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Draft Genome Sequences of Human Pathogenic Fungus *Geomyces pannorum* *Sensu Lato* and Bat White Nose Syndrome Pathogen *Geomyces (Pseudogymnoascus) destructans*

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We report the draft genome sequences of *Geomyces pannorum sensu lato* and *Geomyces (Pseudogymnoascus) destructans*. *G. pannorum* has a larger proteome than *G. destructans*, containing more proteins with ascribed enzymatic functions. This dichotomy in the genomes of related psychrophilic fungi is a valuable target for defining their distinct saprobic and pathogenic attributes.

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Geomyces pannorum is a soil-dwelling fungus common in colder parts of the world (1–3). *G. pannorum* is rarely implicated in the human disease geomycosis, which manifests as skin and nail infections (4–6). *Geomyces destructans* is the etiologic agent of bat geomycosis or white nose syndrome (WNS) (7, 8). *G. destructans* is restricted to caves and mines in the United States and Europe (9, 10). *G. pannorum sensu lato* represents a species complex, while *G. destructans* was recently reclassified as *Pseudogymnoascus destructans* (2, 9). As taxonomy is in a state of flux, *G. destructans* and *G. pannorum* will be used as the organism names throughout this work. Both fungi are adapted to a psychrophilic range (4° to 15°C) and express enzymes implicated in fungal virulence (1, 3, 8, 11). The study of the biology and pathogenicity of psychrophilic fungi is in its infancy due to a lack of experimental tools. This is also true for other eukaryotes inhabiting colder parts of the earth.

Genomic DNA from *G. pannorum* M1372 and *G. destructans* M1379 was obtained by phenol-chloroform extraction of pulverized fungal mycelia. The Illumina HiSeq 2000 was used for 100-base paired-end sequencing. The assemblies were generated using four programs, subsampling 89 million reads for *G. pannorum* and 88 million reads for *G. destructans*. Optimal assemblies representing 100× coverage for *G. pannorum* and 150× coverage for *G. destructans* were generated with MaSuRCA version 1.9.2 (12). The *G. pannorum* assembly is 29.47 Mb, with a G+C content of 50.5%, and comprises 856 scaffolds ranging in length from 300 bases to 839 kb (average, 34.4 kb; median, 7.9 kb; N₅₀, 105 kb). *G. destructans* is 30.49 Mb, with a G+C content of 49.8%, and was assembled into 5,008 scaffolds of length 108 bases to 234 kb (average, 6.1 kb; median, 1.8 kb; N₅₀, 19.2 kb). Fifty-two percent of the *G. destructans* reference DNA shares similarity with *G. pannorum* query DNA, with 45% of it being identical. A custom *ab initio* gene prediction pipeline generated 9,689 *G. pannorum*

proteins and 7,967 *G. destructans* proteins. The difference in the coding density, which is 48% for *G. pannorum* and 37% for *G. destructans*, is attributable to the smaller number of proteins and numerous repeats (25.8% of the genome) in *G. destructans* than in *G. pannorum* (5.40% repeats). CEGMA predicted 96.7% of the 458 conserved genes in *G. destructans* and 98.3% in *G. pannorum* (13). Functional annotation with BLAST against UniProt (14) and HMM searches against TIGRFams/Pfams (15, 16) yielded Gene Ontology annotations (17) for 62.3% of the *G. destructans* proteins and 63.1% of the *G. pannorum* proteins. EC assignments were given to 2,052 *G. destructans* proteins (25.8%) and 2,734 *G. pannorum* proteins (28.2%). Thus, *G. pannorum* contains more proteins than *G. destructans*, including more with ascribed enzymatic functions. This dichotomy in the genomes of related psychrophilic fungi is a valuable target for defining their distinct saprobic and pathogenic attributes.

Nucleotide sequence accession numbers. The *G. (Pseudogymnoascus) destructans* whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AYKP00000000](#). The version described in this paper is [AYKP01000000](#). The *G. pannorum* whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AYKR00000000](#). The version described in this paper is [AYKR01000000](#).

