Draft genome sequence of a Fusarium proliferatum isolate obtained from small cardamom, Elettaria cardamomum

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Data Note

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Abstract

Objectives:

Several *Fusarium* species are well-known plant pathogens responsible for causing wilt and rot diseases across a wide range of crops. We are interested in studying the pathogenicity of *Fusarium* species in economically important crops like small cardamom. In this study, small cardamom plants exhibiting typical wilting symptoms were investigated for *Fusarium* infection in Idukki district of Kerala, India. A *Fusarium*-like fungus was isolated in pure culture from a symptomatic plant and whole-genome sequencing was performed to identify the isolate and examine its genetic makeup. The genome sequence identified it as *Fusarium proliferatum* isolate STSP and provided valuable insights into its genetic composition. Additional experiments and analysis of the genome sequence are underway to determine the pathogenicity of the isolate in small cardamom.

Data description:

A *Fusarium* strain STSP was isolated from symptomatic tissues of *Elettaria cardamomum* (small cardamom). The genomic DNA of the isolate was extracted and sequencing was done using

Illumina and Oxford Nanopore platforms. The isolate STSP belongs to *F. proliferatum* and its draft genome sequence of 33,320,451 bp of nucleotides is presented here.

Objective

Fusarium is a genus of filamentous Ascomycete fungi, many of which are soil-borne vascular-wilt pathogens responsible for destructive plant diseases. Several of these species also produce harmful mycotoxins and can act as opportunistic pathogens in animals. In addition, some *Fusarium* species can persist as dormant endophytes living asymptomatically within plant tissues (1,2). The genus *Fusarium* is typically characterized by features such as pigment production, mycelial growth patterns, septation, hyaline and elongated macroconidia, and the formation of chlamydospores (3). *Fusarium* species have traditionally been identified using morphological and phylogenetic species concepts, together enabling more accurate delineation within the genus

(4). Several *Fusarium* species are economically important plant pathogens with different members such as *F. oxysporum* f. sp. *cubense* (Panama disease in banana), *F. solani* (root rot in cassava),

F. guttiforme (fusariosis in pineapple), *F. sacchari* (pokkah boeng in sugarcane), and *F. oxysporum* Schlecht (root rot in small cardamom). Additionally, *F. proliferatum* is linked to crown rot in banana and root rot in alfalfa, and *F. proliferatum* f. sp. *malus domestica* has been reported to cause apple replant disease (5–10).

Here, we report the complete genome sequence of *Fusarium proliferatum* isolate STSP isolated from *Elettaria cardamomum* (small cardamom) generated using two sequencing platforms. The findings provide foundational genomic information that enhances our understanding of *F. proliferatum* and helps identify existing knowledge gaps. This resource also supports comparative analyses across *Fusarium* species and improves understanding of diversity within the *Fusarium fujikuroi* species complex (FFSC). The FFSC consists of species that are primarily classified based on their plant pathogenicity, many of which are also known to produce a range of mycotoxins. In addition, several members of this group are recognized as opportunistic

human pathogens. Species within the FFSC include *F. verticillioides*, *F. circinatum*, *F. mangiferae*, *F. temperatum*, *F. proliferatum* and several others (11,12)

Data description

The methodology of this study involved several sequential steps, beginning with the collection of infected plant material and concluding with genome assembly and annotation of the fungal isolate. Tiller tissue located above the rhizome was collected from a wilted small cardamom (*Elettaria cardamomum*) plant from the Cardamom Hill Reserve (CHR) in Idukki district, Kerala (9° 40' 9.97" N, 77° 11' 1.94" E) (Data file 1). The plant tissue was surface-sterilized and the sterilized sections were transferred onto Potato Dextrose Agar (PDA) plates and incubated at 25°C for seven days. During incubation, fungal growth gradually emerged from the plant tissue, forming white, cottony mycelia characteristic of *Fusarium* species (Data file 2). To confirm morphological features, a small portion of the culture was mounted on a slide using Lactophenol Cotton Blue (LPCB) stain. Microscopic examination revealed the presence of long, slender macroconidia and short microconidia —key diagnostic traits commonly observed among *Fusarium* species (13). This preliminary morphological identification provided the basis for further molecular confirmation.

