

# **A Genome-Scale Metabolic Draft Reconstruction of *Cannabis sativa* with the integration of non-targeted LC-MS based metabolomics data.**

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In the last two decades, Genome scale model reconstructions has become a fundamental tool taking advantage of the development of high throughput data of omics technologies to study and understand complex interactions of organisms. In plant systems biology, genome-scale modelling has gain considerable progress thanks to reconstruction of *Arabidopsis thaliana*, maize *Zea mays*, sugarcane *Saccharum officinarum*, among others; however, modelling of crops with increasingly importance such as *Cannabis sativa*, could benefit economic growth of specific populations.

Colombia has suffered for the past decades a complex social problematic related to illicit crops which includes forced displacement, violence, environmental damage, among other consequences for vulnerable populations. Even a considerable effort has been made in regulation and legalization of illicit crops, especially *Cannabis sativa*, still exits the necessity to explore new ways and models to approach this problematic such as research and development.

Here we would present a first draft of Genome-Scale Metabolic of *Cannabis sativa* with the integration of non-targeted LC-MS based metabolomics data, which could help to understand their complex interactions toward applications in the anticancer drug development, and other potential applications in food, cosmetic, textile and agrochemical industries. Starting from reference genome avail in NCBI databank, we will annotate and create a semi-automated reconstruction of model using Kraken and Raven respectively. Secondly, we will implement curation steps using gap-filling algorithms such as GapFind and GapFill, and manual curation supported by biochemical data reported in literature. Finally, we will integrate experimental metabolomic data through the mapping of gene-protein-reaction relationships to obtain context-specific model of terpenes and cannabinoids production, using constraint-based reconstruction and analysis.