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PATTERNS OF PHYLOGEOGRAPHY OF DWARF PALM (*CHAMAEROPS HUMILIS* –L.)

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Chamaerops humilis, *microsatellites, landscape genetics*

Chamaerops humilis “dwarf palm”, the only native palm in Italy, is one of two native palms occurring in Europe. The present distribution of *C. humilis* is restricted to the West Mediterranean, both on the European and African sides. In Africa, it occurs mainly in Morocco but also in N Algeria and N Tunisia. In Europe, it occurs on the coasts of S Portugal, S and E Spain, on most of the large islands of the West Mediterranean. In Italy, during 20th century, the anthropic pressure caused a strong reduction of growth areas and presently the dwarf palm distribution is very fragmented and confined to Sicily, Sardinia and few coastal areas still wild.

The purposes of this work, are: (1) to describe the phylogeographic structure of the species throughout its distributional range in Italy and the West Mediterranean region; (2) to infer a biogeographic scenario to explain its present distribution.

For this purpose, leaf materials and herbarium samples of populations coming from Morocco, Spain, Sicily, Campania, Tuscany, and Liguria were analysed with a set of microsatellite markers and a mini plastidal satellite that exploit sequence variability of the species.

General estimates of genetic diversity, marker frequencies and F-statistic in the population data were calculated using the SPAGeDi v1.3a. Statistical significance was determined by Jackknifed estimators after 20,000 permutations. The population data was analyzed using STRUCTURE program v.2.3 and Geneland software v3.0. We used the model-based clustering algorithm implemented in STRUCTURE and the empirical statistic K of Evanno to determine the number of sub-populations (K). The default model parameters and varying K from 1 to 10 were used for both plots to run STRUCTURE. Each run consisted of 250,000 burn-in iterations and 1,000,000 data collection iterations, and was replicated 20 times. We inferred population structure using a Bayesian Monte Carlo Markov Chains method implemented in the Geneland: ten independent MCMC runs were performed with the following settings: 1,000,000 iterations with 100 thinning intervals and a burn-in period of 250,000, using the correlated allele frequencies model. The maximum number of populations was set to 20. A map of posterior probabilities (membership) was obtained by PostProcessChain and PostTessellation functions into Geneland by tesselling the landscape at a resolution of 1 m. Null alleles for nSSRs were also inferred.

The analysis, at the moment on more than 20 populations, has provided very interesting results that point out a distribution of samples from Morocco, Spain, Tuscany, Sicily and Liguria in three groups. The results suggest two different routes of diffusion: an Italian South-West axis and a West one along the coasts of Spain to Liguria.