

# THE EMERALD CONFERENCE

Produced by MJBizScience

February 27 - March 1, 2022  
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## **Genomic Tools for Cannabis sativa and Psilocybe Cubensis**

**Speaker: Kevin J. McKernan, Founder & CSO, Medicinal Genomics**

**Abstract:** With many cannabis reference genomes now public, the search for pathogens that infect the plant has become greatly simplified. RNA sequencing can now be performed and screened against these genome references for novel RNA that can then be assembled and reviewed for viral content. These references greatly accelerated the development of 12 virus/viroid qPCR assays. We describe these assays' utilization in the cannabis industry and our progress building the same genomics foundation in *Psilocybe cubensis*. Using Pacific Biosciences HiFi sequencing and Phase Genomics Proximity ligation assay (HiC), we constructed a chromosome scale, annotated reference genome for *Psilocybe cubensis*. The genome now contains 13 chromosomes, 46Mb with an N50 contig lengths of 3.6Mb. Several chromosomes are tip to tip chromosomes with visible telomeres on each end. Using this reference genome, we have sequenced and mapped an additional 81 *Psilocybe* genomes to catalog the genetic diversity and microbial contaminants frequently found in this genus.