



# Draft Genome Sequence of *Diaporthe* sp. Strain HANT25, an Endophytic Fungus Producing Mycoepoxydiene

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**ABSTRACT** *Diaporthe* sp. strain HANT25 is an endophytic fungus that produces mycoepoxydiene, a rare bioactive natural compound. Here, we report the genome sequence of *Diaporthe* sp. HANT25, comprising 55.3 Mb in 80 scaffolds. The genome sequence should enhance understanding of the biology and bioactive compound production potential of the genus *Diaporthe*.

Fungi in the genus *Diaporthe* (and their *Phomopsis*-like state) are commonly found inhabiting a broad range of plant hosts as nonpathogenic endophytes, pathogens, or saprobes (1). They are capable of producing an array of structurally diverse low-molecular-weight bioactive secondary metabolites with antimicrobial, antiparasitic, or anticancer activities (2). *Diaporthe* sp. strain HANT25 (formerly known as *Phomopsis* sp. strain HANT25) is an endophytic fungus that was isolated from twigs of a Thai medicinal plant, *Hydnocarpus anthelminthicus* Pierre ex Laness, collected from Central Botanical Garden (Pukae), Saraburi Province, Thailand (3). The fungus was initially identified as a *Phomopsis* sp. based on both microscopic morphology and a molecular method using internal transcribed spacer (ITS) sequences (1). The ITS sequences were deposited in GenBank under the accession number [EF635375](https://doi.org/10.1128/MRA.00805-20). This endophytic fungus can produce mycoepoxydiene and derivatives that contain a rare oxygen-bridged cyclooctadiene structure and have cytotoxic activity toward cancer cell lines, as well as anti-inflammatory activities (3–6). The fungus was kept on agar slants under liquid paraffin.

The genomic DNA of *Diaporthe* sp. HANT25 was obtained from a 6-day-old culture of the fungus in 50 ml Sabouraud dextrose broth (Merck) at 25°C under static conditions. The mycelium was collected by filtration and then lyophilized. The genomic DNA extraction, library preparation, sequencing, and *de novo* assembly of the genome were performed by Macrogen (Republic of Korea). The genomic DNA was fragmented and a sequencing library was constructed with the TruSeq DNA PCR Free kit (Illumina, CA, USA) with 350-bp inserts. Whole-genome sequencing was performed using the Illumina HiSeq 2000 platform, generating paired-end reads of 100 bp. A total of 8,136,214,782 bases in 80,556,582 reads were obtained. Sequencing quality was inspected using FastQC (7), and the reads were filtered for pairs of paired-end reads that had >90% of bases with a base quality score of  $\geq$ Q20. The filtered reads, consisting of 6,528,808,872 bases in 64,641,672 reads, were *de novo* assembled using SOAPdenovo2 version 2.0.4-r240 (8) with a k-mer size of 25 estimated with Jellyfish version 1.1.11 (9). The genome sequence of *Diaporthe* sp. strain HANT25 consisted of 55,338,496 bases distributed among 80 scaffolds. The  $N_{50}$  value was 1,996,735 bases, and the GC content was 52.11%. The sequencing depth was estimated to be 89 $\times$ . The genome assembly quality was evaluated using Benchmarking Universal Single-Copy Orthologs (BUSCO)

**Citation** Tulsook K, Isarangkul D, Sriubolmas N, Kittakoop P, Wiyakrutta S. 2020. Draft genome sequence of *Diaporthe* sp. strain HANT25, an endophytic fungus producing mycoepoxydiene. *Microbiol Resour Announc* 9:e00805-20. <https://doi.org/10.1128/MRA.00805-20>.

**Editor** Jason E. Stajich, University of California, Riverside

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**Received** 22 July 2020

**Accepted** 14 August 2020

**Published** 3 September 2020

(10) version 4.0.6 using genome mode with the Sordariomycetes\_odb10 data set (as of 20 November 2019). Of 3,817 BUSCO genes, more than 98% were found in the genome assembly (complete, 98.6% [single, 98.3%; duplicated, 0.3%]; fragmented, 0.3%; missing, 1.1%). The availability of this genome should enhance understanding of the biology and the secondary metabolite production potential of the genus *Diaporthe*.

**Data availability.** The genome sequence of *Diaporthe* sp. strain HANT25 has been deposited in GenBank under the accession number [JACBFG000000000](https://ncbi.nlm.nih.gov/nucl/JACBFG000000000) (version [JACBFG010000000](https://ncbi.nlm.nih.gov/nucl/JACBFG010000000)). The associated BioProject and BioSample accession numbers are [PRJNA642004](https://ncbi.nlm.nih.gov/bioproject/PRJNA642004) and [SAMN15375391](https://ncbi.nlm.nih.gov/biosample/SAMN15375391), respectively. The raw sequence reads were deposited in the SRA under accession number [SRR12145307](https://ncbi.nlm.nih.gov/sra/SRR12145307).

## ACKNOWLEDGMENTS

This research project was supported by Mahidol University. K.T. was supported by the Development and Promotion of Science and Technology Talents Project, Thailand.

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