In vitro antifungal susceptibility profiles and genotypes of 308 clinical and environmental isolates of Cryptococcus neoformans var. grubii and Cryptococcus gattii serotype B from north-western India

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Cryptococcus neoformans and Cryptococcus gattii are aetiological agents of cryptococcosis, a major opportunistic systemic mycosis of increasing global importance. This study reports the antifungal susceptibility profiles of clinical and environmental isolates of C. neoformans var. grubii, genotype VNI/AFLP1 (n=246), and C. gattii serotype B, genotype VGI/AFLP4 (n=62), originating from patients and environmental sources in north-western India. All of the C. neoformans var. grubii and C. gattii isolates were mating type a. Using the broth microdilution method, both species were found to be susceptible to the antifungals tested except for two clinical C. neoformans var. grubii isolates that were resistant to 5-flucytosine (MIC >0.64 μg ml⁻¹).

Data on the geometric mean of MICs revealed that C. gattii was significantly less susceptible than C. neoformans var. grubii to fluconazole, itraconazole and voriconazole (P<0.0001). In addition, the MIC₉₀ of C. gattii was twofold higher than that of C. neoformans var. grubii for fluconazole, itraconazole and voriconazole. However, no statistically significant difference in susceptibility of the two Cryptococcus species was observed against amphotericin B and 5-flucytosine.

Furthermore, the environmental C. neoformans var. grubii isolates were significantly less susceptible to fluconazole, itraconazole and 5-flucytosine (P<0.0001) than the clinical isolates.

A continued surveillance of antifungal susceptibility of clinical and environmental strains of C. neoformans and C. gattii is desirable to monitor the emergence of any resistant strains in order to ensure more successful therapy of cryptococcosis.

INTRODUCTION

Cryptococcosis is a life-threatening, opportunistic fungal infection of worldwide distribution, including India, especially in the human immunodeficiency virus (HIV) positive population (Casadevall & Perfect, 1998; Chakrabarti et al., 2000; Khanna et al., 2000; Lakshmi et al., 2007; Thakur et al., 2008). It has two major aetiological agents, namely Cryptococcus neoformans and Cryptococcus gattii. C. neoformans has serotypes A, D and AD, whereas C. gattii has serotypes B and C. The strains belonging to serotype A represent C. neoformans var. grubii, whereas those of serotype D represent C. neoformans var. neoformans. C. neoformans and C. gattii differ significantly with regard to their geographical distribution and ecological niches (Casadevall & Perfect, 1998; Kwon-Chung et al., 2002). Based on molecular studies, using PCR fingerprinting, amplified fragment length polymorphism (AFLP) analysis, analysis of the orotidine monophosphate pyrophosphorylase (URA5) and phospholipase (PLB1)
genes by RFLP and multilocus sequence typing, C. neoformans and C. gattii have been further classified into several distinct genotypes: VNI/AFLP1 and VNI/AFLP1A/AFLP1B (C. neoformans var. grubii, serotype A), VNI/AFLP2 (C. neoformans var. neoformans, serotype D), VNI/AFLP3 (hybrid serotype AD), VGII/AFLP4, VGII/AFLP6, VGIII/AFLP5, VGIV/AFLP7 and AFLP10 (C. gattii, serotype B/C). In addition, hybrids of C. neoformans var. neoformans and C. gattii and of C. neoformans var. grubii and C. gattii belong to genotypes AFLP8 and AFLP9, respectively.

The vast majority of cryptococcal infections, particularly in immunocompromised patients, are caused by C. neoformans, whereas C. gattii accounts for a smaller proportion of cases, often occurring in immunocompetent patients in tropical and subtropical regions. However, in the past decade, a more virulent genotype of C. gattii, VGII/VGIIc, has emerged as a primary pathogen on Vancouver Island and its adjoining areas in Canada and the USA, indicating extension of its geographical domain to the temperate climate (Kidd et al., 2004; Byrnes et al., 2010). The outbreak of human and animal cryptococcosis on Vancouver Island due to C. gattii indicated that exposure to environmental sources such as colonized trees and soil led to pulmonary and disseminated cryptococcosis. In India, we have reported a widespread colonization of decayed wood inside trunk hollows of diverse tree species by C. neoformans var. grubii and C. gattii serotype B (Randhawa et al., 2006, 2008; Hiremath et al., 2008). The objective of this study was to compare antifungal susceptibility profiles of clinical isolates with those of environmental isolates of C. neoformans var. grubii and C. gattii serotype B originating from decayed wood of diverse tree species and from their surrounding soil in north-western India.

