



# **Review article**

# Searching for clues for eighteen years: Deciphering the ecological determinants of *Cryptococcus gattii* on Vancouver Island, British Columbia

Emily Sohanna Acheson<sup>1,\*</sup>, Eleni Galanis<sup>2,3</sup>, Karen Bartlett<sup>3</sup>, Sunny Mak<sup>2</sup> and Brian Klinkenberg<sup>1</sup>

<sup>1</sup>Department of Geography, University of British Columbia, 1984 West Mall, Vancouver, British Columbia, Canada, V6T 1Z2, <sup>2</sup>British Columbia Centre for Disease Control, Vancouver, British Columbia, Canada, V5Z 4R4 and <sup>3</sup>School of Population and Public Health, University of British Columbia, 2206 East Mall, Vancouver, British Columbia, Canada, V6T 1Z3

\*To whom correspondence should be addressed. Emily Acheson, MSc, PhD candidate, Department of Geography, University of British Columbia, 1984 West Mall, Room 210J, Vancouver, British Columbia, Canada, V6T 1Z2. Tel: +604-822-3534;

E-mail: emily.acheson@gmail.com

Received 11 September 2016; Revised 27 January 2017; Accepted 6 April 2017; Editorial Decision 6 February 2017

# Abstract

Cryptococcus gattii emerged on Vancouver Island in 1999 for unknown reasons, causing human and animal fatalities and illness. The apparent emergence of this fungus in another temperate area, this time in the Pacific Northwest, suggests the fungus may have expanded its ecological niche. Yet studies that directly examine the potential roles of climatic and land use changes on C. gattii are still lacking. We aim to summarize the existing global literature on the ecology of C. gattii, with particular focus on the gap in knowledge surrounding the potential effects of climatic and land use changes. We systematically reviewed English peer-reviewed literature on the ecological determinants of C. gattii. We included studies published from January 1970 through June 2016 and identified 56 relevant studies for our review. We identified environmental isolations of C. gattii from 18 countries, spanning 72 separate regions across six continents. Fifty-three tree species were associated with C. gattii, spanning 10 climate classifications and 36 terrestrial ecoregions. No studies directly tested the potential effects of climatic changes (including climatic oscillations and global climate change) on C. gattii, while only one study directly assessed those of land use change. To improve model predictions of current and future distributions of C. gattii, more focus is needed on the potential effects of climatic and land use changes to help decrease the public health risk. The apparent emergence of C. gattii in British Columbia is also an opportunity to explore the factors behind emerging infectious diseases in Canada and elsewhere.

Key words: climate change, Cryptococcus gattii, human fungal pathogen, land use change, molecular type.

<sup>©</sup> The Author 2017. Published by Oxford University Press on behalf of The International Society for Human and Animal Mycology. All rights reserved. For permissions, please e-mail: journals.permissions@oup.com

#### Introduction

Over recent years, North America has witnessed the emergence or re-emergence of several traditionally tropical and subtropical diseases, such as the introduction of West Nile virus in New York in 1999<sup>1</sup> and the first autochthonous transmission of chikungunya virus in Florida in 2014.<sup>2</sup> It is also experiencing the spread of other diseases, such as Lyme disease in southern Ontario.<sup>3</sup> Accelerating climatic and land use changes are likely key factors driving these trends, though elucidating their specific roles from the web of other interacting drivers (e.g., global trade, migration, and travel) is daunting. Despite this complexity, the task of determining the ecological drivers of infectious organism emergence not only remains but is also becoming increasingly critical with accelerating climate change. Another complication is whether an emergence is a true emergence (i.e., the organism has never before been present in the environment it has been discovered in) or a new recognition (i.e., the organism existed in the environment previously and has only now been detected).

Cryptococcosis is a potentially fatal respiratory and neurological disease caused by inhalation of Cryptococcus fungal spores<sup>4</sup> and causes nearly 625,000 deaths globally each year.<sup>5</sup> Cryptococcosis caused by C. gattii was considered predominantly a tropical and subtropical disease until its discovery on Vancouver Island, British Columbia, in 1999,6 despite clinical, veterinary, and environmental isolations in temperate zones prior to 1999.7-9 Clinical isolation of C. gattii was rare in North America before the Vancouver Island outbreak, with one of the earliest known cases coming from a patient in West Virginia in 1924 (this isolate was only identified as C. gattii VGI decades later).<sup>10</sup> Retrospective analyses of clinical records showed that no clinical cases of C. gattii infections existed in Canada prior to 1999.6 Whether environmental triggers helped C. gattii emerge for the first time or become detectable to humans after years or decades of existence on Vancouver Island in 1999 is unknown and needs to be explored. C. gattii is a facultative parasite; it can remain free-living on trees and in soil but will take advantage of the opportunity of infecting a mammal host, including humans.<sup>11</sup> Despite possible tropical and subtropical origins, now suggested to be in South America or Africa,<sup>12,13</sup> C. gattii has been associated with a variety of native Canadian trees, potentially facilitating its establishment and proliferation in the western Canadian temperate environment.

The *Cryptococcus* species complex is currently comprised of two species: *Cryptococcus neoformans* with serotypes A, D, and AD and *Cryptococcus gattii* with serotypes B and C.<sup>14</sup> Both species have two mating types: MATa and MAT $\alpha$ , where the latter is more frequently found in clinical and environmental isolates.<sup>15,16</sup> Molecular typing techniques of subgroups within the *C. gattii* species have evolved through the decades, with the application of many techniques including DNA<sup>17</sup> and polymerase chain reaction (PCR) fingerprinting,<sup>18</sup> random amplification of polymorphic DNA,<sup>19</sup> restriction fragment length polymorphism (RFLP),<sup>20</sup> amplified fragment length polymorphism (AFLP),<sup>21</sup> and multilocus sequence typing (MLST),<sup>22</sup> among many others. The multitude of molecular typing methods at the global scale created the need to standardize molecular nomenclature for the *C. neoformans* and *C. gattii* species.

