

Microbiological, Epidemiological, and Clinical Characteristics and Outcomes of Patients with Cryptococcosis in Taiwan, 1997–2010

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Abstract

Background: Among members of *Cryptococcus neoformans*-*Cryptococcus gattii* species complex, *C. neoformans* is distributed worldwide whereas *C. gattii* is considered to be more prevalent in the subtropics and tropics including Taiwan. This nationwide study was undertaken to determine the distribution of genotypes, clinical characteristics and outcomes of 219 patients with proven cryptococcosis at 20 hospitals representative of all geographic areas in Taiwan during 1997–2010.

Methods and Findings: Of 219 isolates analyzed, *C. neoformans* accounted for 210 isolates (95.9%); nine isolates were *C. gattii* (4.1%). The predominant genotype was VNI (206 isolates). The other genotypes included VNII (4 isolates), VGI (3 isolates) and VGII (6 isolates). Antifungal minimal inhibition concentrations higher than epidemiologic cutoff values (ECVs) were found in nine VNI isolates (7 for amphotericin B). HIV infection was the most common underlying condition (54/219, 24.6%). Among HIV-negative patients, liver diseases (HBV carrier or cirrhosis) were common (30.2%) and 15.4% did not have any underlying condition. Meningoencephalitis was the most common presentation (58.9%), followed by pulmonary infection (19.6%) and “others” (predominantly cryptococemia) (18.7%). The independent risk factors for 10-week mortality, by multivariate analysis, were cirrhosis of liver ($P = 0.014$) and CSF cryptococcal antigen titer ≥ 512 ($P = 0.020$). All except one of 54 HIV-infected patients were infected by VNI genotype (98.1%). Of the 13 isolates of genotypes other than VNI, 12 (92.3%) were isolated from HIV-negative patients. HIV-infected patients compared to HIV-negative patients were more likely to have meningoencephalitis and serum cryptococcal antigen $\geq 1:512$. Patients infected with *C. gattii* compared to *C. neoformans* were younger, more likely to have meningoencephalitis (100% vs. 57%), reside in Central Taiwan (56% vs. 31%), and higher 10-week crude mortality (44.4% vs. 22.2%).

Conclusions: *Cryptococcus neoformans* in Taiwan, more prevalent than *C. gattii*, has a predominant VNI genotype. Isolates with antifungal MIC higher than ECVs were rare.

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Introduction

Among members of the *Cryptococcus neoformans*-*Cryptococcus gattii* species complex that cause cryptococcosis in humans, *C. neoformans* (comprising var. *grubii* [serotype A] and var. *neoformans* [serotype DJ]) occur worldwide. In contrast, *C. gattii* (serotype B and C) is usually limited to the selected regions, particularly the

Asia-Pacific region before the occurrence of a *C. gattii* outbreak in Vancouver Island, Canada [1]. Based on a large global molecular epidemiologic survey *Cryptococcus* could be divided into eight major genotypes: VNI (serotype A), VNII (serotype A), VNIII (serotype AD), and VNIV (serotype D) of *C. neoformans*; and VGI, VGII, VGIII, and VGIV of *C. gattii* using orotidine monophosphate pyrophosphorylase (*URA5*) gene restriction fragment length

