GENETIC VARIABILITY IN A COLLECTION OF WILD CARDOON 
(CYNARA CARDUNCULUS VAR. SYLVESTRIS) BY USE OF 
MICROSATELLITES MARKERS (SSR)

SABA E.*, RAU D.*, RODRIGUEZ M.**, ATTENE G.*

*) Dipartimento di Scienze Agronomiche e Genetica Vegetale Agraria, Università degli Studi di Sassari, Via de Nicola, 07100 Sassari (Italy)
**) Centro per la Conservazione e Valorizzazione della Biodiversità Vegetale, località Surigheddu, Università degli Studi di Sassari 07100 Sassari (Italy)

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Wild cardoon (Cynara cardunculus var. sylvestris) is a poliennial species which grows spontaneously in different areas of Sardinia. This species can be used to extract biopharmaceutical products, to produce lignocellulosic biomass and oil from seeds as well as for food preparation. Moreover, it is a potential source of useful genes in breeding programs of cultivated globe artichoke.

Thirteen populations were collected from seven different ecogeographic areas according to a hierarchical sampling method: three transects were identified per each population and fifteen plants were sampled from each transect.

A total of 117 individuals (9 per population, 3 per each transect) were analysed with nuSSR and cpSSR molecular markers. For nuSSR, the analysis of the molecular variance (AMOVA) revealed the same level of differentiation both among populations (9.97%) and transects (6.22%). However, a substantial amount of variation was found within population (83.81%). Moreover, molecular analyses revealed a tendency of populations to cluster on the basis of their ecogeographical area of origin.

The analysis of nuSSR polymorphism has evidenced three distinct genetics groups (not uniformly widespread across Sardinia). In eight out of the 13 populations all of the three genetic groups were present, in 4 populations at least two of the genetic groups were present while only one population was constituted by individuals belonging to one genetic group. CpSSR analysis has evidenced a very low level of variability, with only one polymorphic locus out of the 35 analyzed (2.86%). Two chloroplastic haplotypes have been identified, of which one homogeneously distributed across Sardinia and one localized in the Central-North-West area. A significant association between chloroplastic haplotypes and genetics groups was also observed.

Field experiments are in progress to obtain a morphological and biochemical characterization of the genotypes belonging to the different genetic groups. These information will likely be useful to identify populations or genotypes interesting for breeding and research purposes.