MITOCHONDRIAL DNA PART B: RESOURCES
2024, VOL. 9, NO. 9, 1207–1212
https://doi.org/10.1080/23802359.2024.2403411

Taylor & Francis
Taylor & Francis Group

MITOGENOME REPORT

OPEN ACCESS Check for updates

# Complete mitochondrial genome sequence of the white root rot pathogen *Dematophora necatrix* (Xylariaceae: Xylariales)

Magriet A. van der Nest[a,b], Emma T. Steenkamp[b], Lieschen De Vos[b], Raven Wienk[a,b], Velushka Swart[a,b] and Noëlani van den Berg[a,b]

[a]Hans Merensky Chair in Avocado Research, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa; [b]Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa

**ABSTRACT**

The mitochondrial genome of *Dematophora necatrix* is 121,350 base pairs in length with a G + C content of 30.19%. Phylogenetic analysis showed that *D. necatrix* grouped with other members of the Xylariaceae, with which its mitogenome also shares a broadly similar architecture and gene content. The *D. necatrix* mitogenome contains 14 protein-coding and 26 tRNA-encoding genes, as well as one copy each of the *rnl*, *rns*, *rps3* and *nat1* genes. However, as much as 80% of this genome is intronic or non-coding. This is likely due to expansions and rearrangements caused by the large number of group I introns and the homing endonucleases and reverse-transcriptases they encode. Our study thus provides a valuable foundation from which to explore the mitochondrion's role in the biology of *D. necatrix*, and also serves as a resource for investigating the pathogen's population biology and general ecology.

**ARTICLE HISTORY**
Received 19 April 2024
Accepted 8 September 2024

**KEYWORDS**
tRNA gene clusters; homing endonucleases; N-acetyltransferase; Xylariaceae

## Introduction

*Dematophora necatrix* Berl. ex Prill. 1904 (Ascomycota, Sordariomycetes, Xylariales, Xylariaceae), also known as *Rosellinia necatrix*, causes the destructive white root rot (WRR) disease of various plant species (Sawant et al. 2021). In avocado (*Persea americana* Mill.), *D. necatrix* hampers production due to susceptibility of rootstocks to WRR (Figure 1A and 1B) (López et al. 2008; van den Berg et al. 2018; Martínez-Ferri et al. 2019). Severity of the disease is further compounded by the pathogen's resistance to drought and various fungicides (Pérez-Jiménez 2006; Pliego et al. 2009; Magagula et al. 2021). Consequently, *D. necatrix* remains a major concern in avocado-growing regions, globally (van den Berg et al. 2018; Zumaquero et al. 2019).

Effective strategies for curbing the pathogen's establishment and spread require detailed knowledge regarding its pathogenesis mechanisms, population biology and general ecology. As a result, whole genome sequences for several *D. necatrix* strains have been published (Shimizu et al. 2018; Chavarro-Carrero et al. 2024, including one obtained from a diseased avocado tree in South Africa (Wingfield et al. 2022). Despite the availability of these resources, an annotated assembly for the mitogenome of this fungus is not available. Therefore, the aim of the current study was to assemble and annotate the mitogenome for the South African strain of *D. necatrix*.

## Materials and methods

Strain CMW50482 of *D. necatrix* was collected from a symptomatic avocado tree in the Limpopo province (GPS coordinates: 23°44'59.5"S 30°08'02.4"E) of South Africa (Wingfield et al. 2022). A specimen (voucher number CMW50482) was deposited in the culture collection of the Forestry and Agricultural Biotechnology Institute (University of Pretoria) (https://www.fabinet.up.ac.za/index.php/research-groups/fungal-culture-collections) curated by Dr Seonju Marincowitz (Seonju.Marincowitz@up.ac.za).

Whole genome shotgun sequences (251 bp paired-end reads) for strain CMW50482, which we previously generated using Illumina HiSeq (Wingfield et al. 2022), were used in this study. The mitogenome was assembled using NOVOPlasty v4.3.1 with default parameters (Dierckxsens et al. 2017). The *de novo* assembly was annotated using mitochondrial genetic code 4 and GeSeq - Annotation of Organellar Genomes tool (Tillich et al. 2017) with the following parameters: circular sequence, mitochondrial sequence source, 25% BLAST protein search identity and 85% identity for BLAST rRNA, tRNA

CONTACT Noëlani van den Berg Noelani.vandenBerg@up.ac.za Hans Merensky Chair in Avocado Research, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa; Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa.

Supplemental data for this article can be accessed online at https://doi.org/10.1080/23802359.2024.2403411.

