A chemotaxonomic approach to *Moricandia* DC. (Brassiceae) using seed globulin electrophoretic patterns

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INTRODUCTION

The use of electrophoretic methods with seed proteins has become one of the most popular techniques for plant characterisation, taxonomy and phylogeny during the last decades. In this sense, seed proteins banding profiles have proved to be useful complementary information to other biological characters. As consequence, a great number of taxonomic investigations have utilised seed storage proteins, since they are unaffected by environmental conditions, are highly stable and very conservative from an evolutionary point of view. In seeds of crucifers, the most abundant storage proteins are globulins, especially cruciferin, a legumin-like 12S storage protein that has been characterised in *Brassica napus* (Dalgalarrondo et al., 1986, Rödin et al., 1990). The genus *Moricandia* DC. (subtribe *Moricandiinae* of *Brassiceae*) is often considered to belong to the *Brassica* coenospecies on the basis of morphological and cytogenetical similarities (Gómez-Campo, 1999). It is comprised by eight species adapted to tolerate drought and arid conditions in the Mediterranean, Irano-Turanian and Saharo-Sindian regions. The distribution of taxa diversity, at specific and infra-specific level, seems to indicate that the origin center of the genus is found in NW Africa or SE of Iberian Peninsula (Sobrino-Vesperinas, 1997). As a part of a more extensive chemotaxonomic and molecular revision of this genus, in present paper we report preliminary results of the relationships among taxa of *Moricandia* using globulin electrophoretic patterns.

MATERIAL AND METHODS

Plant material - Seeds of 13 studied accessions were collected from their natural habitats and stored under long-term preservation conditions (Gómez-Campo, 1990) at the germplasm bank of the Dept. de Biología Vegetal, E. T. S. de Ingenieros Agrónomos de Madrid (Spain) (Table 1).

Table 1. Plant material studied in the electrophoretic analysis of globulins.

Accession number(*)	TAXON	ORIGIN
GC-9304-96	*Moricandia arvensis* (L.) DC.	Tahal-Tabernas (Almería, Spain)
GC-0863-66	*M. arvensis* (L.) DC.	Jumilla (Murcia, Spain)
GC-6665-84	*M. arvensis* (L.) DC.	Catania (Sicily, Italy)
GC-3660-75	*M. arvensis* (L.) DC. f. *robusta*	El Kantara (Algeria)
GC-3670-75	*M. arvensis* var. *garamantum* Maire	Tamanrasset (Algeria)
GC-4073-76	*M. foetida* Bourgeau	Tabernas (Almería, Spain)
GC-5549-80	*M. foleyi* Batt.	Merzuga (Morocco)
GC-9414-97	*M. moricandioides* (Boiss.) Heywood	Benamejí (Córdoba, Spain)
GC-2276-77	*M. moricandioides* (Boiss.) Heywood	Alcoy (Alicante, Spain)
GC-2129-72	*M. nitens* (Viv.) Durd. & Barr	Botanical Garden of Tohoku Univ. (Japan)
GC-3748-75	*M. sinaica* Boiss.	Behbahan (Iran)
GC-1845-70	*M. spinosa* Pomel	Drahu (Algeria)
GC-9274-96	*M. suffruticosa* (Desf.) Coss. & Dur.	Missur (Morocco)

(*) In the germplasm bank of Departamento de Biología Vegetal, Escuela Técnica Superior de Ingenieros Agrónomos de Madrid (Spain).

Protein extraction and electrophoresis – Five seeds per accession were homogenised and salt soluble proteins (globulins) were extracted in a 0.4M NaCl buffer with 3% mercaptoethanol during 18 h at room temperature. After centrifugation, supernatant was boiled for 4 min under reducing conditions as in Sánchez-Yélamo et al. (1992). Protein electrophoresis (SDS-PAGE) was carried out following Laemmli (1970) system. Three replications were made.

