MITOGENOME ANNOUNCEMENT

The complete mitogenome of Colletotrichum lupini var. setosum

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ABSTRACT

The structure of *Colletotrichum lupini* mitogenome is typical of a fungus from the genus *Colletotrichum* similar to *C. acutatum* and *C. lindemuthianum*. The sequenced mitogenome has a total length of 36 554 bp. The nucleotide composition in the following genome is: 35.7% - A, 16.5% - C, 13.4% - G and 29.9% - T. In the *C. lupini* mitogenome we identified 46 genes: 15 protein coding genes, two ribosomal RNAs and 29 tRNA genes.

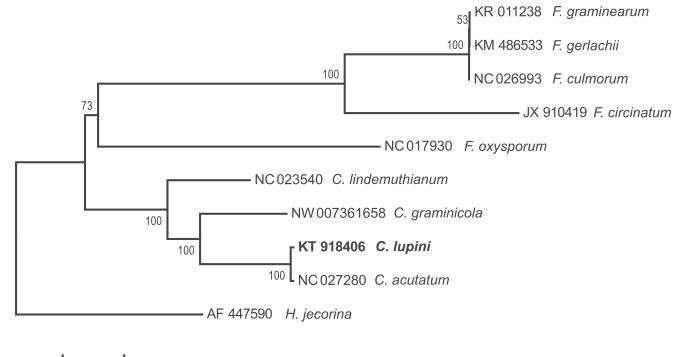
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A variety of species belonging to the genus *Colletotrichum* cause diseases, commonly described as anthracnose, in many crops and wild plants (Damm et al. 2012). *Colletotrichum lupini* was separated as an independent taxon within the *C. acuta- tum* species complex (Nirenberg et al. 2002) and it is an

economically significant pathogen of lupin crops worldwide. Damm et al. (2012) demonstrated that *C. lupini* is a phylogenetically distinct species of the *C. acutatum* complex.

In this study, we sequenced the complete mitogenome (mitochondrial genome) of the *C. lupini* strain CBS 119142



0,2

Figure 1. The phylogenetic tree of the *Colletotrichum lupini* mitogenome and related organisms. The full mitochondrial DNAs of *C. acutatum* (NC_027280 30 892 bp), *C. lindemuthianum* (NC_023540 36 957 bp), *C. graminicola* (NW_007361658 39 649 bp), *C. lupinii* (KT918406 36 554 bp), *Fusarium oxysporum* (NC_017930 34 477 bp), *F. circinatum* (JX910419 67 109 bp), *F. culmorum* (NC_026993 103 844 bp), *F. graminearum* (KR011238 97 460 bp), *F. gerlachii* (KM486533 93 428 bp) and *Hypocrea jecorina* (AF447590 42 130 bp) were aligned using Clustal W algorithm. The phylogenetic analysis was done using the Maximum Likelihood method based on the Tamura and Nei model (1993) in MEGA6 (Tamura et al. 2013). The percentage of trees in which the associated taxa clustered together (for 1000 bootstrap replications) is shown next to the branches. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.

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(GenBank accession number KT918406) isolated from *Lupinus albus* in Elsenburg 33°51′00″S, 18°50′00″E (South Africa, 1995). Genome libraries were prepared from the genomic DNA using a Nextera XT kit (Illumina Inc., San Diego, CA). Genomic DNA was extracted from *C. lupini* mycelium using a Promega Kit (Promega GMBH, Madison, WI). Prepared libraries were sequenced on the Illumina MiSeq platform (Illumina Inc., San Diego, CA) with a 150 bp paired-end read, version 3.

The trimmed reads were mapped to the reference mitogenomes of *C. acutatum* (KR349346) and *C. lindemuthianum* (KF953885) using Geneious Mapper (version 8.0.4) (http:// www.geneious.com, Kearse et al. 2012). Next, we selected contigs containing annotated genes and remapped these contigs to elongate them. After every 10 iterations, we assembled the contigs to obtain scaffolds and finally the full circular sequence. The mitogenome was annotated using PlusMapper (Dong et al. 2004) and was manually adjusted. ORF Finder (http://www.ncbi.nlm.nih.gov/gorf/gorf.html) was used to verify annotated genes and to identify any potential genes in the 27 003–32 670 region. The length and positions of the rRNA large subunit were identified by alignin to numerous fungi reference sequences using Megablast (Morgulis et al. 2008).

The full length of the *C. lupini* mitogenome is 36554 bp. We identified 46 genes: 15 protein-coding genes, two ribosomal RNAs and 29 tRNA genes (for all 20 amino acids). All identified genes have the same direction. The phylogenetic analysis shows that sequenced mitogenome of *C. lupini* is located in the same clade with other *Colletotrichum* full mitogenomes (Figure 1).

Disclosure statement

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

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