

PHYTOCANNABINOID BIOSYNTHESIS DURING EARLY STAGES OF DEVELOPMENT OF YOUNG CANNABIS SATIVA L. SEEDLINGS: INTEGRATING BIOCHEMICAL AND TRANSCRIPTIONAL DATA

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Cannabis sativa (L.) is characterized by great genetic and phenotypic diversity, also expressed in the array of bioactive compounds synthesized. Despite its great potential economic interest, knowledge of the biology and genetics of this crop is incomplete, and still, many efforts are needed for a complete understanding of the molecular mechanisms regulating its key traits. The main bioactive compounds synthesized by *C. sativa* are the phytocannabinoids, terpeno-phenolic compounds accumulating in glandular trichomes in different combinations and amounts characterizing the chemical profile (chemotype) of the plant. To better understand the synthesis of these compounds, we analyzed the transcription levels of phytocannabinoid pathway genes during the early phases of plant development, then compared the transcriptional results with a chemical characterization of the same samples. The work was conducted on both industrial and medicinal *C. sativa* plants, using samples belonging to three different chemotypes. Genes coding for the cannabinoid synthases, involved in the last step of the cannabinoid biosynthetic pathway, were found to be already expressed in the seed, providing a measure of the importance of this metabolism for the plant. However, no phytocannabinoid was produced until the *Prenyl Transferase* (PT)

gene was transcribed at the cotyledonary stage (BBCH 9). Cannabichromenic acid (CBCA) was confirmed to be the first cannabinoid accumulating in the seedlings, shortly after emergence, and it was found that there is a good correspondence between the transcriptional profile of *Cannabichromenic acid synthase* (CBCAS) gene and the accumulation of CBCA in all chemotypes.