


Molecular characterisation and antifungal susceptibility of clinical *Cryptococcus deuterogattii* (AFLP6/VGII) isolates from Southern Brazil

P. F. Herkert^{1,2} · F. Hagen²  · G. L. de Oliveira Salvador³ · R. R. Gomes^{1,4} · M. S. Ferreira⁵ · V. A. Vicente^{1,6} · M. D. Muro⁷ · R. L. Pinheiro⁷ · J. F. Meis^{2,8} · F. Queiroz-Telles⁹

Received: 3 June 2016 / Accepted: 11 July 2016 / Published online: 1 August 2016
© Springer-Verlag Berlin Heidelberg 2016

Abstract Cryptococcosis, caused by *Cryptococcus gattii sensu lato*, is an emerging disease that was initially found in (sub)tropical regions but recently expanded to temperate regions. *Cryptococcus gattii s.l.* infections are mostly encountered in healthy individuals, frequently affecting both lungs and the central nervous system (CNS). Usually, *C. gattii s.l.* is less susceptible to antifungal compounds than its counterpart, *C. neoformans s.l.* We studied 18 clinical *C. gattii s.l.* isolates with amplified fragment length polymorphism (AFLP) fingerprinting, mating-typing, multi-locus sequence typing (MLST) and antifungal susceptibility testing. All

isolates were *C. deuterogattii* (genotype AFLP6/VGII), 14 were mating-type α and four were type a. Amphotericin B, itraconazole, voriconazole, posaconazole and isavuconazole showed high activity, with minimum inhibitory concentration (MIC) ranges of 0.063–0.25, 0.031–0.25, 0.031–0.25, 0.031–0.25 and <0.016–0.25 $\mu\text{g mL}^{-1}$, respectively. Fluconazole and flucytosine had high geometric mean MICs of 2.07 and 3.7 $\mu\text{g mL}^{-1}$, respectively. Most cases occurred in immunocompetent patients ($n = 10$; 55.6 %) and CNS involvement was the most common clinical presentation ($n = 14$; 77.8 %). Three patients (16.7 %) showed sequelae, hyperreflexia, dysarthria, diadochokinesia, anosmia and upper limb weakness. In conclusion, all infections were caused by *C. deuterogattii* (AFLP6/VGII) and the majority of patients were immunocompetent, with the CNS as the most affected site. All antifungal drugs had high in vitro activity against *C. deuterogattii* isolates, except fluconazole and flucytosine.

✉ F. Hagen
f.hagen@cwz.nl

- ¹ Postgraduate Program in Microbiology, Parasitology and Pathology, Biological Sciences, Department of Basic Pathology, Federal University of Parana, Curitiba, PR, Brazil
- ² Department of Medical Microbiology and Infectious Diseases, Canisius-Wilhelmina Hospital, Weg door Jonkerbos 100, 6532 SZ Nijmegen, The Netherlands
- ³ Department of Internal Medicine, Federal University of Parana, Curitiba, PR, Brazil
- ⁴ Department of Biological Science, State University of Parana/ Campus Paranagua, Paranagua, PR, Brazil
- ⁵ Federal University of Uberlandia, Uberlândia, MG, Brazil
- ⁶ Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brasília, DF, Brazil
- ⁷ Laboratory of Mycology, Hospital de Clínicas, Federal University of Parana, Curitiba, PR, Brazil
- ⁸ Department of Medical Microbiology, Radboudumc, Nijmegen, The Netherlands
- ⁹ Communitarian Health Department, Hospital de Clínicas, Federal University of Parana, Curitiba, PR, Brazil

Introduction

Cryptococcosis is caused by basidiomycetous yeast species that belong to the *Cryptococcus gattii*/*Cryptococcus neoformans* species complexes, mainly affecting lungs and the central nervous system (CNS) [1]. The taxonomy of the polyphyletic genus *Cryptococcus* has been thoroughly revised [2–4]. The two varieties of *C. neoformans* were recognised as species, with *C. neoformans* (=formerly *C. neoformans* variety *grubii*) and *C. deneoformans* (=formerly *C. neoformans* variety *neoformans*) [2]. The five *C. gattii* species complex genotypes were raised to the species level as *C. gattii sensu stricto* (AFLP4/VGI), *C. bacillisporus* (AFLP5/VGIII), *C. deuterogattii* (AFLP6/VGII), *C. tetragattii* (AFLP7/VGIV) and *C. decagattii* (AFLP10/VGIV) [2]. *Cryptococcus gattii s.s.*

and *C. deuterogattii* are the main culprits of infections in immunocompetent hosts [2, 5], whereas *C. bacillisporus*, *C. tetragattii* and *C. decagattii* are commonly associated with immunocompromised hosts [2, 6–8].

Members of the *C. gattii* species complex have increasingly been reported from temperate climate regions [5, 9–11]. Trading of tree products, transport of propagules through water currents and via animals, insects and humans may be responsible for the world-wide spread [12, 13]. The first environmental isolation of *C. gattii s.l.* was reported from *Eucalyptus camaldulensis* [14]. Globally, *C. gattii s.l.* has been found on a plethora of other species of trees [13, 15–19].

In Europe, *C. gattii s.s.* is the most frequently encountered species, while few cases of *C. deuterogattii* infection are travel-related [20–22]. In Asia and Australia, *C. gattii s. s.* and *C. deuterogattii* are predominant [23]. *Cryptococcus bacillisporus* is rarely encountered outside North and South America [21, 23, 24], while *C. tetragattii* has mainly been isolated from Africa and India [8, 23]. On the American continent, *C. deuterogattii* is the predominant species among clinical and environmental isolates [23]. In North America, *C. deuterogattii* subgenotypes (AFLP6A/VGIIa, AFLP6B/VGIIb and AFLP6C/VGIIc) were reported as the cause of expanding outbreaks [5, 9, 10, 25]. A recent study showed that, by using coalescence gene genealogy analysis, the ancestral lineage of *C. deuterogattii* originated from South America, specifically from the Brazilian Amazon Rainforest, where mating-types a and α were reported in nearly equal rates, providing evidence of recombination within the Brazilian *C. deuterogattii* population [25].

