

ANALYSIS OF GENE REGULATORY NETWORKS IN PEACH: THE INTERPLAY BETWEEN TRANSCRIPTION FACTORS AND MICRORNAs

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MicroRNAs (miRNAs) are a class of non-coding small RNAs with fundamental roles in key plant biological processes such as development, signal transduction and environmental stress response. MiRNAs act on gene regulation at post-transcriptional level, a phenomenon known in plants as PTGS (Post Transcriptional Gene Silencing), through sequence-based interaction with target mRNAs. Transcription factor families comprise most of the highly conserved miRNA targets. At the same time microRNA genes expression is controlled by transcription factors and both the two types of *trans*-regulators are part of complex regulatory networks thus exerting a widespread impact on gene expression.

In this work the interplay between microRNAs and transcription factors has been studied in peach and complex regulatory networks have been identified. In particular feed-forward loops, involving a transcription factor regulating a target gene together with a microRNA, which is regulated in turn by the same transcription factor have been deeply analyzed.