Proceedings of the 54th Italian Society of Agricultural Genetics Annual Congress
Matera, Italy – 27/30 September, 2010
ISBN **978-88-904570-0-5**

Poster Communication Abstract – 5.22

ISOLATION OF MYB TRANSCRIPTION FACTORS INVOLVED IN THE REGULATION OF PHENYLPROPANOID BIOSYNTHESIS IN ARTICHOKE

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Transcription factors, phenylpropanoids, caffeoylquinic acids, artichoke

The known nutraceutical properties ascribed to artichoke are mainly attributable to the presence of phenylpropanoid compounds, in particular of flavonoids, caffeic acid and its derivatives (caffeoylquinic acids). These metabolites play central roles in plant biology, as they are involved in the protection against various biotic and abiotic stresses, in the regulation of plant reproduction and development, and they act as signalling molecules. Phenylpropanoids have also significant beneficial effects on human health if consumed as part of the diet, as they act as antioxidants, reducing the incidence of cardiovascular disease, certain cancers and age-related degenerative diseases. Hence, there is considerable interest in improving our understanding of phenylpropanoid biosynthesis and its regulation, to enhance the levels of these bioactive molecules in plants used as food.

The biosynthetic pathway leading to the accumulation of phenylpropanoids has been elucidated using genetic and biochemical information from many plant species. The fine regulation of this pathway is achieved by combinatorial actions of transcription factors (TF) belonging to various classes, among which MYB TF.

The metabolic route for the biosynthesis of caffeoylquinic acids, particularly chlorogenic acid (CGA) and its derivatives has been recently studied in artichoke, where several enzymes directly involved in this biosynthetic pathway have been isolated and characterized. However, little is known on the regulation of these genes. We have previously studied the genes coding for phenylalanine ammonio lyase (PAL) and two hydroxycinnamoyl-CoA:quinate hydroxycinnamoyl transferases (HQT) enzymes in artichoke, where we detected different binding sites recognized by MYB TF in their promoter regions, suggesting that, as in other plant species, this class of transcription factors might be involved in the regulation of these artichoke genes.

In order to isolate one or more MYB TF from artichoke, sequences of the ortholog MYB12 from other species (e.g. Arabidopsis, tomato) were used to screen artichoke EST database. Primers were designed to amplify a fragment of putative MYB TF in artichoke cDNA. Sequence completion was performed by means of 5'-RACE and 3'-RACE technology.

This strategy allowed us to isolate two putative TF genes belonging to the MYB family. Further analyses are being performed to assess their role in phenylpropanoid accumulation in artichoke. Heterologous expression in bacteria, transient expression assays, quantitative real-time PCR are being performed to elucidate their function and interaction with phenylpropanoid biosynthetic genes.