Poster Communication Abstract – 7.17

METABOLIC CHARACTERIZATION AND TRANSCRIPTIONAL PROFILING OF PHENYLPROPANOIDS IN CANNABIS SATIVA L. INFLORESCENCES WITH DIVERSE CHEMOTYPE

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Cannabis sativa, inflorescences, phenylpropanoids, UHPLC-HRMS, transcription factor

Among secondary metabolites, phenylpropanoids and flavonoids have been investigated to lesser extent in Cannabis sativa L., compared to phytocannabinoids and terpenoids due to their pharmaceutical properties and role in determining the scent of inflorescences, respectively. Understanding the biochemical composition of phenylpropanoids from Cannabis inflorescences, the molecular basis of flavonoids synthesis and how their content can be modulated by acting on specific transcription factors will shed light on others biologically active metabolites that can be of interest for diverse industries. Furthermore, flavonoids may exert a synergistic effect on phytocannabinoids bioactivity when considering the entire phytocomplex of Cannabis inflorescence. In this work, we used an untargeted metabolomic approach via UHPLC-HRMS to investigate the composition in phenylpropanoids. Inflorescences were collected from 13 Cannabis genotypes, included in a huge collection of C. sativa maintained at CREA- Research Center for Cereal and Industrial Crops (CREA-CI) Bologna and Rovigo, comprising two medical varieties called CINBOL and CINRO, cultivated in open filed trial at CREA-CI Rovigo in 2019. Based on a previous work involving the in silico analysis of Cannabis MYBs and bHLHs, candidate genes for the regulation of flavonoids synthesis and structural enzymes encoding genes were identified and selected for transcriptional analysis via RT-qPCR on the same plant materials. More than 1400 compounds

belonging to phenylpropanoids were identified and categorized in diverse classes of flavonoids and phenolic acids and transcriptional data integrated with the biochemical composition of Cannabis genotypes.