Fusarium oxysporum is a soil borne fungal pathogen which can infect a variety of crops and cause serious crop yield reduction (Favel et al. 2003). There are more than 120 species of F. oxysporum (Armstrong 1981). With the advancement of scientific research and time, over 63 F. oxysporum have been sequenced and compared their mitotic genome. The mitochondrial genome of F. oxysporum is diverse and has many different characteristics from that of other fungi (Brankovics et al. 2017; Chen et al. 2019; Park, Kwon, Huang, et al. 2019; Park, Kwon, Zhu, et al. 2019). Fusarium oxysporum strain KGSJ26F3 (GenBank accession number MK764912) was isolated from wilted potato in northwest China where potato is the most important crop. We carried out a complete mitochondrial genome of F. oxysporum. The results showed the circular molecule is 46,664 bp, and the base composition of the mitogenome is as follows: A (34.3%), T (33.6%), C (14.6%), and G (17.5%). The mitogenome contains 18 protein-coding genes, two ribosomal RNA (rRNA), and 26 transfer RNA (tRNA) genes. The gene order is identical to that of the other Fusarium mitogenomes. The taxonomic status of F. oxysporum mitogenome exhibits a closest relationship with F. oxysporum. However, it varied in the structure of mitochondrial genome.
commune (LT906348) are determined as sisters of *F. oxysporum* with strong support. High bootstrap and posterior probability values show that presented relations are stable. The mitochondrial genome of *F. oxysporum* will contribute to the understanding of phylogeny.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

We confirm that the data supporting the findings of this study are available within the article and its supplementary materials. The data that support the findings of this study are openly available in NCBI GenBank database at [https://www.ncbi.nlm.nih.gov/nuccore/](https://www.ncbi.nlm.nih.gov/nuccore/) with the accession number is MT269799, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

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