Rauwane *et al. BMC Genomic Data* (2025) 26:14
https://doi.org/10.1186/s12863-025-01299-1

BMC Genomic Data

DATA NOTE

Open Access

Draft genome sequence of the fungal pathogen *Penicillium expansum* (PPRI25879) isolated in South Africa

Molemi Rauwane[1,2*], Sandiswa Figlan[2], Wai Yin Chan[3] and Khayalethu Ntushelo[2]

Abstract

Objectives *Penicillium expansum*, a necrotrophic plant pathogen with a wide range of fruit hosts, is an important causal agent of blue mold rot. The fruit business suffers significant financial losses because of blue mold rot that occurs during fruit storage, transportation, and sale. The objective of this work was to generate a high-quality draft genome assembly of *P. expansum*, which will contribute to enhancing the management of blue mold, especially in stone and pome fruits, including grapes, by improving our understanding of the epidemiology of the pathogen and its interactions with the host.

Data description Here, we describe the genome sequence of *Penicillium expansum* isolate PPRI25879, one of the most virulent strains isolated from grapes in South Africa. Sequencing reads from *P. expansum* produced approximately 3.5 Gb. The assembly generated a draft genome of size 32.1 Mb, consisting of 1648 contigs, with an N50 of 508 KB. Examination of the genome completeness with Benchmarking Universal Single-Copy Orthologs (BUSCO) showed the draft genome carries 97.9% of the 746 genes in the Eurotiomycetes_odb10 database. The draft genome sequence will allow improved genomic comparisons among the most important pathogens belonging to the *Penicillium* genus, with the aim of improving our knowledge of their plant-pathogen interactions, population biology, and control.

Keywords *Penicillium Expansum*, Blue mold rot, Genome assembly, Illumina, Pome fruit, Stone fruit

Objectives

Penicillium expansum is a filamentous phytopathogenic fungus belonging to the phylum Ascomycota, class Eurotiomycetes, and the genus *Penicillium*. *Penicillium* species are ubiquitous soil inhabitants that are typically found in decomposing vegetation on the orchard floor or soil [1]. *P. expansum* is the most common and aggressive among the *Penicillium* species [2]. This postharvest pathogen has significant economic importance, causing blue mold rot in a wide range of fruits, particularly pome and stone fruits, and produces carcinogenic mycotoxins that can be dangerous for animals and people [2–4]. Fruits are infected by this common wound parasite

*Correspondence:
Molemi Rauwane
molemi.rauwane@mandela.ac.za
[1]Department of Agriculture and Animal Health, University of South Africa, Private X6, Florida 1710, South Africa
[2]Department of Botany, Nelson Mandela University, P O Box 77000, Gqeberha 6031, South Africa
[3]Wits Diagnostic Innovation Hub, Health Science Research Unit, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg 2193, South Africa

© The Author(s) 2025. **Open Access** This article is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License, which permits any non-commercial use, sharing, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if you modified the licensed material. You do not have permission under this licence to share adapted material derived from this article or parts of it. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativecommons.org/licenses/by-nc-nd/4.0/.

Table 1 Overview of data files/data sets

Label	Name of data file/data set	File types (file extension)	Data repository and identifier (DOI or accession number)
Data File 1	Genome summary of *P. expansum PPRI25879*	Spreadsheet (.xls)	Figshare, https://doi.org/10.6084/m9.figshare.27084043 [13]
Data Set 1	V350082631_L02_PPRI_PE_1.fq.gz.1 V350082631_L02_PPRI_PE_2.fq.gz.1	Fastq (.fq.gz)	NCBI Sequence Read Archive, https://identifiers.org/ncbi/insdc.sra:SRR29916162 [14]
Data Set 2	P. expansum PPRI25879 draft genome assembly	Fasta (.fasta)	NCBI GenBank, https://identifiers.org/ncbi/insdc:JBGBCT000000000.1 [15]

fungus through mechanical injury from rigorous handling during harvest and transportation, as well as by injuries caused by insects, birds, and adverse weather conditions, especially before harvest [5, 6], resulting in light brown discoloration or lesions on the skin as the infection spreads [7]. The infection is typically quick to expand across the fruit surface and inside the tissue, and the pathogen produces blue-green mold spore colonies that may appear on the surface of the fruit at advanced stages of decay [2], resulting in fruit frailty, and may also pose health risks to animal and human consumers [8]. The main source of inoculum is conidia, which can be found in the packinghouse in flume water, on bin surfaces, on fruit, and in the air [9].

The aim of this study was to assemble a high-quality draft genome of *P. expansum* using next-generation sequencing technology. The work presented here provides fundamental genomic information that could be valuable in enhancing the existing knowledge on the general knowledge of *Penicillium* biology and may contribute to the discovery of novel mechanisms of pathogenicity. The genome data also present an opportunity for further comparative genomic analysis of *Penicilium* species.

