commercial bakeries. There are numerous varieties and ecotypes of sesame adapted to various ecological conditions. However, the cultivation of modern varieties is limited due to insufficient genetic information. Many farmers continue to grow local sesame populations with low yields. In 1998, only 2.552 million tons were cultivated on 7.2 million hectares (Escribano et al. 1998). Knowledge of genetic distance among landraces will help the breeding of high yielding, good quality cultivars that will increase production (FAO, 1998).

The multivariate analysis of quantitative and qualitative characters has been used to measure genetic distance within populations of Oat (*Avena sativa* L.)

(Souza and Sorrels, 1991), bean (*Phaseolus vulgaris* L.) (Singh et al. 1991), cotton (*Gossypium hirsutum* L.) (Brown, 1997), *Triticales* (Royo et al. 1995), soybean (*Glycine max* L.) (Perry and McIntosh, 1991) and biserrula (*Biserrula pelecinus* L.) (Loi et al. 1986). Two studies that used morphological characters to group genotypes into clusters (Ganesh and Thangavelu, 1995; Patil and Sheriff, 1994) found a wide genetic diversity in Indian sesame genotypes. Multivariate analysis based on morphological characters provides genetic information that will allow the breeder to improve populations by selecting from specific geographic regions (Souza and Sorrels, 1991).

In our study, both quantitative and qualitative morphological and agronomical traits were evaluated by multivariate analysis to determine genetic distance among 52 landraces of cultivated Turkish sesame which were consequently grouped into four major clusters. Multivariate analysis based on morphological characters provides genetic information that will allow the breeder to improve populations by selecting from specific geographic regions (Souza and Sorrels, 1991).

2. Material and Methods

The 52 sesame landraces were collected from culture areas of the Northwest, West (Aegean), South and Southeast regions of Turkey as illustrated in Figure 1. Each landrace was represented by 10 randomly chosen lines. These sesame landraces have been still grown by local farmers in Turkey.

The 52 landraces were planted in two row plots, 4 m long with 50 cm between rows, in Antalya, in summer of 1998. The cultivated area is situated at 30^0 44' east, 36^0 52' north and 51 m above the sea level. The average temperature in Antalya is 27^0 and the annual rainfall is 40 mm. Data were collected from ten randomly selected plants from each population.

The seven qualitative traits used were time to flowering (TF), branching (B), capsule number per axil (CAN), carpel number per capsule (CNC), seed coat colour (SCC), capsule pubescence (CP) and capsule order (CO). The 6 quantitative traits were plant height to first capsule (HFC), Plant height (PH), number of seeds per capsule (NSC), number of capsules on main stem (NCMS), total number of capsules per plant (TNCP) and 100 seed weight (100SW) (Demir, 1962). Data was measured when the 90 % capsule produce completed, except 100 SW, Time To Flowering, Seed Coat Colour (SCC).They were measured at the post-harvest. Details and units of each trait measurement are given in Table 1.

First, the univariate normality was checked for the 13 traits of each landrace using rankit plots. Intercorrelations among all quantitative and qualitative traits were evaluated by correlation analysis. The resulting 13x13 correlation matrix was used as input for the PCA to remove the effects of scale (Johnson and Wichern, 1998). The 13 variables were reduced to 6 independent linear combinations with a cumulative variance of about 79 %. Then, intra-population variability was evaluated by hierarchical cluster analysis. The 6 retained principle component scores were used as the input for cluster analysis using Ward's method, which minimizes within-cluster variance summed over all variables (hair et al. 1987). JMP 4.02 statistical package was used for the analysis of correlations, PC and cluster analysis (SAS, 2000).