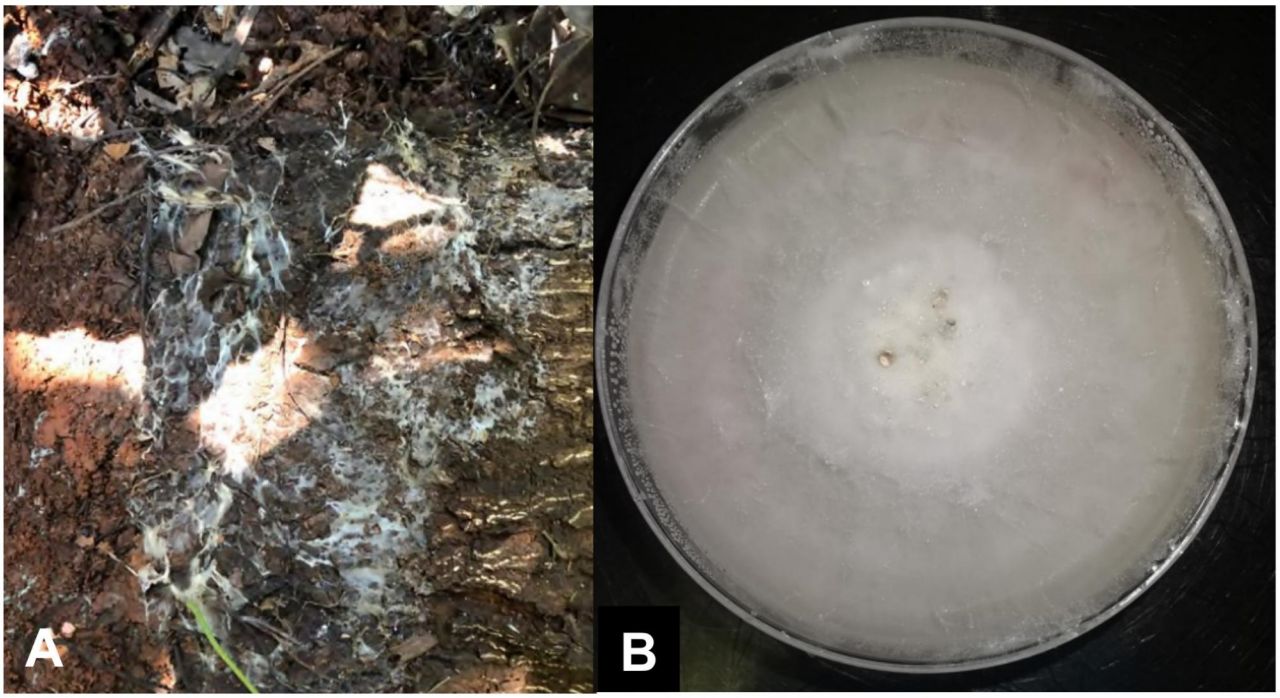


**Figure 1.** Morphological observation of *dematophora necatrix*. Avocado tree roots colonized with *D. necatrix*, forming a white mycelial mass characteristic of the white root rot disease **(a)**. Mycelial growth cultured on PDA medium at 25 °C for 2 weeks **(B).** Photos taken by raven wienk.

and DNA search, third party tRNA annotator ARAGORN v1.2.38 and tRNAScan-SE v2.0, and *Annulohypoxylon stygium* (NC_023117) as Refseq choice. We then used MFannot v1.0 (Lang et al. 2023) and mitochondrial genetic code 4 to assess the gene predictions, while open reading frames (ORFs) and introns were verified using BLAST analyses (https://blast.ncbi.nlm.nih.gov) and the ExPASy translation tool (http://web.expasy.org/translate/).

Size and coding content of the *D. necatrix* mitogenome were compared to those assembled for other Xylariales species using data from GenBank (https://www.ncbi.nlm.nih.gov). Also, protein-coding genes typically found in fungal mitogenomes (Sandor et al. 2018) were subjected to maximum-likelihood (ML) phylogenetic analysis. Here, the inferred protein sequences for *atp6,8,9*, *cox1,2,3*, *nad1,2,3,4,4L,5,6* and *cob* were used. Following alignment with the stand-alone version of MAFFT (–thread 10 –auto –reorder –adjustdirection), the sequences were concatenated using FASconCAT-G v1.04 (Kück and Longo 2014). The concatenated dataset consisted of our *D. necatrix* sequences, as well as those for 25 other filamentous Ascomycota for which relevant data were available in GenBank. Maximum Likelihood (ML) phylogenetic analysis was conducted with IQ-TREE 2 v2.2.2.6 (Minh et al. 2020) using the LG model (Le and Gascuel 2008), while MEGA v11.0 (Tamura et al. 2021) was used for Neighbor-Joining (NJ) phylogenetic analysis based on Poisson distances with rate uniformity among sites. In both cases, branch support was estimated using 1,000 bootstrap replicates.

