

# Study finds likely origin of lung fungus invading Pacific Northwest

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*Cryptococcus gattii*, a virulent fungus that has invaded the Pacific Northwest is highly adaptive and warrants global "public health vigilance," according to a study by an international team led by the Translational Genomics Research Institute (TGen).

*C. gattii*, which likely originated in Brazil, is responsible for dozens of deaths in recent years since it was first found in 1999 on Vancouver Island, British Columbia, Canada, well outside its usual tropical habitats.

"We identified several genes that may make the outbreak strains more capable of surviving colder environments and that make it more harmful in the lungs," said David Engelthaler, Director of Programs and Operations for TGen's Pathogen Genomics Division (TGen North) and lead author of the study published today in the scientific journal *mBio*.

This study should form the basis of additional investigations about how and why *C. gattii* disperses and emerges. It identified several new genomic targets for diagnostic tests, and possible new targets for therapeutic drugs and preventative vaccines.

"By closely analyzing the genomes of dozens of outbreak strains, as well as globally diverse strains, we were able to closely compare and determine the genomic differences that may cause their clinical and ecological changes," said Dr. Paul Keim, one of the study's senior authors. Dr. Keim also is Director of TGen North, and Director of the Microbial Genetics and Genomics Center at Northern Arizona

University (NAU).

TGen, working with the U.S. Centers for Disease Control and Prevention and others, conducted one of the largest global fungal genome analyses of a specific species to understand its emergence in new environments. The collaborative team included 24 researchers from 13 institutions in seven nations who sequenced 115 genomes of *C. gattii* collected from 15 countries.

"By thinking globally, we were able to better understand what was happening locally," Engelthaler said.

*C. gattii* was typically a tropical fungus before it was discovered in the temperate environs of Vancouver Island. It soon evolved into a new, more virulent, pulmonary disease that quickly spread to mainland Canada and south into the state of Washington. That was followed by an outbreak in Oregon of another new strain of *C. gattii*, which also displayed increased lethality and similarly spread throughout the Pacific Northwest.

*C. gattii* previously was associated with neurological disease in strains found elsewhere in the world. But the strains discovered in the Pacific Northwest not only establish a new environmental niche, but also display increased virulence and produce severe lung infections.

"We provide evidence that the Pacific Northwest strains originated from South America, and identified numerous genes potentially related to habitat adaptation, virulence expression and to clinical presentation," said Dr. Wieland Meyer, the study's other senior author.

"Further elucidation and characterization of these genetic features may lead to improved diagnostics and therapies for infections caused by this continually evolving fungus," said Dr. Meyer, who is affiliated with:

Sydney Medical School-Westmead Hospital; the University of Sydney; and the Westmead Millennium Institute for Medical Research.

This study concludes that: "Public health vigilance is warranted for emergence in regions where *C. gattii* is not thought to be endemic."

New tests developed for this study by TGen are making it easier to detect this and other fungi, and could lead to better monitoring and treatments. The same tools used in this study also were used to investigate the cause of a fungal meningitis outbreak associated with steroid back injections, and the recent outbreak of Valley Fever in the state of Washington.

**More information:** "Cryptococcus gattii in North American Pacific Northwest: whole population genome analysis provides insights into species evolution and dispersal," *mBio*, 2014.

Provided by The Translational Genomics Research Institute

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