Poster Abstract – A.45

GENETIC MAPPING IN CYNARA CARDUNCULUS L.

E. PORTIS*, A. ACQUADRO*, R. MAURO**, G. MAUROMICALE **, S. LANTERI*

*) DiVaPRA, Plant Genetics and Breeding, University of Turin, Via L. da Vinci 44, 10095 Grugliasco (TO), Italy - ezio.portis@unito.it

**) Dipartimento di Scienze Agronomiche, Agrochimiche e delle Produzioni Animali – sez. Scienze Agronomiche, University of Catania, Via Valdisavoia 5, I-95123 Catania, Italy

globe artichoke, cardoon, genetic map, QTLs

The complex *Cynara cardunculus*, includes the globe artichoke (var. *scolymus* L.), the cultivated cardoon (var. *altilis* L.) and the wild cardoon (var. *sylvestris* (Lamk) Fiori).

Globe artichoke (*C. cardunculus* var. *scolymus* L.) contributes significantly to the Mediterranean agricultural economy, with an annual production of about 750Mt (more than 60% of global production) from over 80kha of cultivated land. Italy is the leading world producer (about 470Mt) followed by Spain (188Mt), France (52.5Mt) and Greece (35Mt). Although to a lesser extent globe artichoke is also cultivated in the Near East, North Africa, South America, United States (mainly in California), and its cultivation is spreading in China (FAO data 2005: http://faostat.fao.org/).

The *C. cardunculus* genome is as yet poorly investigated. In order to move to a crossing strategy for breeding, a greater knowledge of artichoke and cardoon genetics will be essential. In particular, it will be advantageous to establish a framework of linkage relationships to allow the identification and localization of genes controlling important yield traits or resistance against pathogens.

Recently we generated the first genetic maps of globe artichoke, based on a two-way pseudotestcross strategy. An F_1 population was created by crossing a clone of 'Romanesco C3' (a latematuring, non-spiny type) with 'Spinoso di Palermo' (an early-maturing spiny type), and the progeny were genotyped using AFLP, M-AFLP, SSR and retrotrasposon based SSAP markers. The female map comprised 204 loci, spread over 18 linkage groups and spanned 1330.5cM with a mean marker density of 6.5cM. The equivalent figures for the male parent map were 180 loci, 17 linkage groups, 1239.4cM and 6.9cM. The presence of 78 loci in common to both maps allowed for the alignment of 16 of the linkage groups.

At present we are applying the same strategy to developing further genetic maps on F_1 progenies obtained by crossing the same clone of 'Romanesco C3', previously used as female parent, with either a cultivated cardoon ('Altilis 41') and a wild cardoon ('Creta 4') accessions used as pollen sources. Wide cross populations of this type are suited for the investigation of the genetic control of quantitative characters in exotic genetic backgrounds. Furthermore, both wild and cultivated cardoon represents the most straightforward resource to exploit for globe artichoke improvement, since they are full cross-compatible to it.

A very high molecular variation was detected and a high phenotypic variation was observed for important commercial traits like: size, shape, weight, tightness, presence/absence and length of spines, peduncle length of the capitula, size and branching of the plants, etc. Since *C. cardunculus* is easily vegetatively propagated, the mapping populations are immortalised, and thus will be grown

in contrasting environments to investigate genotype x environment interaction for important commercial traits.