



Complete mitochondrial genome sequence of lettuce pathogenic fungus, *Fusarium oxysporum* f. sp. *lactucae* 16-086

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ABSTRACT

Fusarium oxysporum f. sp. *lactucae* 016-086 is a plant pathogenic filamentous fungus isolated from wilted lettuce in Korea. We reported complete mitochondrial genome sequence of *F. oxysporum* f. sp. *lactucae* 016-086. Total length of this mitogenome is 41,826 bp and it encoded 42 genes (14 protein-coding genes, 2 rRNAs, and 26 tRNAs). Nucleotide sequence of coding region takes over 30.6%, and overall GC content is 32.5%. Phylogenetic tree of *Fusarium* mitochondrial genomes presented distinct clades along with nine *formae speciales*. This mitogenome will contribute distinguishing *formae speciales* of *F. oxysporum* clearly with additional mitogenomes sequenced in the near future.

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Fusarium oxysporum f. sp. *lactucae*; mitochondrial genome; *formae speciales*; Ascomycota

Fusarium oxysporum is an ascomycete, soilborne, and pathogenic fungus (Alabouvette and Couteaudier 1992; Fravel et al. 2003). Owing to next generation sequencing technologies, more than 60 fungal mitogenomes have been assembled (Pantou et al. 2008; Fourie et al. 2013; Brankovics et al. 2017; Park et al., in preparation). These mitogenomes cover only nine out of around 120 *formae speciales*, suggesting mitogenomes of more *formae speciales* should be investigated to understand their genetic diversities as well as host-specificity. *F. oxysporum* f. sp. *lactucae* 16-086 isolated from wilted lettuces in Iksan area, South Korea (36.041085 N, 126.976071 E) and identified based on translation elongation factor 1-a gene sequences (Samson et al. 2004) confirmed strong pathogenicity to lettuces as other *F. oxysporum* did. To understand mitogenomic background of *F. oxysporum* f. sp. *lactucae*, we sequenced its complete mitochondrial genome.

Its DNA was extracted from the hyphae of *F. oxysporum* f. sp. *lactucae* 16-086, taken from Horticultural and Herbal Crop Environment Division (16-086), by using HiGene™ Genomic DNA Prep Kit (BIOFACT, Korea). Raw data generated by HiSeq4000 were subject to *de novo* assembly done by Velvet 1.2.10 (Zerbino and Birney 2008), gap filling with SOAPGapCloser 1.12 (Zhao et al. 2011), and base confirmation with BWA 0.7.17 and SAMtools 1.9 (Li et al. 2009; Li 2013). Geneious R11 11.0.5 (Biomatters Ltd, Auckland, New Zealand) was used to annotate its mitochondrial genome by comparing with that of *F. oxysporum* f. sp. *cucumerinum* (LT906315; Brankovics et al. 2017).

The length of *F. oxysporum* f. sp. *lactucae* 16-086 mitochondrial genome (Genbank accession is MN259514) is 41,826 bp. Its mitochondrial genome encoded 42 genes consisting of 14 protein-coding genes (PCGs), 2 rRNAs, and 26 tRNAs, different from that of *F. oxysporum* f. sp. *cucumerinum* (LT906315). Nucleotide sequence of coding region takes over 30.6%, and overall GC content is 32.5%.

Based on alignment between 16-086 and *F. oxysporum* f. sp. *cucumerinum* (LT906315), 3,889-bp deletion on 16-086 mitogenome covering three genes and one pair of direct repeat sequences were found. Except it, only six single nucleotide polymorphisms (SNPs) and 18 insertions and deletions (INDELs) are identified. There are 62 SNPs and 180 INDELs except 3,861-bp deletion on 16-086 mitogenome based on alignment between 16-086 and *Fusarium oxysporum* f. sp. *cubense* race 1 (LT906350), presenting that *F. oxysporum* f. sp. *lactucae* is very close to *F. oxysporum* f. sp. *cucumerinum*.

