Proceedings of the 52nd Italian Society of Agricultural Genetics Annual Congress
Padova, Italy – 14/17 September, 2008
ISBN **978-88-900622-8-5**

Poster Abstract – D.72

ANALYSIS OF SWEET ORANGE FLESH PROTEOME AT RIPENING TIME AND COMPARISON WITH TRASCRIPTOMIC DATA

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2D electrophoresis, LC-MSMS, anthocyanins, maturity flesh, Citrus sinensis

In Italy the sweet orange production is characterized by red pigmentation, due to the anthocyanin content. On citrus mature fruits anthocyanins are exclusively expressed in blood oranges and its hybrids.

The characterization of proteins isolated from flesh orange tissue is apparently an essential parameter for understanding orange anthocyanin pigmentation at ripening time.

In this work we present the analysis of a nucellar line of Moro (a blood cultivar) and Cadenera (a common orange) flesh orange using a proteomic approach.

For the fist time we succeeded in extracting the whole citrus flesh proteome following a procedure based on phenol extraction coupled with ammonium acetate precipitation.

Proteome maps obtained by 2D electrophoresis were compared to assess the extent to which protein distribution differs in orange flesh ripe of blood pigmented and common cultivar.

The tryptic digest of the spots differential expressed in the blood (23 spots) and in common oranges (39 spots) were characterized by LC-MSMS and the proteins were identified by searching protein and EST databases.

Proteins involved in stress response (chaperones) and primary metabolism were identified as being over-expressed in Cadenera flesh. Proteins involved in the secondary metabolism, such as anthocyanin's pathway, defence mechanism and primary metabolism were identified over-expressed in Moro cultivar.

Results obtained through proteomic analysis were compared with a previous investigation performed using a transcriptomic approach (Licciardello et al., 2008, Tree Genetics & Genomes 4: 315-331) using a subtracted cDNA library. The comparison with transcriptomic studies evidentiated some discrepancies, confirming the necessity to carry on proteomic analysis and to go deeper in the analysis of protein posttranscriptional and translational modifications. This combined study may reveal the need to associate both methodology approaches to have a general and complete perspective for the specific analysed challenge.