Complete mitochondrial genome sequence of the phytopathogenic fungi
Sclerotinia sclerotiorum JX-21

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ABSTRACT

Sclerotinia sclerotiorum JX-21 (Fungi, Ascomycota, Ascomycetidae, Helotiales, Sclerotiniaceae), is one of the most devastating necrotrophic fungal plant pathogens in agriculture (Bary 1886). It can cause diseases in over 400 species of plants including important crops and numerous weeds. In this work, the mitochondrial sequence of S. sclerotiorum with different strain obtained from the infected stems of Brassica campestris L. in Wangjiang County, Anhui Province, China is presented. The mt DNA codes for 14 proteins of the respiratory chain, 1 ribosomal protein, 2 homing endonucleases, 2 rRNAs, 25 tRNAs, and 5 hypothetical proteins ORFs. Phylogenetic analysis with protein-coding gene sequences of reported Ascomycota mt genomes revealed the close relationship of JX-21 with the family of Sclerotiniaceae.

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MITOGENOME ANNOUNCEMENTS

Sclerotinia sclerotiorum JX-21 (Fungi, Ascomycota, Ascomycetidae, Helotiales, Sclerotiniaceae), is one of the most devastating necrotrophic fungal plant pathogens in agriculture (Bary 1886). It can cause diseases in over 400 species of plants including important crops and numerous weeds. In this work, the mitochondrial sequence of S. sclerotiorum with different strain obtained from the infected stems of Brassica campestris L. in Wangjiang County, Anhui Province, China is presented. The mt DNA codes for 14 proteins of the respiratory chain, 1 ribosomal protein, 2 homing endonucleases, 2 rRNAs, 25 tRNAs, and 5 hypothetical proteins ORFs. Phylogenetic analysis with protein-coding gene sequences of reported Ascomycota mt genomes revealed the close relationship of JX-21 with the family of Sclerotiniaceae.

G + C content of 30.6%. All coding genes are transcribed with different polarities and started with the canonical translation initiation codon-AUG. Fourteen of the 15 typical mitochondrial protein-coding genes are involved in energy and oxidative metabolism (cox1, cox2, and cox3, cob, atp6, atp8, atp9, nad1, nad2, nad3, nad4, nad4L, nad5, and nad6). The remaining one encoded the 40S ribosomal protein S3 (rps3).

Fourteen intronic ORFs were located in the five protein-coding genes cox1 (7), nad5 (3), nad1 (1), atp6 (1), cox3 (1), and rnl (1). Ten of the 14 ORFs exhibited similarity in the amino acid sequence to the LAGLIDADG motif and four of them were similar to GIY-YIG motif.

Twenty-five tRNA genes were identified in S. sclerotiorum JX-21 mt DNA genome represented 19 amino acids except tRNA^{Gly} and included three copies of tRNA^{Met}, tRNA^{Ser}, and two copies of tRNA^{Ala}, tRNA^{Thr}. Single-copy genes encoded the remaining tRNAs. Nineteen tRNAs were grouped into four clusters with 6, 5, 3, and 5 tRNA genes each. Two clusters of 6 and 5 tRNAs were located around cox1 gene. The remaining two clusters were located around rRNA gene: five around rnl and three around rps3, while the remaining four tRNA genes occurred, respectively.

The phylogenetic analysis of S. sclerotiorum JX-21 was performed by comparison with 15 core mt proteins of other 21 species in Ascomycota (Mardanov et al. 2014) and was constructed by a maximum-likelihood analysis of MEGA 6.0 (Hachioji, Tokyo, Japan) (Tamura et al. 2013) program using 1000 bootstrap replicates. Result shows JX-21 is closely related to S. sclerotiorum1980 UF-70, S. borealia F-4128, and S. fuckeliana B05.10 which are another three members in the family Sclerotiniaceae with high bootstrap value supported (Figure 1).
In conclusion, the complete mtDNA of *S. sclerotiorum* JX-21 provides essential and important DNA molecular data for further phylogenetic and evolutionary analysis for Sclerotiniaceae.

**Disclosure statement**

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