PHENETIC STUDIES OF ATROPA SPECIES IN IRAN

M. Sheidai, M. Khatamsaz, & M. Goldasteh

Sheidai, M., Khatamsaz, M. & Goldasteh, M. 2001 12 15: Phenetic studies of *Atropa* species in Iran. -*Iran. Journ. Bot. 9(1): 41-46.* Tehran.

Phenetic analyses of morphological characters were performed on 19 populations of two *Atropa* species, namely *A. belladonna* and *A. acuminata*. Different clustering and ordination methods as well as discriminant analysis, supported taxonomic treatment of these species. New morphological characters are suggested for the delimitation of *Atropa* species.

Masoud Sheidai and Maryam Goldasteh, Biology Department, Shahid Beheshti University, Tehran, Iran. -Mahbobeh Khatamsaz, Research Institute of Forests and Rangelands, P.O. Box 13185-116. Tehran, Iran.

Key words. Phenetic analysis, *Atropa,* Iran.

بررسی فنتیکی گونه های Atropa در ایران

مسعود شیدایی، محبوبه خاتم‌ساز و مریم گلدسته

نوزده جمعیت متعلق به دو گونه *Atropa belladonna* و *A. acuminata* مورد بررسی فنتیکی قرار گرفتند. تجزیه خوشه‌ای و رسته‌بندی جمعیتها براساس دو مولفه اول حاصل از تجزیه به مولفه‌های اصلی وجود دو گونه را تایید نمود. جمعیتهای *A. belladonna* تفاوتهای بسیاری را در بعضی از صفات ریختی نشان دادند. روشهای آماری چند متغیره، علاوه بر صفاتی که در کلید شناسایی این گونه‌ها استفاده می‌شوند، صفات ریختی جدیدی را برای شناسایی معرفی نمودند.

Introduction

The *Solanaceae* species grow wild throughout Iran and are considered as economically important plants. A few biosystematic studies of *Solanaceae* species have been carried out in the country and such data is completely lacking for most of the species (Khatamsaz & Zangirian 1988, Sheidai & al. 1999a, b; 2000a, b). The present report is a part of biosystematic investigation carried out on *Solanaceae* species of Iran, considering phenetic analysis of morphological characters in *Atropa* species/ populations, for the first time.

Materials & Methods

Atropa species grow wild in the northern parts of Iran, therefore 19 populations (OTUs) were collected from these regions and used for morphometric studies (Table 1). Five to ten plant specimens were used from each locality for morphological studies.

In total 32 quantitative/qualitative morphological characters were studied for each OTU (based on minimum 5 samples). The mean of quantitative characters were used in the analysis while qualitative characters were treated as multistate characters and coded accordingly (Table 2). Standardized data (mean=0, variance=1) were used for multivariate statistical analysis (Sheidai & Inamdar 1997).

The grouping of OTUs was performed by using cluster analysis and ordination method based on principal components analysis (PCA). Different clustering methods like single linkage, UPGMA (Unweighted Paired Group Mean Average) and WARD (minimum variance spherical clusters) were used to find the actual clusters (Ingroille 1986). Euclidean and squared Euclidean distances were used as the similarity measures.

Discriminant analysis (DA) was performed on morphological characters in order to check the correctness of the groupings obtained (Lefèbvre & Vekemans 1995). For each species/population predicted group membership was estimated from canonical discriminant scores using Bayes' rule (Norusis 1988) and checked against actual group membership, followed by grouping of the species based on discriminant factors.

Factor analysis based on PCA was used to identify the most variable morphological characters among the species/ populations (Chatfield & Collins 1995). Statistical analysis used STATISTICA version 4.3 (1993) and SPSS version 6 (1993) software.

Results and discussion

Khatamsaz (1998) in taxonomic treatment of the genus *Atropa*, based on morphological ground, recognized two species of *A. belladonna* and *A. acuminata*. In order to check such a grouping; cluster analysis and ordination of *Atropa* species/populations were performed (Figs. 1 and 2).

