

## **ISOLATION AND CHARACTERIZATION OF RNA FRACTIONS INVOLVED IN THE MATURATION PROCESS IN *OPUNTIA FICUS-INDICA* (L.) MILL.**

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Recently, an increasing interest towards the genetic mechanism regulating fruit ripening process has been registered (Bartley et al., 2002). Genes involved in different pathways, characterising this process, hold a key role to produce fruits of high nutritional and commercial quality.

This preliminary study has been carried out in order to study, to analyse and to characterize differentially expressed gene fragments during the prickly pear ripening process. Particularly, we focused on biophenol biosynthesis pathways because of the growing interests towards these metabolites, very important as nutraceuticals, due to their antioxidant activity.

*Opuntia ficus-indica* (L.) Mill. is an important crop, native of Mexico and widespread in Mediterranean basin. It is characterised by a high adaptability to the semi-arid environment and by multiple uses of the plants (fruit, vegetable, forage, fence, etc.).

Fruits of three prickly pear genotypes ("Bianca", "Rossa" and "Gialla") at different ripening stages (green, ripening and full ripe) have been collected.

Total RNA extraction from the pulp and peel of cactus fruits at the different ripening stages and stored at -80°C has been performed. Afterwards, cDNA has been synthesised and processed to isolate differentially expressed fragments.

Differentially amplified products have been obtained either among genotypes and the different sampling stages of the same genotype. Differentially expressed fragments have been cloned and sequenced. The sequence were compared to database to evaluate similarity with genes all ready isolated.

The next step will be directed to better outline the trascryptomic activity for some fragments isolated involved in secondary metabolites biosynthesis. In particular, further studies will be directed to carry out a quantitative analyses of the transcript fragments.