Legume Research, 42(2) 2019: 162-167
Print ISSN:0250-5371 / Online ISSN:0976-0571

AGRICULTURAL RESEARCH COMMUNICATION CENTRE
www.arccjournals.com

Determination of morphological variability of different *pisum* genotypes using principal component analysis

Fatih Hanci[1]* and Esra Cebeci[2]

Erciyes University,
Faculty of Agriculture, Kayseri, Turkey.
Received: 29-06-2018 Accepted: 06-09-2018 DOI: 10.18805/LR-438

ABSTRACT

The aim of the study was to evaluate the variation among some *Pisum* genotypes using principal component analysis technique. The plant material covering wild pea accessions (*Pisum fulvum* L., *P. abyssinicum* L., *P. sativum* var. *elatius*), local varieties (*P. sativum* var. *sativum* L. and *P. sativum* var. *arvense* L.) and two commercial varieties were evaluated for 50 morphological traits. According to results, the first eleven principal component with Eigenvalues >1 contributed % 96.95 of the variability. The percentages of cumulative variation accounted for by each of the four principal component are 33.14%, 48.72%, 58.65%, and 66.88% respectively. Based on the principal coordinate analysis, five major groups were formed. In general, the diagram represented an obvious division between taxonomic groups except for *P. sativum* var. *sativum* and *P. sativum* var. *arvense* accessions.

Key words: Characterization, Eigenvalue, Pea, Pisum.

INTRODUCTION

Pea (*Pisum sativum* L.) has the great economic importance and belongs to *Pisum* that is the significant genus in the *Fabaceae* family. The classification of *Pisum* based on karyological and morphological characters has altered in due course. Despite the broad phenotypic and genetic diversity, actual taxonomic classifications are confusing (Korstein and Bogdanova, 2008). According to Govorov (1937), the genus *Pisum* comprises of five species: *P. abyssinicum* ((A. Braun) Govorov), *P. sativum* L., *P. fulvum* (Sibth. *et* Smith.), *P. humile* (Boiss. *et* Noë), and *P. elatius* ((M. Bieb.) Asch. *et* Graebn). Only two species (*P. sativum* and *P. fulvum*) have been recognized by Kupicha (1981) and Davis (1970). These authors did not regard the third supposed species *P. abyssinicum*. In addition to these taxonomic classifications, Vershinin *et al*. (2003) expressed robust relations among *P. sativum, P. humile* and *P. elatius* species and grouped the genus into three main classes: *P. fulvum, P. abyssinicum*, and a complex which consists of *P. humile, P. elatius, P. sativum*.

Maxted and Ambrose (2001) described a phylogenetic organization of taxa in which three species were identified (*P. fulvum, P. sativum, and P. abyssinicum*) and with two subspecies ssp. *Sativum* and ssp *elatius* (Bieb.). According to the actual Integrated Taxonomic Information System database, the *Pisum* genus consists of only two species: *P. fulvum* and *P. sativum* L. According to same data, the *P. sativum* L. species has five varieties: *P. sativum* var. *arvense* (L.) Poir. (field pea, Austrian winter pea), *P. sativum* var. *elatius* (Steven ex M. Bieb.) Alef., *P. sativum* var. *macrocarpon* Ser., *P. sativum* var. *pumilio* Meikle, *P. sativum* var. *sativum* L. (garden pea) (ITIS, 2017).

The determination of genetic variability is a significant part of a successful plant breeding program. The significance of characterization in breeding studies has been emphasized in autogam and allogam plants (Griffing and Lindsstromm, 1954). Conservation of genetic resources intends two main matters: (1) Prevention loss of genetic variability and (2) Prevention costs (Jones, 1984).