3. Results and Discussion

3.1.Analysis of Traits Means

Correlation analysis showed that many pairs of characters were correlated in these populations. Of the agronomical and morphological variables, plant height was positively correlated with height to first capsule ($r= 0.776^{**}$), number of capsules on main stem ($r= 0.780^{**}$) and time to flowering ($r= 0.579^{**}$). Height to first capsule was positively and significantly correlated with number of capsule on main stem ($r= 0.991^{**}$) and time to flowering ($r= 0.591^{**}$). Total number of capsules per plant was positively correlated with the number of

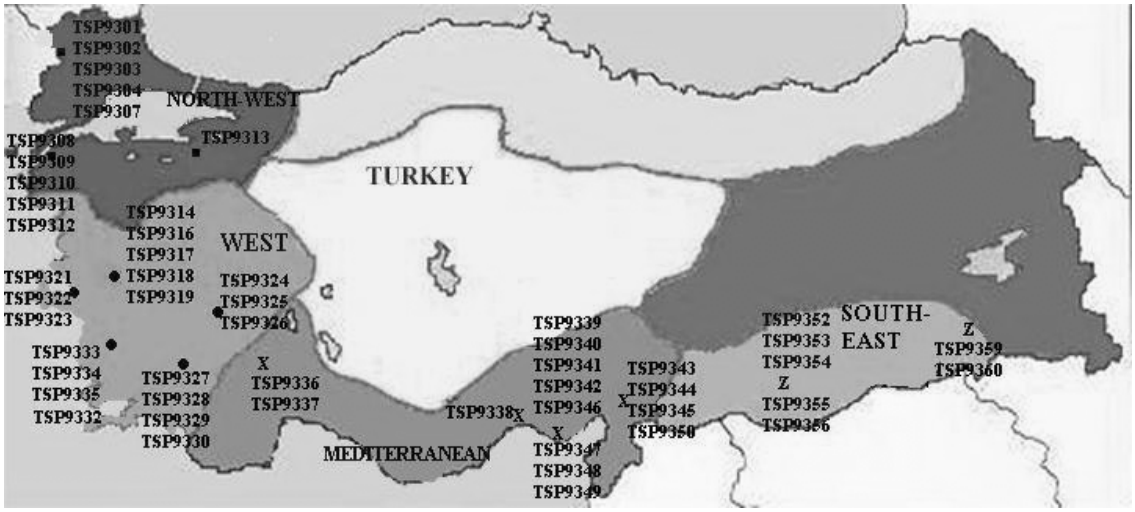

Figure 1. Map Showing the Sampling Sites for the 52 Sesame Landraces. Landraces in the four main geographic regions are indicated with different symbols (■: Northwest, ●: West, X: South, Z: Southeast).

Table 1. Details of how each traits was measured and the units of each measurement are given (* Post-harvest).

Traits	How Measured	Character Unit
Plant Height (PH)	Length of the main stem	cm
Plant Height to First Capsule (HFC)	Length of the main stem from soil to firsth capsule	cm
Number of Seeds per Capsule (NSC)	Total number of seeds were counted in the capsule	number
Number of Capsules on Main Stem (NCMS)	Total capsule number on main stem	number
Total Number of Capsules per Plant (TNCP)	Total capsule number both main stem and branches	number
100 Seed Weight (100SW) *	weigth of 100 seeds	g/100 seeds
Time to Flowering (TF) *	Number of days 50% plants had at least one flower	30-40 days early, 41-50 days mid-early, 51th and after days mid-late
Branching (B)	Number of branch	>3:(branched) <3:(unbranched)
Capsule Number per Axil (CAN)	Monocapsulle Tricapsulle	Numeric
Carpel Number per Capsule (CNC)	Bicarpellatum Quadricarpellatum	Numeric

seeds per capsule (r= 0.681 **), negatively correlated with time to flowering (r= -0.316 *) (Table 2). Correlation between characters was supported by PC analysis (Souza and Sorrels, 1991). In the first PC axes, number of capsules on main stem (0.478) and plant height to first capsule (0.478) had the largest coefficient, plant height (0.449) had the second largest coefficient, followed by the time to flowering (0.401) and 100 seed weight (0.195). Number of seeds per capsule (0.488), total number of capsules per plant (0.469), capsule pubescence (0.401), capsule number per axil (0.309) and capsule order (-0.240) had the largest coefficients in the second PC axes. The first 6 PC axes accounted for 78.93 % of total variation among populations (Table 3). Jolliffe (1986) suggested that when the correlation matrix is used as input data, cumulative variance must be at least 0.75 %. In PC analysis, traits such as number of capsules on main stem, height to first capsule and plant height were the most effective for distinguishing among landraces. These results support the findings of correlation analysis. Studies in North American oat (Souza and Sorrels, 1991) and Mediterranean populations of *Biserrula*

pelecinus (Loi et al. 1986) have supported the high degree of correlation between characters by the PC analysis.