## Results

The *D. necatrix* mitogenome assembled as a circular DNA molecule consisting of 121,350 bp (Figure 2). The G + C content averaged at 30.19%, with mean base compositions for A, C, G, and T of 35.4%, 13.3%, 16.9%, and 34.4%, respectively. The average coverage depth was 3622x (Figure S1).

The *D. necatrix* mitogenome contained the 14 expected protein-coding genes. These included genes encoding the cytochrome oxidase subunits of Complex IV, apocytochrome b of Complex III, NADH dehydrogenase subunits of Complex I and the ATP synthase subunits (Figures 2, S2A and S2B). The assembly also contained genes encoding ribosomal protein S3 (*rps3*) and N-acetyltransferase (*nat1*). In terms of RNA coding genes, the mitogenome contained the large and small subunit ribosomal RNA (rRNA) genes *rnl* and *rns*, respectively, as well as 26 transfer RNA (tRNA) genes that mostly clustered at two regions (Figures 2, S2B and S2C). The tRNA genes occurred as single copies, except for the tRNA-Arg (four copies) and tRNA-Val (two copies) and tRNA-Met genes (three copies) (Figures 2, S2D). A total of 22 introns were detected, of which two represented group II introns. The rest were group I introns and contained ORFs coding for homing endonucleases or reverse-transcriptases (Table S1).

The ML an NJ phylogenies grouped *D. necatrix* with the Xylariales, where it was more closely related to members of the Xylariaceae (i.e. *Nemania diffusa* and *Xylaria hypoxylon*) than to taxa from other families (Figure 3). This close relationship was also evident from the syntenic nature of their mitogenomes (Figures S2B, S2C and SD). Like *D. necatrix*, the *N. diffusa*, *Annulohypoxylon stygium*, and *Apiospora arundinis* mitogenomes also contained *rps3* (albeit within the borders of *rnl*), while the *N. diffusa* and *Pestalotiopsis fici* mitogenomes also contained the *nat1* gene. Additionally, most of the *D. necatrix* mitogenome was non-coding and/or represented by introns, which is similar to other Xylariales. These similarities were despite gene losses in *X. hypoxylon* (Zhou et al. 2019) and *A.*