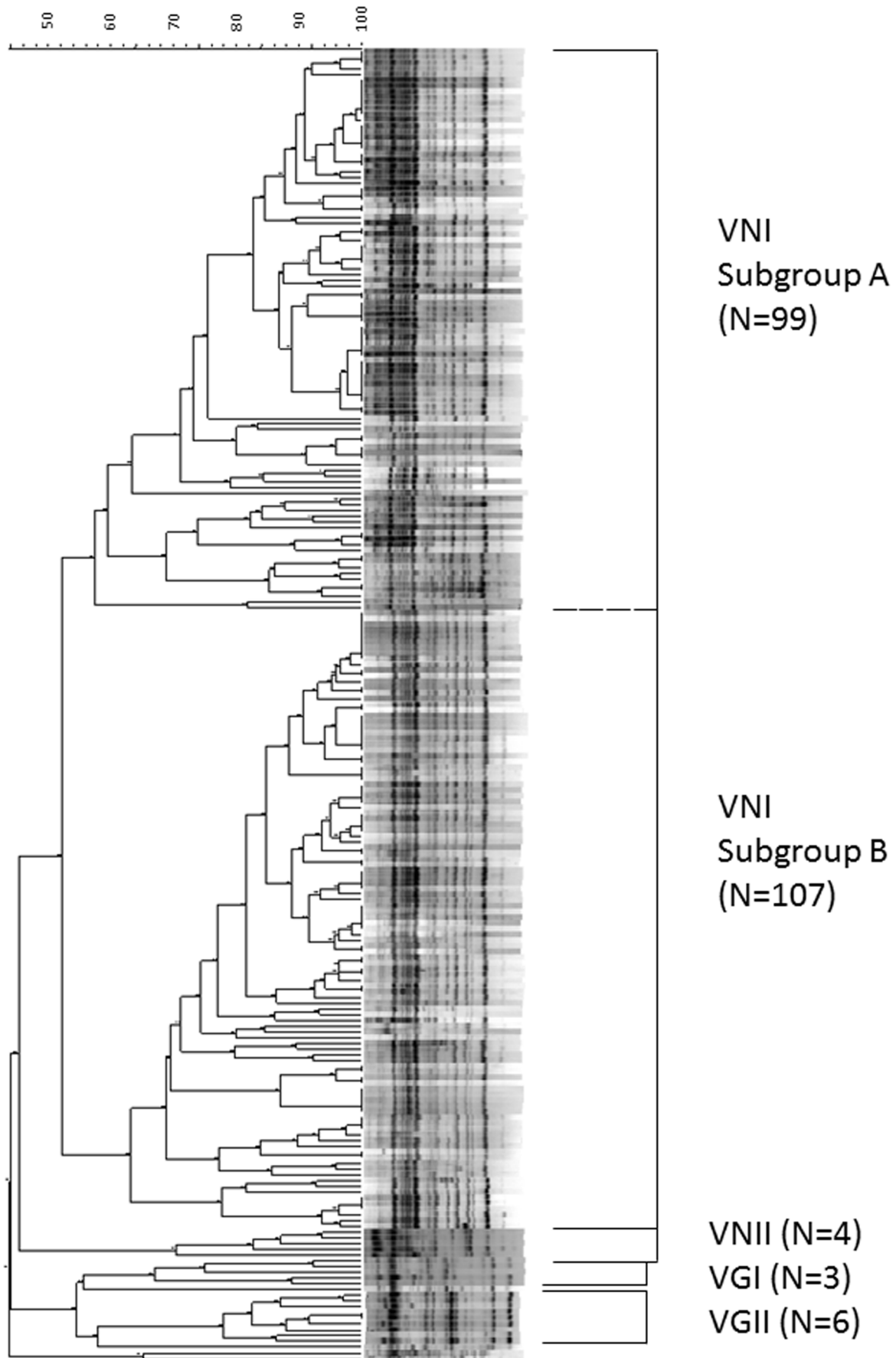


Figure 1. Dendrogram of M13 PCR fingerprint analysis of 219 clinical isolates of *Cryptococcus neoformans*-*Cryptococcus gattii* species complex collected in Taiwan during 1997 to 2010 and 12 reference strains.

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polymorphism (RFLP) analysis and M13 polymerase chain reaction (PCR) fingerprinting [2].

Cryptococcosis is associated with significant morbidity and mortality. It can present as meningoencephalitis, pneumonia and cryptococemia in both immunocompetent and immunocompromised hosts. Outcome and treatment failure are usually associated with underlying conditions, a delay in diagnosis, and absence of a fungicidal drug [3–5]. In addition, the emergence of isolates with resistance or elevated minimum inhibition concentration (MIC) above epidemiologic cutoff values (ECVs) is of concern as well [6,7].

We conducted this nationwide multicenter retrospective study for patients with proven cryptococcosis to address two questions. First, what are the genotypes and antifungal susceptibility of *Cryptococcus* clinical isolates collected from representative regions in Taiwan? Second, are demographic qualities, underlying conditions, and microbiological characteristics associated with cryptococcosis patient mortality?

Population and Methods

This research was approved by the Research Ethics Committees of the National Taiwan University Hospital (No. 201209035RIC), Mackay Memorial Hospital (No.12MMHIS120), Kaohsiung Medical University Hospital (No.KMUH-IRB-20120239), China

Medical University Hospital (No. DMR101-IRB1-240), and National Health Research Institute (No.EC 09602024) and was conducted according to the Declaration of Helsinki. The project involved the use of existing data, records, and clinical isolates without intervention. Informed consent was waived and the data were analyzed anonymously.

Hospital settings and *Cryptococcus* clinical isolates

Cryptococcus clinical isolates were obtained from 219 patients with proven cryptococcosis managed at 20 hospitals located in the four geographic regions of Taiwan during 1997–2010. The initial patient isolate, regardless of anatomical site, was selected and sent to National Taiwan University Hospital (NTUH) for microbiological characterization.

Genotypes

High-molecular-weight DNA was isolated and genotypes were determined by *URA5* gene RFLP analysis [2]. Molecular types were evaluated and compared using M13 PCR-fingerprinting [2]. The computer program BioNumerics version 6.0 (Applied Maths, Kortrijk, Belgium) was used to determine the cluster analysis by the UPGMA method [8]. DNA bands were defined manually with a band position tolerance of 0.8% and an optimization setting of 0.2%. Reference strains included WM 148 (VNI), WM 626

Table 1. Susceptibility of 216 cryptococcal clinical isolates to four antifungal agents in Taiwan, 1997–2010.

Antifungal agent	Genotype	No. of isolates	Minimum inhibitory concentration (µg/mL)					% (No.) above ECV	
			Range	Geometric Mean	MIC ₅₀	MIC ₉₀	ECV	This study	Global studies ^a
Amphotericin B									
	VNI	203	0.03–1	0.48	0.5	0.5	0.5	3.4% (7)	2.8%
	VNII	4	0.13–1	0.42	0.5	1	NA ^a		
	VGI	3	0.25–0.25	0.25	0.25	0.25	0.5	0%	0.8%
	VGII	6	0.06–1	0.31	0.5	1	1	0%	0.8%
Flucytosine									
	VNI	203	0.13–32	1.14	1	2	8	0.5% (1)	3.4%
	VNII	4	0.13–2	0.30	0.19	2	NA ^a		
	VGI	3	0.5–1	0.63	0.5	1	4	0%	4.3%
	VGII	6	1–2	1.59	2	2	16	0%	2.9%
Fluconazole									
	VNI	203	0.03–16	2.35	4	8	8	0.5% (1)	2.9%
	VNII	4	0.13–8	0.84	0.75	8	NA ^a		
	VGI	3	1–4	2	2	4	8	0%	1.2%
	VGII	6	0.13–16	5.04	8	16	32	0%	6.9%
Voriconazole									
	VNI	203	0.03–0.25	0.06	0.06	0.13	0.25	0%	2.4%
	VNII	4	0.03–0.13	0.05	0.05	0.13	NA ^a		
	VGI	3	0.03–0.06	0.04	0.03	0.06	0.5	0%	0%
	VGII	6	0.13–0.25	0.20	0.25	0.25	0.25	0%	4.1%

^aThe epidemiologic cutoff values of VNII to antifungal drugs being tested were not available in global studies [6,7].

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Table 2. Epidemiological and clinical characteristics of 219 patients with proven cryptococcosis hospitalized at 20 hospitals in Taiwan, 1997–2010.

