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Poster Abstract – C.29

A COMBINED PROTEOME AND TRANSCRIPTOME ANALYSIS OF DIURNAL RESPONSES IN CRY2-OX AND WILD-TYPE TOMATO PLANTS

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Most aspects of plant development are regulated in response to different environmental signals, and light is mainly important in this regard as an environmental cue during plant development. Plants respond to their surrounding solar radiation and adjust their growth and development accordingly. The day/night cycling of gene expression is controlled, primarily, by light and temperature and, secondarily, by a free-running internal molecular timekeeper known as the circadian clock. The intimate connection between light signalling pathways and the circadian oscillator allows the anticipation of the environmental transitions and the measurement of day-length as an indicator of changing seasons. Phytochromes, phototropins, and cryptochromes are the three main kinds of photoreceptor proteins in plants. These photoreceptors co-ordinately control seedling establishment, entrainment of the circadian clock, and the transition from vegetative to reproductive growth.

Recent microarray analyses in our lab have established that in wild-type (wt) tomato diurnal rhythms in gene expression affect a large portion of the transcriptome. In addition, comparative transcription analysis between wt and the transgenic tomato overexpressing cryptochrome 2 gene (*CRY2-OX)* has shown that the CRY2 controls the diurnal transcription profiles of several phytochrome and cryptochrome genes.

In order to study possible effects of cryptochrome 2-mediated light signals on the global expression profiles of tomato genes, we performed large scale transcription comparisons in wt and *CRY2-OX* by using the long oligo-based TOM2 microarray. Tomato plants were grown under a daily light cycle of 16h light/8h darkness (LD) and sampled every 4h for 24 hours.

However, mRNA-based screening are not necessarily comprehensive in the context of gene expression at the protein level due to post-transcriptional control and post-translational modifications. Thus a direct screening of the protein profiles by using 2D differential in-gel analysis (DIGE) and mass spectrometry has been carried out to probe proteome expression in wt and *CRY2OX* in a diurnal cycle.

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