Data description

Strain PPRI25879 of *P. expansum* was isolated from grapes at the Agricultural Research Council (ARC) – Plant Health and Protection, Roodeplaat, Tshwane, South Africa. Symptomatic tissues were surface sterilized using 1% bleach and ethanol, and further plated on sugar-free agar and plant count agar + nutrient agar. The isolates were identified by morphological observations and PCR. The culture was stored as agar punches in sterile water and frozen at -80 °C. Prior to DNA sequencing, the culture was replated on ¼ potato dextrose agar and mycelia were scraped into a 2 ml microcentrifuge tube. DNA was extracted using the Quick-DNA miniprep Plus kit (Zymo Research, Irvine, CA, USA). Genomic DNA libraries were prepared using the TruSeq Nano DNA Library Prep Kit, and sequencing was performed using the Illumina MiSeq sequencing platform to produce paired-end sequences of 300 bp. The quality of the raw reads was assessed using FastQC v. 0.11.9, and low-quality bases and adaptor sequences were trimmed using Trim Galore v. 0.6.5. Filtered reads were de novo assembled using SPAdes v 3.15.4 assembler [10], and genome completeness was scored using BUSCO v 5.4.7 [11] against the Eurotiomycetes _odb10 database. The genome assembly quality was assessed using Quast v 5.2.0 [12]. The assembly statistics, raw sequence data and genome assembly data are listed in Table 1, Data file 1 [13], Data set 1 and Data set 2 [14, 15]. A draft genome assembly of 32 116 299 bp of nucleotides and 47.68% GC content were assembled. This draft genome assembly has a sequencing depth of 87.4X with total of 1648 contigs (> 200 bp).

Overall, genome completeness assessment on the draft assembled genome quality showed that a 97.9% complete (742 of complete and single copy gene found / 746 complete BUSCO genes of Eurotiomycetes _odb10).

Limitations

The genome assembly presented in this study was obtained from a single strain of *P. expansum* and has not been annotated.

Abbreviations

NCBI	National Centre for Biotechnology
SRA	Sequence Read Archive
BUSCO	Benchmarking Universal Single-Copy Orthologs

Author contributions

M.R. and K.N. wrote the manuscript, W.Y.C., M.R. and S.F. analysed the data. All authors read and approved the final manuscript.

Funding

No funding.

Data availability

Raw sequence data is obtainable from NCBI database, SRA under BioSample accession SAMN42738374 and BioProject ID PRJNA1138726.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

Received: 29 July 2024 / Accepted: 10 January 2025

Published online: 21 February 2025

References

1. Errampalli D. *Penicillium Expansum* (blue mold). In Postharvest decay 2014 Jan 1 (pp. 189–231). Academic.
2. Luciano-Rosario D, Keller NP, Jurick WM. *PeniciExpansumpansum*: biology, omics, and management tools for a global postharvest pathogen causing blue mould of pome fruit. Mol Plant Pathol. 2020;21(11):1391–404.
3. Pitt JI, Leistner L. Toxigenic *penicillium* species. Mycotoxins and animal foods. Jul. 1991;23:81–99.
4. Ghuffar S, Irshad G, Naz F, Khan MA. Studies of *Penicillium* species associated with blue mold disease of grapes and management through plant essential oils as non-hazardous botanical fungicides. Green Process Synth. 2021;10:021–36.
5. Xiao CL, Boal RJ. Residual activity of fludioxonil and pyrimethanil against *Penicillium Expansum* on apple fruit. Plant Dis. 2009;93(10):1003–8.
6. Van Zeebroeck M, Ramon H, De Baerdemaeker J, Nicolaï BM, Tijskens E. Impact Damage Apples Dur Transp Handling Postharvest Biol Technol. 2007;45(2):157–67.
7. Assaf LR, Pedrozo LP, Nally MC, Pesce VM, Toro ME, de Figueroa LC, Vazquez F. Use of yeasts from different environments for the control of *Penicillium Expansum* on table grapes at storage temperature. Int J Food Microbiol. 2020;320:108520.
8. Bennett JW, Klich M. Mycotoxins Clin Microbiol Rev. 2003;16(3):497–516.
9. Sutton TB, Aldwinckle HS, Agnello AM, Walgenbach JF, editors. Compendium of apple and pear diseases and pests.
10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 2012;19:455–77.
11. Seppey M, Manni M, Zdobnov EM. BUSCO: assessing genome assembly and annotation completeness. Gene Prediction: Methods Protoc. 2019;1962:227–45.
12. Gurevich A, Saveliev V, Vyahhi N, Tesler G. QUAST: quality assessment tool for genome assemblies. Bioinformatics. 2013;29:1072–5.
13. Chan WY. Data file for complete genome of the *Penicillium expansum* strain PPR125879. Figshare. 2024. https://doi.org/10.6084/m9.figshare.27084043
14. National Center for Biotechnology Information. Illumina sequencing reads of *Penicillium Expansum*. Seq Read Archive SRR29916162. (2024). https://identifiers.org/ncbi/insdc.sra:SRR29916162
15. National Center for Biotechnology Information. Genome assembly bioproject PRJNA1138726. (2024). https://identifiers.org/ncbi/insdc:JBGBCT000000000.1

Publisher's note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.