

## **TOMATO PLANTS OVEREXPRESSING CRYPTOCHROME 2 REVEAL MODIFIED EXPRESSION OF CHLOROPLAST GENOME**

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Tomato is a major food commodity especially in the Mediterranean countries. It represents a source of fibres, carbohydrates, proteins, lipids, minerals as well as of several vitamins and antioxidants, namely lycopene, that plays an important role in the prevention of some diseases like prostate cancer. The relative concentration of all these substances is finely regulated by biochemical processes that occur during ripening and which are related to genetic and environmental cues, as light and temperature. The ability to perceive and transduce light is important for normal growth and development of many organisms. Higher plants are able to monitor the environmental light conditions by using multiple wavelength-specific photoreceptors including red/far-red absorbing phytochromes and blue/UVA absorbing cryptochromes and phototropins. Light changes activate, by photo-perceptive proteins, a cascade of biochemical and molecular processes which change the physiological state of plants. Some of these changes may regard the chloroplast genome expression in photosynthetically active tissues. The cryptochromes, UV-A/blue light photoreceptors, play an important role in the monitoring, capturing and transmitting the light stimuli. In tomato four cryptochrome genes have been identified and characterized so far: CRY1a, CRY1b, CRY2 and CRY3. CRY2 gene has a central role in tomato plant development. Its over-expression in the transgenic CRY2-OX line, is of high relevance for the overproduction of anthocyanins and chlorophyll in leaves and fruits, suggesting its role in promoting the photosynthetic performance.

In this study we analysed the effects of CRY2 over-expression on chloroplast genome transcription in tomato, by using a genome tiling array. High density arrays containing 90k 35mer oligonucleotide probes were produced using CustomArray technology. The tiling array consisted of 30 nt overlapping probes, covering the entire chloroplast genome. Total chloroplast RNA extracted from wild type and CRY2-OX plants was used to hybridize the microarrays.

This study allowed to identify genes differentially expressed between CRY2-OX and wild type plants, in particular those involved in photosynthetic activity. We also found genes with complex transcriptional architecture, where transcripts corresponding to different parts of the same gene are detectable at different levels. The analysis also allowed to map the positions of 3' and 5' UTRs of coding genes. Potentially microRNAs could be also identified.