Cryptococcus gattii s.l. is less susceptible to common antifungal compounds than *C. neoformans*; fluconazole and flucytosine show lower in vitro activity against *C. deuterogattii* strains [26–28]. In addition, heteroresistance to azoles in the *C. neoformans/C. gattii* species complexes is an intrinsic mechanism that may contribute to relapse of cryptococcosis during maintenance therapy [29, 30].

In the present study, our aim was to compare the clinical outcome with molecular and antifungal susceptibility data of Brazilian *C. gattii s.l.* isolates.

Materials and methods

Isolates and clinical data

Eighteen clinical *C. gattii s.l.* isolates were isolated at the Hospital de Clínicas, Curitiba, PR, Brazil between 1999 and 2015. A single colony was taken for further microbiological and molecular characterisation. Medical records were accessed to collect clinical information.

Molecular characterisation

Extraction of genomic DNA, mating-type determination, amplified fragment length polymorphism (AFLP) fingerprinting and multi-locus sequence typing (MLST) were performed as described previously [20–22, 31].

Sequences were compared with those deposited in the MLST database (<http://mlst.mycologylab.org>). The alignment was performed with the online MAFFT alignment module [32] and visual inspection by MEGA version 7 [33], followed by a 1000× bootstrapped maximum likelihood analysis on an MLST dataset that comprises all known *C. deuterogattii* sequence types [8].

Antifungal susceptibility testing

Broth microdilution testing [34] included amphotericin B (Bristol Myers Squibb, Munich, Germany), fluconazole (Pfizer, Sandwich, United Kingdom), itraconazole (Janssen Pharmaceutica, Beerse, Belgium), voriconazole (Pfizer), posaconazole (Merck, Kenilworth, NJ, USA), isavuconazole (Basilea Pharmaceutica, Basel, Switzerland) and flucytosine (ICN Pharmaceuticals, Zoetermeer, The Netherlands). The concentration ranges were 0.016–16 $\mu\text{g mL}^{-1}$ for amphotericin B, itraconazole, voriconazole, posaconazole and isavuconazole, and 0.062–64 $\mu\text{g mL}^{-1}$ for fluconazole and flucytosine. *Cryptococcus* isolates were cultured onto Sabouraud dextrose agar for 48 h at 30 °C and the inocula were adjusted to 1×10^3 CFU/mL in 0.9 % NaCl to perform the test. The microdilution plates were incubated at 35 °C for 72 h and the minimal inhibitory concentrations (MICs) were defined as the lowest concentration that produced complete growth inhibition for amphotericin B and prominent decrease of growth (50 %) for other antifungal agents when compared with the drug-free growth control. *Candida parapsilosis* ATCC22019 and *C. krusei* ATCC6258 were used as quality controls [34]. The interpretation of MIC values was based on the epidemiological cut-off value (ECV) [26–28]. MIC₅₀ and MIC₉₀ values were obtained by ordering the data for each antifungal in ascending order and selecting the median and 90th quantile, respectively. Geometric mean MICs were calculated using Microsoft Office Excel 2010 software (Microsoft, Redmond, WA, USA). When the MIC was higher or less than the dilutions tested, 1 log₂ dilution higher or 1 log₂ dilution lower was used to calculate the geometric mean.

Results

Molecular characterisation

Mating-type analysis showed that 14 isolates were mating-type α and four were type a. MLST analysis showed that all 18

isolates clustered with the *C. deuterogattii* AFLP6/VGII reference strain WM178 (Fig. 1). Maximum likelihood analysis showed that most isolates were related with other Brazilian isolates, while isolate UFU986 was genetically indistinguishable from the outbreak genotype AFLP6A/VGIIa (Fig. 1). MLST sequences were deposited in GenBank with the accession numbers KU642658–KU642671, KU642673–KU642676 (*CAP59*), KU642703–KU642716, KU642718–KU642721 (*GPD1*), KU642748–KU642761, KU642763–KU642766

(*IGS1*), KU642793–KU642806, KU642808–KU642811 (*LAC1*), KU642838–KU642851, KU642853–KU642856 (*PLB1*), KU642883–KU642896, KU642898–KU642901 (*SOD1*) and KU642928–KU642938, KU642940–KU652944, KU642946, KU642966 (*URA5*). By AFLP genotyping analysis, four isolates clustered together with the *C. deuterogattii* AFLP6/VGII reference strain WM178, while the remaining isolates clustered in two distinct clades due to the presence of several dominant markers (Fig. 2).