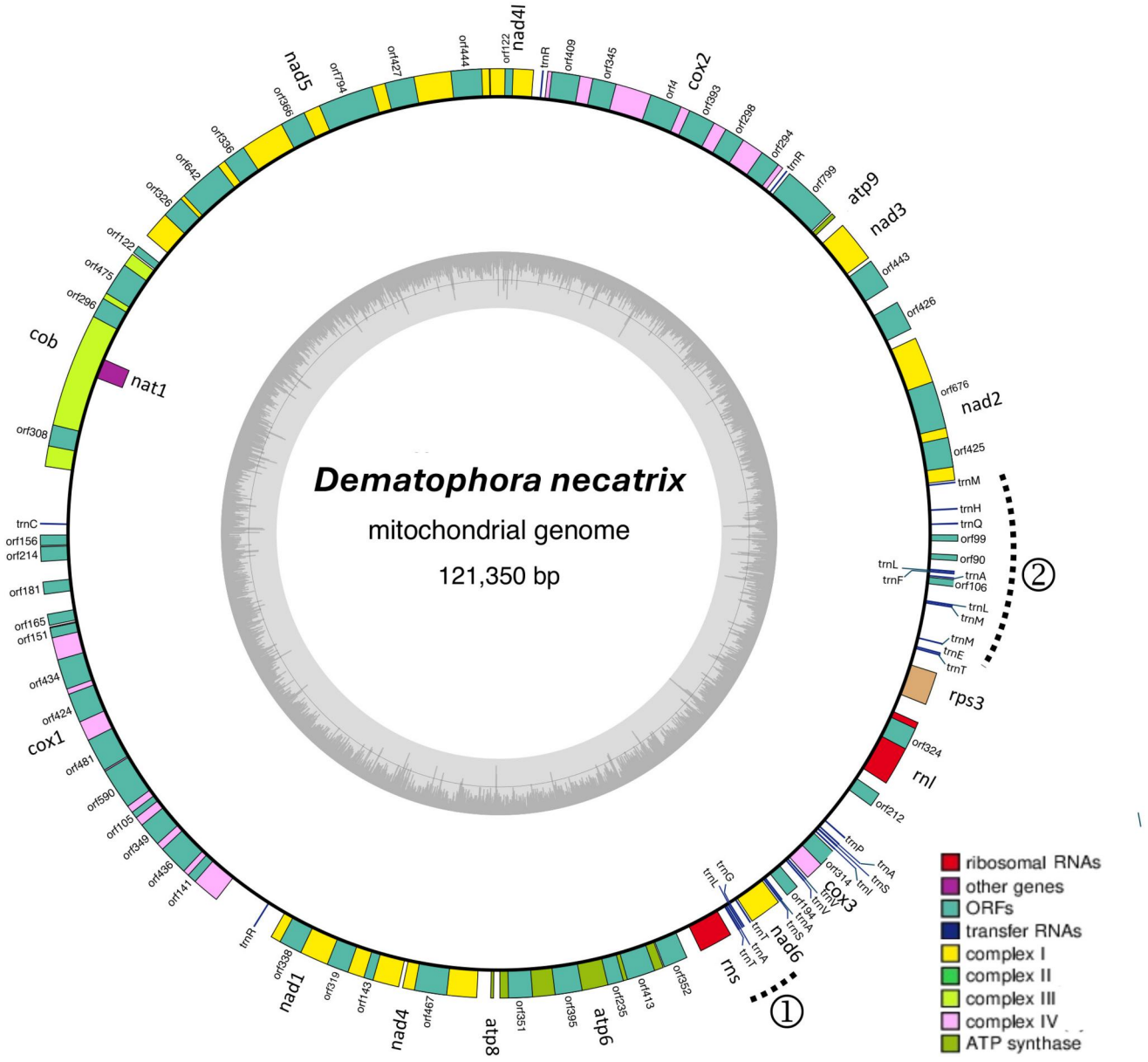


**Figure 2.** Circular map of the mitochondrial genome of *dematophora necatrix* prepared using OGDRAW program (https://chlorobox.mpimp-golm.mpg.de/OGDraw.html). Genes are color-coded by their functional classification. Genes on the outside of each ring indicate that they are on the forward strand, while genes within the ring indicates those located on the reverse strand. The inner, grayscale bar graph shows G + C content (%), with the Middle line marking the 50% threshold. The positions of the two main clusters of tRNA genes are indicated with the dotted brackets (see supplementary figure S2 for details).

*arundinis* (GenBank accession KY775582), and a large inversion in the *N. diffusa* mitogenome (Tang et al. 2020).

## Discussion and conclusion

The *D. necatrix* mitogenome closely resembles those published for other members of the Xylariales (Deng et al. 2018; Zhou et al. 2019; Tang et al. 2020). As in these fungi, the *D. necatrix* mitogenome encoded all of its protein-coding and rRNA genes in the same order and orientation. Likewise, the bulk of the *D. necatrix* tRNA genes occurred in clusters between the *rns* and *nad6* genes, and between the *nrl* and *nad2* genes.

Two notable protein-coding genes annotated in the *D. necatrix* mitogenome are *rps3* and *nat1*. In fungi, the *rps3* gene is often cycled between the nuclear and mitochondrial genomes by mobile genetic elements (Wai et al. 2019), and its product is a vital component of many cellular processes (Graifer et al. 2014; Medina et al. 2020). Not much is known about N-acetyltransferase-encoding genes such as *nat1*, but they have been implicated in mitochondrial turnover and the detoxification of plant defence compounds (Sharma et al. 2020). Therefore, these genes are potential targets for studies aiming to explore the molecular basis of pathogenesis in *D. necatrix*.

The large number of introns predicted in the *D. necatrix* mitogenome is consistent with previous reports from members of the Xylariales (Zhang et al. 2017; Deng et al. 2018) and Sordariomycetes (Medina et al. 2020). Indeed, these elements are implicated in the size variation and expansion of fungal mitogenomes (Wu et al. 2015). As expected for fungi (Mukhopadhyay and Hausner 2021), the *D. necatrix* mitogenome also contained more group I introns than group II introns. Due to their impact on the overall architecture of the