A global standardized approach is crucial for comparison of results in different countries and across years, though this has not been without its challenges. Three of the molecular typing techniques produced the most comparable results when subtyping the C. neoformans and C. gattii species: PCR fingerprinting, AFLP, and MLST.<sup>16</sup> The first, coupled with RFLP of the URA5 gene, differentiated C. gattii into four molecular types: VGI, VGII, VGIII, and VGIV.<sup>20</sup> The high discriminatory power of the AFLP typing method then led to the differentiation of AFLP4, AFLP5, AFLP6, AFLP7, and AFLP10 strains within the C. gattii species (where the last two were variations of VGIV),<sup>21,23</sup> in addition to two AFLP6 subtypes (AFLP6A and AFLP6B) in the Vancouver Island C. gattii outbreak.<sup>24</sup> MLST analyses further confirmed the VGI-VGIV molecular types from the PCR fingerprinting methods as well as the Vancouver Island outbreak subtypes VGIIa and VGIIb.<sup>25</sup> At present, the C. gattii complex is categorized into five molecular types (AFLP4/VGI, AFLP5/VGIII, AFLP6/VGII, AFLP7/VGIV, and AFLP10/VGIV)<sup>26</sup>, now argued to be five separate species called C. gattii sensu stricto, C. bacillisporus, C. deuterogattii, C. tetragattii, and C. decagattii, respectively.<sup>27</sup> Since the VGI-VGIV nomenclature was most prominent in our reviewed literature, with many studies published before the differentiation of VGIV into AFLP7 and AFLP10, we will hereafter use the VGI-VGIV nomenclature for this review.

The ongoing outbreak of *C. gattii* infections in the Pacific Northwest is attributed predominantly to VGIIa and to a lesser extent to VGIIb and VGI.<sup>24,28</sup> Another highly virulent subtype, VGIIc, is currently restricted to Oregon.<sup>29</sup> VGIII also appears to be expanding in the western United States and differs from the Vancouver Island outbreak (VIO) VGII strains by causing infections in immunocompromised individuals in Southern California and the southwestern United States.<sup>30</sup> Of all four molecular types, VGII has been reported as the most virulent and fertile in immune cell and whole animal experiments, demonstrating particularly high virulence in the Pacific Northwest.<sup>24,31</sup> Each molecular type also has a slightly different geographical distribution. VGI



**Figure 1**. Worldwide ecoregions from which *C. gattii* has been isolated from the environment. Ecoregions (in red) where environmental isolations of *Cryptococcus gattii* have been made worldwide, along with insets detailing (a) the Pacific Northwest, (b) Mexico, (c) Puerto Rico, (d) northern South America, (e) southeastern South America, (f) western Europe and the northern coast of Africa, (g) eastern Africa, (h) India, and (i) Australia, based on the terrestrial regions specified by Olson et al.<sup>46</sup> The molecular type(s) found in each ecoregion is/are superimposed. It is important to note that the ecoregions highlighted in red represent entire ecoregions within which *C. gattii* was isolated, and not necessarily the full extent of where *C. gattii* was found. Only areas that were specified in the review papers as environmental isolation areas of *C. gattii* were mapped. This excludes areas where only clinical and/or veterinary isolations have been made, as well as areas where only the country of environmental isolation was specified, and is likely an underrepresentation of the full extent of *C. gattii* in the global environment. This Figure is reproduced in color in the online version of *Medical Mycology*.

and VGII have widespread distributions worldwide, while VGIII and VGIV are more localised and less common.<sup>16,32</sup>

Vancouver Island has one of the highest annual incidences of *Cryptococcus gattii* infections among humans in the world.<sup>33</sup> From 1999 to 2015, 393 cases were reported in British Columbia (Source: BCCDC, 2016). As of 2004, *C. gattii* was discovered in the Pacific Northwestern United States, including Oregon and Washington, at least eight non-Pacific Northwest states, including California<sup>34</sup> and, most recently, in Nova Scotia, Canada.<sup>35</sup> Predictions of the full environmental extent of *C. gattii* are likely underestimates due to the lack of successful environmental isolations (see Fig. 1). For example, *C. gattii* VGIIa (identical to the Vancouver Island outbreak strain R265) was isolated from a Japanese patient in 2007 with no recent history of travel to disease-endemic areas.<sup>36</sup> To our knowledge, environmental isolations of *C. gattii* in Japan are still lacking but the local acquisition of infection indicates more environmental sampling needs to be done. If Vancouver Island witnessed a new emergence of C. gattii in 1999, then its emergence in this temperate area and others in the Pacific Northwest suggests the fungus may have expanded its ecological niche. Yet, studies that directly examine the potential effects of climatic and land use changes on C. gattii are lacking. This gap in the literature exists despite the possibilities of importation, warming of ambient air, and deforestation playing roles in C. gattii's Vancouver Island emergence.<sup>6,37</sup> Warmer temperatures can increase a plant's susceptibility to fungal colonization,<sup>38</sup> further supporting the need to study the potential effects of climatic changes. Aerosolization of C. gattii spores is aided by felling of colonized trees,<sup>37</sup> possibly explaining why C. gattii emerged on Vancouver Island in an area of expanding neighbourhoods and following construction of a new highway through forested areas in

131

the mid-1990s.<sup>6</sup> This further supports the need to study the possible effects of land use changes on *C. gattii* emergence and spread.

A previous review of the global distribution of C. gattii<sup>32</sup> found published work on clinical and veterinary isolations of the fungus nearly always outnumbered that for environmental isolations (see Springer and Chaturvedi<sup>32</sup>, Table 1). However, the movement of individuals who become infected and the lengthy incubation period of C. gattii currently estimated to last up to 3 years<sup>39</sup> complicates determining the actual location of exposure. There have also been tourists who contracted C. gattii after visiting Vancouver Island and were later diagnosed in their respective home countries.<sup>40–43</sup> For these reasons, this article focuses solely on environmental isolations, or isolations taken directly from an environmental source, of C. gattii. Through this review, we aim to summarize the existing global literature on the ecology of Cryptococcus gattii, with particular focus on the potential effects of climatic and land use changes.