Characteristics	<i>Cryptococcus neoformans</i> (N = 210)		<i>Cryptococcus gattii</i> (N = 9)	
	No.	(%)	No.	(%)
Geographic distribution				
Northern	119	(56.7)	1	(11.1)
Central	65	(30.9)	5	(55.6)
Southern	21	(10.0)	1	(11.1)
Eastern	5	(2.4)	2	(22.2)
Demographic data				
Age, range, years	12 to 94		22 to 68	
Age, mean \pm SD, years	53.1 \pm 18.4		38.6 \pm 13.0	
Age \geq 60 years	75	(35.7)	1	(11.1)
Male	143	(72.2)	5	(55.6)
Underlying conditions				
HIV infection	53	(27.3)	1	(11.1)
Liver diseases				
Hepatitis B virus carrier	46	(21.9)	0	(0.0)
Cirrhosis of liver	31	(14.8)	0	(0.0)
Malignancy				
Hematological malignancy	13	(6.2)	0	(0.0)
Other malignancy	31	(14.8)	0	(0.0)
Diabetes mellitus	39	(18.6)	1	(11.1)
Kidney diseases				
Systemic lupus erythematosus and other rheumatologic diseases	11	(5.2)	0	(0.0)
Cerebrovascular accident	8	(3.8)	1	(11.1)
Tuberculosis	6	(2.9)	0	(0.0)
Solid organ transplantation ^a	3	(1.4)	1	(11.1)
Idiopathic CD4 lymphocytopenia	3	(1.4)	0	(0.0)
Other diseases	3	(1.4)	0	(0.0)
No underlying conditions	19	(9.0)	4	(44.4)
Classification of cryptococcosis				
Meningoencephalitis	120	(57.1)	9	(100.0)
Pulmonary cryptococcosis	43	(20.5)	0	(0.0)
Others ^b	47	(22.4)	0	(0.0)
Serum cryptococcal capsular antigen				
Antigen titer \geq 512	73	(34.8)	4	(44.4)
Antigen titer < 512	57	(27.1)	3	(33.3)
Not done	80	(38.1)	2	(22.2)
CSF cryptococcal capsular antigen				
Antigen titer \geq 1:512	76	(36.2)	7	(77.8)
Antigen titer < 1:512	40	(19.0)	2	(22.2)
Not done	94	(44.8)	0	(0.0)
Intracranial pressure				
Opening pressure \geq 250 mmH ₂ O	48	(22.9)	6	(66.7)
Opening pressure < 250 mmH ₂ O	42	(20.0)	2	(22.2)
Not done or not available	120	(57.1)	1	(11.1)
Neurosurgical intervention	19	(9.0)	3	(33.3)
All-cause mortality				
2-week mortality	22	(10.5)	2	(22.2)
10-week mortality	60	(28.6)	4	(44.4)

Abbreviations: SD: standard deviation; CSF: cerebrospinal fluid; HIV: human immunodeficiency virus.

^aSolid organ transplantation included two liver transplantations and one heart transplantation in *C. neoformans* infected patients; and one kidney transplantation in *C. gattii* infected patient.

^b“Others” included 36 patients with cryptococemia.

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(VNII), WM 628 (VNIII), WM 629 (VNIV), WM 179 (VGI), WM 178 (VGII), WM 161 (VGIII), WM 779 (VGIV) [2], two Australia clinical strains T184 (VNI) and T185 (VGI), and Vancouver Island outbreak strains R265 (VGIIa) and R272 (VGIIb).

Antifungal susceptibility

Susceptibility, as displayed by MIC ($\mu\text{g/ml}$) levels, to amphotericin B, flucytosine, fluconazole, and voriconazole was determined following the Clinical Laboratory Standards Institute (CLSI) M27-A3 broth microdilution method and incubated at 35°C [9]. All results were read visually at 72 h. The reference strains *C. neoformans* ATCC 90112, *Candida albicans* ATCC 90028, and *Candida parapsilosis* ATCC 22019 were used as internal controls. The ECVs are the MIC values that captured >95% of the observed population in RPMI medium provided in recent studies [6,7].

Clinical characteristics and outcomes of patients with cryptococcosis

Data were collected retrospectively after isolates were sent for microbiological characterization and included gender, age, underlying conditions such as human immunodeficiency virus (HIV) status and lowest CD4 count during hospitalization, hepatitis B virus (HBV) carrier defined by positive surface antigen (HBsAg) status, and cirrhosis of liver determined by sonography; clinical characteristics included presentation, initial cryptococcal capsular polysaccharide antigen titer in cerebrospinal fluid (CSF) or serum, baseline intracranial opening pressures, neurosurgical intervention, all-cause mortality at 2- and 10-weeks. One patient could possess more than one underlying condition. We did not collect and record treatment details.

Case definition

Proven cryptococcosis was defined and classified into cryptococcal meningoencephalitis, pulmonary cryptococcosis, and others as described previously [10].

Data analysis

The categorical variables were analyzed by number (No.) (%) and the continuous variables were presented as mean \pm standard deviation (SD). The association between categorical variables was analyzed with the Chi-square test or Fisher's exact test if the expected number was less than five. The independent and joint effects of several variables to identify significant predictors of mortality were investigated by univariate and multivariate logistic regression analyses. Two-sided P value <0.05 was considered statistically significant. All statistical analyses were performed using the SAS software, version 9.2 (SAS Institute Inc., Cary, NC, US).

Results

Cryptococcus genotypes

Of 219 *Cryptococcus* clinical isolates, 210 were *C. neoformans* (95.9%) and 9 were *C. gattii* (4.1%). VNI genotype accounted for 206/210 (98.1%) of *C. neoformans*. Four isolates were VNII. Among the nine isolates of *C. gattii*, three were VGI and six were

VGII. The details of patients with VNII and *C. gattii* are shown in **Table S1** and **Table S2**, respectively.

Figure 1 shows the M13 PCR-fingerprinting dendrogram of the 219 cryptococcal isolates (details are presented in **Figure S1**). Genotype VNI can be divided into two subgroups. Subgroup A accounted for 48.1% (99/206) of VNI with 57.4% similarity and subgroup B accounted for 51.9% (107/206) of VNI with 63.2% similarity.