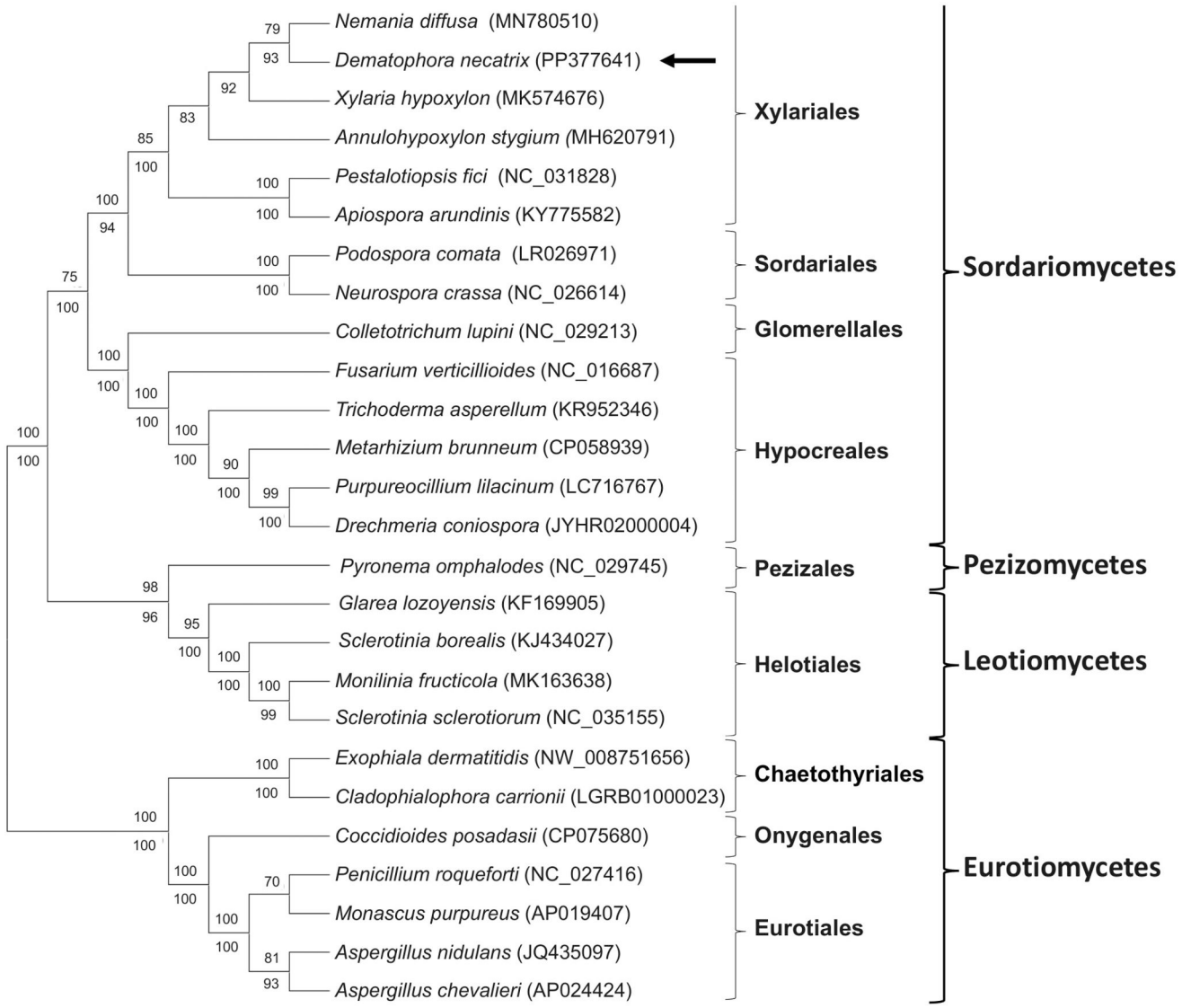


**Figure 3.** Maximum likelihood (ML) phylogenetic tree showing the relationships between *dematophora necatrix* strain CMW50482 and other members of the ascomycota, which were inferred from the concatenated amino acid sequences of the 14 conserved protein-coding genes encoded on the mitogenome. Similar clustering patterns were observed in our Neighbor-Joining (NJ) phylogeny. ML bootstrap support values are indicated above the nodes, while NJ bootstrap support values are indicated below the nodes. Accession numbers are indicated after the species names. Species used include the following: *Xylaria hypoxylon* (MK574676) (Zhou et al. 2019), *Dematophora necatrix* (PP377641) (this paper), *Nemania diffusa* (MN780510) (Tang et al. 2020), *Annulohypoxylon stygium* (MH620791) (Deng et al. 2018), *pestalotiopsis fici* (NC_031828) (unpublished), *Apiospora arundinis* (KY775582) (Yuan et al. 2019), *Podospora comata* (LR026971) (Unpublished), *Neurospora crassa* (NC_026614) (Monteiro et al. 2021), *Colletotrichum lupini* (NC_029213) (Pszczółkowska et al. 2020), *Fusarium verticillioides* (NC_016687) (Al-Reedy et al. 2012), *Trichoderma asperellum* (KR952346) (Unpublished), *Metarhizium brunneum* (CP058939) (Unpublished), *Purpureocillium lilacinum* (LC716767) (Unpublished), *Drechmeria coniospora* (JYHR02000004) (Unpublished), *Glarea lozoyensis* (KF169905) (Youssar et al. 2013), *Monilinia fructicola* (MK163638) (Unpublished), *Sclerotinia borealis* (KJ434027) (Mardanov et al. 2014), *Sclerotinia sclerotiorum* (NC_035155) (Unpublished), *Pyronema omphalodes* (NC_029745) (Unpublished) and *Aspergillus chevalieri* (AP024424) (Kadooka et al. 2021).

mitogenome (Mukhopadhyay and Hausner 2021), intron activity may also impact the overall biology of the fungus harboring them. In certain fungi, for example, a particular allele of the group I type D intron occurring in *cob* has been shown to confer resistance to QoI (quinone outside inhibitor) fungicides (Cinget and Bélanger 2020).

The mitogenome assembled and characterized in this study provides many opportunities to improve our understanding of the biology and ecology of *D. necatrix* in South Africa. Apart from providing a sound foundation from which to explore the role of this organelle in the biology of the species, our findings would also serve as a valuable resource for exploring the genetic diversity and population biology of this important pathogen.

