

CHARACTERIZATION OF ENDIVE SESQUITERPENE PATHWAY THROUGH ANALYSES OF RNA-SEQ DIFFERENTIAL GENE EXPRESSION AND METABOLITE CONTENT VARIATION

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The CISIA project (<http://www.ibba.mlib.cnr.it/Projects/Cisia/Project.html>) provided tools to enhance valorization and traceability of endives (*Cichorium endivia*), which are consumed as fresh or minimally processed foods. Sesquiterpene lactones (SL) and phenolics complexly regulate the bitter flavor of these vegetables. The SL content of lactucin-like (lactucin, 1,3-dihydrolactucin, 8-deoxylactucin, 11(s),13-dihydro-8-deoxylactucin) and lactucopicrin-like (lactucopicrin, 11(s),13-dihydrolactucopicrin) compounds was measured in seven cultivars. Principal component analysis of SL content variation could mostly discriminate curly- from smooth-leafed (syn. escaroles) types and pointed at a strong positive correlation among curly-leafed genotypes, high amounts of lactucin- and lactucopicrin-like molecules and bitterness predictive scores. An endive reference transcriptome, previously assembled from a curly-cultivar, allowed the annotation of unigenes in the sesquiterpenoid and triterpenoid biosynthesis pathway. Out of 22 unigenes, the *germacrene A-synthase* (*GAS*), which acts in the branch leading to the key SL precursor costulonide, showed significant differential expression in those cultivars with most divergent SL contents ('Myrna' vs 'Domari' in the curly group; 'Confiance' vs 'Flester' in the smooth group; 'Myrna' vs 'Flester'). The very strong positive correlation ($r \geq 0.9$) between SL contents and the transcriptions of three different *GAS* genes suggested a key role of these, consistently with the finding that terpene accumulation and synthase gene expression go in parallel.