Antifungal susceptibility

Among the 219 isolates, the susceptibility data of three VNI isolates (T203, T205, and T262) were indeterminate due to very poor growth in RPMI broth at 35°C. The MIC levels of 216 isolates to amphotericin B, flucytosine, fluconazole, and voriconazole are shown in **Table 1**. Seven of 203 VNI isolates (3.4%) had amphotericin B MIC levels higher than ECV. One VNI isolate had a flucytosine MIC level higher than ECV. Two of six VGII isolates and one of 203 VNI isolates had fluconazole MIC levels >8 $\mu\text{g/ml}$, but there were none above this level for 4 VNII isolates and 3 VGI isolates. Fluconazole ECV was 8 $\mu\text{g/ml}$ for VNI and VGI, and was 32 $\mu\text{g/ml}$ for VGII. Therefore, only one VNI isolate of 219 isolates had fluconazole MIC higher than ECV. Detailed information regarding cryptococcosis due to *Cryptococcus* VNI isolates with antifungal MICs higher than ECVs is shown in **Table S3**.

Epidemiological and clinical characteristics

Table 2 shows the epidemiological and clinical characteristics of the 219 patients with proven cryptococcosis. More than half of the patients were in Northern Taiwan. However, 5 of 9 isolates of *C. gattii* (55.6%) were from Central Taiwan. The most common five underlying conditions were HIV infection (54 patients, 24.6%), HBV carrier (46 patients, 21.0%), malignancies (44 patients, 20.1%), diabetes mellitus (40 patients, 18.2%), and cirrhosis of liver (31 patients, 14.1%). No underlying condition was identified in 23 patients (10.5%). Meningoencephalitis was the most common presentation (58.9%), followed by pulmonary infection (19.6%) and “others” (predominantly cryptococemia) (18.7%). The nine patients with *C. gattii* infection, compared to 210 patients with *C. neoformans*, were younger (mean 38.6 years vs. 53.1 years) and more likely to have no underlying conditions (44.4% vs. 9.0%), to have meningoencephalitis (100.0% vs. 57.1%) and to undergo neurosurgical intervention (33.3% vs. 9.0%). They also had a higher 10-week mortality (44.4% vs. 22.2%), as seen in **Table 2**.

Of 54 HIV-infected patients, 53 were infected by the VNI genotype (98.1%) and one was infected by the VGI genotype, as seen in **Table 3**. Excluding five patients without recorded CD4 data, the mean CD4 of 49 HIV-infected patients was $50.0 \pm 68.3/\text{mL}$ (ranging from 2 to 318/ mL). Of 13 isolates of genotypes other than VNI, twelve (92.3%) were isolated from HIV-negative patients (**Table 3**, **Table S1**, and **Table S2**). The 54 HIV-infected patients, as compared to the 149 HIV-negative patients, were younger, predominantly male, and more likely to have meningoencephalitis and serum cryptococcal antigen ≥ 512 . Compared to HIV infected patients, HIV-negative patients were more likely to have pulmonary infection and liver diseases (either

Table 3. Comparisons of genotype distribution and clinical characteristics of cryptococcosis by HIV status, Taiwan, 1997–2010.

Characteristics	HIV-negative patients (N = 149) ^a		HIV-infected patients (N = 54) ^a		P value
	No.	(%)	No.	(%)	
Genotype distribution					
VNI	137		53		
VNII	4		0		
VGI	2		1		
VGII	6		0		
Geographic distribution					
Northern	84	(56.4)	34	(63.0)	
Central	43	(28.9)	14	(25.9)	
Southern	16	(10.7)	5	(9.3)	
Eastern	6	(4.0)	0	(0.0)	
Demographic data					
Age ≥60 years	75	(50.3)	1	(1.9)	<0.001
Male	94	(63.1)	51	(94.4)	<0.001
Underlying conditions					
Liver diseases					
Hepatitis B virus carrier	33	(22.1)	13	(24.1)	0.845
Cirrhosis of liver ^b	30	(20.1)	1	(1.9)	0.001
Diabetes mellitus	40	(26.8)	0	(0.0)	<0.001
Malignancy					
Hematological malignancy	5	(3.4)	3	(5.6)	0.686
Other malignancy	33	(22.1)	3	(5.6)	0.005
Kidney diseases					
Solid organ transplantation	4	(2.7)	0	(0.0)	0.576
No underlying conditions	23	(15.4)	0	(0.0)	0.002
Classification of cryptococcosis					
Meningoencephalitis	80	(53.7)	44	(81.5)	0.002
Pulmonary cryptococcosis	35	(23.5)	3	(5.6)	
Others ^c	34	(22.8)	7	(13.0)	
Serum cryptococcal capsular antigen					
Antigen titer ≥512	43	(28.9)	34	(63.0)	0.001
Antigen titer <512	49	(32.9)	11	(20.4)	
Not done ^d	57	(38.3)	9	(16.7)	
CSF c cryptococcal capsular antigen					
Antigen titer ≥1:512	50	(33.6)	33	(61.1)	0.661
Antigen titer <1:512	27	(18.1)	15	(27.8)	
Not done ^d	72	(48.3)	6	(11.1)	
Intracranial pressure					
Opening pressure ≥250 mmH ₂ O	32	(21.5)	22	(40.7)	0.101
Opening pressure <250 mmH ₂ O	33	(22.1)	11	(20.4)	
Not done or not available ^d	84	(56.4)	21	(38.9)	
Neurosurgical intervention	15	(10.1)	7	(13.0)	0.592
All-cause mortality					
2-week mortality	19	(12.8)	5	(9.3)	0.468
10-week mortality	52	(34.9)	12	(22.2)	0.100

Abbreviation: HIV: human immunodeficiency virus.

^aOf 219 patients with cryptococcosis, the HIV status of 16 patients was not available. Therefore, 203 cases were included for analysis.

^bOne patient could possess more than one underlying condition; 18 HIV-negative patients had both cirrhosis of liver and HBV infection.

^c“Others” included 25 patients with cryptococcemia in HIV-negative group and seven cryptococcemia in HIV-infected group.

^dData which were not done or not available were excluded from statistical analysis.

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HBV carrier or cirrhosis of liver) as the most common underlying conditions (45 patients, 30.2%).

Of nine patients infected by the VNI genotype and with antifungal MICs above ECVs, five patients had HIV infections, six had meningoencephalitis, and three had cryptococemia. The all-cause mortality at 10 weeks was 33.3% (3/9), as shown in **Table S3**. We did not collect data, such as prior use of antifungal agent or drug interaction, to explain the reason for elevated MICs.

