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Poster Abstract – F.25

TRANSCRIPTIONAL FACTORS IDENTIFICATION ON *CITRUS SINENSIS* L. DURING RIPENING PROCESS

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DNA expression, fruit development, transcriptional factors

Transcript DNA fractions analysis of fruit development point out as many metabolic pathway were involved in this process. Environmental conditions (temperature, light, etc.) could influence the metabolic activity.

Ripening has an impact on fibre content and composition, lipid metabolism, levels of vitamins and antioxidant compounds. The ability to understand and manipulate, through traditional breeding or biotechnological approaches, process key control points or regulatory points such as carotenoids, flavonoids, vitamins, and flavour volatiles biosynthesis, will allow the genetic control of the traits involved in the quality and nutritional aspects linked to ripening process.

The present work was direct to isolate transcriptional factor and differentially expressed DNA fractions during ripening in *Citrus sinensis* L.

Fruits from different cultivars and at three different ripening stages, from green to Physiological ripe, were collected. RNA was isolated from fruit tissue and cDNA was obtained in order to perform several experiments to isolate differentially fractions. Specific and random primers were applied both in order to isolate sequences of gene involved in ripening process.

All fragments differentially expressed isolated were sequenced. The sequences obtained were compared to databases to evaluate similarity with genes all ready isolated.

Sequences showed high homology with genes encoding protein with known activity as epimerase, carotene desaturase, zinc metabolism enzymes etc. Several transcriptional factors were found in particular some of them involved in sugar metabolism. All fragments isolated were used to produce specific cDNA library. Few sequences were submitted and accepted to EMBL data base.