## Ethical approval

The Ethics Committee of the Faculty of Natural and Agricultural Sciences (NAS) at the University of Pretoria (Pretoria, South Africa) approved the work conducted in this study (reference number: NAS173/2020).

## Authors' contributions

MAV, VS and NV conceived of the research; MAV, LD, RW and ETS analyzed and interpreted the data; MAV and ETS drafted the paper; NV, VS, RW and LD revised the paper critically for intellectual content; all authors approved the final version to be published and agreed to be responsible for all aspects of the work.

## Disclosure statement

No potential conflict of interest was reported by the authors.

## Funding

The author(s) declare financial support was received for the research, authorship, and/or publication of this article. Funding for the publication was generously provided by the Hans Merensky Foundation.

## Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/. The associated BioProject, BioSample, Genbank, and SRA numbers are PRJNA884201, SAMN31015769, PP377641 and SRR28283158.

## References

Al-Reedy RM, Malireddy R, Dillman CB, Kennell JC. 2012. Comparative analysis of Fusarium mitochondrial genomes reveals a highly variable region that encodes an exceptionally large open reading frame. Fungal Genet Biol. 49(1):2–14. doi:10.1016/j.fgb.2011.11.008.

Arjona-Lopez JM, Telengech P, Jamal A, Hisano S, Kondo H, Yelin MD, Arjona-Girona I, Kanematsu S, Lopez-Herrera CJ, Suzuki N. 2018. Novel, diverse RNA viruses from Mediterranean isolates of the phytopathogenic fungus, *Rosellinia necatrix*: insights into evolutionary biology of fungal viruses. Environ Microbiol. 20(4):1464–1483. doi:10.1111/1462-2920.14065.

Chavarro-Carrero EA, Snelders NC, Torres DE, Kraege A, López-Moral A, Petti GC, Punt W, Wieneke J, García-Velasco R, López-Herrera CJ, et al. 2024. The soil-borne white root rot pathogen *Rosellinia necatrix* expresses antimicrobial proteins during host colonization. PLOS Pathog. 20(1):e1011866. doi:10.1371/journal.ppat.1011866.

Cinget B, Bélanger RR. 2020. Discovery of new group ID introns leads to creation of subtypes and link to an adaptive response of the mitochondrial genome in fungi. RNA Biol. 17(9):1252–1260. doi:10.1080/15476286.2020.1763024.

Deng Y, Hsiang T, Li S, Lin L, Wang Q, Chen Q, Xie B, Ming R. 2018. Comparison of the mitochondrial genome sequences of six *Annulohypoxylon stygium* isolates suggests short fragment insertions as a potential factor leading to larger genomic size. Front Microbiol. 9:2079. doi:10.3389/fmicb.2018.02079.

Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45(4):e18. doi:10.1093/nar/gkw955.