## Methods

We performed systematic searches in three databases for peer-reviewed English journal literature on the ecology of Cryptococcus gattii: Google Scholar (http:// scholar.google.com), ScienceDirect (http://www.science direct.com/), and Web of Science (http://thomsonreuters. com/thomson-reuters-web-of-science). We included studies published from January 1970 up to and including June 2016. Each search varied based on the search engine input options but included the following three sets of inputs for topics: the first inputs for the species was "either/or" for "Cryptococcus gattii," "Cryptococcus neoformans var. gattii," or "Cryptococcus bacillisporus" (the last being synonymous with C. gattii in the late 1970s and early 1980s)44; the second inputs for the ecological or geographical study of C. gattii was "either/or" for "ecolog"," "geograph"," "distribution"," "ecological niche," or "niche"; the third inputs for the effects of climate and land use changes was "either/or" for "climate," "climate change," "climat\* oscillation," "land use," "land use change," or "environmental change\*." The initial searches yielded a total of 402 papers. Studies were included if they successfully sampled for C. gattii in the environment. We therefore excluded any clinical studies where the fungus was isolated from a human or animal only. We also only included studies where ecological determinants of C. gattii were tested for. Based on these criteria, our search yielded 56 publications for review.

We identified climate characteristics where *C. gattii* was environmentally isolated using the Köppen-Geiger climate classification scheme,<sup>45</sup> the most frequently used climate classification system. We used the most recent map based on observed climate characteristics for 1976–2000 (http:// koeppen-geiger.vu-wien.ac.at/shifts.htm). We also identified the corresponding terrestrial ecoregions of the world where these samples were taken, based on the ecoregions classification map developed by Olson et al.<sup>46</sup> (Table S1) (https://databasin.org/datasets/68635d7c77f1475f9b6c1d1 dbe0a4c4c). We overlaid each map over the mapped *C. gattii* sample regions in ArcMap v.10.1 (ESRI 2012, Redlands, CA, USA). Coordinates for the sample regions were taken based on the centroid of the city, town, or region where sampling occurred, unless exact coordinates were specified by the study.

# The geographical distribution of *C. gattii* worldwide

Retrospective analyses currently suggest that the earliest documented human case of C. gattii infection may have been from a patient in Europe in 1895.<sup>10,47</sup> However, C. gattii was first recognized as a variety of C. neoformans after it was isolated from a 7-year-old Congolese Bantu boy in 1970,48 differentiated by its elongated, cigar-shaped form that was atypical of the round shape characteristic of C. neoformans.<sup>49</sup> Following the 1970 differentiation of C. gattii from C. neoformans, reports of C. gattii infections predominantly originated in tropical and subtropical regions, including parts of Africa, South America, Asia, and Australia. This led to the long-standing hypothesis that C. gattii is a tropical and subtropical pathogen,<sup>50,51</sup> despite isolations also being made in temperate areas. These included multiple C. gattii outbreaks in goats in Spain between 1990 and 1994,<sup>7</sup> as well as outbreaks in sheep and horses in southwestern Australia in the early 1990s.<sup>8</sup> The 1999 Vancouver Island outbreak of C. gattii renewed investigations into the ecological niche of the fungus, dismantling the hypothesis that the fungus was mainly restricted to tropical and subtropical regions.<sup>24</sup> Soon, clinical and/or veterinary isolations of C. gattii were made in temperate regions of the United States, Europe, and Asia<sup>31,52,53</sup> as well as Eastern Canada.<sup>35</sup> Human, veterinary, and environmental isolations of C. gattii are now widespread, found on every continent except Antarctica.

# **Environmental isolations**

Based on the present review of the peer-reviewed literature from 1970 to 2016, 56 publications identified isolations of *C. gattii* from the environment in 18 different countries, spanning 72 separate regions and six continents

Country	Reference	Region	Molecular type	Mating type	Source	Collection year(s)
Argentina	(55)	Buenos Aires City	:.	÷	Tree hollows	2001
	(09)	Republica de Chile Park, de los Patricios Park, Centenario	NGI	:	Tree hollows	2002
	(59)	Fark, and N. Avenancua Fark, Duenos Anes Cuty Resistencia Chaco	NGIII		T tee hollows	2006-2007
	100			•		1007-007
		Rosario, Santa Fe	NGI	:	I ree hollows	7006-2007
		Parque España, La Paz, Entre Rios	IDV	•	Tree hollows	2006–2007
Australia	(77)	Barossa Valley (Barossa Reservoir and Nuriootpa), SA <sup>a</sup>	:	:	Bark, woody and leaf debris	1989
		Balranald, NSW	:	:	Bark, woody debris	1989
		Hay, NSW	:	:	Bark, woody debris	1989
	(83)	Currumbin, Gold Coast, QLD	:	:	Bark and woody debris in tree	1991
					hollows	
		Mt. Annan, Greater Sydney, NSW	:	:	Plant debris	1991
	(9)	Balranald, NSW	NGI	:	Bark, fruit, soil, woody debris	1989 - 1990
		Tocumwal, NSW	IDV	:	Woody debris	1991
		Mt. Annan, Greater Sydney, NSW	IDV	:	Woody debris	1991 - 1994
		Currumbin, Gold Coast, QLD	NGI	:	Woody debris	1991-1993
		Barossa Valley, SA	NGI	:	Air, bark, fruit, soil, woody and	1989–1992
					leaf debris	
		Busselton, WA	NGII	:	Plant debris	1993
	(79)	Balranald, NSW	NGI	$\alpha$ , a	Bark, soil, woody debris	1989-1996
		Hay, NSW	NGI	α	Soil, woody debris	1989-1990
		Adelaide, SA	NGI	α	Woody debris	1996
		Gold Coast, QLD	NGI	α	Woody debris	1996
		Renmark, SA	NGI	$\alpha$ , a	Woody debris	1998
		St. Ives, Sydney, NSW	NGI	α	Tree detritus, woody debris	1997-1998
		Port Macquarie, NSW	NGI	α	Woody debris	1998
		Pilliga, NSW	NGI	α	Leaf debris	1998
		Breza, NSW	NGI	α	Leaf debris	1998
	(91)	Coffs Harbour, NSW	:	α	Branches, leaves, wood	1997 - 2000
		Port Macquarie, NSW	:	α	Branches, leaves, wood	1997 - 2000
		Sydney, NSW	:	$\alpha$ , a	Branches, leaves, wood	1997 - 2000
	(61)	Glenbrook, Blue Mountains National Park, Sydney	NGI	α	Tree hollows	2000
	(100)	Mt. Druitt, Sydney, NSW	VGI, VGII	σ	Insect frass on bark of tree	<2003
Botswana	(62)	Francistown	:	:	Bark, tree hollows, soil	2012

Table 1. Overview of positive global environmental isolations of Cryptococcus gattii.

