

REGULATORY NETWORKS CONTROLLING PHOTOSYNTHESIS IN LEAVES OF THE MEDITERRANEAN SPECIES *CICHORIUM ENDIVIA*

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Cichorium endivia is a typical Mediterranean species that has been cultivated since ancient times in the Mediterranean basin. *C. endivia* leaves represent an excellent source of health benefiting plant nutrients and are widely consumed as fresh, minimally processed and cooked traditional food. *C. endivia* commercial varieties show a high degree of intraspecific morphological variation, and two major varieties can be distinguished: var. *latifolium* with broad leaves (escarole) and var. *crispum* with narrow curly/crisp leaves (endive).

Due to the striking morphological diversity of the leaves in escarole and endive, *C. endivia* represents a good model to study the relationship between leaf shape and function. A standing question, that is both of fundamental and applied interest, is the adaptive value of leaf shape in relation with its photosynthetic activity.

We used transcriptomic data from leaves of two commercial cultivars of endive and two of escarole to explore regulatory networks of transcription factors (TFs) involved in leaf development and leaf function through cluster analysis and construction of Gene Co-expression Networks (GCN). We identified modules of functionally related TF genes acting in *C. endivia* leaves and regulatory networks that are differential between broad and curly leaves. We then analyzed how genes related to photosynthetic activity, as well as to molecules involved in energy dissipation and reactive oxygen species (ROS) detoxification (flavonoids, carotenoids and ascorbic acid), enter into the GCN networks and relate to the TF modules identified with a guide-gene approach. This allowed to predict the regulatory networks controlling photosynthesis in *C. endivia* leaves, their relationship with leaf morphological characteristics and the genetic hubs that are at the boundaries between shape and function. Physiological analysis of the photosynthesis properties linked to different leaf shapes were carried out to corroborate predictive models of the regulatory networks identified. Finally, target genes to be used in breeding selection programs and biotechnology were predicted based on network topological properties and node ranking.