Graifer D, Malygin A, Zharkov DO, Karpova G. 2014. Eukaryotic ribosomal protein S3: a constituent of translational machinery and an extraribosomal player in various cellular processes. Biochimie. 99:8–18. doi:10.1016/j.biochi.2013.11.001.

Kadooka C, Mori K, Okutsu K, Yoshizaki Y, Takamine K, Tashiro K, Tamaki H, Futagami T. 2021. Chromosome-level genome sequence of *Aspergillus chevalieri* M1, isolated from Katsuobushi. Microbiol Resour Announc. 10(37):e0038521. doi:10.1128/MRA.00385-21.

Kück P, Longo GC. 2014. FASconCAT-G: extensive functions for multiple sequence alignment preparations concerning phylogenetic studies. Front Zool. 11(1):81. doi:10.1186/s12983-014-0081-x.

Lang BF, Beck N, Prince S, Sarrasin M, Rioux P, Burger G. 2023. Mitochondrial genome annotation with MFannot: a critical analysis of gene identification and gene model prediction. Front Plant Sci. 14:1222186. doi:10.3389/fpls.2023.1222186.

Le SQ, Gascuel O. 2008. An improved general amino acid replacement matrix. Mol Biol Evol. 25(7):1307–1320. doi:10.1093/molbev/msn067.

López M, Ruano-Rosa D, López-Herrera CJ, Monte E, Hermosa R. 2008. Intraspecific diversity within avocado field isolates of *Rosellinia necatrix* from south-east Spain. Eur J Plant Pathol. 121(2):201–205. doi:10.1007/s10658-007-9253-2.

Magagula P, Taylor N, Swart V, van den Berg N. 2021. Efficacy of potential control agents against *Rosellinia necatrix* and their physiological impact on avocado. Plant Dis. 105(11):3385–3396. doi:10.1094/PDIS-08-20-1751-RE.

Mardanov AV, Beletsky AV, Kadnikov VV, Ignatov AN, Ravin NV. 2014. The 203 kbp mitochondrial genome of the phytopathogenic fungus *Sclerotinia borealis* reveals multiple invasions of introns and genomic duplications. PLOS One. 9(9):e107536. doi:10.1371/journal.pone.0107536.

Martínez-Ferri E, Moreno-Ortega G, Van den Berg N, Pliego C. 2019. Mild water stress-induced priming enhance tolerance to *Rosellinia necatrix* in susceptible avocado rootstocks. BMC Plant Biol. 19(1):458. doi:10.1186/s12870-019-2016-3.

Medina R, Franco MEE, Bartel LC, Martinez Alcántara V, Saparrat MCN, Balatti PA. 2020. Fungal mitogenomes: relevant features to planning plant disease management. Front Microbiol. 11:978. doi:10.3389/fmicb.2020.00978.

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, Von Haeseler A, Lanfear R. 2020. IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. Mol Biol Evol. 37(5):1530–1534. doi:10.1093/molbev/msaa015.

Monteiro J, Pratas D, Videira A, Pereira F. 2021. Revisiting the *Neurospora crassa* mitochondrial genome. Lett Appl Microbiol. 73(4):495–505. doi:10.1111/lam.13538.

Mukhopadhyay J, Hausner G. 2021. Organellar introns in fungi, algae, and plants. Cells. 10(8):2001. doi:10.3390/cells10082001.

Pérez-Jiménez RM. 2006. A review of the biology and pathogenicity of *Rosellinia necatrix* - The cause of white root rot disease of fruit trees and other plants. J Phytopathology. 154(5):257–266. doi:10.1111/j.1439-0434.2006.01101.x.

Pliego C, Kanematsu S, Ruano-Rosa D, De Vicente A, López-Herrera C, Cazorla FM, Ramos C. 2009. GFP sheds light on the infection process of avocado roots by *Rosellinia necatrix*. Fungal Genet Biol. 46(2):137–145. doi:10.1016/j.fgb.2008.11.009.

Pszczółkowska A, Androsiuk P, Jastrzębski JP, Paukszto Ł, Okorski A. 2020. rps3 as a candidate mitochondrial gene for the molecular identification of species from the *Colletotrichum acutatum* species complex. Genes. 11(5):552. doi:10.3390/genes11050552.

Sandor S, Zhang Y, Xu J. 2018. Fungal mitochondrial genomes and genetic polymorphisms. Appl Microbiol Biotechnol. 102(22):9433–9448. doi:10.1007/s00253-018-9350-5.

Sawant SS, Choi ED, Song J, Seo H. 2021. Current status and future prospects of white root rot management in pear orchards: a review. Res Plant Dis. 27(3):91–98. doi:10.5423/RPD.2021.27.3.91.