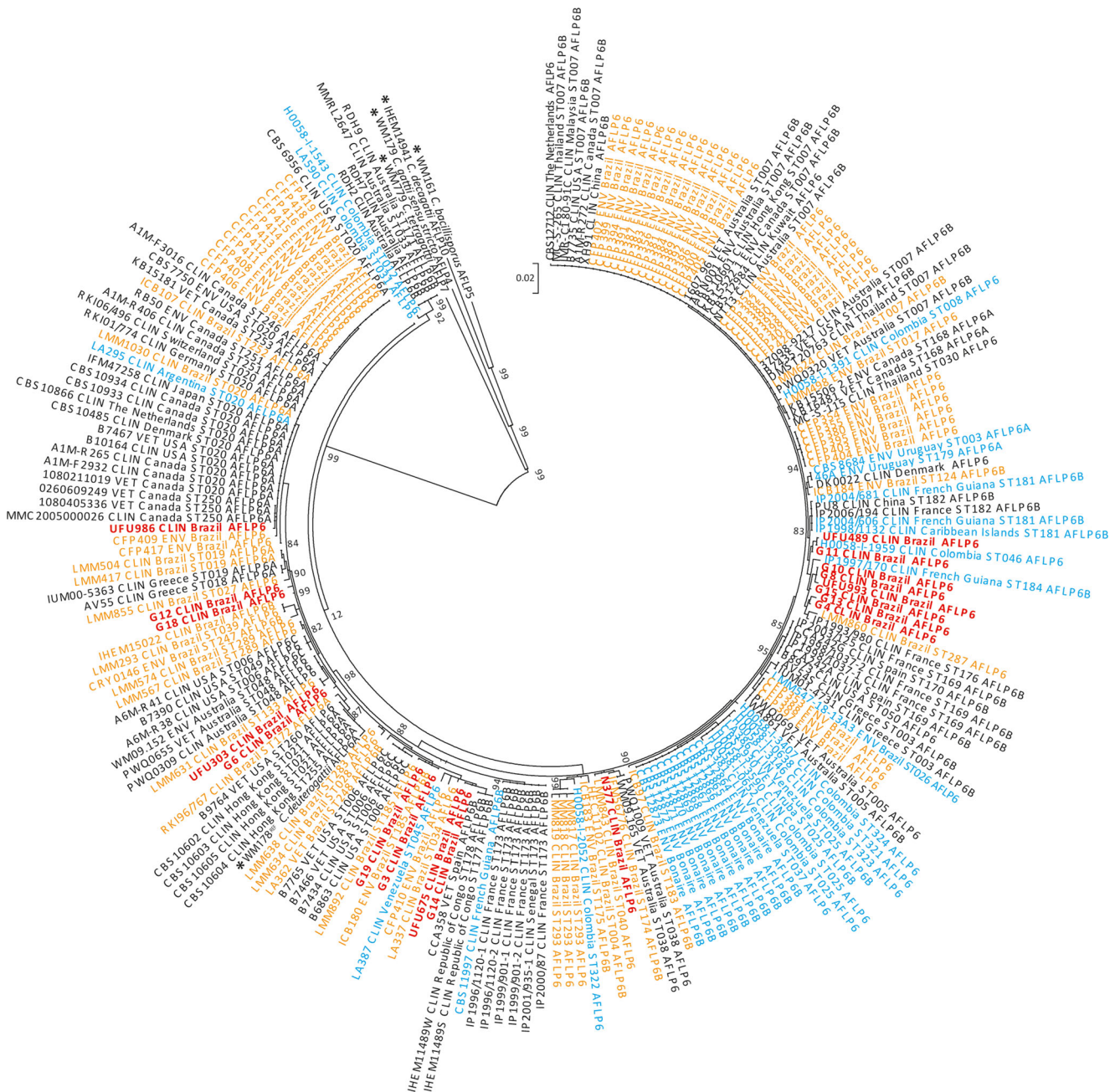


Fig. 1 Phylogenetic 1000× bootstrapped maximum likelihood analysis of *Cryptococcus deuterogattii* isolates based on the ISHAM consensus MLST dataset. *Cryptococcus gattii sensu stricto* (WM179), *C. bacillisporus* (WM161), *C. tetragattii* (WM779) and *C. decagattii*

(IHEM14941) were used as an outgroup. Bold red, isolates from the present study; orange, other Brazilian isolates; blue, other Latin American isolates; black, global isolates; *, reference strains

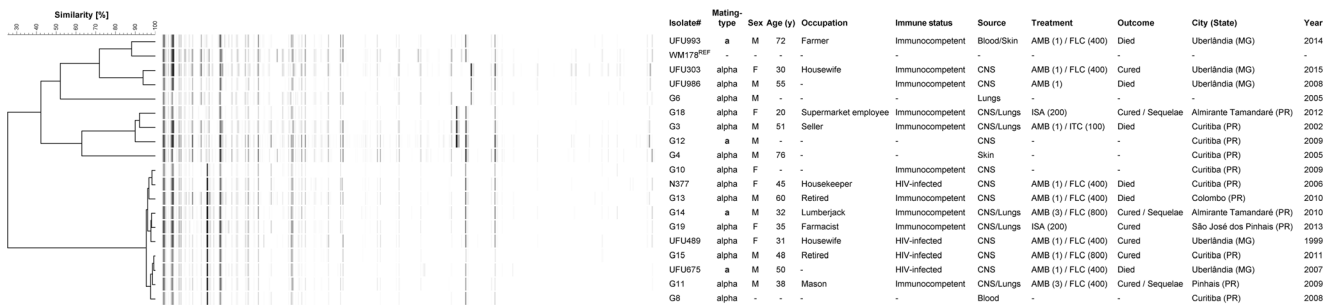


Fig. 2 Amplified fragment length polymorphism (AFLP) fingerprint patterns of 18 Brazilian *C. deuterogattii* (AFLP6/VGII) isolates, including clinical and epidemiological characteristics of the patients. WM178 (*C. deuterogattii* AFLP6/VGII) serves as a reference strain; AMB,

amphotericin B; FLC, fluconazole; ITC, itraconazole; ISA, isavuconazole; treatment doses, AMB (mg/kg/day) and FLC, ITC and ISA (mg/day); –, data not available; F, female; M, male; CNS, central nervous system. PR, Paraná State; MG, Minas Gerais State

Antifungal susceptibility profiles

The MIC values are presented in Table 1. Itraconazole, voriconazole, posaconazole, isavuconazole and amphotericin B showed high activity against *C. deuterogattii*. Fluconazole and flucytosine had the highest geometric mean MICs of 2.07 and 3.7 $\mu\text{g mL}^{-1}$, respectively.