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REFERENCES

1. Marshall WA. 1998. Aerial transport of keratinaceous substrate and distribution of the fungus *Geomyces pannorum* in Antarctic soils. *Microb. Ecol.* 36:212–219.
2. de Hoog GS, Guarro J, Gené J, Figueras MJ. 2009. Atlas of clinical fungi, 3rd edition (pilot version). CBS/Universitat Rovira i Virgili, Utrecht, the Netherlands.
3. Kochkina GA, Ivanushkina NE, Akimov VN, Gilichinskii DA, Ozerskaia SM. 2007. Halo- and psychrotolerant *Geomyces* fungi from Arctic cryopegs and marine deposits. *Mikrobiologiya* 76:39–47. (Article in Russian.)
4. Christen-Zaech S, Patel S, Mancini AJ. 2008. Recurrent cutaneous *Geomyces pannorum* infection in three brothers with ichthyosis. *J. Am. Acad. Dermatol.* 58:S112–S113.
5. Gianni C, Caretta G, Romano C. 2003. Skin infection due to *Geomyces pannorum* var. *pannorum*. *Mycoses* 46:430–432.
6. Zelenková H. 2006. *Geomyces pannorum* as a possible causative agent of dermatomycosis and onychomycosis in two patients. *Acta Dermatovenereol. Croat.* 14:21–25.
7. Blehert DS, Hicks AC, Behr M, Meteyer CU, Berlowski-Zier BM, Buckles EL, Coleman JT, Darling SR, Gargas A, Niver R, Okoniewski JC, Rudd RJ, Stone WB. 2009. Bat white-nose syndrome: an emerging fungal pathogen? *Science* 323:227. doi:10.1126/science.1163874.
8. Chaturvedi V, Springer DJ, Behr MJ, Ramani R, Li X, Peck MK, Ren P, Bopp DJ, Wood B, Samsonoff WA, Butchkoski CM, Hicks AC, Stone WB, Rudd RJ, Chaturvedi S. 2010. Morphological and molecular characterizations of psychrophilic fungus *Geomyces destructans* from New York bats with white nose syndrome (WNS). *PLoS One* 5:e10783. doi:10.1371/journal.pone.0010783.
9. Minnis AM, Lindner DL. 2013. Phylogenetic evaluation of *Geomyces* and allies reveals no close relatives of *Pseudogymnoascus destructans*, comb. nov., in bat hibernacula of eastern North America. *Fungal Biol.* 117: 638–649.
10. Puechmaille SJ, Wibbelt G, Korn V, Fuller H, Forget F, Mühldorfer K, Kurth A, Bogdanowicz W, Borel C, Bosch T, Cherezy T, Drebet M, Göröfö T, Haarsma AJ, Herhaus F, Hallart G, Hammer M, Jungmann C, Le Bris Y, Lutsar L, Masing M, Mulkens B, Passior K, Starrach M, Wojtaszewski A, Zöphel U, Teeling EC. 2011. Pan-European distribution of white-nose syndrome fungus (*Geomyces destructans*) not associated with mass mortality. *PLoS One* 6:e19167. doi:10.1371/journal.pone.0019167.
11. Marchisio VF, Fusconi A, Rigo S. 1994. Keratinolysis and its morphological expression in hair digestion by airborne fungi. *Mycopathologia* 127:103–115.
12. Zimin AV, Marçais G, Puiu D, Roberts M, Salzberg SL, Yorke JA. 2013. The MaSuRCA genome assembler. *Bioinformatics* 29:2669–2677.
13. Parra G, Bradnam K, Korf I. 2007. CEGMA: a pipeline to accurately annotate core genes in eukaryotic genomes. *Bioinformatics* 23:1061–1067.
14. UniProt Consortium. 2013. Update on activities at the Universal Protein Resource (UniProt) in 2013. *Nucleic Acids Res.* 41:D43–D47. doi:10.1093/nar/gks1068.
15. Punta M, Coghill PC, Eberhardt RY, Mistry J, Tate J, Boursnell C, Pang N, Forslund K, Ceric G, Clements J, Heger A, Holm L, Sonnhammer EL, Eddy SR, Bateman A, Finn RD. 2012. The Pfam protein families database. *Nucleic Acids Res.* 40:D290–D301.
16. Haft DH, Selengut JD, White O. 2003. The TIGRFams database of protein families. *Nucleic Acids Res.* 31:371–373.
17. Gene Ontology Consortium, Blake JA, Dolan M, Drabkin H, Hill DP, Li N, Sitnikov D, Bridges S, Burgess S, Buza T, McCarthy F, Peddinti D, Pillai L, Carbon S, Dietze H, Ireland A, Lewis SE, Mungall CJ, Gaudet P, Chrisolm RL, Fey P, Kibbe WA, Basu S, Siegele DA, McIntosh BK, Renfro DP, Zweifel AE, Hu JC, Brown NH, Tweedie S, Alam-Faruque Y, Apweiler R, Auchinchloss A, Axelsen K, Bely B, Blatter M-, Bonilla C, Bouguerleret L, Boutet E, Breuza L, Bridge A, Chan WM, Chavali G, Coudert E, Dimmer E, Estreicher A, Famiglietti L, Feuermann M, Gos A, Gruaz-Gumowski N, et al. 2013. Gene ontology annotations and resources. *Nucleic Acids Res.* 41:D530–D535. doi:10.1093/nar/gks1050.