Risk factors for mortality at 2 weeks and 10 weeks

The outcomes of 19 patients at 2-weeks and 24 patients at 10-weeks were not available as patients transferred to other hospitals. All-cause mortality at 2-weeks and 10-weeks were shown in **Table 1**. The significant risk factors for 2-week mortality of cryptococcosis, according to univariate analysis, were geographic distribution in Eastern Taiwan ($P=0.041$), and classification of “others” (predominantly cryptococemia) ($P=0.011$). Under multivariate analysis the risk factors for 2-week mortality were geographic distribution in Eastern Taiwan ($P=0.043$; odds ratio (OR), 10.7; 95% confidence interval (CI), 1.1–106.1) and classification of “others” ($P=0.018$; OR, 13.3; 95% CI, 1.6–112.4).

Risk factors associated with 10-week mortality for 195 patients with cryptococcosis are shown in **Table 4**. The significant factors under univariate analysis were age ≥ 60 years ($P=0.016$), cirrhosis of liver ($P=0.001$), kidney diseases ($P=0.035$), meningoencephalitis ($P=0.038$), other cryptococcosis ($P<0.001$) and CSF cryptococcal antigen titer $\geq 1:512$ ($P=0.019$). Multivariate analysis showed cirrhosis of liver ($P=0.014$; OR, 3.8; 95% CI, 1.3–11.16) and CSF antigen titer $\geq 1:512$ ($P=0.020$; OR, 3.3; 95% CI, 1.2–9.0) as independent predictors for mortality.

Discussion

The current study provides the first nationwide description of the microbiological and clinical epidemiology of cryptococcosis in Taiwan. The majority of isolates in Taiwan were *C. neoformans* genotype VNI (96%). This is in agreement with the worldwide distribution of *Cryptococcus* which is VNI in Ibero-America (68%) [2], Vietnam (71%) [11], India (89%) [12], Malaysia (89%) [13], China (93%) [14] and Korea (96%) [15].

Cryptococcosis in HIV-negative patients was common (73%) in Taiwan (this study) as well as in China (84% to 96%) [14,16,17]. However, HIV-negative patients accounted for 60% in an Indian study [12], 57% in Australia and New Zealand [18], 23% of a

Table 4. Risk factors associated with 10-week mortality for 195 patients with cryptococcosis in Taiwan.

Characteristics	Died (N=64)		Lived (N=131)		Odds ratio	95% confidence interval	P value
	No.	(%)	No.	(%)			
Demographic data							
Age ≥ 60 years	32	(50.0)	42	(32.1)	2.2	1.1–3.9	0.016
Male	41	(64.1)	98	(74.8)	0.6	0.3–1.1	0.12
Underlying conditions							
HIV infection	12	(18.8)	39	(29.8)	0.5	0.3–1.1	0.10
Hepatitis B virus carrier	15	(23.4)	28	(21.4)	1.1	0.5–2.3	0.76
Cirrhosis of liver	18	(28.1)	12	(9.2)	3.9	1.7–8.7	0.001
Kidney diseases	11	(17.2)	9	(6.9)	2.7	1.1–7.0	0.03
Classification of cryptococcosis							
Pulmonary	5	(7.8)	33	(25.2)	1.0		
Meningoencephalitis	37	(57.8)	83	(63.4)	2.9	1.1–8.1	0.04
Others ^a	22	(34.4)	15	(11.4)	10.4	3.3–32.9	<0.001
Serum cryptococcal capsular antigen							
Antigen titer $\geq 1:512$	26	(40.6)	47	(35.9)	1.4	0.7–2.9	0.41
Antigen titer $<1:512$	17	(26.6)	42	(32.1)	1.0		
Not done ^b	21	(32.8)	42	(32.1)			
CSF cryptococcal capsular antigen							
Antigen titer $\geq 1:512$	29	(45.3)	51	(38.9)	3.2	1.2–8.6	0.02
Antigen titer $<1:512$	6	(9.4)	34	(26.0)	1.0		
Not done ^b	29	(45.3)	46	(35.1)			
Intracranial pressure							
Opening pressure ≥ 250 mmH ₂ O	16	(25.0)	37	(28.2)	1.0	0.4–2.6	0.92
Opening pressure <250 mmH ₂ O	12	(18.8)	29	(22.1)	1.0		
Not done or not available ^b	36	(56.3)	65	(49.6)			
Neurosurgical intervention	9	(14.1)	13	(9.9)	1.5	0.6–3.7	0.43

Abbreviation: CSF: cerebrospinal fluid.

^a“Others” included 19 patients with cryptococemia died and 12 patients with cryptococemia lived.

^bData which were not done or not available were excluded from statistical analysis.

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French cohort [19] and 18% in Mexican [20]. Only 15% patients were no underlying condition in Taiwan (this study). This was very different from reports in China (68%) [16] and Vietnam (81%) [11]; and yet was close to a study in Korea (19%) [15], USA (22%) [10] and results of another review from China (16%) [17]. Regarding the distribution of underlying conditions and their impact on 10-week mortality, this study showed that HIV infection was the most common underlying condition (25%), but not a risk factor associated with mortality of cryptococcosis (**Table 4**). Liver diseases (either HBV carrier or cirrhosis) were the most common underlying conditions among HIV-negative patients in Taiwan (30%, **Table 3**) and in China (12%) [17]. Furthermore, cirrhosis of liver was an independent predictor of mortality in this study (**Table 4**) and our previous single center study of cryptococemia [21]. High CSF antigen titers have been associated with death at 10 weeks in a cohort of Italian HIV-positive patients [22] and HIV uninfected patients in Vietnam [11] and our previous study [23]. Our current study confirmed this finding as well. Thus, a threshold of 1:512 or higher should help monitor patients with cryptococcosis, regardless of their HIV status.