METHODS

Fungal isolates. Three hundred and eight isolates, comprising 246 C. neoformans var. grubii and 62 C. gattii serotype B, originating from clinical and environmental sources were included in the study. All of the C. neoformans isolates (n=246) were serotype A, genotype VNI/AFLP1 and mating type α, whereas all of the C. gattii isolates belonged to serotype B, genotype VGII/AFLP4 and mating type α. Of the 246 C. neoformans var. grubii isolates, 160 were clinical, originating from 130 patients, and the remaining 86 were from decayed wood of trees and soil. Among the 62 C. gattii isolates, 60 were from environmental and two were from clinical sources. The clinical isolates had been collected and stocked during our investigation of decayed wood samples in proximity to some of the positive trees (Randhawa et al., 2006; 2008; Hiremath et al., 2008). Also included for comparison were eight reference strains procured from global culture collections. These were C. neoformans (serotype A) ATCC 90112, C. gattii (serotype B) CBS1930 and CDC 3175 (Centers for Disease Control and Prevention, Atlanta), C. gattii (serotype B) B4495 and B4499 and C. gattii (serotype C) B4546, JF109 and JF101 (McMaster University, Hamilton, Ontario, Canada).

All isolates of C. neoformans var. grubii and C. gattii tested here were identified by standard mycological procedures (Randhawa et al., 2006, 2008; Hiremath et al., 2008). Their genotypes were determined based on two methods: (i) PCR fingerprinting using (GACA)4 and M13 phage core sequences as single primers (Meyer et al., 1999); and (ii) DNA sequences at the URAS locus (Meyer et al., 2009). The mating type of isolates was determined by PCR amplification, using primer pairs designed from the sequences of the mating type-specific STE12 and STE20 genes (Hiremath et al., 2008).

Antifungal susceptibility testing. In vitro antifungal susceptibility testing was carried out using the Clinical and Laboratory Standards Institute (CLSI) broth microdilution method (CLSI, 2008). The antifungal drugs tested were amphotericin B (Sigma), fluconazole, voriconazole (Pfizer), itraconazole (LeePharma) and 5-flucytosine (Sigma). Stock solutions were prepared in water (fluconazole and 5-flucytosine) or DMSO (itraconazole, voriconazole and amphotericin B). Further dilutions of each antifungal agent were prepared with RPMI 1640 with glutamine without bicarbonate (Sigma), buffered to pH 7 with 0.165 M MOPS (Sigma). The drug dilutions were dispensed in 96-well microdilution plates, sealed and frozen at −70 °C until needed. The final concentrations of the drugs ranged from 0.125 to 64 μg ml−1 for fluconazole and 5-flucytosine, 0.03 to 16 μg ml−1 for amphotericin B and 0.015 to 8 μg ml−1 for itraconazole and voriconazole. The yeast inoculum was adjusted to a concentration of 0.5 × 102–2.5 × 103 cells ml−1 in RPMI 1640 as measured by spectrophotometry, and an aliquot of 0.1 ml was added to each well containing various concentrations of the antifungal drugs. Drug-free and yeast-free controls were included, and microplates were incubated at 35 °C for 72 h.

Following the CLSI recommendations, two quality-control strains, Candida krusei (ATCC 6258) and Candida parapsilosis (ATCC 22019), were used with each test. The reproducibility of the in vitro results was assessed by determining MICs for all strains twice on two different days. The MIC end points were read visually after 72 h and defined for fluconazole, voriconazole, itraconazole and 5-flucytosine as the lowest drug concentration that caused a prominent decrease in growth (50%) compared with the controls. For amphotericin B, the MIC was defined as the lowest concentration at which there was 100% inhibition of growth compared with the drug-free control wells.

Statistical analysis. Statistical differences between MIC values of various groups of strains were assessed using the Mann–Whitney test. Statistical significance was defined as P<0.05. Statistical analyses were performed with GraphPad Prism version 5.00 (GraphPad Software).

