Proceedings of the 50th Italian Society of Agricultural Genetics Annual Congress
Ischia, Italy – 10/14 September, 2006
ISBN **88-900622-7-4**

Oral Communication Abstract – 2.03

CHARACTERIZATION OF STRAWBERRY FLAVONOID PATHWAY BY MOLECULAR AND BIOCHEMICAL APPROACHES

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strawberry, fruits, flavonoids, gene expression, in vitro essays

Strawberry (*Fragaria x ananassa* Duch.) fruits are an excellent source of antioxidants, among which flavonoids are very effective in scavenging of free radicals. Biochemical and molecular analyses were carried out to characterise the flavonoid pathway in strawberry. Strawberry fruits of different genotypes were analyzed to determine the relative content of the major classes of flavonoids such as anthocyanins, flavan-3-ols and PAs. The analyses show remarkable differences in flavonoid accumulation pattern not only among genotypes but also within the same genotype grown in different geographical areas.

In parallel, structural genes encoding ANR, ANS, DFR, FHT, FGT, FLS and LAR were cloned from cv. Queen Elisa, and properties of encoded recombinant proteins were studied by means of *in vitro* assays. Microarray and quantitative Real-Time PCR experiments were carried out to determine the expression pattern of strawberry flavonoid genes. The results show fine modulations of the transcript abundance of genes involved in flavonoid biosynthesis and of a number of other coding sequences related to fruit quality. Finally structural genes of the flavonoid pathway are being analysed in genotypes with contrasting flavonoid pattern.

The ultimate goal of this study is the identification of key factors controlling flavonoid metabolism in strawberry fruit. The results could support breeding programs for the selection of strawberry genotypes with higher nutraceutical value.