Using the Principal Component analysis also to estimate inter-landrace variation, we found that the landraces of the west (Aegean) region were closely associated with the landraces of the Northwest, South and Southeast regions. The Aegean and Southeast regions showed comparatively more variability than the South region. The landraces of the Northwest showed the least variability as indicated by their tight accumulation in the tree-dimensional plot of the components (Figure 2).

3.2. Cluster Analysis of landraces based on similarity characters

In hierarchical cluster analysis, landraces were grouped based on Ward's minimum variance method using quantitative and qualitative traits. Using only quantitative traits produced the same results (data not shown). Harch et al. (1997) and Escribano et al. (1998) used quantitative and qualitative traits to determine genetic diversity among the world groundnut collection and common bean, respectively. The 52 populations were clustered into four groups based on similarity of coefficients in the first six PC axes. The number of genotypes included in clusters I, II, III and IV were 2, 4, 1 and 45 respectively (Figure 3). Group IV was divided into 6 subgroups by classification. The genetic distance among all populations was narrow ranging between 0.18 % and 6.38 %. Diaz et al. (1999) evaluated sesame accessions collected from Undra, Korea, Western Asia, Africa, China-Japan and Central Asia, using isozyme systems. The results showed that the total diversity was lower for sesame that than the mean of other cultivated self-pollinated species (0.1194-0.1890).

The general description of each of the clusters in this classification is as follows: Group I includes two landraces from the Aegean region. This group includes non-branching landraces, with white and light yellow seed coat colour. Both landraces are tricapsule and bicarpellatum, therefore have high 100 seed weight. Group II contains two landraces each from Aegean and Southeast regions. These bicarpellatum, monocapsule and branching landraces have dark-yellow and brown seed coat colour, and a high 100 seed weight. Group III has just one bicapsulle, quadricarpellatum landrace with a high 100 seed weight from the Aegean region. Group IV is divided into subgroups based on genetic distance. Subgroup 1 includes six landraces from the South region with dark-yellow and dark-brown seed coat and one landrace from the Southeast regions with dark-brown and black seed coat. Landraces in this subgroup have the lowest

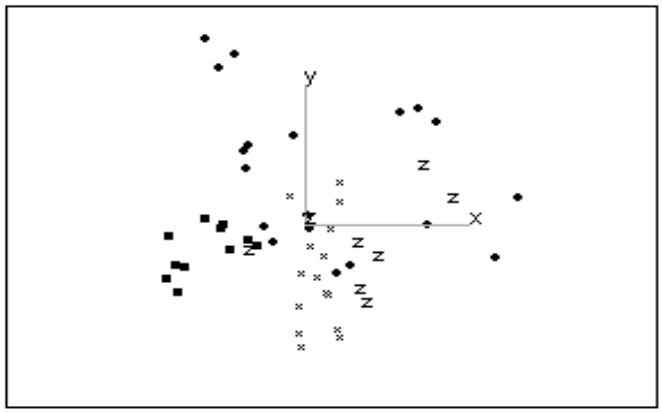

Figure 2. Results of the PC Analysis, showing a plot of the first three components.
(■ Northwest, ●: West, X: South, Z: Southeast)

Table 2. Correlation matrix obtained from agronomical and morphological traits (character abbreviations as defined in material and methods).

