

CONSTRUCTION OF A NEW GENETIC LINKAGE MAP OF *CYNARA CARDUNCULUS* L.

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globe artichoke, cardoon, linkage analysis, genetic map, pseudo-testcross

Cynara cardunculus (*Compositae*, $2n=2x=34$) is a perennial allogamous species, native to the Mediterranean Basin, with an estimated genome size of 1078Mbp. It includes globe artichoke (var. *scolymus* L.), cultivated cardoon (var. *altilis* DC.) and their progenitor wild cardoon [var. *sylvestris* (Lamk) Fiori]. *C. cardunculus* improvement through breeding has been rather limited and, unlike other crop species belonging to the same botanical family (such as sunflower, lettuce and chicory), its genome organization remains largely unexplored. To move towards a modern breeding it is compulsory to generate genetic maps for identifying the genetic bases of key resistance and agronomic traits. Due to the high level of heterozygosity of the species, and the marked inbreeding depression following selfing, the most suitable strategy for linkage analyses is the two-way pseudo-testcross.

We produced three F_1 progenies obtained by crossing a globe artichoke clone of ‘Romanesco C3’, as female parent, with three pollen sources: a genotype of globe artichoke ‘Spinoso di Palermo’ (progeny A); one of cultivated cardoon (progeny B) and one of wild cardoon (progeny C). The first genetic maps were developed by genotyping progeny A and applying AFLP, M-AFLP, retrotransposon based SSAP as well as the first available set of SSR markers. They comprised 204 (female map) and 180 (male map) loci spread over 18 and 17 linkage groups respectively; furthermore, the presence of 78 markers in common to both maps allowed the alignments of 16 linkage groups. Recently a new set of microsatellites has been developed and 35 SSR loci were suitable to implement these maps, of which 19 shared between parents.

Here we report on the development of a new consensus map on progeny B, based on more than 700 AFLPs and 60 SSRs markers, the latter representing a set of robust and informative anchor points between the segregating populations. Another map, based on progeny C, is currently under construction and markers suitable for mapping in the three F_1 progenies will be used as point of reference to locate important genes to a particular LG.

C. cardunculus is easily vegetatively propagated, thus the mapping populations are immortalised, and are at present growing in contrasting environments to investigate genotype x environment interactions. The generated maps will open the way for QTL analyses and future application of a marker assisted selection breeding strategies.