In this study, we found clinical presentation of patients with *C. gattii* infection were more likely than those with *C. neoformans* infection to have meningoencephalitis, were younger, and were less likely to have underlying conditions (**Table 2**), which was concordant with an Australian study [18]. The past studies from a center in northern Taiwan (i.e. NTUH) revealed that clinical cases

of *C. gattii* decreased from 59% (17/29) during 1982–1994 to 13% (4/30) during 1995–1997 [24], and 1% (1/100) during 1999–2004 [25]. Another report from a center in southern Taiwan showed 15% (5/34) clinical cases during 1998–2002 were *C. gattii* [26]. Although the ecological niches of *C. gattii* are poorly defined in Taiwan [27], Chaturvedi V. et al. suggested a hypothetical lifecycle of *C. gattii* whereby it cycles through plants, soil, air, and water [28]. Loss of tree coverage in mountainous areas following numerous landslides washed into the estuaries in recent years might explain part of the reason why there has been a decrease in *C. gattii* in Taiwan. We speculate that the global distribution of *C. gattii*, as shown in **Table 5**, might be related to ocean circulation to allow distribution and thriving of *C. gattii* propagules into new ecological niches.

Recently, Espinel-Ingroff A. et al. suggested the epidemiologic cutoff values (ECVs) (highest wild type susceptibility endpoint) of antifungal susceptibility for reference [6,7] as the Clinical and Laboratory Standards Institute (CLSI) does not provide clinical breakpoints (CBPs) for *Cryptococcus* species [9]. While CBPs predict the clinical outcome of therapy, the ECVs could monitor the emergence of strains with reduced susceptibility (due to mutation) to the agent being evaluated. In the current study, only nine of 219 isolates had MICs higher than ECVs (**Table 1**). Of them, seven isolates (3.4%) of the VNI genotype had amphotericin B MIC levels higher than ECV, while the global study showed 2.8% [6]. Regarding fluconazole MIC, the values of MIC₅₀ and MIC₉₀ in

Table 5. The global distribution of clinical isolates of *Cryptococcus gattii* by genotype in the literature reviewed.

Report year	Collection year	Region	No. of isolates					Reference
			Total	VGI	VGII	VGIII	VGIV	
1996	1965–1994	Australia	48	44	3	1	0	[33]
2003	1961–2001	South American	33	3	13	16	1	[2]
2004	1999–2002	Canada, BC	21	1	20	0	0	[8]
2005	NA	Papua New Guinea	37	31	2	4	0	[34]
2005	NA	Australia, NT	21	9	12	0	0	[34]
2005	NA	India	5	0	5	0	0	[12]
2006	1987–2004	Colombia	16	1 ^a	14 ^b	1	0	[35]
2006	1998–2003	Hong Kong	3	1	2	0	0	[36]
2007	2004–2005	USA, Northwest	5	1	4	0	0	[37]
2008	1994–2006	China, 16 provinces	9	9	0	0	0	[16]
2008	1981–2005	China, Southeastern	9	8	1	0	0	[14]
2009	2006–2008	USA, Northwest	14	0	14	0	0	[38]
2009	1994–2004	Mexico	8	2	2	2	2	[20]
2009	2007	USA, Southeastern	1	1	0	0	0	[39]
2010	2003–2004	Malaysia	11 ^c	4	4	0	0	[13]
2010	1998–2007	Vietnam	10	9	1	0	0	[11]
2010	1990–2008	Korea	2	0	1	1	0	[15]
2010	2007	Japan	1	0	1	0	0	[40]
2012	2005–2007	India	4	0	0	0	4	[41]
2012	2011	USA, Southeastern	1	1	0	0	0	[42]
2012	1997–2010	Taiwan	9	3	6	0	0	Current Study

Abbreviations: NT: Northern Territory; BC: British Columbia; NA: not available.

^aMating type **a**.

^b11 strains with mating type **a** were included.

^cThree untyped *C. gattii* were included.

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this study (**Table 1**) and ECVs in global studies [7] were higher for VGII than for VGI, VNI, and VNII. This indicates antifungal susceptibility for *Cryptococcus* should be species-specific and molecular type-specific [6,7]. It seems likely that the differences seen among the *C. neoformans*-*C. gattii* species complex are due to intrinsic heteroresistance to fluconazole [29], chromosome duplication during prolonged azole therapy [30], and possible involvement of phosphoinositide-dependent kinase (PDK1), protein kinase C (PKC), and target of rapamycin (TOR) signaling pathways in basal fluconazole tolerance [31].

The strengths of this study are the large number of cryptococcal clinical isolates collected from hospitals representative of all regions of Taiwan during a 13 year period, the use of molecular methods for genotyping, assessment of antifungal susceptibility, and characterization of the risk factors for 10-week mortality. The weaknesses inherent in a study of this kind were the inability to collect sufficient isolates of rare genotypes or those with MICs higher than ECV to determine the impact on outcome. Generally only one isolate per infection is tested, although it has been revealed that 20% of patients with cryptococcosis can be infected by multiple strains or molecular types [32]. The geographic distribution according to hospital location might not represent the places where exposure to *Cryptococcus* occurred. Besides, we could not evaluate treatment responses of an individual drug because antifungal regimens and dosages were modified in many of the patients and confounded by the underlying conditions.

In conclusion, the major genotype of *Cryptococcus* clinical isolates in Taiwan was VNI. Only nine of 219 patients were infected by *C. gattii*. Isolates with antifungal MICs higher than ECVs were rare. HIV infection was the most common underlying condition and all except one such patient was infected by the VNI genotype. Liver diseases were the most common underlying conditions in HIV-negative patients. Cirrhosis of liver and high CSF cryptococcal antigen levels were independent predictors of 10-week mortality.

