Cryptococcus neoformans carried by Odontomachus bauri ants

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Cryptococcus neoformans is the most common causative agent of cryptococcosis worldwide. Although this fungus has been isolated from a variety of organic substrates, several studies suggest that hollow trees constitute an important natural niche for C. neoformans. A previously surveyed hollow of a living pink shower tree (Cassia grandis) positive for C. neoformans in the city of Rio de Janeiro, Brazil, was chosen for further investigation. Odontomachus bauri ants (trap-jaw ants) found inside the hollow were collected for evaluation as possible carriers of Cryptococcus spp. Two out of 10 ants were found to carry phenoloxidase-positive colonies identified as C. neoformans molecular types VNI and VNII. The ants may have acted as a mechanical vector of C. neoformans and possibly contributed to the dispersal of the fungi from one substrate to another. To the best of our knowledge, this is the first report on the association of C. neoformans with ants of the genus Odontomachus.

Key words: Cryptococcus neoformans - Odontomachus bauri - insect association - hollow tree habitat

Hollows from tree trunks have been investigated as potential sources of Cryptococcus gattii and Cryptococcus neoformans, the two causative agents of cryptococcosis, a life-threatening systemic mycosis affecting humans and a wide range of animals (Kwon-Chung & Perfect 2000). In addition to these surveys, there have been other investigations on the hollow trunks of living trees, where they interact with plants (Passos & Oliveira 2004, Gibernau et al. 2007, Spagna et al. 2009). These pathogenic capsulated yeasts, which have as their teleomorphic state the genus Filobasidiella, belong to the class Tremellomycetes of the phylum Basidiomycota (Kirk et al. 2008). Like other members of this phylum, these yeasts also produce laccase, a ligninolytic enzyme that allows them to grow on decaying wood and other lignified substrates (Lazéra et al. 1998, Chan & Tay 2010). Fungi can also be associated with many insect species. The exoskeletons of some insects can harbour several species of yeasts, promoting their survival or dispersal to new substrates (Rosa et al. 2003, Pagnocca et al. 2008). Species of Odontomachus ants, a predatory genus from the subfamily Ponerinae (family Formicidae), known as trap-jaw ants, are highly common in neotropical countries, where they interact with plants (Passos & Oliveira 2004, Gibernau et al. 2007, Spagna et al. 2009).

To test the hypothesis that ants can act as carriers of C. neoformans, we examined 10 of these insects collected from a hollow of a living pink shower tree (Cassia grandis) that has been positive for this pathogen for nearly 15 years (Lazéra et al. 1996).

MATERIALS AND METHODS

Ant collection - The ants were collected in sterilised tubes from the hollow of a pink shower tree (C. grandis) located on the campus of the Oswaldo Cruz Foundation (Fiocruz) in the city of Rio de Janeiro (Fig. 1). The ants were transferred to the laboratory for immediate fungal isolation.

Fungal isolation from ant exoskeletons - Each ant was allowed to walk for 24 h on niger seed agar (NSA) plate supplemented with chloramphenicol (400 mg l-1) and amikacin (800 mg l-1). The plates were incubated at 25°C and examined daily for four days. During this period, phenoloxidase-positive yeast colonies were isolated and pure cultures were obtained after serial transfers on NSA. The isolates were subcultured on Sabouraud dextrose agar, stored at 4°C and cryopreserved in 15% glycerol at -70°C.
**Ant characterisation** - The ants collected from the studied hollow were morphologically characterised and identified according to the literature (Kempf 1972, Brown 1976, Baccaro 2006, Bolton et al. 2006).

**Yeast identification** - Morphological and physiological characterisations were conducted, including phenoloxidase production on NSA, thermostolerance at 37°C, cycloheximide sensitivity, urease production and assimilation tests performed with the VITEK-32 (bio-Mérieux, France). Canavanine-glycine-bromothymol blue medium was used to identify the species as *C. gattii* and *C. neoformans* (Kwon-Chung et al. 1982).

