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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the bambusicolous fungus *Fusarium bambusae* (Nectriaceae, Ascomycota)

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ABSTRACT

The complete nucleotide sequence of the mitochondrial genome of the bambusicolous fungus *Fusarium bambusae* was determined using the next-generation sequencing technology. The circular molecule is 63,593 bp long with a GC content of 31.92%. Gene prediction revealed 44 genes encoding 15 conserved proteins, 27 tRNAs, and the large and small ribosomal RNAs. All genes are located on the same strand. The tRNA genes contain codons for all 20 standard amino acids. It turns out to be similar to the previously sequenced mitochondrial genomes of *Fusarium circinatum* and *F. verticillioides*. The differences lie in the number of introns embodied in protein-coding genes. Four introns exist in the mitochondrial genome of *F. verticillioides*, 10 in *F. bambusae*, and 14 in *F. circinatum*. The phylogenetic analysis confirmed *F. bambusae* as a member of *Fusarium* (Nectriaceae). The mitochondrial genome of *F. bambusae* will contribute to the understanding of phylogeny and evolution of the genus and family.

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Hypocreales; mitogenome; next-generation sequencing (NGS); phylogeny

Fusarium bambusae is a bambusicolous fungus discovered on culm of bamboo or rotten bamboo in eastern China, including Anhui, Henan, and Zhejiang provinces. It is characterized by soft-textured dark purple ascomata, two-layered perithecial wall, and clavate asci with 4–8 ascospores (Zhang and Zhuang 2003; Zhuang 2013). Formerly, this fungus was known as *Gibberella bambusae*, but recently transferred to *Fusarium* (Zeng and Zhuang 2017) according to genera in Bionectriaceae, Hypocreaceae, and Nectriaceae proposed for acceptance or rejection (Rossman et al. 2013). Its life circle and applicability have not been well investigated.

The *F. bambusae* strain 5137 was isolated from an ascoma living on rotten bamboo from the Jigong Mountain (N31°49′, E114°04′), Henan Province, China. The specimen is deposited in the Mycological Herbarium, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China (HMAS 86476). DNA extraction, library construction, and sequencing were performed as described in the previous studies (Wang et al. 2016, 2017). The 125 bp pair-end reads were assembled using CLC Genomics Workbench (Version 8.0.3; CLC Bio, Aarhus, Denmark). The mitochondrial genome of *Trichoderma reesei* (NC_003388) was served as a reference to identify the assembled scaffolds belonging to mitochondrial genome. After filtering with BLAST, only one scaffold was obtained. Manual comparison of the ends of the scaffold helped to link them into a circular molecule. This mitochondrial genome was annotated using MFannot (Lang et al. 2014). Ten mitochondrial genomes belonging to Nectriaceae and Bionectriaceae released on the public database were included in the Neighbour-joining phylogenetic analysis using MEGA6 (Tamura et al. 2013).

The complete sequence of *F. bambusae* mitochondrial genome (GenBank accession number MH684411) is 63,593 bp long with the GC content of 31.92%. It encodes 15 conserved proteins, 27 tRNAs, and the large and small ribosomal RNAs. All structural genes are located on the same strand. The tRNA genes contain codons for all 20 standard amino acids. Most amino acids are represented by only one tRNA gene; however, two *trnL* (*trnL-UAA* and *trnL-UAG*), two *trnS* (*trnS-GCU* and *trnS-UGA*), three *trnM-CAU* and four *trnR* (*trnR-ACG*, *trnR-UCG,* and double copies of *trnR-UCU*) genes are found in this mitochondrial genome. Eleven introns are detected in five genes, i.e. each in *rnl*, nad2, and cox2, three in *cob* and five in *cox1*.

As shown in Figure 1, 10 members of Nectriaceae are included in the phylogenetic analysis, including eight taxa of *Fusarium*. *Fusarium circinatum* (NC_022681) and *F. verticillioides* (NC_016687) are determined as sisters of *F. bambusae* with strong support. The three share the same composition and order of protein, rRNA and tRNA genes. However, they differ in the number of introns embodied in protein-coding genes. Four introns exist in the mitochondrial genome of *F. verticillioides*, 10 in *F. bambusae*, whereas 14 in *F. circinatum*. The mitochondrial genome of *F. bambusae* will contribute to the understanding of phylogeny and evolution of Nectriaceae.

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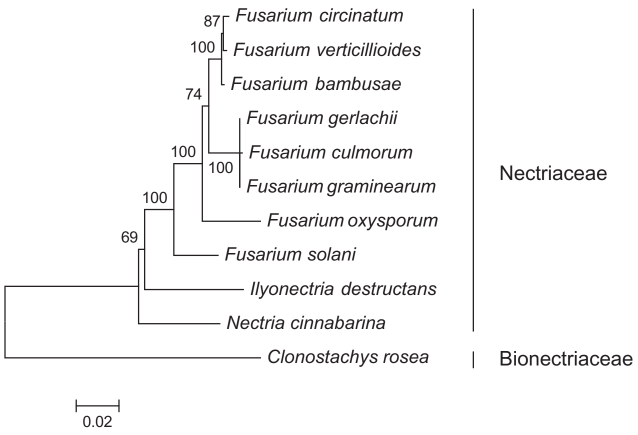

Figure 1. Phylogenetic relationship of 10 taxa of Nectriaceae (Hypocreales, Ascomycota) determined by Neighbour-joining analysis based on concatenated sequences of 15 translated mitochondrial proteins. The 15 proteins included subunits of the respiratory chain complexes (*cob, cox1*, *cox2*, *cox3*), ATPase subunits (*atp6*, *atp8*, and *atp9*), NADH: quinone reductase subunits (*nad1*, *nad2*, *nad3*, *nad4*, *nad4L*, *nad5*, *nad6*), and ribosomal protein S3 (*rps3*). The concatenated sequences were aligned using MAFFT. The following mitogenomes were used in this analysis: *Fusarium circinatum* (NC_022681), *F. culmorum* (NC_026993), *F. gerlachii* (NC_025928), *F. graminearum* (NC_009493), *F. oxysporum* (NC_017930), *F. solani* (NC_016680), *F. verticillioides* (NC_016687), *Ilyonectria destructans,* and *Nectria cinnabarina* (NC_030252). *Clonostachys rosea* (NC_036667, Bionectriaceae) was served as outgroup. The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. Bootstrap values no less than 50% are shown.

Disclosure statement

No potential conflict of interest was reported by the authors.

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