Table 1. ( <i>C</i>	ontinued).					
Country	Reference	Region	Molecular type	Mating type	Source	Collection year(s)
Brazil	(101)	Rio de Janeiro	IDV	:	Bat guano	<1993
	(58)	Teresina	NGII	α	Tree hollows	1993
	(57)	Teresina	NGII	α	Tree hollows	1993-1997
	(82)	Ibirapuera Park, Sao Paulo	:	:	Bark, flowers, fruits, leaves, plant	1996-1997
					detritus, soil	
	(56)	Ilha de Maracá	NGII	:	Tree hollows	1998
	(54)	Belém, Parà	NGII	:	Tree hollows	<2009
	(72)	Botafogo district, Rio de Janeiro	NGI	:	Tree hollows	2008-2010
	(66)	Santa Isabel do Rio Negro, Amazonas state	NGII	a, $\alpha$	Dust from wooden houses	<2015
Canada	(24)	Rathtrevor Beach Provincial Park (Parksville), MacMillan Park (Cathedral Grove), Vancouver Island	VGII	σ	Air, bark, tree hollows, soil	2001-2002
	(74)	Victoria, Duncan, Nanaimo, Parksville, Courtenay, Cameron	VGI, VGII	÷	Air, bark, leaf debris, living trees,	2001-2003
		Lake, and Campbell River, Vancouver Island			soil	
	(37)	Vancouver Island	VGI, VGII	α	Air, bark, footwear, leaves, soil,	2003-2005
					tree hollows, water, wheel wells of	
					cars, woody debris	
	(87)	Courtenay, Duncan, Nanaimo, Parksville, Port Alberni,	VGI, VGII	α	Air, bark, tree hollows, leaves,	2001-2006
		Victoria, Vancouver Island			soil, water, woody debris	
		Mainland, British Columbia	NGII	÷	Air	2001–2006
	(31)	Gulf Islands	VGI, VGII	:	Bark, soil, tree hollows, water, woody debris	2001-2005
		Mainland. British Columbia	NGII	::	Air	2001 - 2005
		Vancouver Island	NGII	σ	Air, soil,	2001-2005
Colombia	(75)	Cúcuta	:	:	Air, bark, flowers, leaves, seeds,	1997
					tree detritus	
	(95)	La Calera	:	ы	Tree detritus	2003
	(71)	Bogota	:	:	Bark, soil, tree hollows	2003
	(85)	Bogota	NGII	а	Tree detritus, soil	2002-2003
		Cali	NGII	а	Tree detritus, soil	2002-2003
		Cúcuta	VGI, VGIII, VGIV	α	Tree detritus, soil	2002-2003
		Cundinamarca	NGII	а	Tree detritus, soil	2002-2003
			VGIV	α		
		Medellin	NGII	а	Tree detritus, soil	2002-2003
	(93)	Bogota	VGIII	в	Flowers and detritus	2007
	(86)	Cúcuta	VGI	а	Soil	2008–2009
			NGIII	0		

Country	Reference	Region	Molecular type	Mating type	Source	Collection year(s)
Egypt	(81)	Qutur and Tanta areas, Gharbia Governorate	:	:	Bark, flowers, living trees, soil, wood	1998
Greece	(73)	Athens Salamina Island	NGI	σ	Soil, tree hollows Tree hollows	2013
India	<ul> <li>(92)</li> <li>(67)</li> <li>(65)</li> <li>(69)</li> <li>(63)</li> <li>(63)</li> <li>(63)</li> </ul>	Ferozepur Delhi/New Delhi (northwestern India) Delhi (northwestern India) Jabalpur City (Central India) Delhi/New Delhi (northwestern India) Delhi, Union Territory; Trivuvannamalai, Tamil Nadu Guindy National Park, Chennai, South India Delhi (northwestern India) Delhi (northwestern India)	  VGI, VGII VGI, VGII	: : : : : : : : : : : : : : : : : : :	Tree flowers Tree hollows Flowers Tree hollows Air, tree hollows Soil, tree hollows Bark, debris of living trees Tree hollows Soil, tree hollows	1995-1996 2000-2002 1999-2000 2002-2004 2000-2007 <2007 <2009 2002-2007 2002-2007
Italy	(98) (73) (96)	Apulia Route Gallipoli–Collepasso Route Brindisi–Fasano Ragaina, Catania Reggio Calabria (southern Italy)	IDN 	6 8 m m	Debris of living trees, samples from animals, soil Tree hollows Debris of living trees and tree detritus	1997 2013 2009
Kenya	(99)	Nairobi	IDV	:	Bird nesting sites, tree hollows	2012-2013
Mexico	(06)	Mexico City	:	:	Debris of living trees, flowers, leaves, tree detritus	<1999
The Netherlands Bonaire (Dutch Caribbean)	(52) (70)	Berg en Dal Lagun Goto Rincon village Hato village	NGI VGI	8 n	Tree hollows Tree hollows, woody debris	2011 2013
Puerto Rico	(94)	Guanica Dry Forest, and western and southern regions	VGII, VGIV	α	Soil, tree detritus, tree hollows	<2010

Table 1. (Continued).