Supporting Information

Figure S1 Details of dendrogram of M13 PCR fingerprint analysis of 219 clinical isolates of *Cryptococcus neoformans*-*Cryptococcus gattii* species complex collected in Taiwan during 1997 to 2010 and 12 reference strains. (TIF)

References

- Harris J, Lockhart S, Chiller T (2012) *Cryptococcus gattii*: where do we go from here? *Med Mycol* 50: 113–129. doi:10.3109/13693786.2011.607854.
- Meyer W, Castaneda A, Jackson S, Huynh M, Castaneda E, et al. (2003) Molecular typing of Ibero-American *Cryptococcus neoformans* isolates. *Emerg Infect Dis* 9: 189–195. doi:10.3201/eid0902.020246.
- Nucci M, Perfect JR (2008) When primary antifungal therapy fails. *Clin Infect Dis* 46: 1426–1433. doi:10.1086/587101.
- Bicanic T, Meintjes G, Wood R, Hayes M, Rebe K, et al. (2007) Fungal burden, early fungicidal activity, and outcome in cryptococcal meningitis in antiretroviral-naïve or antiretroviral-experienced patients treated with amphotericin B or fluconazole. *Clin Infect Dis* 45: 76–80. doi:10.1086/518607.
- Dromer F, Bernede-Bauduin C, Guillemot D, Lortholary O, French Cryptococcosis Study G (2008) Major role for amphotericin B-flucytosine combination in severe cryptococcosis. *PLoS ONE* 3: e2870. doi:10.1371/journal.pone.0002870.
- Espinel-Ingroff A, Chowdhary A, Cuenca-Estrella M, Fothergill A, Fuller J, 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, Aller AI, Canton E, Castanon-Olivares LR, Chowdhary A, 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.
- Kidd SE, Hagen F, Tschärke RL, Huynh M, Bartlett KH, 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.
- Clinical and Laboratory Standards Institute (2008) Reference method for broth dilution antifungal susceptibility testing of yeasts; approved standard. Wayne, PA: CLSI.
- Pappas PG, Perfect JR, Cloud GA, Larsen RA, Pankey GA, et al. (2001) Cryptococcosis in human immunodeficiency virus-negative patients in the era of effective azole therapy. *Clin Infect Dis* 33: 690–699. doi:10.1086/322597.
- Chau TT, Mai NH, Phu NH, Nghia HD, Chuong LV, et al. (2010) A prospective descriptive study of cryptococcal meningitis in HIV uninfected patients in Vietnam - high prevalence of *Cryptococcus neoformans* var *grubii* in the absence of underlying disease. *BMC Infect Dis* 10: 199. doi:10.1186/1471-2334-10-199.
- Jain N, Wickes BL, Keller SM, Fu J, Casadevall A, et al. (2005) Molecular epidemiology of clinical *Cryptococcus neoformans* strains from India. *J Clin Microbiol* 43: 5733–5742. doi:10.1128/JCM.43.11.5733-5742.2005.
- Tay ST, Rohani MY, Hoo TS, Hamimah H (2010) Epidemiology of cryptococcosis in Malaysia. *Mycoses* 53: 509–514. doi:10.1111/j.1439-0507.2009.01750.x.
- Feng X, Yao Z, Ren D, Liao W, Wu J (2008) Genotype and mating type analysis of *Cryptococcus neoformans* and *Cryptococcus gattii* isolates from China that mainly originated from non-HIV-infected patients. *FEMS Yeast Res* 8: 930–938. doi:10.1111/j.1567-1364.2008.00422.x.

Table S1 Microbiological, epidemiological, and clinical characteristics and outcomes of cryptococcosis due to VNII genotype in Taiwan, 1997 to 2010.

(DOC)

Table S2 Microbiological, epidemiological, and clinical characteristics and outcomes of *Cryptococcus gattii* in Taiwan, 1997 to 2010.

(DOC)

Table S3 Microbiological, epidemiological, and clinical characteristics and outcomes of cryptococcosis due to *Cryptococcus* VNI isolates with antifungal minimum inhibition concentration above epidemiologic cutoff values in Taiwan, 1997 to 2010.

(DOC)

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Author Contributions

Conceived and designed the experiments: YCC. Performed the experiments: YCC HKT. Analyzed the data: HKT YCC WLC. Contributed reagents/materials/analysis tools: YCC CPL MWH YHL PLL HJL. Wrote the paper: HKT YCC.