Different clustering methods produced similar results and grouped the species/ populations in two major clusters. The specimens identified as different populations of *A. belladonna* formed the first major cluster while *A. acuminata* populations formed the second cluster, supporting Khatamsaz (1998) taxonomic treatment. However much of variations were observed among populations of A. *belladonna* (Fig. 1) which was also revealed in their seed proteins (unpublished data). Ordination of the species/ populations based on PCA supported the clustering results.

Factor analysis of morphological characters revealed that the first 5 factors comprise about 70% of total variance. The first factor comprised about 25% of total variance, separating the two species of

Table. 1. Species/ populations and their localities.

Species/ population	Code	Locality
Atropa belladonna L.	b1	Noshahr
A. belladonna	b2	Gorgan
A. belladonna	b3	Gorgan
A. belladonna	b4	Bandpay
A. belladonna	b5	Gorgan
A. belladonna	b6	Ramsar
A. belladonna	b7	Kelardasht
A. belladonna	b8	Kheyroodkenar
A. belladonna	b9	Noshahr
A. belladonna	b10	Alamdeh
A. belladonna	b11	Chaloos
A. belladonna	b12	Tonekabon
A. belladonna	b13	Noshahr
A. belladonna	b14	Ramsar
A. belladonna	b15	Asalem
A. belladonna	b16	Polesefid
A. acuminata Royle ex Lindl	a1	Gorgan
A. acuminata	a2	Abshar
A. acuminata	a3	Golestan

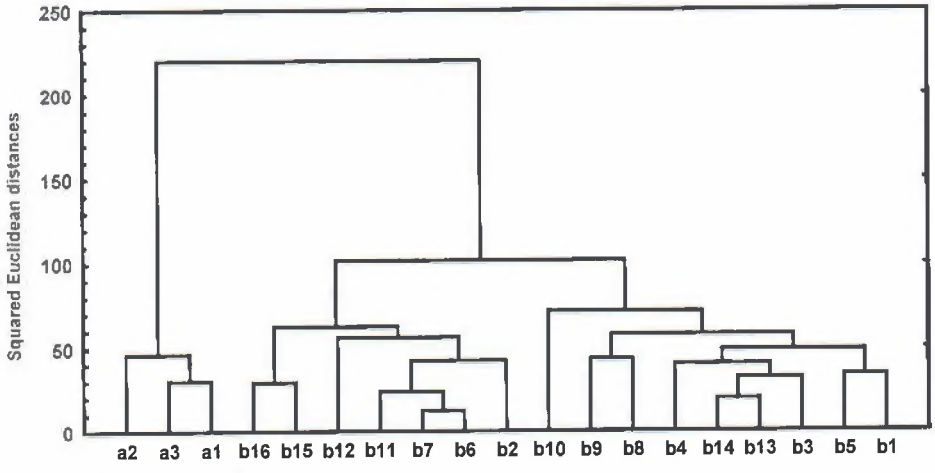

Fig. 1. Cluster analysis (WARD) of morphological data in *Atropa* species/ populations. Species/ populations code as in Table. 1.

Table. 2. Morphological characters of *Atropa* species and their coding.

1- Stem base, angular = 1, circular = 2
2- Leaf length (cm)
3- Leaf width (cm)
4- Petiole length (cm)
5- Petiole indumentum, tomentose = 1, glandular = 2, absent = 3
6- Pedicel indumentum, tomentose = 1, glandular = 2, absent = 3
7- Pedicel length (cm)
8- Pedicel diameter in flower (cm)
9- Pedicel length in fruit (cm)
10-Pedicel diameter in fruit (cm)
11-Calyx length in flower (cm)
12-Calyx diameter in flower (cm)
13-Amount of indumentum in calyx, low = 1, medium = 2, high = 3
14-Calyx indumentum, glandular-tomentose = 1, glandolar = 2
15-Apex of calyx teeth, acute = 1, acuminate = 2
16-Length of calyx teeth in flower (cm)
17-Calyx gland in fruit, very few = 1, few = 2
18-Corolla shape, funnel-shaped = 1, campanulate = 2, funnel-shaped- campanulate = 3
19-Corolla length (cm)
20-Corolla color, yellow = 1, yellow with pinkish reticulation = 2
21-Corolla diameter (cm)
22-Corolla indumentum, very low tomentose = 1, low tomentose = 2, medium tomentose = 3, glandular-tomentose = 4
23-Length of corolla teeth (cm)
24-Fruit diameter (cm)
25-Ratio of calyx to corolla, 1/4 = 1, 1/5 = 2, 1/4-1/5 = 3
26-Number of flowers, solitary = 1, 2-3 = 2, more than 3 = 3
27-Branches bearing flowers, present = 1, absent = 2