Country	Reference	Region	Molecular type	Mating type	Source	Collection year(s)
pain	(64)	Alicante	IDA	σ	Bark, tree hollows	<2012
		Barcelona	NGI	α	Tree detritus, tree hollows	<2012
	(27)	El Perello, Tarragona	VGIV	α	Woody debris	<2015
		Campello, Alicante	NGI	α	Tree hollows	2014
	(73)	El Perello, Tarragona	VGIV	σ	Tree hollows	2013
		Mendivil, Navarra	NGI	α	Bark	2014
<b>Funisia</b>	(84)	Sfax region (southern Tunisia)	÷	ø	Bark, flowers, fruits, soil, woody debris	<2011
Inited States	(112)	Fort Point San Francisco California				1990
	(6)	San Francisco, California	NGII		Woody debris	<1996
		San Diego Zoo area, San Diego, California	VGIII, VGI	:	Woody debris	<1996
	(20)	California	:	:	Bark	<2000
	(31)	Northern Washington	NGII	:	Bark, fence post, soil, tree	2001-2005
					hollows, woody debris	
	(87)	Lynden, Washington	NGII	:	Soil	2001-2006
	(89)	Los Angeles, California	NGI	α	Debris of living trees, soil	2011-2012
			VGIII	a, $\alpha$	Debris of living trees, soil	2011-2012
	(78)	Oregon	VGI, VGII	:	Bark, soil	2010-2011
Jruguay	(102)	:	NGII		Wasp nest	<1993

the collection was made prior to the study's publication year. <sup>a</sup>NSW, New South Wales; QLD, Queensland; SA, South Australia; WA, Western Australia.

Table 1. (Continued).

worldwide (Table 1). Isolations were most commonly made on or around various tree species, with positive samples most often taken by swabbing inside or sampling debris from hollows of living trees.<sup>24,37,54–73</sup> Other isolations were made through analyses of tree bark, 9,24,31,37,62,64,71,73-84 soil, 9,24,31,37,62,63,71,73,74,78,79,82,85-89 leaves, 37,75,82,87,90, flowers,<sup>65,81,84,90,92-94</sup> fruit,<sup>9,82,84,94</sup> plant detri-91 tus,<sup>64,75,82,85,90,93,95,96</sup> woody debris,<sup>9,31,37,77,79,80,83</sup>, 84,87,89,90,96-98 air.<sup>9,24,31,37,53,74,75,87</sup> and water.<sup>31,37,87</sup> C. gattii was also isolated from indoor dust in wooden houses,<sup>99</sup> wheel wells of cars,<sup>37</sup> insect and bat faeces,<sup>100,101</sup> animal enclosures,<sup>98</sup> bird nesting sites,<sup>66</sup> and wasp nests.<sup>102</sup> C. gattii has often been harder to isolate in the environment than C. neoformans, likely due to lower concentrations.<sup>84</sup> It is important to note that this review encompasses a variety of isolation methods from different environmental sources, making direct comparisons between studies more difficult.

Despite this collection of primary sources, the true global distribution of *C. gattii* is still likely underrepresented because environmental monitoring is often patchy.<sup>32</sup> Certain locations have, for instance, been excluded from this review due to clinical isolations but not environmental ones. For example, *C. gattii* has been clinically isolated in eight non-Pacific Northwest states since 2009, yet tests for *C. gattii* in the natural environment of these areas have not yet been attempted.<sup>34</sup>

#### Variations in distributions of molecular types

The geographical distribution of C. gattii continues to evolve and patterns in the locations of the different molecular types are emerging. Molecular type VGI appears relatively widespread. Environmental isolations of VGI were made on six continents, excluding Antarctica (Fig. 1; Table 1). VGII is still primarily found in more tropical and subtropical areas,<sup>16</sup> though it appears to have adapted to the more temperate climates of areas such as southern Australia,9 British Columbia, and parts of the Pacific Northwest.<sup>24</sup> Environmental isolations of molecular type VGIII are relatively less common, with positive samples in Argentina,<sup>59</sup> Colombia,<sup>85,86</sup> India,<sup>68</sup> and the United States<sup>9</sup> (Table 1). Molecular type VGIV shows the fewest positive environmental isolations worldwide, so far located in Columbia,<sup>85</sup> Puerto Rico,<sup>94</sup> and Spain.<sup>97</sup> This molecular type has yet to be environmentally isolated from North America. Mating type  $\alpha$  is more common both clinically and environmentally than mating type  $a_{2}^{24}$  though reasons for this are still unknown. The ecological reasons for the distributions of each molecular type, including the possible ecological niche of each molecular type, are also still unknown.

# C. gattii in British Columbia

The emergence of *C. gattii* on Vancouver Island in 1999 contributed to dismantling the long-held hypothesis that the species was mainly restricted to tropical and subtropical niches.<sup>24</sup> The fungus infected immunocompetent individuals, including local residents, visiting tourists, as well as wild and domestic animals.<sup>24</sup> The search for the ecological niche of *C. gattii* on Vancouver Island began in 2001.<sup>74,103</sup> Animal, human, and environmental cases were found to be clustered along the eastern side of Vancouver Island in the rain shadow.<sup>104,105</sup> This area is defined by flora and soil unique to the Coastal Douglas Fir and Western Hemlock biogeoclimatic zone.<sup>105</sup> In this zone, summers are dry and average 17.6°C, while winters are mild, average 2.7°C<sup>24</sup> and rarely go below freezing.<sup>104</sup>

Vancouver Island not only gained worldwide scientific attention for the unexpected emergence of *C. gattii* in a new temperate zone but also for one of the highest reported incidences of *C. gattii* infections in the world.<sup>106</sup> Nearly all *C. gattii* isolates from the VIO (>97%) fall under the VGII molecular type,<sup>24</sup> with VGI also being isolated.<sup>31,37,87</sup> Every study of Canadian isolates included in this review also isolated VGII (Table 1). Whether *C. gattii* was recently introduced to the Canadian environment or existed undetected for years is still unclear. However, the match between a clinically isolated 1970s Seattle strain and the 1999 Vancouver Island outbreak VGII strain may suggest the latter.<sup>107</sup>