	PH	HFC	NCMS	TNCP	NSC	100SW	CAN	CNC	B	SCC	TF	CO	CP
HFC	0.776**	1.000											
NCMS	0.781**	0.992**	1.000										
TNCP	-0.102	-0.055	-0.037	1.000									
NSC	-0.147	-0.108	-0.111	0.682**	1.000								
100SW	0.249	0.229	0.233	-0.092	-0.066	1.000							
CAN	-0.035	-0.067	-0.053	0.397**	0.224	0.036	1.000						
CNC	-0.033	-0.068	-0.060	0.213	0.240	-0.017	-0.028	1.000					
B	0.229	0.226	0.216	-0.011	0.137	0.160	-0.058	-0.040	1.000				
SCC	0.202	0.140	0.186	-0.109	-0.241	0.042	-0.105	-0.165	0.161	1.000			
TF	0.580**	0.591**	0.588**	-0.316*	-0.392**	0.190	-0.189	-0.132	-0.019	0.162	1.000		
CO	-0.064	-0.008	-0.005	-0.185	-0.059	-0.068	-0.141	-0.225	-0.075	0.029	-0.002	1.000	
CP	0.159	0.277*	0.255	0.097	0.287*	0.355**	0.165	0.115	0.238	-0.103	-0.048	-0.156	1.000

P<0.05 (**), P>0.01 (*)

Table 3. PC Analysis of sesame landrace Traits. First six PC axes and eigenvectors of characters were showed. (character abbreviations as defined in material and methods).

	PC1	PC2	PC3	PC4	PC5	PC6
Eigenvalue	3.582	2.310	1.191	1.136	1.041	1.002
Cumulative proportion of variation	27.559	17.743	9.169	8.740	8.011	7.711
Total Variation	27.559	45.302	54.471	63.211	71.222	78.933
Characters		Eigenvectors				
PH	0.450	0.115	0.157	0.007	0.048	0.028
HFC	0.478	0.161	0.182	0.042	0.001	0.129
NCMS	0.478	0.159	0.196	0.060	0.011	0.097
TNCP	0.166	0.470	0.338	0.228	0.073	0.080
NSC	0.187	0.488	0.087	0.193	0.139	0.278
1000SW	0.196	0.144	0.521	0.174	0.358	0.074
CAN	0.098	0.309	0.154	0.242	0.505	0.427
CNC	0.089	0.245	0.120	0.585	0.390	0.106
B	0.146	0.188	0.485	0.298	0.449	0.038
SCC	0.163	0.155	0.110	0.396	0.390	0.475
TF	0.401	0.149	0.214	0.171	0.097	0.050
CO	0.001	0.241	0.025	0.436	0.186	0.663
CP	0.115	0.401	0.422	0.100	0.200	0.143

100 seed weight among all groups and subgroups. Subgroup 2 consists of four landraces from the same city in the West (Aegean) region characterized by tall plants with dark yellow seed coat. Subgroup 3 has three non-branching landraces from the Southeast with dark-yellow and dark-brown seed coat colour and high 100 seed weight. Subgroup 4 includes five landraces from the West and South regions that have high 100 seed weight and number of seeds per capsule. Subgroup 5 also contains landraces from the West and South regions except that they are non-branching and their height to first capsule is high. Subgroup 6 includes all Northwest landraces, one from the Southeast and two landraces from the West regions. Plant height and height to first capsule in this group are the lowest among all groups. Their flowering time is early, capsule number and seed number in capsule are high.

In both PC analyses (Figure 2) and hierarchical clustering analyses (Figure 3), most of the landraces of the South, Southeast and West regions did not follow a pattern of aggregation based on their geographical origin. This finding is in agreement with the earlier reports of Ganesh and Thangavelu (1995); Patil and Sheriff (1994) who found the distribution of Indian sesame landraces was not according to their geographic origin. In our study, landraces from the Southeast, for example, were clustered with landraces from the distant regions of the West (Aegean) and the Northwest as well as the neighboring South (Mediterranean) region. As seen in Figure 1, Aegean and Mediterranean regions lie between the Northwest and Southeast regions. Landraces from the Southeast may have been introgressed into the Northwest region through the South and West regions. Narrow genetic distance among all landraces may have played another role in the lack of aggregation based on geographic origin (Royo et al. 1995).

