

Draft Genome Sequence of the Filamentous Fungus *Penicillium paxilli* (ATCC 26601)

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***Penicillium paxilli* ATCC 26601 is an asexual filamentous fungal species known for its production of the mycotoxin paxilline. We present here the 35-Mb draft genome sequence for this organism.**

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Penicillium paxilli is an asexual saprophytic fungus, and isolate ATCC 26601 originates from insect-damaged pecans in Georgia, USA (1). *P. paxilli* is known for its production of the indole-diterpene paxilline, a potent tremorgen (1) that inhibits calcium-activated potassium channels (2). Due to the high rate of growth, sporulation, and ease of genetic modification, *P. paxilli* has been utilized as a model organism for studying indole-diterpene biosynthesis (3–8). The paxilline biosynthetic machinery is encoded by the *PAX* gene cluster, and the promoter from the *paxM* gene of this cluster has been successfully used for the heterologous expression of indole-diterpene biosynthetic genes from the fungal grass endophyte *Epichloë festucae* (9). The genome sequence of *P. paxilli* was sequenced to investigate its suitability as a heterologous expression system for fungal nonribosomal peptide synthetases (NRPS).

P. paxilli genomic DNA was prepared by phenol-chloroform extraction (10) and treated with RNase A. Two runs with 150-bp paired-end fragment reads were done on an Illumina MiSeq instrument by New Zealand Genomics Limited (NZGL), obtaining approximately 182-fold genome coverage. The reads were dynamically trimmed using the SolexaQA package to their longest fragment, such that the base call error rates did not exceed a *P* value of 0.05, and paired-end reads of <100 bp were discarded. *De novo* assembly was performed on all data using ABySS version 1.3.0, with the parameters *n* = 2, *c* = 10, and *k* = 79. The final assembly consisted of 635 contigs, with 414 contigs >500 bp in size, an average contig length of 84,079 bp, a maximum contig length of 732,567 bp, an *N*₅₀ of 189,821 bp, and a total of 34,808,516 residues.

Blast+ was used to identify a 4'-phosphopantetheinyl transferase (DDBJ/EMBL/GenBank accession no. KP233470) and a type II thioesterase (accession no. KP233471) in the *P. paxilli* genome that are likely to be functional. These proteins are required to produce and maintain functional NRPS enzymes, indicating that *P. paxilli* has the potential to be a suitable heterologous expression system for fungal NRPSs.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. AOTG00000000. The version described in this paper is the first version, AOTG01000000.

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