

## **CRF (CYTOKININ RESPONSE FACTOR) TRANSCRIPTION FACTORS IN ABIOTIC-STRESS AND FLOWERING TIME: FROM ARABIDOPSIS THALIANA TO LACTUCA SATIVA AND SOLANUM LYCOPERSICUM**

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The abiotic stresses brought about by climate change, such as drought, floods, alterations in temperature and others, are altering important agronomic traits, such as flowering time in horticultural species. This can have a negative impact on the abundance and organoleptic properties of these crops.

Adaptation to environment involves the accumulation of random mutations that can be fixed if they confer an evolutionary advantage. Genetic diversity in natural and domesticated plants populations is the richest source of allelic variants that are "tested" naturally by evolutionary mechanisms, and therefore is the most important resource for genetic improvement. More than 60% of adaptive mutations are associated with polymorphisms in transcription factors (TFs) DNA sequences that leads to variations in the way they regulate their target genes in response to environmental and developmental signals. In facts, transcription represents the primary regulation level in determining an organism phenotype starting from his genotype. TFs are thus the main targets on which the process of adaptation of genotypes to the environment acts.

CRFs (CYTOKININ RESPONSE FACTORS) are ubiquitous TFs of the plant kingdom and are central in the hormonal crosstalk between auxins and cytokinins, being induced by cytokinins (CK) and being at the same time regulators of

auxin transporters (PINs). These TFs play fundamental roles both in plant development and abiotic stress responses and are at the core of the trade-off that takes place in plant adaptation to the environment.

In this study, clade III CRFs orthologs of *Arabidopsis thaliana* have been identified in the agriculturally relevant species *Lactuca sativa* (model for the Asteraceae family) and *Solanum lycopersicum* (model for the Solanaceae family) through phylogenetic analyses. CRFs gene expression has been analysed in silico in different tissues and conditions. Selected transcriptomic data, available in public databases such as NCBI's GEO or published, have been analysed by k-means clustering to identify co-expression modules related to stress response and flowering to compare transcriptional networks amongst the three different species in the crosstalk between CKs and auxin. In addition, collections of natural and domesticated varieties of the three species are being explored in silico, in search of mutations "selected" by the evolutionary process, which can improve plant resilience and adaptation to stress. The knowledge developed will be used for the genetic improvement of *Lactuca sativa* and *Solanum lycopersicum*, to create molecular markers that can be used to accelerate the breeding of new resilient crops that maintains their productive and organoleptic characteristics in the more variable and extreme environmental conditions that will characterize the upcoming decades.