# The ecology of C. gattii

The ecology of *C. gattii* remained unknown until its discovered association with *Eucalyptus* trees in Australia in 1990.<sup>77,108</sup> This led to a plethora of investigations worldwide into *C. gattii* ecology, with focus primarily on plant debris, including particular emphasis on the hollows of tree trunks.<sup>9,56,59</sup> Despite the observation of expanding geographic distributions of *C. gattii* in the Pacific Northwest and the urgent need to better understand *C. gattii* ecology in order to forecast its expansion and possible reasons for its emergence in temperate areas, there is still minimal research on the biophysical determinants that strongly influence *C. gattii* dynamics.<sup>104,109</sup>

#### Abiotic factors

#### Temperature

Most studies that directly test the temperature thresholds of *C. gattii* appear to focus on the Vancouver Island outbreak VGII strains. The *C. gattii* strains in Vancouver have been found to be sensitive to temperatures below freezing<sup>104,105</sup>

but showed high survival rates in seawater at  $4^{\circ}$ C.<sup>87</sup> The VGIIa and VGIIb subtypes within the VGII molecular type involved in the VIO also have the ability to grow at  $37^{\circ}$ C, the core human body temperature.<sup>110</sup> Their ability to infect a variety of mammals further suggests their tolerance exceeds  $37^{\circ}$ C, given that many mammals have body temperatures several degrees higher than those of humans.<sup>111</sup> In addition, they are also able to produce melanin to deal with stressors such as sunlight radiation and temperature.<sup>104</sup> Areas with greater amounts of solar radiation appear to promote *C. gattii* in air and trees.<sup>71,104</sup> This may explain how *C. gattii* has also been found in dry, hostile environments with constant sun exposure, with isolations of the fungus taken from succulent plants.<sup>94</sup>

Our use of the Köppen-Geiger climate classification map<sup>45</sup> revealed 28 studies with positive environmental sampling of *C. gattii* in other "warm temperate" climates as early as 1991 in California<sup>112</sup> (Table S1). Increased temperatures caused by climatic changes may also have facilitated the emergence of *C. gattii* into Vancouver's temperate environment,<sup>107</sup> though this has not yet been explored. Likewise, climate change in other parts of the world may shrink *C. gattii*'s ecological niche in tropical and subtropical areas as temperatures gradually exceed tolerable ranges for the fungus.

#### Water and air

Environmental isolations of C. gattii from water, including water bodies, precipitation, and moisture, were of the VGII strains from the VIO.31,37,87,113 C. gattii was first isolated in freshwater and saltwater on Vancouver Island.<sup>87</sup> Saltwater, either filtered or unfiltered, better supported C. gattii, though the organism is not considered a true halophile.<sup>87</sup> The route of cryptococcal infection in sea animals is still unclear but could be due to runoff or air transport.<sup>24</sup> Yet, C. gattii also appears to grow in drier conditions, with clinical, veterinary, and environmental samples predominantly located in the rain shadow of Vancouver Island. Our use of the Köppen-Geiger classification scheme <sup>45</sup> revealed that the fungus can survive in a range of precipitation conditions, from "equatorial rainforest" climates to "arid" climates (Fig. 1, Table S1). Ecological niche modeling of this fungus in British Columbia forecasted that optimal ecological conditions fall within the Coastal Douglas-Fir and Coastal Western Hemlock regions.<sup>103</sup> These biogeoclimatic zones are defined by relatively drier conditions (650-1250 mm of annual precipitation) compared to British Columbia or Vancouver Island averages,<sup>114</sup> suggesting C. gattii does not require, or may even prefer, less moisture. This would support the hypothesis that C. gattii relies on aerolization of its spores for transfer to other locations or potential hosts; dry conditions would facilitate aerolization.

Aerosolization of spores may also facilitate the fungus' transport to colonize other trees and soil. Though literature directly studying aerosolization of C. gattii is rare, concentrations of airborne cryptococci appear to show a seasonal pattern; concentrations peaked in August, the warmest and driest month in British Columbia.87 In addition, cooler, wetter months, such as December, experienced a drop in concentrations of airborne cryptococci. This is likely due to the fungal propagules being washed out of the air during precipitation; no positive air samples of C. gattii were made during or shortly after rainy periods.<sup>87</sup> Relative humidity was also negatively correlated with airborne concentrations of C. gattii. Air sampled from inside tree hollows has also led to positive isolations of C. gattii,<sup>53</sup> but more analyses are needed to determine whether air is the predominant method of C. gattii transport to new locations.

#### Soil

Trees were originally suggested to be the principal reservoir of *C. gattii* colonization, with particular emphasis on eucalypts.<sup>9,77,82,91</sup> However, first-attempt sampling of *C. gattii* on Vancouver Island revealed a greater proportion of positive isolations from soil samples than from swab samples of trees, stumps, shrubs, and cut logs.<sup>87</sup> In our review, 22 of the 56 studies isolated *C. gattii* from soil close to trees. Like many fungal species, concentrations of *C. gattii* are greatest in the top 15 cm of soil, usually due to temperature, humidity, and nutrient requirements.<sup>87</sup> This may also be due to their increased aerosolization when near the surface of the soil, as moderate winds may mobilize surface soil and increase *C. gattii* airborne concentrations.<sup>104</sup>

The soil in the Coastal Douglas Fir biogeoclimatic zone is acidic, with *C. gattii* and other acidophilic or acidotolerant fungi being isolated from soil samples with pH ranges of 4.3 to 7.5.<sup>87</sup> One sampling method of trees in the Coastal Douglas Fir region of Vancouver Island and mainland British Columbia measured both tree swabs as well as sampled soil associated with the root zone. Across trees where only the swab or soil sample was positive, positive soil samples were nearly twice as common (65%) as positive tree samples (35%).<sup>87</sup> Yet, whether a tree or its surrounding soil was first to be colonized remains difficult to determine.