Clinical data

The majority of isolates were recovered from immunocompetent patients ($n = 10$; 55.6 %). Fourteen (77.8 %) had CNS involvement and four (22.2 %) of them were HIV-positive. Furthermore, six patients (33.3 %) had lung infection, including five (27.7 %) with associated CNS symptoms, while two patients (11.1 %) had cutaneous cryptococcosis. Three (16.7 %)

Table 1 Minimal inhibitory concentrations (MICs) of all the *Cryptococcus deuterogattii* isolates studied

Isolate code	Minimal inhibitory concentration ($\mu\text{g mL}^{-1}$)						
	AMB	FLC	ITC	VOR	POS	ISA	5FC
G3	0.063	0.5	0.063	0.063	0.063	0.031	4
G4	0.125	8	0.25	0.25	0.25	0.25	8
G6	0.031	8	0.125	0.125	0.125	0.063	2
G8	0.031	2	0.125	0.063	0.063	0.063	4
G10	0.125	4	0.125	0.125	0.125	0.125	8
G11	0.063	0.5	0.031	0.031	0.031	<0.016	1
G12	0.063	0.5	0.063	0.063	0.063	0.063	4
G13	0.031	4	0.063	0.063	0.063	0.063	2
G14	0.063	4	0.125	0.125	0.125	0.125	4
G15	0.125	4	0.125	0.125	0.125	0.125	4
G18	0.125	2	0.125	0.063	0.063	0.063	4
G19	0.125	16	0.25	0.25	0.25	0.25	4
N377	0.125	0.5	0.063	0.063	0.063	0.031	8
UFU303	0.125	8	0.125	0.125	0.125	0.063	4
UFU489	0.063	0.5	0.063	0.063	0.063	0.031	2
UFU675	0.125	0.5	0.063	0.063	0.063	0.063	4
UFU986	0.063	4	0.25	0.125	0.125	0.125	4
UFU993	0.125	1	0.063	0.063	0.063	0.063	4
MIC range	0.063–0.25	0.5–16	0.031–0.25	0.031–0.25	0.031–0.25	<0.016–0.25	1–8
MIC ₅₀	0.063	2	0.125	0.063	0.063	0.063	4
MIC ₉₀	0.125	8	0.25	0.125	0.125	0.125	8
Geometric mean	0.0788	2.0785	0.0994	0.0853	0.0853	0.0651	3.7034

AMB, amphotericin B; FLC, fluconazole; ITC, itraconazole; VOR, voriconazole; POS, posaconazole; ISA, isavuconazole; 5FC, flucytosine

developed neurological sequelae after the cryptococcal infection, one left-sided hyperreflexia, dysarthria and diadochokinesia, one had motor sequelae in the upper limbs and one developed anosmia. Nine patients (50 %) were treated with a combination of amphotericin B and fluconazole, one received amphotericin B and itraconazole, one amphotericin B and two were treated with isavuconazole. Two patients received liposomal amphotericin B after development of nephrotoxicity. Treatment dosing and outcome data are summarised in Fig. 2.

Discussion

Infections caused by members of the *C. gattii* species complex have a wide spectrum of clinical presentations, including pneumonia, meningoencephalitis, skin lesions and pulmonary and cerebral cryptococcoma formation, and surgical intervention may be necessary in certain cases [6, 35–38]. CNS disease is associated with neurological sequelae such as visual impairment, deafness, limb weakness and dysphasia [39]. We observed hyperreflexia, dysarthria, diadochokinesia, anosmia and upper limb weakness. Some studies reported that 60–90 % of patients with *C. gattii* species complex cryptococcosis have pulmonary symptoms with or without CNS involvement [10, 39, 40]. These data differ from this study, where the majority of patients ($n = 14$; 77.8 %) had CNS disease, five (27.7 %) also had lung involvement and a solitary patient (5.5 %) had only a lung infection.

All isolates were found to be *C. deuterogattii*, which is in concordance with the literature data, as it is predominant among clinical, veterinary and environmental isolates in Brazil [18, 41–50]. *Cryptococcus gattii* s.s. is more often reported in southern Brazil [51, 52] and the southeastern region [52, 53], and *C. bacillisporus* in the southeastern and north-eastern part [52]. Despite increasing epidemiological surveys in Brazil, information about the species distribution are fragmented and underrepresented from several Brazilian states. This is mainly due to the lack of proper diagnosis and the absence of an efficient reporting system [43].

We found that four out of 18 *C. deuterogattii* were mating-type a. The presence of both mating types within the South American *C. deuterogattii* population demonstrates that recombination events are a common phenomenon, causing high genetic diversity compared to other localities [25]. Globally, the majority of clinical isolates were found to be mating-type α , and with respect to *C. deuterogattii*, this is also the case for the ongoing outbreaks in North America [6, 25]. Recently, the first Australian *C. deuterogattii* mating-type a isolate was reported [54]. The absence or low number of mating-type a isolates within study populations suggests that *C. deuterogattii* is either clonal or reproduces by same-sex mating [55].

Antifungal susceptibility testing showed that amphotericin B had high activity, which is in concordance with other studies

[27, 48, 56–58]. Fluconazole had the lowest activity among the triazoles tested, with an MIC range of 0.5–16 $\mu\text{g mL}^{-1}$. Nevertheless, all MIC values were in the susceptible range [26, 59]. Hagen et al. [58] observed lower fluconazole activity against all *C. gattii* species complex members, with European and North American isolates showing higher MIC values (0.125 to >64 $\mu\text{g mL}^{-1}$ and 0.5–64 $\mu\text{g mL}^{-1}$, respectively). A recent Brazilian study reported high MICs (2–64 $\mu\text{g mL}^{-1}$), with a geometric mean of 6.08 $\mu\text{g mL}^{-1}$ for *C. deuterogattii* [60]. We also observed low MICs of itraconazole and new triazoles [26, 27, 56, 58].

