Draft Genome Sequence of *Daldinia eschscholzii* Isolated from Blood Culture

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*Daldinia eschscholzii* is an invasive endophyte that is most commonly found in plant tissues rich in secondary metabolites. We report the draft genome sequence of *D. eschscholzii* isolated from blood culture. The draft genome is 35,494,957 bp in length, with 42,898,665 reads, 61,449 contigs, and a G+C content of 46.8%. The genome was found to contain a high abundance of genes associated with plant cell wall degradation enzymes, mycotoxin production, and antifungal drug resistance.

The genomic DNA was sequenced to a 100-fold depth of coverage on the Illumina Genome Analyzer IIX sequencer. From our analysis, the estimated genome size of *D. eschscholzii* UM1020 is ∼42.66 Mb. The genome was assembled into 61,449 contigs using the SOAPdenovo version 1.05 assembler (9). All contigs generated were scaffolded into 599 large scaffolds (∼1,000 bp; N50, 115 kb). The resulting draft genome is 35,494,957 bp, with an overall G+C content of 46.8%. Subsequent gene prediction analysis using GeneMark-ES version 2.3 (11) yielded a total of 11,445 predicted protein-coding genes with 92% (10,578) longer than 100 amino acids. The predicted gene model has an exon frequency of 2.82 exons per gene. Genome annotation on predicted genes was carried out by BLAST similarity searches against Swiss-Prot, with a total of 56.75% genes successfully annotated.

The genome is found to contain a high abundance of genes associated with plant cell wall degradation enzymes such as xylanase, endoglucanase, β-glucosidase, and cellobiohydrolase, which are important for survival, as an endophyte lives inside plant tissues (7, 8, 10). These genes are essentially absent or in low abundance in host-dependent endogenous fungi such as *Candida albicans* (4). A plethora of genes which are essential in heavy metal, toxic compound, and pesticide resistance were detected in *D. eschscholzii* UM1020, indicating its adaptation ability and also the origin of this species from the external environment. Genes associated with the production of potent human carcinogens, such as aflatoxins and sterigmatocystin, commonly produced by *Aspergillus* species (5, 13) were detected, together with HC-toxin, an inhibitor of histone deacetylase commonly secreted by the filamentous fungus *Cochliobolus carbonum* (6, 12). The subsequent discovery of genes associated with resistance to the antifungal drugs fluconazole, fluoroocytosine, and benomyl, as well as methotrexate resistance (1, 2, 3), present an interesting opportunity to study molecular mechanisms that lead to antifungal drug resistance.

The draft genome of *D. eschscholzii* UM1020 represents the first reported genome sequence of a wood-inhabiting fungus isolated from a patient’s blood culture. The understanding of the *D. eschscholzii* UM1020 genome provides insights into the genetic potential of nonhuman endogenous fungal infection and delivers an excellent basis for the further study of human-fungal interactions.

**Nucleotide sequence accession number.** The nucleotide sequence of the *D. eschscholzii* genome has been deposited in DDBJ/EMBL/GenBank under accession no. AIID00000000.

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