



(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>, Kears e 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 27003–32670 region. The length and positions of the rRNA large subunit were identified by aligning to numerous fungi reference sequences using Megablast (Morgulis et al. 2008).

The full length of the *C. lupini* mitogenome is 36 554 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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