Isavuconazole is a second-generation triazole antifungal, with a broad spectrum of activity against many important fungal pathogens [61]. Antifungal susceptibility tests have shown potent in vitro activity against members of *C. neoformans*/*C. gattii* species complexes, even for those that are less susceptible to fluconazole [28, 62, 63]. We observed that isavuconazole had excellent activity against *C. deuterogattii*, showing the lowest geometric mean MIC (0.065 $\mu\text{g mL}^{-1}$) among the antifungal compounds tested. Two immunocompetent female patients were included in a multi-centre international clinical trial with isavuconazole (ClinicalTrials.gov, NCT00634049) [64]. The first was 20 years old and working in a supermarket, where she had continuous contact with wood, fruits and vegetables. After the diagnosis, she received amphotericin B deoxycholate therapy for 16 days, but without response. The therapy was switched to isavuconazole, resulting in a complete clinical, radiological and microbiological response after 6 months of treatment. Anosmia was observed as a sequel. The second patient was a pharmacist, who received isavuconazole as primary therapy for a total of 176 days, resulting in a complete response without any sequelae.

Flucytosine had the lowest in vitro activity, showing the highest geometric mean MIC (3.7 $\mu\text{g mL}^{-1}$) among the antifungals tested, but the MICs for all isolates were within the wild-type range. It is known that resistance to flucytosine is rare [58, 65], but the use as monotherapy could lead to acquired resistance [66]. There are studies showing less susceptibility to flucytosine in *Cryptococcus* [58, 67, 68], but since flucytosine is not registered in Brazil, we supposed that the patients did not receive previous treatment with this drug. Higher MICs of flucytosine were also reported in other Brazilian studies [45, 48, 53, 60].

In conclusion, the majority of cases occurred in immunocompetent patients, with the CNS as the most affected site. All infections were caused by *C. deuterogattii* (AFLP6/VGII) and all antifungal drugs had in vitro activity against this species, except fluconazole and flucytosine.

Acknowledgments The work of Patricia Fernanda Herkert was financially supported by ‘Coordenação de Aperfeiçoamento de Pessoal de Nível Superior’ and ‘Conselho Nacional de Desenvolvimento Científico e Tecnológico’, Brazil.

Compliance with ethical standards

Conflict of interest JFM served as a consultant to and has received research grants from Astellas, Basilea, Gilead Sciences and Merck. All of the other authors declare no conflicts of interest.

