

MOLECULAR CHARACTERIZATION OF THE WIDER EUROPEAN CYNARA COLLECTION BY MEANS OF MARKERS

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The wider *Cynara* germplasm collection has been build up from former germplasm collections present in Italy, France, and Spain, in the frame of the 'CYNARES' project, sponsored by the AGRI GEN RES Community Programme (European Commission, Directorate-General for Agriculture and Rural Development, under Council Regulation (EC) No 870/2004). The full global artichoke collection include germplasm from all the four artichoke typologies (Violet de Provence, Catanese, Spinoso Sardo, Romanesco), for a total of 151 accessions. A core collection was analyzed for morphological and biochemical traits, while the whole collection was characterized at the molecular level to assess the diversity present, to measure the genetic distance among accessions and to cluster them. In the present paper are reported the results of molecular analyses. SSR, ISSR and AFLP markers were used, for a total of 2403 loci on 543 genotypes. Genomic DNA was extracted from plant leaves and shared among partners; each partner analysed the whole collection using different markers. The total data were used to detect several genetic information such as: Nei's genetic distance, level of polymorphism, observed and expected heterozygosity, presence of private alleles, polymorphism information content (PIC) of each marker. The different marker typologies were also analysed separately. Finally, accessions were clustered and discriminant analysis was undertaken to detect the correct assignment of each genotype with respect to country of origin and artichoke typologies. The majority of genetic diversity was within accession. The Nei's genetic distance is able to cluster together all the accessions with cardoon germplasm; but on the other hand, are located far apart in the dendrogramm accessions called with the same names and obtained by different Institutions; this highlight the not proper Cultivars definition, over years of cultivation in various locations.