The molecular types were determined by restriction fragment length polymorphism (RFLP) of the gene *URA5* according to Meyer et al. (2003). The following standard strains representing each molecular type of *C. neoformans* (VN) and *C. gattii* (VG) were included in the analysis: WM 148 (serotype A, VNI/AFLP1), WM 626 (serotype A, VNII/AFLP1A), WM 628 (serotype AD, VNIII/AFLP2), WM 629 (serotype D, VNIV/AFLP3), WM 179 (serotype B, VGI/AFLP4), WM 178 (serotype B, VGII/AFLP6), WM 175 (serotype B, VGIII/AFLP5) and WM 779 (serotype C, VGV/AFLP7).

Genomic DNA was extracted as previously described by Ferrer et al. (2001) with some modifications. Half of an inoculation loop of culture was frozen at -20°C for 1 h and incubated at 65°C for 1 h in 0.5 mL of extraction buffer (50 mM Tris-HCl, 50 mM ethylenediaminetetraacetic acid, 3% sodium dodecyl sulphate, 1% 2-mercaptoethanol). The lysate was extracted with phenol-chloroform-isooamy alcohol (25:24:1). The DNA was recovered by isopropanol precipitation and then washed with 70% ethanol and diluted in sterile water.

The polymerase chain reaction (PCR) of the *URA5* gene was performed in a final volume of 50 μL. Each reaction contained 50 ng of DNA, 1 x PCR buffer [160 mM (NH₄)₂SO₄, 670 mM Tris-HCl (pH 8.8 at 25°C), 0.1% Tween-20 (Bioline), 0.2 mM each of dATP, dCTP, dGTP and dTTP (Roche Diagnostics GmbH), 3 mM magnesium chloride, 1.5 U BioTaq DNA polymerase (Bioline) and 50 ng each of the primers URA5 (5’ ATGTCCTCCCAAGCCCTCGACTCCG 3’) and SJ01 (5’TTAAGACCTCCTGAAACCCGTACTC 3’) (Meyer et al. 2003). The target sequence was amplified in a Perkin-Elmer thermal cycler (model 480) using the following cycling program: 94°C for 2 min (initial denaturation), 35 cycles of 45 s at 94°C (denaturation), 1 min at 61°C (annealing) and 2 min at 72°C (extension) and a final extension cycle for 10 min at 72°C. A total of 30 μL of the PCR products was double digested with *Sau*96I (10 U/μL) and *Hha*I (20 U/μL) for 3 h and the fragments were separated by 3% agarose gel electrophoresis at 100 V. The RFLP patterns were assigned visually by comparison with patterns obtained from the standard strains described above.

**RESULTS**

Two out of the 10 collected ants, later morphologically identified as *Odontomachus bauri* Emery, 1892, were found to carry phenoloxidase-positive yeasts. Two NSA plates allowed the growth of one dark brown colony each, later identified as *C. neoformans* molecular types VNII and VNI (Fig. 2). These isolates were deposited in the Pathogenic Fungal Collection (CFP), Clinical Research Institute Evandro Chagas, Fiocruz, as CFP 216 and CFP 217, respectively.
DISCUSSION

Fourteen hollows of living trees were formerly investigated at the Fiocruz campus. Serial scrapings taken from the inner surfaces of the hollows of two living C. grandis trees (family Fabaceae, subfamily Caesalpinioideae), popularly known as pink shower trees, yielded isolates of *C. neoformans* (Lazéra et al. 1996). The pink shower tree that provided the most isolates of *C. neoformans* (hollow A) and was continuously positive for *C. neoformans* until recently (M Lazéra, unpublished observations) was chosen for the current investigation. These yeasts are commonly found in this habitat, probably due to their ligninolytic enzyme laccase, which allows the yeasts to grow on decaying wood (Lazéra et al. 1998, Chan & Tay 2010).