There are several techniques to determine genetic diversity in a germplasm. One of them is the principal components analysis (PCA). This is a multivariate statistical technique and, has the capability to convert a lot of likely correlated factors into a fewer factors named principal components (Ziegel, 2002). Each principal component is a linear transformation of the original factor and could be respective of a specific sense (Jobson, 1991). Principal component analysis (PCA) is one of the beneficial statistical techniques that has been used in various areas of science. The PCA is a prevalent method for detecting models in data of large dimensions and in specifying key components of diversity in a data set (Yared, 2011). Each principal component (PC) shows varied properties of the original data and may be commented independently because it is orthogonal and free of each other. Therefore, the cumulative

*Corresponding author's e-mail: *Corresponding Email: tanerfatih@gmail.com
[1]Erciyes University, Faculty of Agriculture, 38280, Melikgazi, Kayseri, Turkey.
[2]Department of Vegetable Breeding, Batı Akdeniz Agricultural Research Institute, Antalya, Turkey.

variation in the original data set may be grouped intosubcomponents (Mohammadi, 2003). The goal of the present study was to detect the effects of some morphological features on genetic variability in diverse *Pisum* genotypes using principal components analysis method in Pea breeding program. It is assumed that the results of the study will provide some helpful knowledge for the preservation and the use of these *Pisum* genotypes in the breeding project.

MATERIALS AND METHODS

The experiments were carried out at the Atatürk Central Horticultural Research Institute, Yalova. Six genotypes were kindly obtained from Western Regional Plant Introduction Station, USDA, Pullman, (USA); two from John Innes Centre (JIC, UK), five from Gene Bank of the Aegean Agricultural Research Institute (AARI, TR) (Table 1).

On 10th November 2015; and 12th November 2016, fifteen *Pisum* accessions were planted. The experimental scheme was randomized block design with three replications. Twenty individual plants randomly selected in each plot to obtain data on different morphological features according to the International Union for the Protection of New Varieties of Plants (UPOV) (Table 2).

Table 1: List of accessions and their origins.

Accession name	Geographical Origin	Taxonomic Name	Resource
65PA099	Ethiophia	*P. abyssinicum*	ARS-USDA, USA
66PA099	Yemen	*P. abyssinicum*	ARS-USDA, USA
67PF099	Antalya, Turkey	*P. fulvum*	ARS-USDA, USA
68PF099	South Anatolia, Turkey	*P. fulvum*	ARS-USDA, USA
69PSE099	Denizli, Turkey	*P. sativum* var *elatius*	ARS-USDA, USA
70PSE099	Mardin, Turkey	*P. sativum* var. *elatius*	ARS-USDA, USA
BOOGIE	Com. Variety	*P. sativum* var. *sativum*	Commercial Cultivar
75PSE098	Mersin, Turkey	*P. sativum* var. *elatius*	JIC, UK
105PSC098	Aydın, Turkey	*P. sativum* var. *arvense*	JIC, UK
115PSA097	Mardin, Turkey	*P. sativum* var. *arvense*	AARI, TR
116PSA097	Kastamonu, Turkey	*P. sativum* var *arvense*	AARI, TR
117PS097	Çorum, Turkey	*P. sativum* var. *sativum*	AARI, TR
122PSA097	Bayburt, Turkey	*P. sativum* var. *arvense*	AARI, TR
141PS097	Çanakkale, Turkey	*P. sativum* var. *sativum*	AARI, TR
RONDO	Com. Variety	*P. sativum* var. *sativum*	Commercial Cultivar

Table 2: Morphological traits regarding leaf-stem, flower, pod-seed characters.

Leaf-Stem (LS)	Flower (F)	Seed-Pod (SP)
Length of leaflet (LS1)	Time of flowering (F1)	Shape of seed (SP1)
Width of leaflet (LS2)	Maximum number of flowers	Color of cotyledon of seed (SP2)
Size of leaflet (LS3)	per node (F2)	Marbling of testa (SP3)
Length of stipule (LS4)	Color of wing (F3)	Violet or pink spots on testa
Width of stipule (LS5)	Intensity of color of wings (F4)	(SP4)
Color of leaflet (LS6)	Intensity of color of standard	Hilum color on seed (SP5)
Intensity of color of leaflet (LS7)	(F5)	Color of testa (SP6)
Leaflets (absent or present) (LS8)	Color of standard (F6)	Wrinkling of seed cotyledon
Waxiness of upper leaflet (LS9)	Width of standard (F7)	(SP7)
Dentations of leaflet (LS10)	Shape of base of standard (F8)	Type of starch grains (SP8)
Degree of dentations of leaflet (LS11)	Undulation of standard (F9)	Width of seed (SP9)
Size of stipule (LS12)	Width of upper sepal (F10)	Curvature on pod (SP10)
Shape of stipule (LS13)	Shape of apex of upper sepal	Type of curvature of pod (SP11)
Flecking of stipule (LS14)	(F11)	Shape of distal part of
Density of flecking of stipule (LS15)	Length of peduncle	pod (SP12)
Anthocyanin coloration of stem (LS16)	(from to first flower) (F12)	Color of pod (SP13)
Length of plant (LS17)		Intensity of green color of pod
Fasciation of stem (LS18)		(SP14)
Intensity of color of foliage (LS19)		Anthocyanin coloration
Stem length (LS20)		of parchment (SP15)
Number of nodes up to first fertile		Anthocyanin coloration of
node (LS21)		pod (SP16)
Length from axil to first leaflet or		
tendr (LS22)		