RESULTS

The results of antifungal susceptibility testing of C. neoformans var. grubii, genotype VNI/AFLP1, and C. gattii of the 25 patients yielding the remaining isolates of C. neoformans var. grubii was unknown.

Among the 146 environmental isolates, 86 (59%) were C. neoformans var. grubii and 60 (41%) were C. gattii serotype B. They had been collected and stocked during our investigation of decayed wood inside trunk hollows of a wide spectrum of tree species and soil samples in proximity to some of the positive trees (Randhawa et al., 2006; 2008; Hiremath et al., 2008). Also included for comparison were eight reference strains procured from global culture collections. These were C. neoformans (serotype A) ATCC 90112, C. gattii (serotype B) CBS1930 and CDC 3175 (Centers for Disease Control and Prevention, Atlanta), C. gattii (serotype B) B4495 and B4499 and C. gattii (serotype C) B4546, JF109 and JF101 (McMaster University, Hamilton, Ontario, Canada).

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Table 1. *In vitro* antifungal susceptibilities of clinical and environmental isolates of *C. neoformans* var. *grubii* (*n* = 246) and *C. gattii* (*n* = 62) to amphotericin B, 5-flucytosine and some azoles

MIC values are given in μg ml\(^{-1}\).

<table>
<thead>
<tr>
<th>Test species and source</th>
<th>Amphotericin B</th>
<th>Fluconazole</th>
<th>Itraconazole</th>
<th>Voriconazole</th>
<th>5-Flucytosine</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>GM</td>
<td>MIC</td>
<td>MIC(_{50})</td>
<td>MIC(_{90})</td>
<td>GM</td>
</tr>
<tr>
<td><em>C. neoformans</em> var. <em>grubii</em></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Clinical (<em>n</em> = 160)</td>
<td>0.235</td>
<td>0.031–1</td>
<td>0.250</td>
<td>0.5</td>
<td>2.190</td>
</tr>
<tr>
<td>Environmental (<em>n</em> = 86)</td>
<td>0.232</td>
<td>0.062–0.5</td>
<td>0.250</td>
<td>0.5</td>
<td>3.639</td>
</tr>
<tr>
<td>Total (<em>n</em> = 246)</td>
<td>0.235</td>
<td>0.031–1</td>
<td>0.250</td>
<td>0.5</td>
<td>2.614</td>
</tr>
<tr>
<td><em>C. gattii</em> serotype B</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Clinical (<em>n</em> = 2)</td>
<td>0.125</td>
<td>0.125</td>
<td>0.125</td>
<td>0.125</td>
<td>1.545</td>
</tr>
<tr>
<td>Environmental (<em>n</em> = 60)</td>
<td>0.256</td>
<td>0.125–1</td>
<td>0.250</td>
<td>0.250</td>
<td>7.379</td>
</tr>
<tr>
<td>Total (<em>n</em> = 62)</td>
<td>0.250</td>
<td>0.125–1</td>
<td>0.250</td>
<td>0.250</td>
<td>6.996</td>
</tr>
</tbody>
</table>
serotype B, genotype VGI/AFLP4, are summarized in Table 1. All of the isolates of *C. neoformans* var. *grubii* and *C. gattii* showed low MICs for all the antifungals tested except for two clinical isolates of *C. neoformans* var. *grubii*, which had high MICs against 5-flucytosine (MIC >64 μg ml⁻¹). However, there were some notable differences in antifungal susceptibility of the two species and within each species depending on the origin of strains from environmental or clinical sources. Specifically, the geometric means (GMs) of MICs for the *C. gattii* serotype B sample were significantly higher than those of *C. neoformans* var. *grubii* for fluconazole (GM 6.996 vs 2.614 μg ml⁻¹, *P*<0.0001), itraconazole (GM 0.244 vs 0.112 μg ml⁻¹, *P*<0.0001) and voriconazole (GM 0.138 vs 0.056 μg ml⁻¹, *P*<0.0001). Similarly, the MIC₉₀ values for *C. gattii* were twofold higher than those for *C. neoformans* var. *grubii* for fluconazole (8 vs 4 μg ml⁻¹), itraconazole (0.5 vs 0.25 μg ml⁻¹) and voriconazole (0.25 vs 0.125 μg ml⁻¹). However, no statistically significant difference in susceptibility of the two *Cryptococcus* species was observed against amphotericin B and 5-flucytosine. Interestingly, in comparison with clinical isolates, the environmental *C. neoformans* var. *grubii* isolates exhibited significantly reduced susceptibility to fluconazole (GM 3.639 vs 2.190 μg ml⁻¹, *P*<0.0001), itraconazole (GM 0.142 vs 0.099 μg ml⁻¹, *P*<0.0001) and 5-flucytosine (GM 3.785 vs 1.450 μg ml⁻¹, *P*<0.0001).