Fungi can be associated with different insects, such as ants, as previously demonstrated by Pagnocca et al. (2008), who isolated several species of yeasts, including *Cryptococcus laurentii*, from the exoskeletons of two ant species, *Atta laevigata* and *Atta capiguara*. In an earlier study, other representatives of the *Cryptococcus* genus were isolated from stingless bees (Rosa et al. 2003) and from the guts of insects belonging to the order Neuroptera (Nguyen et al. 2007). In another investigation, two different molecular types of *C. gattii* (VGI and VGI) were isolated from fresh insect frass (order Lepidoptera, family Oecophoridae) in a shallow cavity in the bark of a living *Eucalyptus tereticornis* tree (Kidd et al. 2003).

To date, there have been no reports on the association of fungi with the genus *Odontomachus*, although the association of these ants with bacteria has been studied (Caetano et al. 2009, dos Santos et al. 2009). The role of ants, including *Odontomachus* spp, as mechanical vectors of pathogenic bacteria within hospitals was recently demonstrated by dos Santos et al. (2009), uncovering a public health problem because these bacteria can be directly associated with nosocomial infections. In another study, bacteria were found in the digestive tract of *O. bauri*, the same species of ant as investigated in the present study, suggesting the participation of these bacteria in the food digestion of this ant (Caetano et al. 2009).

The finding that only two out of the 10 ants were positive for *C. neoformans* may be due to the non-homogeneous presence of these pathogens in the hollow tree; these pathogens likely have a focal distribution. During sample collection, either by swabbing or scraping, it is very common to find only 10-25% that are positive. In addition, it is necessary to consider the detection limitations of the method, which can be low, in addition to the competition with other microorganisms (Mitchell et al. 2011).

The fact that the *C. grandis* tree from which the *O. bauri* ants were collected (hollow A) is very close to another *C. grandis* tree (hollow B) previously studied that is also positive for *C. neoformans* (Lazéra et al. 1996) suggests that the ants could be acting as mechanical vectors of *C. neoformans* and may be responsible for the dispersal of these yeasts from one tree to another. In any case, this yeast-ant association deserves more research.

In Teresina, the capital of the state of Piauí, Northeast Region, Brazil, the *C. neoformans* strains isolated from several trees in a single downtown square showed a high level of molecular similarity values (> 95%) in their amplified fragment length polymorphism patterns, suggesting that cryptococcal populations may be clonally dispersed among neighbouring trees and nearby animal-related habitats (Trilles et al. 2003).

Based on molecular typing, *C. neoformans* can be subdivided into the VNI, VNII, VNIII and VNI V types (Meyer et al. 1999). The *C. neoformans* isolates presently investigated were characterised as molecular types VNI and VNII. However, Trilles et al. (2008) molecularly typed 5 isolates of *C. neoformans* originating from two *C. grandis* trees investigated by Lazéra et al. (1996), one of which was the tree used in this study and found that all five isolates were molecular type VNI. Thus, from the first sampling (Lazéra et al. 1996) to the more recent sampling in the same hollow tree, a change in the community may have occurred, with *C. neoformans* VNII being added to the previously identified *C. neoformans* VNI. In their study, Trilles et al. (2008) analysed 320 *C. neoformans* isolates and 123 *C. gattii* isolates from various parts of Brazil, demonstrating that the most common molecular type in the southern region, which includes Rio de Janeiro, was VNI (64%) and that VNII had a minor incidence (5%), occurring exclusively in this region from clinical and environmental sources.

This study indicates the need for a thorough investigation with more samplings of insects, inside and around hollow trees, over an extended period of time at regular intervals to confirm that *O. bauri* and/or other insects are acting as mechanical vectors of *C. neoformans* and are responsible for the dispersal of these yeasts to other substrates. The interaction of fungi with hollow trees and insects forms a system that may be useful for understanding their ecology.

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