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The complete mitochondrial genome for Cannabis sativa

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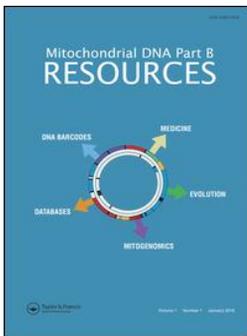


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The complete mitochondrial genome for *Cannabis sativa*

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ABSTRACT

The following report details the first annotated mitochondrial genome for the Carmagnola variety of *Cannabis sativa*, the first reference genome for the Cannabaceae family. The total length is 415,499 bp and contains 54 genes, which sub-divide into 38 protein-coding genes, 15 tRNA genes, and 3 rRNA genes.

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Cannabis sativa has been an important agricultural crop throughout human history. Despite its multiple uses, *C. sativa* has been classified as a drug in many countries, a political aspect that has impeded scientific investigation on the plant (Li 1973; Russo 2007). *C. sativa* belongs to the family Cannabaceae, which is composed of 10 different genera and ~100 species (Bell et al. 2010). The *C. sativa* plants are wind-pollinated, usually annual and most individuals are dioecious, but monoecious individuals occur (Li 1973). In addition to the critical functions of the mitochondrion, its genome can reveal important evolutionary patterns. Further, there are a disproportionately low number of assembled plant mtDNA genomes on NCBI due, in part, to inherent difficulties in assembly. Thus, the availability of a complete assembled, and annotated *C. sativa* mitochondrial genome provides a useful tool for a variety of studies in diverse biological fields.

DNA from a female plant from the Carmagnola variety of *C. sativa* grown in Colorado (39°58'47.90" N, 105°4'30.05" W) was extracted using a Quiagen DNeasy plant kit (Germantown, MD). The whole-genome library of genomic DNA was sequenced using the Illumina HiSeq2500 platform (San Diego, CA) and yielded 40,963,006, 130bp paired-end reads with an average insert size of 150bp. The published *Cannabis* genome assembly includes a partially assembled mitochondrion of the Purple Kush variety (van Bakel et al. 2011), which we downloaded from the short-read archives of Genbank and used as a reference to generate an improved, error-corrected, and annotated *Cannabis* mitochondrial genome. The mitochondrion was then assembled *denovo* using SPAdes genome assembler v.3.1.1 (Bankevitch et al. 2012). We merged the contigs that overlapped, filled remaining gaps, and extended the end of the assembled contig until we had a circularized sequence

resulting in the complete genome. Subsequently, we performed error correction by aligning the trimmed reads to the draft genome. The 54 genes present in our genome were annotated using Mitofy (Alverson et al. 2010).

We downloaded 17 genes (*atp1*, *atp6*, *atp9*, *cox1*, *cox2*, *cox3*, *matR*, *nad1*, *nad2*, *nad4*, *nad4L*, *nad5*, *nad6*, *nad7*, *nad9*, *rps3*, and *rps12*) shared among 11 species from the public repository NCBI (Table 1). These CDS (coding sequences) were aligned using the software Clustal X with default parameters (Larkin et al. 2007). The 17 alignments were concatenated and a maximum likelihood tree (Figure 1) was constructed using MEGA v. 6.0612 (Takamura et al. 2013). The alignment of these 17 CDS from the 11 species was ~16,173 bp.

This phylogenetic analysis illustrates the relationship between the species within each order. Once we collapse the low bootstrap orders into polytomies, our phylogenetic tree reflects the most accepted relationship between the orders in the angiosperms. Using zPicture10 (Ovcharenko et al. 2004), we aligned our assembled genome to the unannotated Purple Kush13 and LA Confidential (<http://www.medicinalgenomics.com/chloroplast-and-mitochondrial-haplotypes-of-cannabis>) genomes.

Our fully error-corrected assembly differs from both, with 69 mismatches and 271 inserted/deleted bases relative to Purple Kush; or 164 mismatches and 212 inserted/deleted bases relative to LA Confidential. As our genome assembly and error correction algorithms differ, it is not clear if these discrepancies represent biological distinctions or instead errors in sequencing or assembly. We are confident that our assembly, KR059940, represents the best possible one given in the current technology.

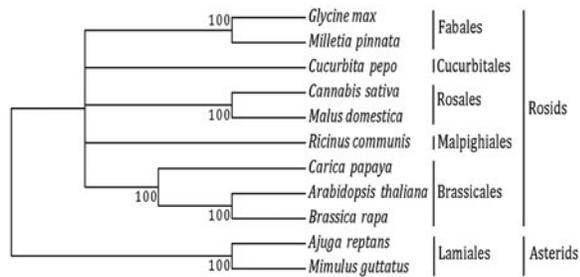


Figure 1. Maximum likelihood tree. We used 17-shared genes from nine species from the subclass Rosids: Order Brassicales – *Arabidopsis thaliana* (NC_001284), *Brassica rapa* (NC_016125), and *Carica papaya* (NC_012116); Order Cucurbitales – *Cucurbita pepo* (NC_014050); Order Fabales – *Glycine max* (NC_020455), and *Millettia pinnata* (NC_016742); Order Malpighiales – *Ricinus communis* (NC_015141); and Order Rosales – *Malus domestica* (NC_018554), and *Cannabis sativa* (KR_059940). We used two species from the subclass Asterids and order Lamiales as outgroups: *Ajuga reptans* (NC_023103), and *Mimulus guttatus* (NC_018041).

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Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content.

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