THE EMERALD CONFERENCE
Produced by MJBizScience

March 1-3, 2023
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Exploring the full spectrum of genetic variation in Cannabis with Pantograph

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Abstract: The complex genetic makeup of the Cannabis genome and the huge genetic diversity between diverse strains prompt larger sequencing efforts to assemble whole Cannabis genomes. Multiple sequences can be summarized as a pangenome, and recent algorithmic advances now enable the generation of genome graphs that contain the full spectrum of genetic variation between sequences. Compared to analyzing small nucleotide changes based on a single reference sequence, pangenomes help identify more large-scale and complex variation as well as sequence not contained in the reference genome. This extends and improves the set of markers important for traits and contributes to a better understanding especially of the still underexplored genetic diversity of Cannabis as the basis to develop tailored strains.

This wealth of genomic information evokes the need to visually explore the genetic variance and to evaluate associations to phenotypic differences. For this purpose, we are developing Pantograph, an interactive browser of pangenome graphs capable of visualizing the entirety of genetic variation in multiple zoom levels from single nucleotide level to whole chromosome views. We will introduce Pantograph and show how it represents SNPs, Indels, SVs, copy number variation, and complex rearrangements, incl. cannabinoid and terpene synthase genes, in one framework. Arbitrary meta data like phenotypic values or environmental factors can be shown alongside the sequences to help link genetic variation to phenotypic traits and to inspect QTL regions. The functional impact of variants can be assessed by the simultaneous display of multiple genome annotations.