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Poster Abstract – A.44

CHARACTERIZATION OF NEWLY ISOLATED MICROSATELLITE MARKERS FROM ARTICHOKE

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Artichoke, *Cynara cardunculus* L. var. *scolymus* (L.) Fiori is a diploid outcrossing species, originated in the Mediterranean basin, whose value is much recognised since ancient times both for its tasty heads and for pharmaceutical properties.

Only a few varieties are widely cultivated in Italy; nevertheless, a number of landraces are diffused on a small scale which have been poorly characterized to date. Some problems arise for variety identification, due to the fact that landraces are normally topologically named irrespectively of their genetic constitution or morphological characters, thus resulting in synonymy and/or duplications. To overcome this problem, molecular markers able to fingerprint the varieties can be developed. One class of such markers are microsatellites (SSRs). They consist of tandem repeats of di-, tri- or tetra-nucleotide patterns, are frequent and usually well distributed in plant genomes, and can be exploited to develop locus-specific codominant markers, useful for studies on genetic diversity and mapping.

In artichoke, only few SSRs have been isolated to date. For this reason, a genomic library produced from the variety "Locale di Mola", was used in order to identify microsatellite regions. Hundreds of recombinant phages were screened by using oligonucleotides labelled with digoxygenin and containing SSR sequences. Positive clones were obtained with $(CAT)_8$ and $(GATA)_5$ probes. The nucleotide sequence of the insert was determined and the repetitive stretches of di- and tri- nucleotides were identified. Primers specific to SSR flanking regions were designed and DNA fragments in the range 150-350 bp were amplified, cloned and sequenced, in order to ascertain the repetitive nature of the sequences. A set of artichoke accessions belonging to the main morpho-agronomic groups and from various geographical origins was selected, together with some wild *C. cardunculus* and other *Cynara* species. A total of 20 microsatellite regions were amplified using one of the primers fluorescently labelled; the amplification product was then analysed using an automated sequencer. Most of the SSRs produced more than two alleles and for some of them allele distribution was related to morpho-agronomic traits.