References

- Kwon-Chung KJ, Fraser JA, Doering TL, Wang Z, Janbon G, Idnurm A et al (2014) *Cryptococcus neoformans* and *Cryptococcus gattii*, the etiologic agents of cryptococcosis. *Cold Spring Harb Perspect Med* 4(7):a019760. doi:10.1101/cshperspect.a019760
- Hagen F, Khayhan K, Theelen B, Kolecka A, Polacheck I, Sionov E et al (2015) Recognition of seven species in the *Cryptococcus gattii*/*Cryptococcus neoformans* species complex. *Fungal Genet Biol* 78:16–48. doi:10.1016/j.fgb.2015.02.009
- Liu XZ, Wang QM, Göker M, Groenewald M, Kachalkin AV, Lumbsch HT et al (2015) Towards an integrated phylogenetic classification of the *Tremellomycetes*. *Stud Mycol* 81:85–147. doi:10.1016/j.simyco.2015.12.001
- Liu XZ, Wang QM, Theelen B, Groenewald M, Bai FY, Boekhout T (2015) Phylogeny of tremellomycetous yeasts and related dimorphic and filamentous basidiomycetes reconstructed from multiple gene sequence analyses. *Stud Mycol* 81:1–26. doi:10.1016/j.simyco.2015.08.001
- Kidd SE, Hagen F, Tschärke RL, Huynh M, Bartlett KH, Fyfe M et al (2004) A rare genotype of *Cryptococcus gattii* caused the cryptococcosis outbreak on Vancouver Island (British Columbia, Canada). *Proc Natl Acad Sci U S A* 101:17258–17263. doi:10.1073/pnas.0402981101
- Byrnes EJ 3rd, Bartlett KH, Perfect JR, Heitman J (2011) *Cryptococcus gattii*: an emerging fungal pathogen infecting humans and animals. *Microbes Infect* 13:895–907. doi:10.1016/j.micinf.2011.05.009
- Springer DJ, Billmyre RB, Filler EE, Voelz K, Pursall R, Mieczkowski PA et al (2014) *Cryptococcus gattii* VGIII isolates causing infections in HIV/AIDS patients in Southern California: identification of the local environmental source as arboreal. *PLoS Pathog* 10, e1004285. doi:10.1371/journal.ppat.1004285
- Nyazika TK, Hagen F, Meis JF, Robertson VJ (2016) *Cryptococcus tetragattii* as a major cause of cryptococcal meningitis among HIV-infected individuals in Harare, Zimbabwe. *J Infect* 72:745–752. doi:10.1016/j.jinf.2016.02.018
- Datta K, Bartlett KH, Baer R, Byrnes E, Galanis E, Heitman J et al (2009) Spread of *Cryptococcus gattii* into Pacific Northwest region of the United States. *Emerg Infect Dis* 15:1185–1191. doi:10.3201/eid1508.081384
- Galanis E, Macdougall L, Kidd S, Morshed M; British Columbia *Cryptococcus gattii* Working Group (2010) Epidemiology of *Cryptococcus gattii*, British Columbia, Canada, 1999–2007. *Emerg Infect Dis* 16:251–257. doi:10.3201/eid1602.090900
- Hagen F, Boekhout T (2010) The search for the natural habitat of *Cryptococcus gattii*. *Mycopathologia* 170:209–211. doi:10.1007/s11046-010-9313-6
- Kidd SE, Bach PJ, Hingston AO, Mak S, Chow Y, MacDougall L et al (2007) *Cryptococcus gattii* dispersal mechanisms, British Columbia, Canada. *Emerg Infect Dis* 13:51–57. doi:10.3201/eid1301.060823
- Springer DJ, Chaturvedi V (2010) Projecting global occurrence of *Cryptococcus gattii*. *Emerg Infect Dis* 16:14–20. doi:10.3201/eid1601.090369
- Ellis DH, Pfeiffer TJ (1990) Natural habitat of *Cryptococcus neoformans* var. *gattii*. *J Clin Microbiol* 28:1642–1644
- Kidd SE, Chow Y, Mak S, Bach PJ, Chen H, Hingston AO et al (2007) Characterization of environmental sources of the human and animal pathogen *Cryptococcus gattii* in British Columbia, Canada, and the Pacific Northwest of the United States. *Appl Environ Microbiol* 73:1433–1443. doi:10.1128/AEM.01330-06
- Chowdhary A, Rhandhawa HS, Prakash A, Meis JF (2012) Environmental prevalence of *Cryptococcus neoformans* and *Cryptococcus gattii* in India: an update. *Crit Rev Microbiol* 38:1–16. doi:10.3109/1040841X.2011.606426
- Hagen F, Chowdhary A, Prakash A, Yntema J-B, Meis JF (2014) Molecular characterization of *Cryptococcus gattii* genotype AFLP6/VGII isolated from woody debris of divi-divi (*Caesalpinia coriaria*), Bonaire, Dutch Caribbean. *Rev Iberoam Micol* 31:193–196. doi:10.1016/j.riam.2013.10.007
- Anzai MC, Lazera MDS, Wanke B, Trilles L, Dutra V, de Paula DAJ et al (2014) *Cryptococcus gattii* VGII in a *Plathymenia reticulata* hollow in Cuiabá, Mato Grosso, Brazil. *Mycoses* 57:414–418. doi:10.1111/myc.12177
- Linares C, Colom MF, Torreblanca M, Esteban V, Romera Á, Hagen F (2015) Environmental sampling of *Ceratonia siliqua* (carob) trees in Spain reveals the presence of the rare *Cryptococcus gattii* genotype AFLP7/VGIV. *Rev Iberoam Micol* 32:269–272. doi:10.1016/j.riam.2014.11.002
- Hagen F, van Assen S, Luijckx GJ, Boekhout T, Kampinga GA (2010) Activated dormant *Cryptococcus gattii* infection in a Dutch tourist who visited Vancouver Island (Canada): a molecular epidemiological approach. *Med Mycol* 48:528–531. doi:10.3109/13693780903300319
- Hagen F, Colom MF, Swinne D, Tintelnot K, Iatta R, Montagna MT et al (2012) Autochthonous and dormant *Cryptococcus gattii* infections in Europe. *Emerg Infect Dis* 18:1618–1624. doi:10.3201/eid1810.120068
- Colom MF, Hagen F, Gonzalez A, Mellado A, Morera N, Linares C et al (2012) *Ceratonia siliqua* (carob) trees as natural habitat and source of infection by *Cryptococcus gattii* in the Mediterranean environment. *Med Mycol* 50:67–73. doi:10.3109/13693786.2011.574239
- Cogliati M (2013) Global molecular epidemiology of *Cryptococcus neoformans* and *Cryptococcus gattii*: an atlas of the molecular types. *Scientifica (Cairo)* 2013:675213. doi:10.1155/2013/675213
- Chowdhary A, Prakash A, Randhawa HS, Kathuria S, Hagen F, Klaassen CH et al (2013) First environmental isolation of *Cryptococcus gattii*, genotype AFLP5, from India and a global review. *Mycoses* 56:222–228. doi:10.1111/myc.12039
- Hagen F, Ceresini PC, Polacheck I, Ma H, van Nieuwerburgh F, Gabaldón T et al (2013) Ancient dispersal of the human fungal pathogen *Cryptococcus gattii* from the amazon rainforest. *PLoS One*. doi:10.1371/journal.pone.0071148
- Espinel-Ingroff A, Aller AI, Canton E, Castañón-Olivares LR, Chowdhary A, Córdoba S et al (2012) *Cryptococcus neoformans*–*Cryptococcus gattii* species complex: an international study of wild-type susceptibility endpoint distributions and epidemiological cutoff values for fluconazole, itraconazole, posaconazole, and voriconazole. *Antimicrob Agents Chemother* 56:5898–5906. doi:10.1128/AAC.01115-12
- Espinel-Ingroff A, Chowdhary A, Cuenca-Estrella M, Fothergill A, Fuller J, Hagen F et al (2012) *Cryptococcus neoformans*–*Cryptococcus gattii* species complex: an international study of wild-type susceptibility endpoint distributions and epidemiological cutoff values for amphotericin B and flucytosine. *Antimicrob Agents Chemother* 56:3107–3113. doi:10.1128/AAC.06252-11
- Espinel-Ingroff A, Chowdhary A, Gonzalez GM, Guinea J, Hagen F, Meis JF et al (2015) Multicenter study of isavuconazole MIC distributions and epidemiological cutoff values for the