15. Choi YH, Ngamskulrungron P, Varma A, Sionov E, Hwang SM, et al. (2010) Prevalence of the VNc genotype of *Cryptococcus neoformans* in non-HIV-associated cryptococcosis in the Republic of Korea. *FEMS Yeast Res* 10: 769–778. doi:10.1111/j.1567-1364.2010.00648.x.
16. Chen J, Varma A, Diaz MR, Litvinseva AP, Wollenberg KK, et al. (2008) *Cryptococcus neoformans* strains and infection in apparently immunocompetent patients, China. *Emerg Infect Dis* 14: 755–762. doi:10.3201/eid1405.071312.
17. Yuchong C, Fubin C, Jianghan C, Fenglian W, Nan X, et al. (2012) Cryptococcosis in China (1985–2010): review of cases from Chinese database. *Mycopathologia* 173: 329–335. doi:10.1007/s11046-011-9471-1.
18. Chen S, Sorrell T, Nimmo G, Speed B, Currie B, et al. (2000) Epidemiology and host- and variety-dependent characteristics of infection due to *Cryptococcus neoformans* in Australia and New Zealand. Australasian Cryptococcal Study Group. *Clin Infect Dis* 31: 499–508. doi:10.1086/313992.
19. Dromer F, Mathoulin-Pelissier S, Launay O, Lortholary O, French Cryptococcosis Study G (2007) Determinants of disease presentation and outcome during cryptococcosis: the CryptoA/D study. *PLoS Med* 4: e21. doi:10.1371/journal.pmed.0040021.
20. Olivares LR, Martinez KM, Cruz RM, Rivera MA, Meyer W, et al. (2009) Genotyping of Mexican *Cryptococcus neoformans* and *C. gattii* isolates by PCR-fingerprinting. *Med Mycol* 47: 713–721. doi:10.3109/13693780802559031.
21. Jean SS, Fang CT, Shau WY, Chen YC, Chang SC, et al. (2002) Cryptococcaemia: clinical features and prognostic factors. *QJM* 95: 511–518.
22. Antinori S, Galimberti L, Magni C, Casella A, Vago L, et al. (2001) *Cryptococcus neoformans* infection in a cohort of Italian AIDS patients: natural history, early prognostic parameters, and autopsy findings. *Eur J Clin Microbiol Infect Dis* 20: 711–717.
23. Shih CC, Chen YC, Chang SC, Luh KT, Hsieh WC (2000) Cryptococcal meningitis in non-HIV-infected patients. *QJM* 93: 245–251.
24. Chen YC, Chang SC, Shih CC, Hung CC, Luhbd KT, et al. (2000) Clinical features and in vitro susceptibilities of two varieties of *Cryptococcus neoformans* in Taiwan. *Diagn Microbiol Infect Dis* 36: 175–183. doi:S0732-8893(99)00137-6 [pii].
25. Liaw SJ, Wu HC, Hsueh PR (2010) Microbiological characteristics of clinical isolates of *Cryptococcus neoformans* in Taiwan: serotypes, mating types, molecular types, virulence factors, and antifungal susceptibility. *Clin Microbiol Infect* 16: 696–703. doi:10.1111/j.1469-0691.2009.02930.x.
26. Chang WN, Huang CR, Lei CB, Lee PY, Chien CC, et al. (2004) Serotypes of clinical cerebrospinal fluid *Cryptococcus neoformans* isolates from southern Taiwan and their in vitro susceptibilities to amphotericin B, fluconazole, and voriconazole. *Jpn J Infect Dis* 57: 113–115.
27. Lee CK (2011) [Isolation of *Cryptococcus* species and *Tricosporon asahii* from environment in southern Taiwan] [master thesis]. Kaohsiung City, Taiwan (R.O.C.): National Sun Yat-Sen University. 52 p.
28. Chaturvedi V, Chaturvedi S (2011) *Cryptococcus gattii*: a resurgent fungal pathogen. *Trends Microbiol* 19: 564–571. doi:10.1016/j.tim.2011.07.010.
29. Varma A, Kwon-Chung KJ (2010) Heteroresistance of *Cryptococcus gattii* to fluconazole. *Antimicrob Agents Chemother* 54: 2303–2311. doi:10.1128/AAC.00153-10.
30. Sionov E, Lee H, Chang YC, Kwon-Chung KJ (2010) *Cryptococcus neoformans* overcomes stress of azole drugs by formation of disomy in specific multiple chromosomes. *PLoS Pathog* 6: e1000848. doi:10.1371/journal.ppat.1000848.
31. Lee H, Khanal Lamichhane A, Garraffo HM, Kwon-Chung KJ, Chang YC (2012) Involvement of PDK1, PKC and TOR signalling pathways in basal fluconazole tolerance in *Cryptococcus neoformans*. *Mol Microbiol* 84: 130–146. doi:10.1111/j.1365-2958.2012.08016.x.
32. Desnos-Ollivier M, Patel S, Spaulding AR, Charlier C, Garcia-Hermoso D, et al. (2010) Mixed infections and In Vivo evolution in the human fungal pathogen *Cryptococcus neoformans*. *MBio* 1. doi:10.1128/mBio.00091-10.
33. Sorrell TC, Chen SC, Ruma P, Meyer W, Pfeiffer TJ, et al. (1996) Concordance of clinical and environmental isolates of *Cryptococcus neoformans* var. *gattii* by random amplification of polymorphic DNA analysis and PCR fingerprinting. *J Clin Microbiol* 34: 1253–1260.
34. Campbell LT, Currie BJ, Krockenberger M, Malik R, Meyer W, et al. (2005) Clonality and recombination in genetically differentiated subgroups of *Cryptococcus gattii*. *Eukaryot Cell* 4: 1403–1409. doi:10.1128/EC.4.8.1403-1409.2005.
35. Escandon P, Sanchez A, Martinez M, Meyer W, Castaneda E (2006) Molecular epidemiology of clinical and environmental isolates of the *Cryptococcus neoformans* species complex reveals a high genetic diversity and the presence of the molecular type VGII mating type a in Colombia. *FEMS Yeast Res* 6: 625–635. doi:10.1111/j.1567-1364.2006.00055.x.
36. Lui G, Lee N, Ip M, Choi KW, Tso YK, et al. (2006) Cryptococcosis in apparently immunocompetent patients. *QJM* 99: 143–151. doi:10.1093/qjmed/hcl014.
37. MacDougall L, Kidd SE, Galanis E, Mak S, Leslie MJ, et al. (2007) Spread of *Cryptococcus gattii* in British Columbia, Canada, and detection in the Pacific Northwest, USA. *Emerg Infect Dis* 13: 42–50. doi:10.3201/eid1301.060827.
38. Byrnes EJ 3rd, Bildfell RJ, Frank SA, MitchellTGMarrKA, et al (2009) Molecular evidence that the range of the Vancouver Island outbreak of *Cryptococcus gattii* infection has expanded into the Pacific Northwest in the United States. *J Infect Dis* 199: 1081–1086. doi:10.1086/597306.
39. Byrnes EJ 3rd, Li W, Lewit Y, Perfect JR, Carter DA, et al (2009) First reported case of *Cryptococcus gattii* in the Southeastern USA: implications for travel-associated acquisition of an emerging pathogen. *PLoS ONE* 4: e5851. doi:10.1371/journal.pone.0005851.
40. Okamoto K, Hatakeyama S, Itoyama S, Nukui Y, Yoshino Y, et al. (2010) *Cryptococcus gattii* genotype VGIIa infection in man, Japan, 2007. *Emerg Infect Dis* 16: 1155–1157. doi:10.3201/eid1607.100106.
41. Cogliati M, Chandrashekar N, Esposto MC, Chandramuki A, Petrini B, et al. (2012) *Cryptococcus gattii* serotype-C strains isolated in Bangalore, Karnataka, India. *Mycoses* 55: 262–268. doi:10.1111/j.1439-0507.2011.02082.x.
42. Sellers B, Hall P, Cine-Gowdie S, Hays AL, Patel K, et al. (2012) *Cryptococcus gattii*: an emerging fungal pathogen in the southeastern United States. *Am J Med Sci* 343: 510–511. doi:10.1097/MAJ.0b013e3182464bc7.