#### **Biotic interactions**

#### Trees and eucalypt associations

We found 53 tree species associated with *C. gattii*, spanning 10 climate classifications<sup>45</sup> and 36 terrestrial ecoregions<sup>46</sup> (Table S1). Association with eucalyptus plants was originally considered the reason for *C. gattii* presence, including

in nonendemic areas.<sup>9,77</sup> However, Fortes et al.<sup>56</sup> noted that other areas where cryptococcosis is endemic, such as British Columbia, central Africa and Papua New Guinea, have shown negative sampling for the fungus from Eucalvptus species. C. gattii was soon found in wild tropical rainforests of Brazil without anthropic interference nor presence of eucalyptus tree species.<sup>56</sup> Over 60% of the papers (37/56) in this review isolated C. gattii from noneucalypt trees (Table S1). Other studies also noted no Eucalyptus species in areas where environmental isolates of C. gattii were positive,<sup>74</sup> or found that even with *Eucalyptus* species present, C. gattii was isolated on other trees endemic to the study region.<sup>61,73,87,88</sup> This suggested that the association between C. gattii and eucalypt species did not represent the total environmental niche of the fungal species, with more habitats open for colonization around the world.<sup>56</sup> C. gattii has also been found on trees in the middle of bustling urban centres,<sup>60,90</sup> as well as environments with nearly no anthropogenic disturbance nor introduced vegetation.<sup>56</sup> The natural degradation of trees has been hypothesized to be the precursor for the primary niche of C. gattii,<sup>57,86</sup> though this remains to be tested.

On Vancouver Island, *C. gattii* was isolated from a variety of noneucalypt species, including alder (*Alnus rubra*), western red cedar (*Thuja plicata*), Douglas fir (*Pseudotsuga menziesii*), Garry oak (*Quercus garryana*), and grand fir trees (*Abies grandis*) (all native to Canada).<sup>24</sup> *Eucalyptus* species are not native to Canada but have been introduced as ornamentals.<sup>74</sup> While some eucalypt species are able to withstand the USDA Zone 8 characteristics of the eastern side of Vancouver Island (where 'zones' are a horticultural guide to how well plants can tolerate cold temperatures), several of the eucalypt species from which *C. gattii* has been isolated, such as *Eucalyptus camaldulensis*, are intolerant to these conditions.<sup>74</sup>

#### Potential vectors of C. gattii

*C. gattii* could be introduced to new locations through passive transport of the spores by bird and other animal migrations on their extremities or in their faeces.<sup>37,100,101</sup> The list of potential animal vectors is increasing. In addition to companion animals such as cats and dogs,<sup>31</sup> *C. gat*-*tii* infections have been identified in other species, such as marine mammals,<sup>115</sup> ferrets,<sup>116</sup> llamas,<sup>31</sup> horses,<sup>117</sup> goats,<sup>7</sup> koalas,<sup>118</sup> deer,<sup>35</sup> insects,<sup>100,102</sup> and birds.<sup>119</sup> In addition to their potential role as vectors, both companion and wild animals often act as important sentinels for human *C. gattii* infection.<sup>113,115,120</sup> The isolation of *C. gattii* from companion animals and wild animals with limited mobility is comparable to isolations taken directly from environmental sources (e.g., trees, soil) due to the animals' limited range

and frequent to constant exposure to outdoor airborne organisms.<sup>120</sup> The relationship of insects with C. gattii is unclear, but insect frass and nests have been found in association with the fungus.<sup>100</sup> The fungus may have arrived after the frass or nest were produced, taking advantage of the digested organic material.<sup>100</sup> In addition, the presence of C. gattii in cactus lesions in the Guanica Dry Forest of Puerto Rico may be linked with birds and insects which create the lesions.<sup>94</sup> Isolations have also been made in droppings of caged birds, such as parrots.<sup>121</sup> C. gattii is not generally associated with bird excrement,<sup>74</sup> while C. neoformans is often isolated from the nests of birds, where there is an accumulation of faeces, limited exposure to sunlight and UV radiation,<sup>122,123</sup> and insufficient aeration.<sup>84</sup> The dispersal capacity of these various vectors is not vet clear, but anthropogenic dispersal of C. gattii through vehicles (e.g., car wheels) and footwear is possible.<sup>37</sup>

# **Changing environments**

While mechanical vectors may contribute to the expansion of *C. gattii* into Canada and other temperate zones, climatic and land use changes may play a greater role in creating hospitable environments where previous colonization may not have been possible. These changes may also improve environmental conditions to encourage the proliferation of already-existing *C. gattii* populations. Analysis of the emerging colonization of *C. gattii* in the Pacific Northwest and its associated clinical cases helps explore whether climatic and land use changes played a role in its emergence.<sup>74</sup>

#### **Climatic changes**

The proposed tropical and subtropical origins of C. gat $tii^{12,13}$  followed by an apparent emergence in a temperate Canadian climate in 1999 renewed global interest in the ecological niche of C. gattii and the possibility that climatic changes may have played a role. Climatic changes (including large-scale climatic oscillations, such as the El Niño Southern Oscillation, as well as global climate change) may have contributed to the establishment or proliferation of C. gattii in the Pacific Northwest. None of the reviewed studies directly tested the potential effects of climatic changes on C. gattii establishment or spread. In addition, only one study mentioned climate change as a possible factor in its emergence and facilitated spread of C. gattii in the Pacific Northwest.<sup>24</sup> To our knowledge, the effects of climatic changes on C. gattii distributions have not been directly studied in any region worldwide. However, association between C. gattii dynamics and seasonal or monthly regional weather patterns have been studied (e.g., Uejio et al.<sup>104</sup>). The relatively recent environmental isolations of C. gattii in temperate regions such as Vancouver<sup>24</sup> and The Netherlands,<sup>52</sup> in addition to the clinical isolation of the fungus in humans with no recent travel history to disease-endemic areas (e.g., Japan),<sup>36</sup> suggest this organism is either expanding its geographical range into previously uncolonized areas or increasing in concentrations leading to enhanced environmental detection due to one or more environmental triggers, such as climatic or land use changes. Focus on climatic changes and their potential association with C. gattii, as well as their measured effects on other infectious organism distributions, has been urged.<sup>107,124</sup> One possibility is that C. gattii existed for several decades in the Pacific Northwest, only becoming detectable with increasingly favorable conditions, such as climatic changes. Another may be that introductions of C. gattii into the Pacific Northwest have occurred more than once, but warming conditions over the past decades, particularly the warming trend on the east coast of Vancouver Island,<sup>6</sup> eventually created an optimal environment for its establishment and spread. These hypotheses continue to be debated and need to be addressed with climatic change analyses for British Columbia, with particular focus on the initial area of emergence and any environmental changes it underwent before the first detection of C. gattii in 1999.