- Cryptococcus neoformans*–*Cryptococcus gattii* species complex using the CLSI M27-A3 broth microdilution method. Antimicrob Agents Chemother 59:666–668. doi:10.1128/AAC.04055-14
29. Sionov E, Chang YC, Garraffo HM, Kwon-Chung KJ (2009) Heteroresistance to fluconazole in *Cryptococcus neoformans* is intrinsic and associated with virulence. Antimicrob Agents Chemother 53:2804–2815. doi:10.1128/AAC.00295-09
 30. Varma A, Kwon-Chung KJ (2010) Heteroresistance of *Cryptococcus gattii* to fluconazole. Antimicrob Agents Chemother 54:2303–2311. doi:10.1128/AAC.00153-10
 31. Illnait-Zaragozi MT, Martínez-Machín GF, Fernández-Andreu CM, Perurena-Lancha MR, Theelen B, Boekhout T et al (2012) Environmental isolation and characterisation of *Cryptococcus* species from living trees in Havana city, Cuba. Mycoses 55:e138–e144. doi:10.1111/j.1439-0507.2012.02168.x
 32. Katoh K, Misawa K, Kuma K, Miyata T (2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res 30:3059–3066
 33. Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Mol Biol Evol 33:1870–1874. doi:10.1093/molbev/msw054
 34. Clinical and Laboratory Standards Institute (CLSI) (2008) Reference method for broth dilution antifungal susceptibility testing of yeasts; Approved standard—Third edition. CLSI document M27-A3 (ISBN 1-56238-666-2). Clinical and Laboratory Standards Institute, 940 West Valley Road, Suite 1400, Wayne, Pennsylvania 19087-1898, USA
 35. Marques SA, Bastazini I Jr, Martins ALGP, Barreto JA, Barbieri D'Elia MP, Lastória JC et al (2012) Primary cutaneous cryptococcosis in Brazil: report of 11 cases in immunocompetent and immunosuppressed patients. Int J Dermatol 51:780–784. doi:10.1111/j.1365-4632.2011.05298.x
 36. Cicora F, Petroni J, Formosa P, Roberti J (2015) A rare case of *Cryptococcus gattii* pneumonia in a renal transplant patient. Transpl Infect Dis 17:463–466. doi:10.1111/tid.12371
 37. Franco-Paredes C, Womack T, Bohlmeier T, Sellers B, Hays A, Patel K et al (2015) Management of *Cryptococcus gattii* meningoencephalitis. Lancet Infect Dis 15:348–355. doi:10.1016/S1473-3099(14)70945-4
 38. Perfect JR, Dismukes WE, Dromer F, Goldman DL, Graybill JR, Hamill RJ et al (2010) Clinical practice guidelines for the management of cryptococcal disease: 2010 update by the Infectious Diseases Society of America. Clin Infect Dis 50:291–322. doi:10.1086/649858
 39. Chen SC-A, Slavin MA, Heath CH, Playford EG, Byth K, Marriott D et al (2012) Clinical manifestations of *Cryptococcus gattii* infection: determinants of neurological sequelae and death. Clin Infect Dis 55:789–798. doi:10.1093/cid/cis529
 40. Chen SC-A, Korman TM, Slavin MA, Marriott D, Byth K, Bak N et al (2013) Antifungal therapy and management of complications of cryptococcosis due to *Cryptococcus gattii*. Clin Infect Dis 57:543–551. doi:10.1093/cid/cit341
 41. dos Santos WRA, Meyer W, Wanke B, Costa SPSE, Trilles L, dos Nascimento JLM et al (2008) Primary endemic cryptococcosis *gattii* by molecular type VGII in the state of Pará, Brazil. Mem Inst Oswaldo Cruz 103:813–818
 42. do Costa PSE, do Lazéra M, Santos WRA, Morales BP, Bezerra CCF, Nishikawa MM et al (2009) First isolation of *Cryptococcus gattii* molecular type VGII and *Cryptococcus neoformans* molecular type VNI from environmental sources in the city of Belém, Pará, Brazil. Mem Inst Oswaldo Cruz 104:662–664
 43. Martins LMS, Wanke B, dos Lazéra M, Trilles L, Barbosa GG, de Macedo RCL et al (2011) Genotypes of *Cryptococcus neoformans* and *Cryptococcus gattii* as agents of endemic cryptococcosis in Teresina, Piauí (northeastern Brazil). Mem Inst Oswaldo Cruz 106:725–730
 44. Freire AKL, dos Santos BA, de Lima SI, Matsuura ABJ, Ogusku MM, Salem JI et al (2012) Molecular characterisation of the causative agents of cryptococcosis in patients of a tertiary healthcare facility in the state of Amazonas-Brazil. Mycoses 55:e145–e150. doi:10.1111/j.1439-0507.2012.02173.x
 45. Matos CS, de Souza Andrade A, Oliveira NS, Barros TF (2012) Microbiological characteristics of clinical isolates of *Cryptococcus* spp. in Bahia, Brazil: molecular types and antifungal susceptibilities. Eur J Clin Microbiol Infect Dis 31:1647–1652. doi:10.1007/s10096-011-1488-3
 46. Silva DC, Martins MA, Szeszs MW, Bonfietti LX, Matos D, Melhem MSC (2012) Susceptibility to antifungal agents and genotypes of Brazilian clinical and environmental *Cryptococcus gattii* strains. Diagn Microbiol Infect Dis 72:332–339. doi:10.1016/j.diagmicrobio.2011.11.016
 47. Cardoso PHM, de Baroni F, Silva EG, Nascimento DC, Martins MDA, Szeszs W et al (2013) Feline nasal granuloma due to *Cryptococcus gattii* type VGII. Mycopathologia 176:303–307. doi:10.1007/s11046-013-9686-4
 48. Favalella OC, de Paula DAJ, Dutra V, Nakazato L, Tadano T, dos Lazera M et al (2014) Molecular typing and in vitro antifungal susceptibility of *Cryptococcus* spp from patients in Midwest Brazil. J Infect Dev Ctries 8:1037–1043
 49. Brito-Santos F, Barbosa GG, Trilles L, Nishikawa MM, Wanke B, Meyer W et al (2015) Environmental isolation of *Cryptococcus gattii* VGII from indoor dust from typical wooden houses in the deep Amazonas of the Rio Negro basin. PLoS One 10, e0115866. doi:10.1371/journal.pone.0115866
 50. Headley SA, Di Santis GW, de Alcântara BK, Costa TC, da Silva EO, Pretto-Giordano LG et al (2015) *Cryptococcus gattii*-induced infections in dogs from Southern Brazil. Mycopathologia 180:265–275. doi:10.1007/s11046-015-9901-6
 51. Abegg MA, Cella FL, Faganello J, Valente P, Schrank A, Vainstein MH (2006) *Cryptococcus neoformans* and *Cryptococcus gattii* isolated from the excreta of psittaciformes in a southern Brazilian zoological garden. Mycopathologia 161:83–91. doi:10.1007/s11046-005-0186-z
 52. Trilles L, dos Lazéra M, Wanke B, Oliveira RV, Barbosa GG, Nishikawa MM et al (2008) Regional pattern of the molecular types of *Cryptococcus neoformans* and *Cryptococcus gattii* in Brazil. Mem Inst Oswaldo Cruz 103:455–462
 53. Nascimento E, Bonifácio da Silva MEN, Martinez R, von Zeska Kress MR (2014) Primary cutaneous cryptococcosis in an immunocompetent patient due to *Cryptococcus gattii* molecular type VGI in Brazil: a case report and review of literature. Mycoses 57:442–447. doi:10.1111/myc.12176
 54. Carriconde F, Gilgado F, Arthur I, Ellis D, Malik R, van de Wiele N et al (2011) Clonality and α -a recombination in the Australian *Cryptococcus gattii* VGII population—an emerging outbreak in Australia. PLoS One 6, e16936. doi:10.1371/journal.pone.0016936
 55. Fraser JA, Giles SS, Wenink EC, Geunes-Boyer SG, Wright JR, Diezmann S et al (2005) Same-sex mating and the origin of the Vancouver Island *Cryptococcus gattii* outbreak. Nature 437:1360–1364. doi:10.1038/nature04220
 56. Iqbal N, DeBess EE, Wohlrle R, Sun B, Nett RJ, Ahlquist AM et al (2010) Correlation of genotype and in vitro susceptibilities of *Cryptococcus gattii* strains from the Pacific Northwest of the United States. J Clin Microbiol 48:539–544. doi:10.1128/JCM.01505-09
 57. Pasa CR, Chang MR, Hans-Filho G (2012) Post-trauma primary cutaneous cryptococcosis in an immunocompetent host by *Cryptococcus gattii* VGII. Mycoses 55:e1–e3. doi:10.1111/j.1439-0507.2011.02058.x
 58. Hagen F, Illnait-Zaragozi M-T, Bartlett KH, Swinne D, Geertsen E, Klaassen CHW et al (2010) In vitro antifungal susceptibilities and amplified fragment length polymorphism genotyping of a

