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Genome Sequence of an Unclassified *Pleosporales* Species Isolated from Human Nasopharyngeal Aspirate

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***Pleosporales* is the largest order in the fungal class *Dothideomycetes*. We report the 36,814,818-bp draft genome sequence and gene annotation of UM1110, a *Pleosporales* isolate associated with unclassified genera that is potentially a new fungal species. Analysis of the genome sequence led to the finding of genes associated with fungal adhesive proteins, secreted proteases, allergens, and pseudohyphal development.**

Pleosporales is the largest order in the fungal class *Dothideomycetes*, which is estimated to comprise more than 4,700 species (9). Isolate UM1110, cultured from human nasopharyngeal aspirate, was identified as a *Pleosporales* species by macro- and microscopic morphology, internal transcribed spacer (ITS)-based PCR amplification, and ITS sequence-based phylogenetic analysis. It shows septate branched hyphae falling apart into rectangular arthroconidia and is potentially a new species of an unclassified *Pleosporales* genus.

The *Pleosporales* isolate UM1110 genomic DNA was sequenced to a 100-fold depth of coverage using the Illumina Genome Analyzer GAIIX by employing the next generation sequencing strategy on a 300-bp DNA insert-size library. The genome was assembled into 491 scaffolds (1 kb; N_{50} , 312 kb) comprising 60,208 contigs by using the SOAPdenovo version 1.05 assembler (2). The assembled genome size is 36,814,818 bp, with a G+C content of 51.14%. A total of 14,074 genes, 13,165 (93.54%) of which are longer than 100 amino acids, was predicted using GeneMark-ES version 2.3 (7). Putative functions were successfully assigned to 7,400 (52.58%) genes based on sequence similarity searches against Swiss-Prot protein sequence database.

A preliminary analysis revealed an abundance of genes encoding serine-rich adhesion platelet proteins, which are key components in platelet adhesion commonly found in staphylococcal and streptococcal bacteria (10). These adhesive proteins probably contribute toward host cell adhesion and binding. Also present were genes encoding secreted proteases, like subtilisins and metalloproteases (8), which constitute a significant part of fungal secretomes (4) and are likely to be virulence-related factors, as well as genes associated with allergic reactivity, such as those encoding aldehyde dehydrogenase (Alt a 10), a putative glycosidase (*crf1* [coding for Asp f 9]), and thioredoxin-like protein (Fus c 2), commonly known as fungal allergens (1). An interesting feature noted was the presence of hyphal growth protein 1, flocculation (*FLO11*), and pseudohyphal development (*EPD1*) genes, which are involved in fungal pseudohyphal development (3, 5). This suggests that UM1110 could have the ability to exist as both filamentous pseudohyphae and yeast cells, a pathogenicity mechanism employed by dimorphic fungi to survive inside mammalian hosts (6).

Nucleotide sequence accession number. The nucleotide sequence of the *Pleosporales* isolate UM1110 genome has been deposited in DDBJ/EMBL/GenBank under accession no. [AJMS00000000](http://ajms00000000).

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K.P.N., Y.F.N., and H.H. conceived the project and contributed to the writing and editing of the manuscript. K.P.N., T.S.S.-H., C.L.C., and S.L.N. were responsible for the isolation, identification, and DNA extraction. S.M.Y., C.C.H., K.W.L., and W.Y.Y. performed the genome sequencing and bioinformatics analysis.

REFERENCES

- Knutsen AP, et al. 2012. Fungi and allergic lower respiratory tract diseases. *J. Allergy Clin. Immunol.* 129:280–291.
- Li R, Kristiansen K, Wang J. 2008. SOAP: short oligonucleotide alignment program. *Bioinformatics* 24:713–714.
- Lo WS, Dranginis AM. 1998. The cell surface flocculin Flo11 is required for pseudohyphae formation and invasion by *Saccharomyces cerevisiae*. *Mol. Biol. Cell* 9:161–171.
- Muszewska A, Taylor JW, Szczesny P, Grynberg M. 2011. Independent subtilases expansions in fungi associated with animals. *Mol. Biol. Evol.* 28:3395–3404.
- Nakazawa T, Horiuchi H, Ohta A, Takagi M. 1998. Isolation and characterization of *EPD1*, an essential gene for pseudohyphal growth of a dimorphic yeast, *Candida maltosa*. *J. Bacteriol.* 180:2079–2086.
- Nemecek JC, Wüthrich M, Klein BS. 2006. Global control of dimorphism and virulence in fungi. *Science* 312:583–588.
- Ter-Hovhannisyan V, Lomsadze A, Chernoff Y, Borodovsky M. 2008. Gene prediction in novel fungal genomes using an ab initio algorithm with unsupervised training. *Genome Res.* 18:1979–1990.
- Vermout S, et al. 2008. Pathogenesis of dermatophytosis. *Mycopathologia* 166:267–275.
- Zhang Y, et al. 2009. Multi-locus phylogeny of Pleosporales: a taxonomic, ecological and evolutionary re-evaluation. *Stud. Mycol.* 64:85–102.
- Zhou M, Wu H. 2009. Glycosylation and biogenesis of a family of serine-rich bacterial adhesins. *Microbiology* 155:317–327.

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