Sharma S, Ahmed M, Akhter Y. 2020. Fungal acetyltransferases structures, mechanisms and inhibitors: a review. Int J Biol Macromol. 157:626–640. doi:10.1016/j.ijbiomac.2019.11.214.

Shimizu T, Kanematsu S, Yaegashi H. 2018. Draft genome sequence and transcriptional analysis of *Rosellinia necatrix* infected with a virulent mycovirus. Phytopathology. 108(10):1206–1211. doi:10.1094/PHYTO-11-17-0365-R.

Tamura K, Stecher G, Kumar S. 2021. MEGA11: molecular evolutionary genetics analysis version 11. Mol Biol Evol. 38(7):3022–3027. doi:10.1093/molbev/msab120.

Tang D, Zhang G, Wang Y, Zhang M, Wang Y, Yu H. 2020. Characterization of complete mitochondrial genome of *Nemania diffusa* (Xylariaceae, Xylariales) and its phylogenetic analysis. Mitochondrial DNA Part B Resour. 5(1):459–460. doi:10.1080/23802359.2019.1704665.

Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq–versatile and accurate annotation of organelle genomes. Nucleic Acids Res. 45(W1):W6–W11. doi:10.1093/nar/gkx391.

van den Berg N, Hartley J, Engelbrecht J, Mufamadi Z, Van Rooyen Z, Mavuso Z. 2018. First report of white root rot caused by *Rosellinia necatrix* on *Persea americana* in South Africa. Plant Dis. 102(9):1850. doi:10.1094/PDIS-10-17-1637-PDN.

Wai A, Shen C, Carta A, Dansen A, Crous PW, Hausner G. 2019. Intron-encoded ribosomal proteins and N-acetyltransferases within the mitochondrial genomes of fungi: here today, gone tomorrow? Mitochondrial DNA Part A DNA Mapp Seq Anal. 30(3):573–584. doi:10.1080/24701394.2019.1580272.

Wingfield BD, Berger DK, Coetzee MPA, Duong TA, Martin A, Pham NQ, van den Berg N, Wilken PM, Arun-Chinnappa KS, Barnes I, et al. 2022. IMA genome-F17: draft genome sequences of an *Armillaria* species from Zimbabwe, *Ceratocystis colombiana, Elsinoë necatrix, Rosellinia necatrix*, two genomes of *Sclerotinia minor*, short-read genome assemblies and annotations of four *Pyrenophora teres* isolates from barley grass, and a long-read genome assembly of *Cercospora zeina*. IMA Fungus. 13(1):19. doi:10.1186/s43008-022-00104-3.

Wu B, Buljic A, Hao W. 2015. Extensive horizontal transfer and homologous recombination generate highly chimeric mitochondrial genomes in yeast. Mol Biol Evol. 32(10):2559–2570. doi:10.1093/molbev/msv127.

Youssar L, Grüning BA, Günther S, Hüttel W. 2013. Characterization and phylogenetic analysis of the mitochondrial genome of *Glarea lozoyensis* indicates high diversity within the order Helotiales. PLOS One. 8(9): e74792. doi:10.1371/journal.pone.0074792.

Yuan XL, Cao M, Li PP, Cheng S, Liu XM, Du YM, Zhang ZF, Shen GM, Zhang P. 2019. The mitochondrial genome of *Arthrinium arundinis* and its phylogenetic position within Sordariomycetes. Int J Biol Macromol. 121:956–963. doi:10.1016/j.ijbiomac.2018.10.150.

Zhang S, Wang XN, Zhang XL, Liu XZ, Zhang YJ. 2017. Complete mitochondrial genome of the endophytic fungus *Pestalotiopsis fici*: features and evolution. Appl Microbiol Biotechnol. 101(4):1593–1604. doi:10.1007/s00253-017-8112-0.

Zhou H, Abuduaini A, Xie H, Kang R, Suo F, Huang L. 2019. The complete mitochondrial genome of wood-rotting fungus *Xylaria hypoxylon*. Mitochondrial DNA Part B Resour. 4(2):3848–3849. doi:10.1080/23802359.2019.1687025.

Zumaquero A, Martínez-Ferri E, Matas AJ, Reeksting B, Olivier NA, Pliego-Alfaro F, Barceló A, van den Berg N, Pliego C. 2019. *Rosellinia necatrix* infection induces differential gene expression between tolerant and susceptible avocado rootstocks. PLOS One. 14(2):e0212359. doi:10.1371/journal.pone.0212359.