Data analysis – The banding patterns obtained were analysed to estimate the relationship among taxa. Each polypeptide (band on the gel) was considered as a qualitative character, and treated as a binary character in a data matrix (coded presence or absence as 1 and 0 respectively). Clustering analysis were made by UPGMA method using the Jaccard' coefficient, and a dendrogram was also obtained using NTSYS computer programs (Rohlf, 1993).

RESULTS AND DISCUSSION

Electrophoretic analysis of *Moricandia* taxa globulins showed two banded-zones on gels corresponding with heavy α chains (aprox. 30 KDa) and light β chains (aprox. 20 KDa) groups of cruciferins, founded by Rödin et al. (1990) in *B. napus*. In our case, as many of 15 different and clearly resolved bands of polypeptides were detected on gels of *Moricandia* taxa studied, and several qualitative differences have been observed among some of them. *M. foleyi* showed the most distinctive electrophoretic pattern; all *M. arvensis* accessions showed identical pattern, and the same is true with respect to *M. nitens, M. spinosa* and *M. suffruticosa*. A great similarity between *M. arvensis* f. *robusta* and *M. arvensis* patterns was observed. However, they could be observed quantitative and qualitative differences between the two accessions of *M. moricandioides*. They were detected specific patterns in the rest of taxa. None quantitative differences respect to the width of the bands were detected respect to ploidy level of the species.

The dendrogram (Fig. 1), shows the relationships of taxa on the basis of their globulin profiles. In a general way, these results are in agreement with the work of Sobrino-Vesperinas (1983) from a morphological and caryological point of view. The endemic taxon *M. foleyi* appears to be the most distinctive respect to the rest of species. Its lowest value of similarity compared to the other taxa in globulins polypeptides (very conservative) together with other caryological and morphological features, as well as geographic distribution (it is endemic in Morocco), possibly point it this species involved in the origin of this genus.

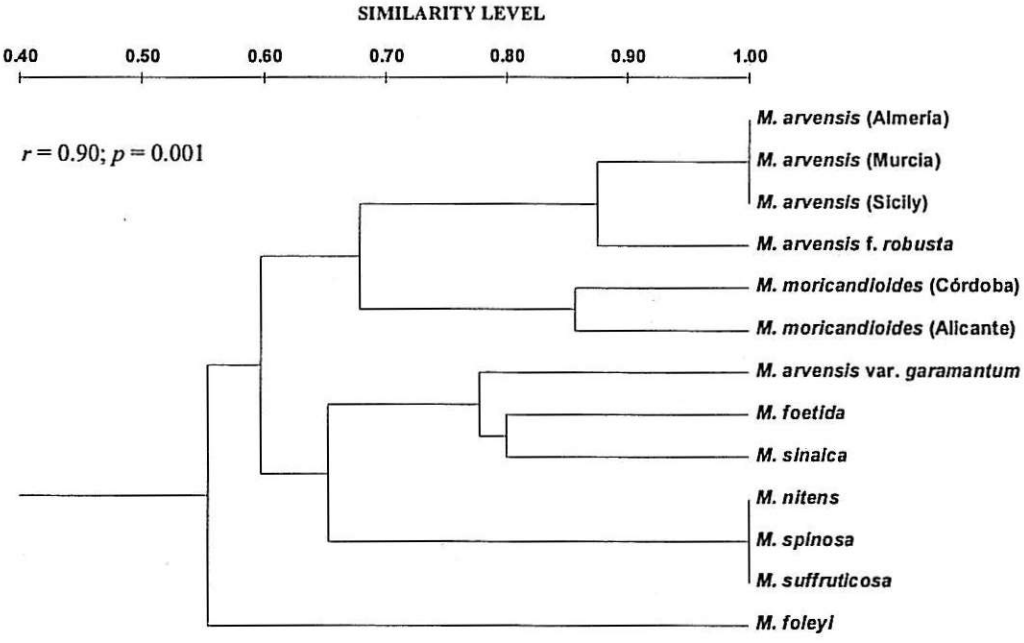

Figure 1. Dendrogram derived from a UPGMA cluster analysis, using Jaccard's coefficient based on the globulin patterns.

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