Of the 53 serial isolates of *C. neoformans* var. *grubii* in this study, collected at least 1 month apart from 23 patients, four serial isolates obtained from four patients receiving antifungal therapy of amphotericin B for 3 weeks and followed by fluconazole prophylaxis (400 mg daily) showed a fourfold increase in fluconazole MICs over a period of 1.5–2.5 months. However, the MIC values did not exceed 4 μg ml⁻¹. Likewise, one serial *C. neoformans* var. *grubii* isolate from a patient showed a fourfold increase in itraconazole MIC but not in fluconazole MIC. A similar increase in amphotericin B MICs was found, which ranged from fourfold in two serial isolates to eightfold in four serial isolates over 1–3 months for strains originating from six patients who had received this antifungal drug for 3 weeks. Here again, the increase in the amphotericin B MICs did not exceed 1 μg ml⁻¹. Interestingly, three serial isolates from three patients showed a fourfold increase in 5-flucytosine MICs, although none of the patients had received 5-flucytosine previously.

**DISCUSSION**

This study is noteworthy for documenting the antifungal susceptibility profiles of the highest number of *C. gattii* genotype VGI/AFLP4 isolates investigated in any study reported so far from India, employing the microbroth dilution method. An earlier study from India reported only the fluconazole susceptibility profiles and genotypes of 57 clinical isolates, comprising 51 *C. neoformans* var. *grubii*, genotype VNI/AFLP1, one *C. neoformans* var. *neoformans*, genotype VNIV/AFLP2, and five *C. gattii*, genotype VGI/AFLP6 (Jain et al., 2005). The reported MICs ranged from 8 to 16 μg ml⁻¹ for *C. neoformans* var. *grubii* and 2 to 64 μg ml⁻¹ for *C. gattii*, whereas in the present study none of the 160 clinical and 86 environmental isolates of *C. neoformans* var. *grubii* revealed MICs >8 μg ml⁻¹ for *C. neoformans* var. *grubii* (range 0.5–8 μg ml⁻¹) and 1–16 μg ml⁻¹ for *C. gattii* serotype B. The low MICs observed in our clinical isolates of both species may be attributed to the fact that the majority originated from patients without history of exposure to fluconazole.

The results demonstrated that *C. gattii* isolates were significantly less susceptible to azoles than *C. neoformans* var. *grubii*, which agrees with several previous reports (Fernandes et al., 2003; Trilles et al., 2004; Khan et al., 2007, 2009; Gomez-Lopez et al., 2008). However, there is divergence of results concerning the antifungal susceptibility patterns of the two species in some other studies, which reported no such difference (Chen et al., 2000; Calvo et al., 2001; Morgan et al., 2006; Tay et al., 2006; Thompson et al., 2009). This divergence in results may be due to a possible lack of uniformity in the methodologies of testing adopted by different investigators. Although the Etest has been recommended as a good alternative to the CLSI microbroth dilution method for antifungal susceptibility of yeasts, the results obtained with *Cryptococcus* species have been inconsistent (Khan et al., 2007). It should be pointed out that the reported discrepancies in results pertain to antifungal drugs that inhibit or bind ergosterol in the cell membrane. Therapy of cryptococcosis due to *C. gattii* with these antifungals has also been reported to be more difficult than therapy of the disease caused by *C. neoformans* (Mitchell et al., 1995; Speed & Dunt, 1995). Attention should be given to the report by Varma & Kwon-Chung (2000), showing that 86 % of the *C. gattii* strains expressed a heteroresistance level of >16 μg ml⁻¹ to fluconazole compared with 46 % of *C. neoformans* strains. They found that all of the clinical isolates not exposed to azoles as well as the environmental strains manifested heteroresistance to fluconazole. Furthermore, this heteroresistance of the test strains was an intrinsic character that was associated with their virulence. Thus, the inherently higher level of heteroresistance to fluconazole of *C. gattii* strains may be another factor that influences the MICs of the strains resulting in the variability of results of *in vitro* antifungal susceptibility reported in different studies.