Table 3: Eigen values and percentage of variation for each principal components.

Principal Component	Eigenvalue	Variance(%)	Cumulative Variance (%)
1	16.57	33.14	33.14
2	7.79	15.58	48.72
3	4.97	9.93	58.65
4	4.12	8.23	66.88
5	3.52	7.04	73.93
6	3.01	6.02	79.95
7	2.44	4.88	84.82
8	2.15	4.30	89.13
9	1.58	3.16	92.28
10	1.21	2.42	94.71
11	1.12	2.24	96.95

To identify the weight of each character principal component analysis (PCA) was applied. The data set was transformed to standardize units before analysis. The number of principal components was determined using the minimum Eigen value. All the statistical procedures for morphological traits were obtained using the SAS Institute Inc. JMP® and IBM SPSS® Statistics Ver. 221.

RESULTS AND DISCUSSION

Out of the total fifteen PCs, eleven principal components (PC1 to PC11) with Eigenvalues >1 accounted with individual variance values and contributed 96.95 % of the total variation of *Pisum* genotypes (Table 3). The proportion of total variation explained by these principal components more than 2/3 is used for next step (Hanci and Gökçe, 2016). The percentages of cumulative variation accounted for by each of the four PCs are 33.14%, 48.72%, 58.65%, and 66.88% respectively.

The first principal component shows for highest variability in the data with respect to succeeding components (Leilah and Al-Khateeb, 2005). The value of any character in the first principal component has never been above |0,3|. This component (PC_1) has high value (|0.22|) for width of leaflet (LS_2), size of leaflet (LS_3), width of seed (SP_9), Width of stipule (LS_5), maximum number of flowers per node (F_2), and width of upper sepal (F_{10}).

Only one character has reached the value |0,3| in the second principal component (wrinkling of seed cotyledon, SP_7). The second principal component had high value for color of leaflet LS_{16}: |0.28|, intensity of color of foliage LS_{19}: |0.26|, intensity of color of wings F_4: |0.26| (Table 4).

These results are similar to the study of Ouafi *et al.* (2016). They reported the presence of a great genetic variability for the same characters. Also, our results represent that specification of genetic diversity of *Pisum* genotypes based on taxonomic groups can possibly be acquired by choosing these characters. Esposito *et al.* (2007) studied PCA on pea accessions and noted that on these genotypes the first and second components explained 67.7% of the variability in the first season of experiment and 69.8% in the second

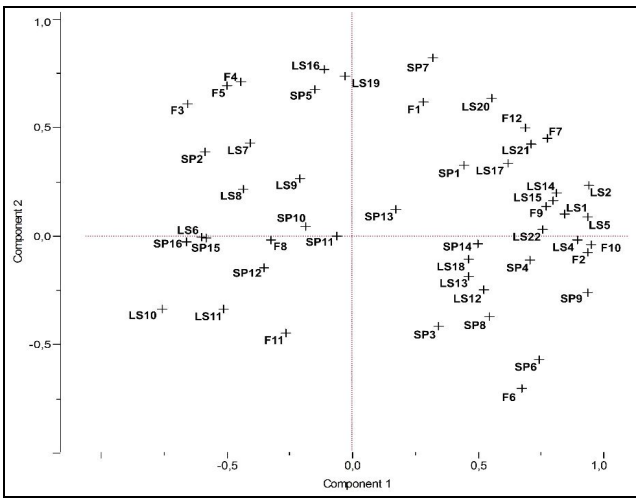


Fig 1: Distribution of observed characters based on the first and component. Abbreviations: As in table 2.

