

GENETIC VARIATION IN THE SICILIAN ENDANGERED *BRASSICA RUPESTRIS*F.M. RAIMONDO¹, A. SCIALABBA¹, G. ZECCA², F. GRASSI², G. CASAZZA³, L. MINUTO³

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Brassica rupestris Raf. is an endemic plant belonging to the *Brassica* section. It grows in rocky places and cliffs of the Central-Western Sicily (Italy). Rare and endangered species are susceptible to loss of genetic variation through genetic drift in small populations. Management decisions for the conservation of rare taxa necessitate an understanding of their biology and other factors, including genetic variability. For this reason the gathering of data on population genetic structure of rare species has become a common prelude to their conservation planning (Ellstrand and Elam, 1993).

In the present study the ISSR technique was used to examine natural populations of *B. rupestris* (both subsp. *rupestris* and subsp. *hispidata*) for the following purposes: 1) to evaluate the genetic diversity both at species and subspecies levels, 2) to assess the genetic differentiation of populations and 3) to provide suggestions for effective conservation programs.

Six natural populations of *B. rupestris* subsp. *rupestris* and two populations of *B. rupestris* subsp. *hispidata*, covering the whole range of the two subtaxa, were investigated and mapped using GPS (Garmin) in order to evaluate their genetic diversity. Six were from Palermo province: S. Calogero, Capo Zafferano, P.so Scuro - Castelbuono, Mt. Pellegrino, Mt. Kumeta, Mt. Pizzuta; one from Agrigento province: Gole Tardara - Sciacca; one from Reggio Calabria province: Stilo. ISSR were used to detect the genetic diversity within and among populations representative of the species distribution range. From each site, a variable number ($8 < N < 10$) according to the availability of individuals were randomly sampled ($n = 76$); 1-2 leaves per plant were dried *in situ* in silica gel, washed in laboratory and total genomic DNA extracted by using DNeasy Plant Mini Kit (Qiagen) following the manufacturer's instructions.

High levels of genetic diversity were revealed both at population ($PPB = 53.88\%$, $H_s = 0.2115$, $Sh = 0.3085$) and at species level ($PPB = 96.55\%$, $H_T = 0.3070$, $Sh = 0.4638$). The correlation between genetic and geographic distances was negative (Mantel test, $r = -0.23$). Our data on *B. rupestris* revealed that about 67% of genetic variation is detectable within the population while 23% among populations within infraspecific taxa. This fact is also confirmed by the quite good value of migration rate among populations and it could be explained by hypothesizing the self-incompatibility systems, often found in many *Brassica* populations (Geraci *et al.*, 2004).

The information on the pattern of genetic variation obtained in the present work bear important inferences for conservation management, and in particular for *ex situ* conservation programmes. The populations showing local markers (Gole Tardara, San Calogero, and Mt. Pellegrino) deserve particular attention for their important presence in a seeds bank.

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