Sequence alignment of 14 conserved PCGs extracted from twenty-five *Fusarium* mitochondrial genomes was conducted by MAFFT 7.388 (Katoh and Standley 2013). The bootstrapped neighbor joining and maximum likelihood phylogenetic trees were constructed using MEGA X (Kumar et al. 2018) and IQ-TREE 1.6.6 (Nguyen et al. 2014), respectively. Based on phylogenetic tree, nine *formae speciales* of *F. oxysporum* show distinct phylogenetic position and it is clearly distinct with *Fusarium commune* (Figure 1). In addition, *F. oxysporum* f. sp. *lactucae* and *F. oxysporum* f. sp. *cucumerinum* (LT906315) are clustered tightly, agreeing with number

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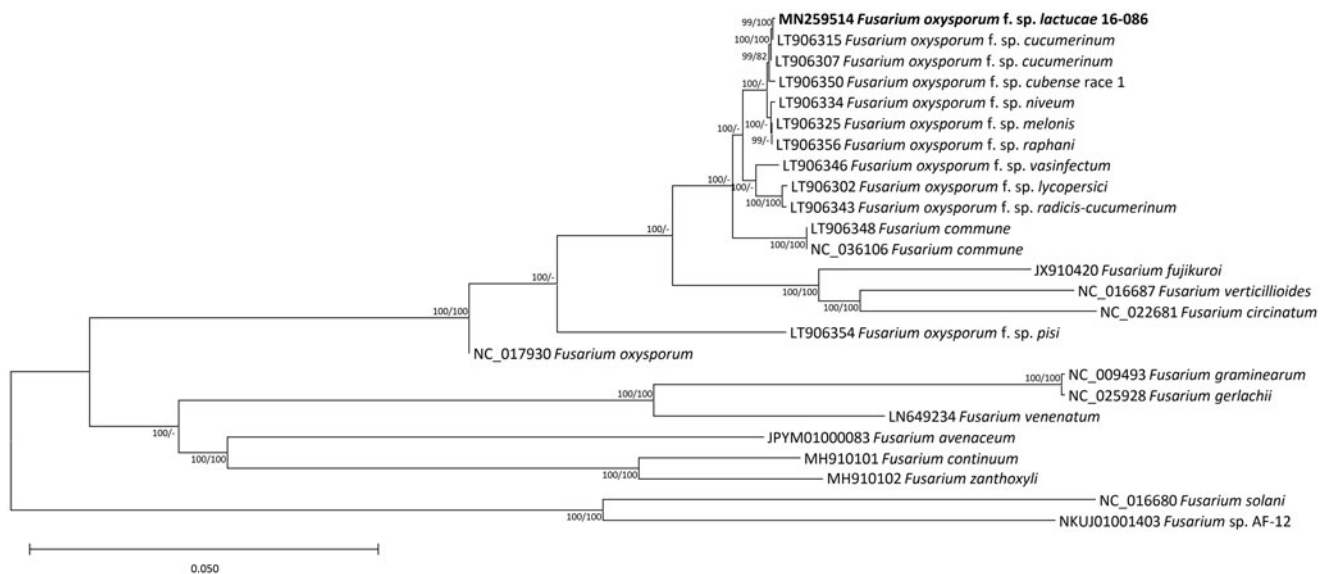


Figure 1. Neighbor joining (bootstrap repeat is 10,000) and maximum likelihood (bootstrap repeat is 1,000) phylogenetic trees of *Fusarium* based on 25 *Fusarium* mitochondrial genomes: *F. oxysporum* f. sp. *lactucae* (MN259514 in this study), *F. oxysporum* f. sp. *cucumerinum* (LT906315, LT906307), *F. oxysporum* f. sp. *cubense* race 1 (LT906350), *F. oxysporum* f. sp. *niveum* (LT906334), *F. oxysporum* f. sp. *melonis* (LT906325), *F. oxysporum* f. sp. *raphani* (LT906356), *F. oxysporum* f. sp. *vasinfectum* (LT906346), *F. oxysporum* f. sp. *lycopersici* (LT906302), *F. oxysporum* f. sp. *radices-cucumerinum* (LT906343), *F. oxysporum* f. sp. *pisi* (LT906354), *F. oxysporum* (NC_017930), *F. commune* (LT906348, NC_036106), *F. fujikuroi* (JX910420), *F. verticillioides* (NC_016687), *F. circinatum* (NC_022681), *F. graminearum* (NC_009493), *F. gerlachii* (NC_025928), *F. venenatum* (LN649234), *F. avenaceum* (JPYM01000083), *F. continuum* (MH910101), *F. zanthoxyli* (MH910102), *F. solani* (NC_016680), and *Fusarium* sp. AF-12 (NKUJ01001403). Phylogenetic tree was drawn based on neighbour joining tree from alignment of complete mitochondrial genomes. The numbers above branches indicate bootstrap support values of neighbor joining and maximum likelihood phylogenetic trees, respectively.

of SNPs and INDELS between two mitogenomes. Our mitogenome can contribute for distinguishing *formae speciales* clearly with more *F. oxysporum* mitogenomes in the near future.

Disclosure statement

The authors declare that they have no competing interests.

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