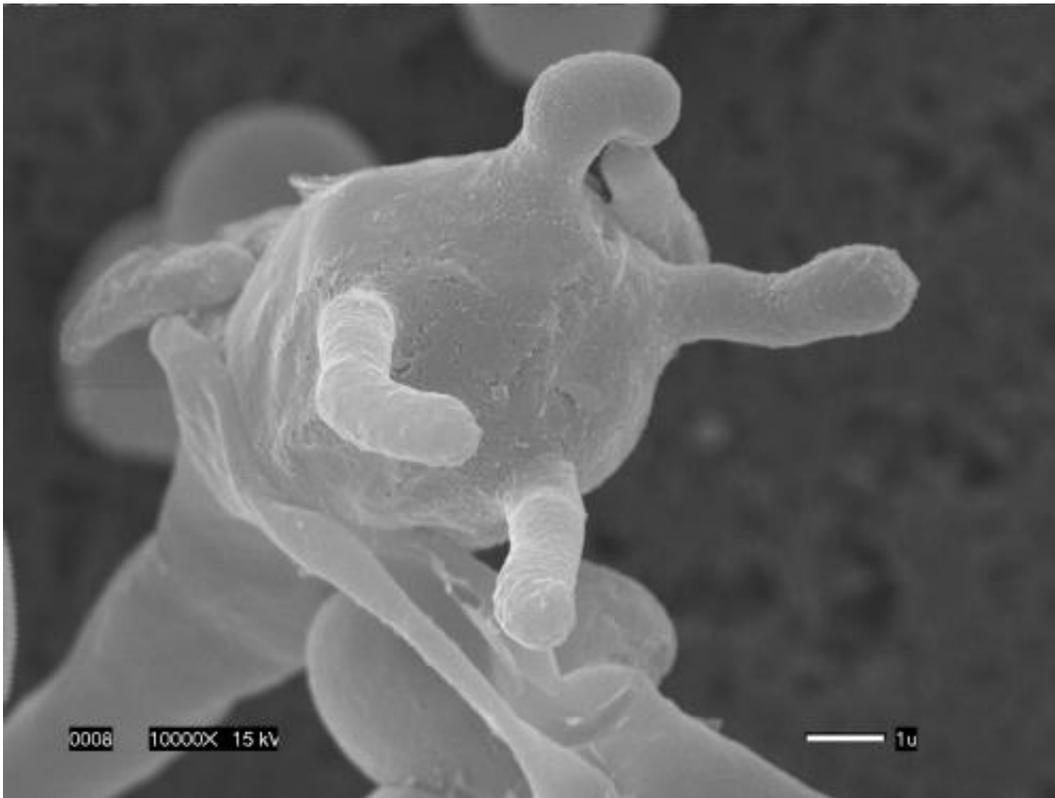


Disease-causing genes spread easily in emerging lethal fungus infection

September 5 2013



Scanning electron micrograph of infectious spores produced by *Cryptococcus gatti* during its sexual cycle, which are readily aerosolized and inhaled to cause infections in humans. Credit: Edmond Byrnes and Joseph Heitman, Duke University

A rare, emerging fungal disease that is spreading throughout Canada and Northwestern USA can easily pass its deadly genes to related fungal

strains within the species but less readily to more distant relatives, according to a study part-funded by the Wellcome Trust.

The findings will help to understand the origins of infectious outbreaks and predict the likelihood of the disease spreading to other populations and geographical areas.

Cryptococcus gattii is a type of [fungus](#) that was previously only found in warmer climates throughout the tropics. However, since 1999 outbreaks of highly [virulent strains](#) of the fungus have been reported in the cooler climates of Canada and Northwestern USA, causing serious illness in otherwise healthy people and domestic and [wild animals](#) and proving fatal in some cases.

To try to understand how likely it is that the disease will spread further, a team of researchers in the US and UK interbred different [strains](#) of the fungus to test how easily the characteristics of these more dangerous strains can be transferred to other less harmful strains.

The results show that genes conferring traits that make the fungus more dangerous are easily passed to the offspring when the two parent strains are closely related. When the strains are distantly related to each other, the genes are much less likely to spread.

Professor Robin May from the University of Birmingham, who co-led the study with Dr. Joseph Heitman, MD, PhD from Duke University, said: "That the fungus can easily pass on the genes that make it more dangerous means that we could potentially see new strains of *C. gattii* cropping up spontaneously, causing outbreaks of disease in areas that were previously unaffected.

"Although this is still a very [rare disease](#), with only around 400 people having been affected in the last decade, the results of our study show that

surveillance efforts will be vital to stop it from spreading."

Part of the reason the 'hypervirulent' strains are so dangerous is that they have the unusual ability to survive inside cells of the infected person's immune system, where they rapidly reproduce.

The findings reveal that these characteristics can be inherited from the parent fungi through the genome and also through genetic material contained within the mitochondria, tiny structures inside the fungal cells. Mitochondrial DNA is normally inherited from only one parent but the team show that this particular strain of fungus can get mitochondrial genes from both parents.

"We were surprised to see that *C. gattii* could inherit mitochondrial [genes](#) from either or even both parents. This may make it easier for the fungus to spontaneously develop disease-causing traits that make it more of a threat," added lead researcher Dr. Kerstin Voelz.

C. gattii is found in the soil and in association with certain trees such as eucalyptus, pine or fir trees. It is transmitted to humans and other animals by inhaling spores of the fungus that are carried in the air. After infecting the lungs, cells of the fungus can travel through the bloodstream to infect other areas of the body, including the brain. The most common symptoms are shortness of breath, coughing, fatigue, fever, and headache.

More information: K. Voelz et al. Transmission of hypervirulence traits via sexual reproduction within and between lineages of the human fungal pathogen *Cryptococcus gattii*. *PLOS Genetics*, 5 September. [epub ahead of print]

Provided by Wellcome Trust

Citation: Disease-causing genes spread easily in emerging lethal fungus infection (2013, September 5) retrieved 19 April 2024 from <https://phys.org/news/2013-09-disease-causing-genes-easily-emerging-lethal.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.