As reported previously (Yildiran et al., 2000; van Duin et al., 2004; Souza et al., 2005; Khan et al., 2007), voriconazole exhibited the highest inhibitory activity against the isolates of *C. neoformans* var. *grubii* (GM 0.056 μg ml⁻¹) and *C. gattii* (GM 0.138 μg ml⁻¹). Itraconazole MICs were in the range of 0.25–0.5 μg ml⁻¹ in 84 % of *C. gattii* serotype B and in 14 % of *C. neoformans* var. *grubii* isolates. This is in agreement with the results of Iqbal et al. (2010), who tested 43 clinical isolates of *C. gattii* from patients in Oregon, USA. Twenty-three per cent of their isolates had itraconazole MICs >1 μg ml⁻¹, whereas 55.8 % revealed MICs in the range of 0.25–0.5 μg ml⁻¹.
Interestingly, their VGI and VGIII isolates had comparatively low fluconazole MICs, whilst the majority with MICs of 16–32 μg ml\(^{-1}\) were of subtype VGIc. Similarly, all of our VGI/AFLP4 C. gattii isolates revealed MICs of ≤16 μg ml\(^{-1}\), consistent with the report by Hagen et al. (2010) on C. gattii, which showed lower MICs for AFLP4/VGI isolates (1.401 and 2.467 μg ml\(^{-1}\)) versus the higher MICs for AFLP6/VGII isolates (4.961 and 5.638 μg ml\(^{-1}\)) against 5-flucytosine and fluconazole, respectively. Concerning the susceptibility to 5-flucytosine, <2 % of C. neoformans isolates have been reported as resistant to this drug prior to treatment (Scholer & Polak, 1984), which is comparable to our results of 1.2% (2/162) for clinical C. neoformans var. grubii isolates. However, concern about the emergence of resistance during treatment with this drug alone has led to its use in combination with amphotericin B in patients with cryptococcosis (Perfect et al., 2010). All of the patients whose serial isolates showed an increase in azole and amphotericin B MICs were HIV-positive. It may be added in this context that relapses in patients with AIDS-associated cryptococcosis are often due to deterioration of the host immune function rather than to an increase in MICs (Witt et al., 1996). However, a rising MIC of fluconazole has been implicated in clinical relapse in patients with AIDS-associated cryptococcal meningitis (Paugam et al., 1994; Birley et al., 1995; Currie et al., 1995; Armengou et al., 1996; Berg et al., 1998; Davey et al., 1998; Aller et al., 2000).

Our significantly lower susceptibility of environmental C. neoformans var. grubii isolates to fluconazole, itraconazole and 5-flucytosine compared with that of the clinical isolates is in contrast to the findings of some investigators who found that antifungal susceptibility was not related to the clinical or environmental origin of strains (Franzot & Hamdan, 1996; Moraes et al., 2003; Trilles et al., 2004). Of relevance here is the report by Soares et al. (2005) stating that a solitary isolate of C. neoformans var. grubii from pigeon excreta was resistant to fluconazole (MIC 64 μg ml\(^{-1}\)). Likewise, in another report from Brazil, one of their environmental isolates of C. neoformans var. neoformans was found to be resistant to itraconazole and three additional isolates exhibited high MICs of 16–32 μg ml\(^{-1}\) against fluconazole (Costa et al., 2010). Furthermore, a fluconazole-resistant strain isolated from an immunocompetent patient without exposure to thisazole has also been reported, indicating the existence of primary resistance in environmental strains to fluconazole (Orni-Wasserlauf et al., 1999). Keeping in mind these emerging reports of resistance in environmental strains, continued surveillance for the emergence of antifungal resistance in clinical and environmental strains of C. neoformans and C. gattii is desirable for more successful therapy of cryptococcosis.

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