- worldwide collection of 350 clinical, veterinary, and environmental *Cryptococcus gattii* isolates. Antimicrob Agents Chemother 54: 5139–5145. doi:10.1128/AAC.00746-10
59. Lockhart SR, Iqbal N, Bolden CB, DeBess EE, Marsden-Haug N, Worhle R et al (2012) Epidemiologic cutoff values for triazole drugs in *Cryptococcus gattii*: correlation of molecular type and in vitro susceptibility. Diagn Microbiol Infect Dis 73:144–148. doi:10.1016/j.diagmicrobio.2012.02.018
60. Trilles L, Meyer W, Wanke B, Guarro J, Lazéra M (2012) Correlation of antifungal susceptibility and molecular type within the *Cryptococcus neoformans/C. gattii* species complex. Med Mycol 50:328–332. doi:10.3109/13693786.2011.602126
61. Miceli MH, Kauffman CA (2015) Isavuconazole: a new broad-spectrum triazole antifungal agent. Clin Infect Dis 61:1558–1565. doi:10.1093/cid/civ571
62. Illnait-Zaragozi M-T, Martínez GF, Curfs-Breuker I, Fernández CM, Boekhout T, Meis JF (2008) In vitro activity of the new azole isavuconazole (BAL4815) compared with six other antifungal agents against 162 *Cryptococcus neoformans* isolates from Cuba. Antimicrob Agents Chemother 52:1580–1582. doi:10.1128/AAC.01384-07
63. Datta K, Rhee P, Byrnes E 3rd, Garcia-Effron G, Perlin DS, Staab JF et al (2013) Isavuconazole activity against *Aspergillus lentulus*, *Neosartorya udagawae*, and *Cryptococcus gattii*, emerging fungal pathogens with reduced azole susceptibility. J Clin Microbiol 51: 3090–3093. doi:10.1128/JCM.01190-13
64. Thompson GR 3rd, Rendon A, Dos Santos RR, Queiroz-Telles F, Ostrosky-Zeichner L, Azie N et al (2016) Isavuconazole treatment of cryptococcosis and dimorphic mycoses. Clin Infect Dis 63:356–362. doi:10.1093/cid/ciw305
65. Chen SC-A, Meyer W, Sorrell TC (2014) *Cryptococcus gattii* infections. Clin Microbiol Rev 27:980–1024. doi:10.1128/CMR.00126-13
66. Hospenthal DR, Bennett JE (1998) Flucytosine monotherapy for cryptococcosis. Clin Infect Dis 27:260–264
67. Illnait-Zaragozi MT, Martínez-Machín GF, Fernández-Andreu CM, Hagen F, Boekhout T, Klaassen CHW et al (2010) Microsatellite typing and susceptibilities of serial *Cryptococcus neoformans* isolates from Cuban patients with recurrent cryptococcal meningitis. BMC Infect Dis 10:289. doi:10.1186/1471-2334-10-289
68. Chowdhary A, Randhawa HS, Sundar G, Kathuria S, Prakash A, Khan Z et al (2011) 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. J Med Microbiol 60:961–967. doi:10.1099/jmm.0.029025-0