

WHEN CANNABIS SATIVA L. TURNS PURPLE: BIOSYNTHESIS AND ACCUMULATION OF ANTHOCYANINS

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Environmental cues elicit anthocyanin synthesis in plant vegetative and reproductive tissues. Their accumulation in different organs accounts for their diverse biological functions, mainly related to their antioxidant properties, and it depends on a temporally and spatially regulated mechanism controlled by the action of a well-known multi-transcription factor complex. Despite the highly recognizable value of *Cannabis sativa L.* as a natural biorefinery of phytochemicals, very little information is known on anthocyanin pigmentation in this species. In this work, a targeted quantification of anthocyanins via HPLC-MS/MS, combined with the transcriptional profile via RT-qPCR of genes encoding for structural (CsF3'H, CsF3'5'H, CsDFR, CsANS) and decorating (Cs3GT, CsOMT) enzymes and regulatory transcription factors (CsMYB82, CsMYB87, CsbHLH112, CsbHLH114) in different *C. sativa* tissues, help gain insights into the anthocyanin pathway in this species. To the best of our knowledge, this is the first report on the identification of cyanidin-3-rutinoside (keracyanin) as the major anthocyanin in *C. sativa* vegetative and floral tissues. Keracyanin amounts were higher than in small berries, suggesting that *Cannabis* biomass is a valuable source of colored antioxidants to be exploited in diverse applications. Furthermore, a gene putatively encoding for an anthocyanin DTX35 type transporter and CsTTG1 were identified *in silico* and their transcriptional levels were assessed via RT-qPCR. A correlation analysis of the expression profiles of anthocyanins genes, reinforced our results and allow us to provide the first model of anthocyanin regulation in *C. sativa*,

revealing candidate genes that could be addressed for breeding purposes and metabolic engineering strategies. Moreover, the valuable amounts of keracyanin in Cannabis genotype shed light on a new research scenario for phytochemical exploitation in a circular economy context.