CAFFEOLQUINIC ACID BIOSYNTHESIS STRUCTURAL GENES IN CYNARA CARDUNCULUS L.: ISOLATION, HETEROLOGOUS EXPRESSION AND GENOME MAPPING

COMINO C., MENIN B., MOGLIA A., PORTIS E.

DIVAPRA, Plant Genetics and Breeding, University of Torino, Via L. da Vinci 44, 10095 Grugliasco (TO), Italy

secondary metabolites, caffeoylquinic acid biosynthesis, SNP marker development, genetic mapping

Plant secondary metabolites are highly evolved compounds performing different functions, and have been widely exploited from food to medicine. A constant supply of phenols, a class of secondary metabolites, provides preventive and defensive mechanisms to reduce the risk of chronic diseases in human beings; among them caffeoylquinic acids (CQAs) have attracted a growing academic and industrial interest in recent years. In various pharmacological test systems, extracts of plants with a high content of CQAs exhibit hepatoprotective, anticarcinogenic, antioxidative, antibacterial, anti-HIV activities as well as the ability to inhibit cholesterol biosynthesis and LDL oxidation. However, at present, fragmentary information are available on CQAs biosynthesis in plants.

Cynara cardunculus L. includes globe artichoke (var. scolymus L.), cultivated cardoon (var. altilis DC.) and their progenitor wild cardoon [var. sylvestris (Lamk) Fiori] and represents a very interesting model species for studying CQAs, due to the exceptionally high natural content and diversity of these compounds. In previous works, the full-length cDNAs of two transferases (HCT and HQT) and a hydroxylase (C3'H) have been identified and characterized by our group and they have been positioned on genetic maps.

Here we report on the analysis of a set of 19000 globe artichoke unigenes (made available by the Compositae Genome Project, http://compgenomics.ucdavis.edu/), that allowed the identification of 7 genes (i.e. a 4-coumarate:coenzyme A ligase, a cinnamate-4-hydroxylase, a MYB12 like gene and four transferases) putatively involved in CQA biosynthesis. The allelic forms of these genes were sequenced in the parental genotypes (the globe artichoke clone ‘Romanesco C3’ and a genotype of cultivated cardoon ‘Altilis 41’) of a F1 progeny used for the construction of a linkage map based on a two-way pseudo-testcross strategy. SNPs were detected and the analysis of their segregation made possible gene positioning in the genetic map. Their linkage group distribution will be the starting point for gaining a better knowledge of the genetic bases (i.e. Quantitative Trait Loci, QTL) of the CQA biosynthesis.

The full-length cDNAs of the four identified transferases, characterized by a high similarity with the C. cardunculus acyltransferases (HCT and the HQT), have been isolated by means of 5’ and 3’ RACE technique and heterologously expressed in E. coli. HPLC analyses of the reactions catalysed by these isolated enzymes are at present in progress, in order to investigate their role in CQA biosynthesis.