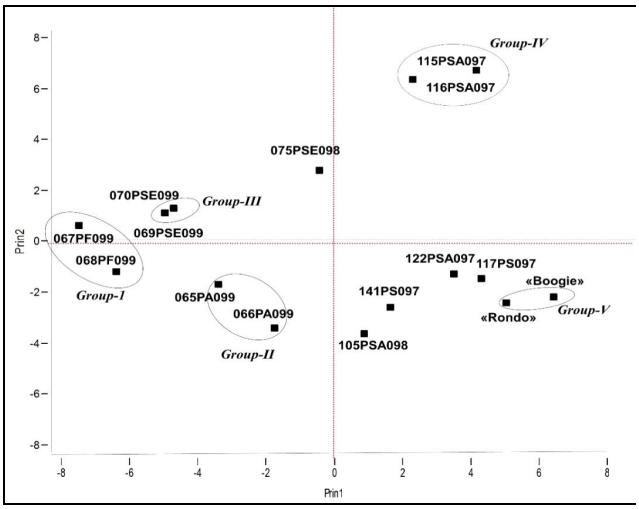


Fig 2: Distribution of P*isum* genotypes based on the first and second component.

one. The results showed that length and width of stipule, width of the leaflet, length, length and width of the pod, number of days to flowering clarified most of the variaiton. In another study, Gixhari *et al*. (2014) applied the PCA technique to determine genetic diversity in Albanian pea genotypes. At end of the study, the authors mentioned that some of the features such as leaflet length and width, number of seed per pod, the weight of 1000 seeds and yield per genotype subscribed to a large part of diversity. Umar *et al*. (2014) reported that pod length and width have big effects

Table 4: Eigen values of each morphological character.

Morphological Traits	Principal Component-1	Principal Component-2	Principal Component-3	Principal Component-4
F1	0,06	0,22	-0,27	-0,15
F2	0,22	-0,03	0,02	-0,07
F3	-0,15	0,22	0,16	0,01
F4	-0,10	**0,26**	-0,01	0,02
F5	-0,12	0,25	-0,03	-0,04
F6	0,15	-0,25	-0,01	-0,02
F7	0,18	0,16	0,09	0,09
F8	-0,08	-0,01	0,02	**-0,29**
F9	0,18	0,05	-0,14	0,05
F10	0,22	-0,01	-0,02	0,02
F11	-0,06	-0,16	0,26	0,00
F12	0,16	0,18	-0,09	-0,16
LS1	0,19	0,04	0,02	0,06
LS2	0,22	0,08	0,07	-0,01
LS3	0,22	0,08	0,07	-0,01
LS4	0,21	-0,01	-0,01	0,08
LS5	0,22	0,03	0,03	0,01
LS6	-0,14	0,00	-0,09	0,24
LS7	-0,09	0,15	0,00	0,23
LS8	-0,10	0,08	-0,05	-0,20
LS9	-0,05	0,09	-0,25	0,25
LS10	-0,18	-0,12	0,01	0,13
LS11	-0,12	-0,12	-0,04	0,25
LS12	0,12	-0,09	0,16	0,03
LS13	0,11	-0,07	-0,03	0,24
LS14	0,19	0,07	0,04	-0,22
LS15	0,18	0,06	0,02	-0,19
LS16	-0,03	**0,28**	0,03	0,14
LS17	0,14	0,12	0,19	-0,05
LS18	0,11	-0,04	0,15	-0,11
LS19	-0,01	**0,26**	0,20	0,10
LS20	0,13	0,23	0,01	0,08
LS21	0,16	0,15	0,03	-0,14
LS22	0,17	0,01	-0,02	0,08
SP1	0,10	0,12	-0,02	**0,28**
SP2	-0,14	0,14	-0,19	-0,23
SP3	0,08	-0,15	-0,03	0,24
SP4	0,16	-0,04	0,07	0,10
SP5	-0,04	0,24	0,25	0,14
SP6	0,17	-0,21	0,04	-0,13
SP7	0,07	**0,30**	0,10	0,10
SP8	0,13	-0,13	0,06	0,12
SP9	0,22	-0,09	0,00	0,08
SP10	-0,04	0,02	-0,28	-0,06
SP11	-0,01	0,00	-0,23	-0,11
SP12	-0,08	-0,05	0,25	0,09
SP13	0,04	0,04	**-0,34**	0,12
SP14	0,12	-0,01	-0,23	0,13
SP15	-0,14	0,00	0,13	-0,10
SP16	-0,15	-0,01	0,29	-0,04