A. belladonna and *A. acuminata* (Fig. 2). Characters like leaf length, size of calyx in fruit, the length of teeth in fruit calyx and corolla possessed the highest correlation (>0.70) in the first factor, therefore these are the most variable morphological characters separating the two species of *A. belladonna* and A. *acuminata*.

The second factor comprised about 12% of total variance, mainly separating different populations of *A. belladonna* (Fig. 2). Characters like the length and diameter of fruit pedicel and diameter of fruit possessed the highest correlation (>0.70) in this factor, therefore these are the most variable morphological characters among *A. belladonna* populations. Characters like corolla and calyx diameter, corolla color and calyx indumentum possessed high correlation (>0.70) in the other factors.

In identification of *Atropa* species characters like stem base, leaf shape, fruit diameter, and shape and color of corolla are used, however factor analysis indicates the importance of other morphological characters like the leaf length, size of calyx in fruit, the length of teeth in fruit calyx and corolla, length and diameter of fruit pedicel, corolla and calyx diameter, and calyx indumentum in taxonomy of *Atropa*.

Due to high variation observed among *A. belladonna* populations, a discriminant analysis (DA) was performed to check the groupings suggested by cluster/ ordination methods. DA produced a single factor on

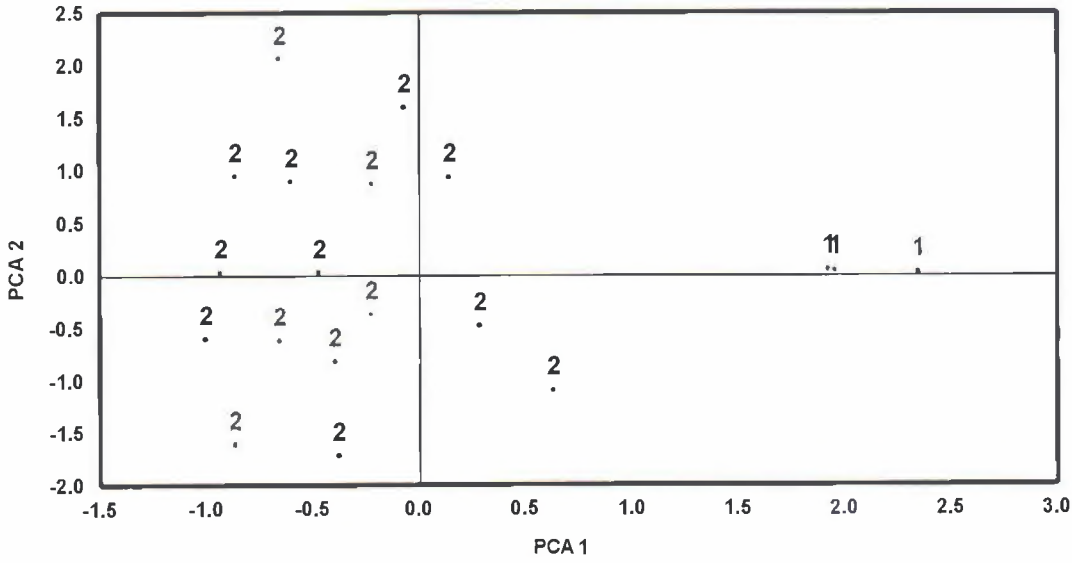

Fig. 2. Ordination of *Atropa* species/ populations on the first two PCA axes. 1 = *A. acuminata*, 2 = *A. belladonna*

