

**INTEGRATED “OMICS” OF LEAF ENDIVES STRESSED BY DOWNPOUR-INDUCED WATERLOG REVEAL INSIGHTS IN NUTRIENT VARIATION AND MOLECULAR ASPECTS OF KESTOSE AND INULIN PATHWAY.**

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Curly- and smooth- leafed endives (*Cichorium endivia* var. *crispum* and var. *latifolium*) are consumed worldwide as fresh or minimally processed salads that provide healthy nutrients. In Italy, endive is mostly cultivated outdoors in autumn-winter cycles because it is a low input and cold-tolerant vegetable, though very sensitive to waterlogging. Phenotypic, metabolic and transcriptomic analyses were used to study variations in leaves of curly ('Domari', 'Myrna') and smooth cultivars ('Flester', 'Confiance') grown in short-term waterlog due to unexpected rainfall excess before harvest. After recording loss of head weights in all cultivars (6-35%), which was minimal in 'Flester', NMR untargeted profiling revealed variations as influenced by genotype, environment and interactions, and included drop of total carbohydrates (6–50%) and polyols (3–37%), gain of organic acids (2–30%) and phenylpropanoids (98–560%), and cultivar-specific fluctuations of amino acids (–37 to +15%). The enhancement of endive transcriptome by a lettuce-genome driven assembly together with the analysis of differential transcription (RNA-seq, Illumina) in stressed vs non stressed leaves collected at harvest allowed the identification of cultivar-specific (minimal in the least affected 'Flester') and cultivar-independent differentially expressed genes (DEGs). The latter DEGs were enriched in GO terms consistent with those of leaves of waterlogged crops, and inclusive of carbohydrate metabolic process. The loss of sucrose, kestose and inulin recurred in all cultivars and the sucrose-inulin route

was investigated by covering over 50 genes of sucrose branch and key inulin synthesis (*fructosyltransferases*) and catabolism (*fructan exohydrolases*) genes. The narrow down on the sucrose-inulin branch showed that the lowered expression of a sucrose gene set in parallel with that of *SUCROSE:SUCROSE-1-FRUCTOSYLTRANSFERASE* (*1-SST*) accounted for sucrose and kestose contents drop of stressed leaves. Two anti-correlated modules harbouring candidate hub-genes, including *1-SST*, were identified by weighted gene correlation network analysis, and proposed to control positively and negatively kestose levels. In silico analysis further pointed at transcription factors of GATA, DOF, WRKY types as putative regulators of *1-SST*.