on genetic variability in pea genotypes from different origins. These characters are connected to the first component which expressed 40.29% of the diversity. Kanwar and Mehta (2018) reported that a large genetic diversity among the French bean (*Phaseolus vulgaris* L.) landraces of Himachal Pradesh. They mentioned that this diversity would demonstrate a simple primary place in germplasm recognition action for future breeding programmes. The rich genetic diversity in *Pisum* was reported by Bhuvaneswari *et. al.* (2017) and Singh *et al.* (2017).

The projections of the 15 genotypes in a 2-dimensional graph have been shown in Fig 1. The first (PC1) and second (PC2) coordinates of the PCA implemented using morphological data accounted for 48.72 % of the diversity monitored. Based on the Principal Coordinate analysis, five main groups were composed (Fig 2). The first and second groups occurred of *P. fulvum* and *P. abyssinicum* genotypes respectively. The third group contained two of the *P. sativum* var. *elatius* accessions except for 75PSE098. Similarly, the fourth group consisted of two *P. sativum* var. *arvense* accessions. However, other two *P. sativum* var. *arvense* accessions did not include any group. Commercial varieties located into same group. In general, the graph represented an obvious division between taxonomic groups except for *P. sativum* var. *sativum* and *P. sativum* var. *arvense* genotypes.

CONCLUSION

Genetic diversity can be estimated using various markers. Evaluating the morphological features can provide a basic method for quantifying genetic diversity while simultaneously defining genotype performance under suitable growing conditions (Shuaib *et al.* 2007). The results of the present study provided significant knowledge on the genetic diversity of different *Pisum* accessions.

In this study, the variation between different *Pisum* genotypes was analyzed by using the data obtained from 50 different morphological observations. The demonstration of the low variability of the first three principal components proved that the diversity of this gene pool was very high. Similarly, in the first four principal components, only two morphological characters have the weight coefficient | 0.3 | or greater.

These results provide an important contribution to morphological characterization of polymorphic patterns from several morphological traits groups (stem and leaf, flower, seed and pod) of *Pisum*, which can help breeders in the future for inter-specific crossing attempts.

ACKNOWLEDGEMENT

The authors thank to Western Regional Plant Introduction Station, USDA, Pullman (USA), John Innes Centre (JIC, UK), Plant Gene Bank of the Aegean Agricultural Research Institute (AARI, TR), and "ALFA Tohum" Seed Company for providing *Pisum* seeds. This work is the part of Project No: TAGEM/BBAD/16/A09/P05/05, supported by General Directorate of Agricultural Research and Policies, Ministry of the Food, Livestock and Agriculture, the Republic of Turkey.

REFERENCES

Bhuvaneswari, S., Sharma, S. K., Punitha, P., Shashidhar, K.S., Naveenkumar, K.L. and Prakash, N. (2017). Evaluation of morphological diversity of field pea [*Pisum sativum* subsp. *arvense* (L.)] germplasm under sub-tropical climate of Manipur, *Legume Research*, **40:** 215-223.

Davis, P.H. (1970). *Pisum* L. In: *Flora of Turkey and the East Aegean Islands*, (ed. P. H. Davis). **3**: 370–373. Edinburgh University Press, Edinburgh.

Esposito, M.A., Milanesi, L.A., Martin, E.A., Cravero, V.P., Lopez, A.F.S. and Cointry, E.L., (2007). Principal component analysis based on morphological characters in pea (*Pisum sativum* L.). *Int J Plant Breed*, **1**: 135- 137.

Ghixari, B., Vrapi, H., Hobdari, V. (2014). Morphological characterization of pea (*Pisum sativum* L.) genotypes stored in Albanian genebank. *Albanian J Agric Sci* (special edition).