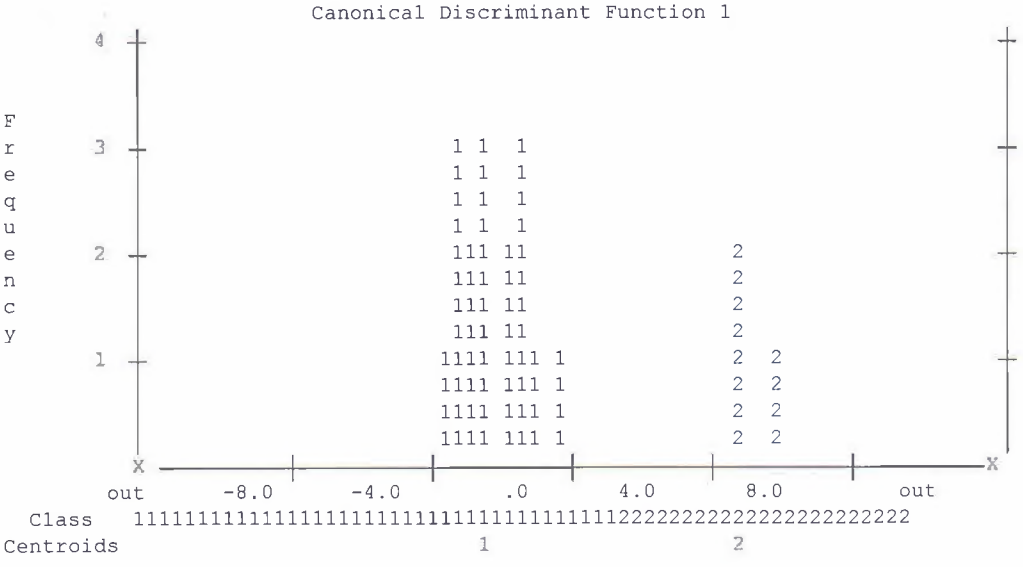

Fig. 3. Stacked histogram of *Atropa* species/populations based on DA of morphological characters. -Abbreviations: 1 = *A. belladonna*, 2 = *A. acuminata* (Note: each four number i.e. 1 or 2 represents a single taxon.

which the species/ populations were plotted (Fig. 3). Separation of populations belonging to either species is evident and the analysis revealed 100% correctness for predicted versus actual membership, supporting the clustering and ordination results. Moreover seed protein analysis of these species/ populations also supported the morphological results (unpublished data).

References

Chatfield, C. & A. J. Collins 1995: Introduction to Multivariate Analysis. -Chapman & Hall. New York.

Ingroille M. J. 1986: The construction of cluster webs in numerical taxonomic investigations. - Taxon 35: 541-545.

Khatamsaz, M. 1998: Flora of Iran. no. 24. Solanaceae. - Research Institute of Forests and Rangelands, I. R. Iran.

Khatamsaz, M. & E. Zangirian 1998: SEM survey of pollen morphology in Iranian species of Hyoscyamus L. (Solanaceae). -Iran. J. Bot. 7: 151-163.

Lefèbvre, C. & X. Vekemans 1995: A numerical taxonomic study of Armeria maritima (Plumbaginaceae) in North America and Greenland. -Can. J. Bot. 73: 1583-1595.

Norusis, M. J. 1988: SPSS/ PC Advanced Statistics. SPSS Inc. -Chicago.

Sheidai, M. & A. C. Inamdar 1997: Cytomorphology of Asparagus taxa using multivariate statistical analysis. -The Nucleus 40: 7-12.

Sheidai, M., Z. Narengi, & M. Khatamsaz 1999a: Karyotype and seed protein analysis of Lycium (Solanaceae) in Iran. -Edinb. J. Bot. 56: 253-264.

Sheidai, M., M. Mosalanejad, & M. Khatamsaz 1999b: Karyological studies in Hyoscyamus species of Iran. -Nordic. J. Bot. 19:369-373.

Sheidai, M., M. Honarvar, & M. Khatamsaz 2000a: Cytology, morphometry and seed protein analysis of Solanum species in Iran. - Iran. J. Bot. 8: 187-208.

Sheidai, M., M. Mosalanejad, & M. Khatamsaz 2000b: Numerical taxonomy and seed protein analysis of Hyoscyamus species in Iran. -J. Sci. I. R. Iran. 11: 83-91