Genomic DNA was extracted from actively growing preculture mycelium using a CTAB–phenol:chloroform protocol followed by column purification to obtain high-purity DNA suitable for sequencing. DNA quality and concentration were assessed using spectrophotometry and agarose gel electrophoresis. Molecular identification of the isolate was performed through amplification and sequencing of the fungal ITS1 region, which confirmed its taxonomic classification within the *Fusarium* genus.

Whole-genome sequencing of the isolate was carried out using a hybrid approach combining both Illumina short-read and Oxford Nanopore Technologies (ONT) long-read platforms. Illumina sequencing produced 10,878,898 read pairs, comprising approximately 2.94 Gb of high-quality filtered data, while ONT sequencing yielded around 6.16 Gb of long-read data, providing the depth and continuity required for robust genome assembly. Raw reads from both platforms underwent demultiplexing, adapter trimming, and quality filtering using Trimmomatic v0.39 (14) to ensure high-quality input data.

High-quality trimmed Illumina reads and long Nanopore reads were used for *de novo* hybrid genome assembly using MaSuRCA assembler, which integrates the strengths of both short and long reads to produce a high-quality hybrid assembly. The resulting scaffolds were further polished and refined using RagTag for reference-guided scaffolding and LR-Gapcloser for filling remaining gaps, producing a draft genome of approximately 33.32 Mb assembled into 84 scaffolds (Data set 1) (15–17). The assembly had a scaffold N50 of 1.03 Mb, with the longest scaffold measuring 1.97 Mb. The average scaffold length was 396 kb. Genome assembly statistics were subsequently computed (Data file 3).

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	Root rot in cardamom	Joint Photographic Experts Group (.jpg)	EBI Biostudies database https://www.ebi.ac.uk/biostudies/studies/S-BSST2324 (18)
Data file 2	*Fusarium proliferatum* plate image 1	Joint Photographic Experts Group (.jpg)	EBI Biostudies database https://www.ebi.ac.uk/biostudies/studies/S-BSST2324 (18)
Data file 3	Genome Assembly Statistics	Webpage (.html)	EBI Biostudies database https://www.ebi.ac.uk/biostudies/studies/S-BSST2324 (18)
Data set 1	*Fusarium proliferatum* draft genome.fasta	Fasta file (.fasta)	NCBI GenBank Database (JBTNMN000000000) (19)
Data set 2	*Nanopore reads of F.proliferatum*	Fastq file (.fastq)	Sequence Read Archive (SRX31921887) (20)
Data set 3	*Illumina raw reads of F.proliferatum*	Fastq file (.fastq)	Sequence Read Archive (SRX31921885) (21)
Data set 4	*Illlumina HQ reads of F.proliferatum*	Fastq file (.fastq)	Sequence Read Archive (SRX31921886) (22)
Supplementary file	*QC Agarose gel FP*	Portable Network Graphics (.png)	EBI Biostudies database https://www.ebi.ac.uk/biostudies/studies/S-BSST2324 (18)

Limitations

Although *Fusarium proliferatum* was isolated from a wilted cardamom plant, its role as a pathogen or endophyte remains uncertain. Pathogenicity must be validated through controlled infection assays in cardamom plants, following Koch's postulates, to conclusively determine whether the isolate is capable of causing wilt disease in cardamom. Experiments to assess the pathogenic potential of the isolate are currently underway, and only after completing these studies can the organism be definitively classified as a pathogen or an endophyte.

Abbreviations

ONT – Oxford Nanopore Technology

BLAST- Basic Local Alignment Search Tool ITS- Internal Transcribed Spacer

LPCB- Lactophenol Cotton Blue

MaSuRCA- Maryland Super-Read Celera Assembler

LR-Gapcloser- Long- Read gapcloser

Declarations

Availability of data and materials

The data described in this Data note can be freely and openly accessed on , NCBI Sequence Read Archive under accession numbers SRX31921887, SRX31921885, and SRX31921886 EBI Biostudies database NCBI GenBank Database under https://doi.org/10.6019/S-BSST2324, JBTNMN000000000 respectively. Please see table 1 and references (18,19) for details and links to the data.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare having no competing interests.

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Authors' contributions

ST: Fungal isolation, Formal analysis, Data curation and uploading, Writing original draft, Review and editing. SG: Review and editing. SP: Conceptualization, Funding acquisition and resources, Formal analysis, Data curation and uploading, Review and editing. All authors reviewed and approved the manuscript.

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