Govorov L.I. (1937). Pisum (N.I. Vavilov, E.V. Wulff), *Flora of Cultivated Plants. IV. Grain Leguminosae*. State Agricultural Publishing Company, Moscow, Leningrad. 231-336.

Griffing, B. and Lindsstromm, E.W. (1954). A study of combining ability of corn inbred having proportion of corn belt germplasm, *Agron J*, **46**: 545-552.

Hanci, F. and Gokce, A.F. (2016). Genetic diversity evaluations in Turkish onion (*Allium cepa* L.) genotypes: principal component analyses (PCA) for breeding strategies. *Acta Hort*. (ISHS) **1143**:227-234.

ITIS, Integrated Taxonomic Information System. (2017). Integrated Taxonomic Information System on-linedatabase. http://www.itis.gov. (accessed 26 January 2018).

Jobson, D. (1991). Confidence regions for the mean variance set: An alternative approach to estimation risk. *Rev Quant Finance Account*, **1**: 235–257.

Jones, Q. (1984). *A national plant germplasm system*, in conservation of crop germplasm an international perspective, Crop Science Society of America, 27– 33.

Kanwar, R. and Mehta, D.K. (2018). Survey, collection and seed morphometric characterization of French bean (*Phaseolus vulgaris* L.) landraces of Himachal Pradesh, *Legume Reseach*, **41:** 333-341

Kosterin O.E. and Bogdanova V.S. (2008). Relationship of wild and cultivated forms of *Pisum* L. as inferred from an analysis of three markers, of the plastid, mitochondrial and nuclear genomes. *Genet Resour Crop Evol*, **55**: 735-755.

Kupicha, F.K. (1981). Tribe 21, Vicieae. In: Advances in Legume Systematics, Polhill, R.M. and P.H. Raven (Eds.), *Royal Botanic Gardens*, Kew. 377–381.

Leilah, A.A. and Al-Khateeb, S.A. (2005). Statistical analysis of wheat yield under drought conditions. *J Arid Environ*, **61**: 483-496.

Maxted, N. and Ambrose M. (2001). Peas (*Pisum* L.) *Plant Genetic Resources of Legumes in the Mediterranean*. Kluwer Academic Publishers. The Netherlands.

Mohammadi, S.A. (2003). Analysis of genetic diversity in crop plants salient statistical tools and considerations. *Crop science,* **43**: 1235.

Ouafi, L., Alane, F., Rahal-Bouziane and H., Abdelguerfi, A. (2016). Agro-morphological diversity within field pea (*Pisum sativum* L.) genotypes. *Afr J Agric Res*, **11**: 4039-4047.

Singh, S.R., Ahmed, N., Singh, D.B., Srivastva, K.K., Singh, R.K. and Mir, A. (2017). Genetic variability determination in garden pea (*Pisum sativum* L sub sp. hortense Asch. and Graebn.) by using the multivariate analysis, *Legume Research*, **40**: 416-422.

Shuaib, M., Alam, A., Zahir, A., Waqar, A., Taufiq, A. and Ikhtiar, K. (2007). Characterization of wheat varieties by seed storage protein electrophoresis. *Afr J Biotechnol,* **6**: 497- 500.

Umar, H.M.I., Ur-rehman, S., Bilal, M., Atif, S., Naqvi, H., Manzoor, S.A. *et al*. (2014). Evaluation of genetic diversity in pea (*Pisum sativum*) based on morpho-agronomic characteristics for yield and yield associated traits. *J Biodivers Environ Sci*, **4**: 323-328.

Vershinin, A.V., Allnutt, T.R., Knox, M.R., Ambrose, M.J., Ellis, T.H.N. (2003). Transposable elements reveal the impact of introgression, rather than transposition, in *Pisum* diversity, evolution, and domestication. *Mol Biol Evol*, **20**: 2067-2075.

Yared, B.S. (2011). Genetic variability, correlation and path analysis studies in Ethiopian mustard (*Brassica carinata* A. Brun) genotypes. *Int J Plant Breed Genet*, **5**: 328-338.

Ziegel, E. (2002). Editor' s report on Encyclopedia of Environmetrics, Vols. 1– 4, (A. El Shaarawi and W. Piegorsch, *Technometrics*,) **44**: 408-409.