In addition, morpho-agronomic traits have shortcomings in evaluating genetic diversity. First, they are phenotypic markers and genetically distant landraces may be morphologically similar. Second, the genetic control of many morpho-agronomic traits is complex due to the number of genes and environmental influence, thus preventing the precise determination of the

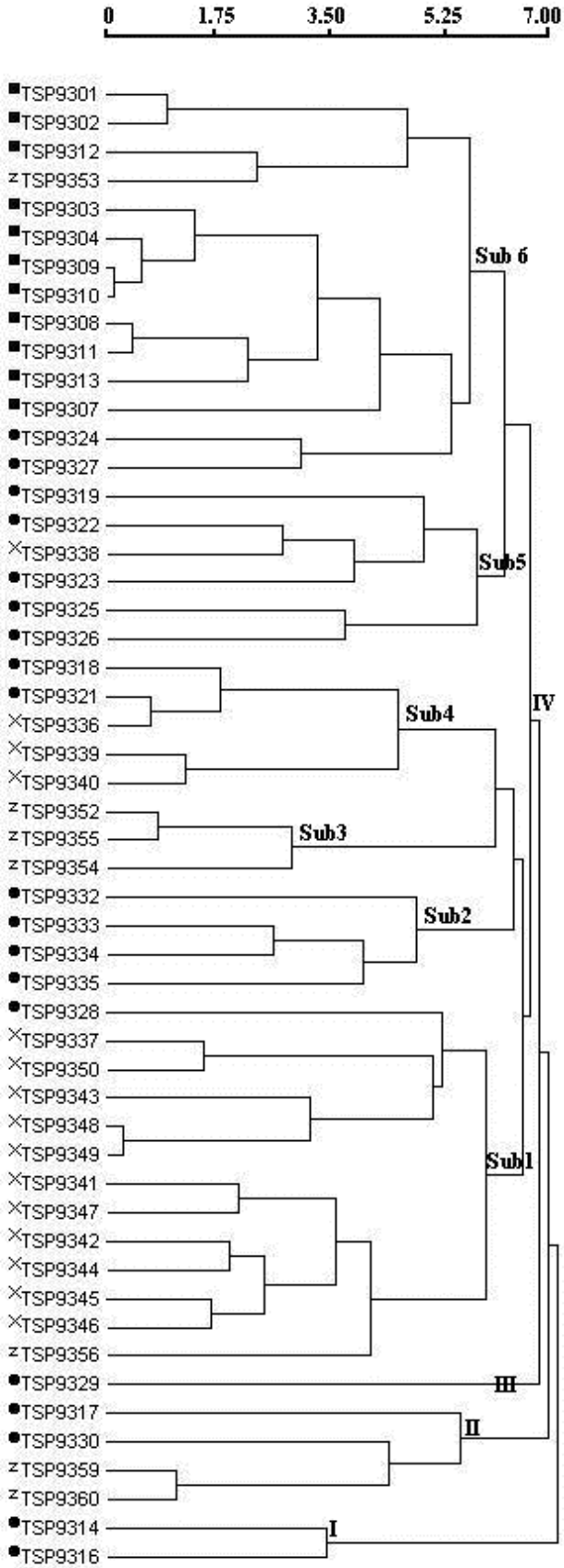

Figure 3. Cluster Analysis of 52 sesame landraces based on quantitative and qualitative characters. (■: Northwest, ●: West, X: South, Z: Southeast)

underlying genotype (Singh et al. 1991). Further research should be done with molecular markers which can be used determine genetic distance easily and successfully. DNA markers should provide more accurate measures of genetic similarity (van Beuningen and Busch, 1997).

This study provides a morpho-agronomic based classification of genetic diversity that can help breeders understand the genetic structure of Turkish sesame landraces. Genetic distance information can be used for parental selection as greater differences between the parents will better allow different favourable alleles to be combined in the hybrid.

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