#### Land use change

We found one study that directly tested the effects of land use change on C. gattii dispersal by analyzing levels of airborne C. gattii following forestry and municipal activities.<sup>37</sup> The possible effects of soil disturbance on C. gattii spread was explored in infected dogs and cats on Vancouver Island from 2001 to 2003 through a case-control study, finding that the animals living or active near commercial environmental disturbance areas had increased risk of C. gattii infection.<sup>125</sup> Companion animals serve as crucial sentinels of human risk to C. gattii infection, and wild animals may be considered even better environmental indicators due to their continuous exposure to the outdoors and, therefore, airborne infectious organisms.<sup>113,115,120</sup> Changes in land use have been speculated as one of the risk factors underlying increases in fungal spread and infection.<sup>126</sup> The spread of other fungal species has been found to be aggravated by soil disruption. For instance, the spread of the fungal Fusarium genus in Brazil has been encouraged by agricultural practices.<sup>126,127</sup> Similarly, the spread of Coccidioides species in and around California that cause coccidioidomycosis has also been correlated with soil disruption activities, such as agricultural, archaeological, and military practices.<sup>128</sup>

Aerosolization of *C. gattii* occurs through deforestation activities such as tree cutting, limb removal, and chipping.<sup>37</sup> Analyses of *C. gattii*-positive red alder and Douglas fir trees

before and after they were felled revealed increased airborne fungal concentrations for the red alder and increased concentrations for both trees after branch chipping.<sup>37</sup> Such activities increase aerosolization of the fungal spores, increasing risk of spread as well as exposure to nearby humans and other animals. Aerosolization would be further aggravated with wind. The effects of land use changes such as forestry need further exploration, particularly at larger spatial scales, to determine the spatial extent of land use effects on *C. gattii* dispersal.

#### **Future opportunities**

*Cryptococcus gattii* is one of the primary aetiological agents of cryptococcosis and is of increasing global importance. Yet, 18 years after its emergence on Vancouver Island, the reasons behind its outbreak are still lacking. Specifically, did climatic changes and land use changes play a role in the 1999 VIO of *C. gattii* and its subsequent spread to the mainland of British Columbia in 2004? If so, what were their roles? Would the longer-term changes in climate have greater or lesser impacts than the more immediate effects of land use change?

In our review of environmental isolations of C. gattii, we found the fungus can survive in a variety of climates, including humid and arid conditions, as well as in association with at least 53 different tree species native to these sampled regions across six continents. Its ecological niche is therefore likely very flexible, suggesting the fungus may continue to expand its distribution. Analyses of ecological factors such as tree and soil associations with C. gattii, as well as the potential role of animals in increasing the extent and distribution of C. gattii colonization,<sup>91,100,102</sup> are needed. Analyses of the potential effects of climatic and land use changes on the geographical distribution of C. gattii, as well as possible interactions between changing environmental factors and ecological factors, are also needed to increase understanding of its ecological niche and what may drive its possible expansion into new areas. Which ecological factors (e.g., temperature, precipitation) changed prior to the 1999 C. gattii outbreak on Vancouver Island? What land use changes occurred on the area of C. gattii emergence? How did these factors change over time, and were these changes associated with the spread of C. gattii through the Pacific Northwest?

Spatiotemporal modeling of *C. gattii* is one method that may help answer these questions, and the 1999 VIO may serve as a unique opportunity to study its emergence and subsequent expansion. Improved modeling of *C. gattii* distributions will improve predictions of areas *C. gattii* will likely emerge in or expand to in the future. These methods may also shed light on the factors behind emerging environmental infectious diseases in Canada and elsewhere. By increasing understanding in the ecology and dispersal mechanisms of *C. gattii*, as well as the potential effects of climatic and land use changes on its emergence and distribution, *C. gattii* could serve as a model for other infectious organisms around the world.

## Supplementary material

Supplementary data are available at MMYCOL online.

## Acknowledgments

This work was supported by a University of British Columbia Four-Year Fellowship and Vanier Canada Graduate Scholarship for NSERC to E. A. This work was also supported by the Health Research Scholar program from the Michael Smith Foundation as well as grant support from the British Columbia Lung Association to K. B. We would also like to thank our two anonymous reviewers for their valuable assistance with the editing process.

#### Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and the writing of the paper.

# References

- Lanciotti RS, Roehrig JT, Deubel V et al. Origin of the West Nile virus responsible for an outbreak of encephalitis in the northeastern United States. *Science*. 1999; 286: 2333–2337.
- Kendrick K, Stanek D, Blackmore C. Notes from the field: Transmission of chikungunya virus in the continental United States—Florida, 2014. CDC Morb Mortal Wkly Rep. 2014; 63: 1137.
- Ogden NH, Radojevic M, Wu X et al. Estimated effects of projected climate change on the basic reproductive number of the Lyme disease vector *Ixodes scapularis*. *Environ Health Perspect*. 2014; 122: 631– 638.
- Carter D, Campbell LA, Saul N et al. Sexual reproduction of *Cryptococcus gattii*: A population genetics perspective. In: Heitman J, Kozel TR, Kwon-Chung KJ, Perfect JR, Casadevall A, eds. *Cryptococcus: From Human Pathogen to Model Yeast*. Washington, DC: ASM Press; 2011.
- Park BJ, Wannemuehler KA, Marston BJ et al. Estimation of the current global burden of cryptococcal meningitis among persons living with HIV/AIDS. AIDS. 2009; 23: 525–530.
- Fyfe M, Macdougall L, Romney M et al. *Cryptococcus gattii* infections on Vancouver Island, British Columbia, Canada: Emergence of a tropical fungus in a temperate environment. *Can Commun Dis Rep.* 2008; 34: 1–12.
- Baro T, Torres-Rodriguez JM, De Mendoza MH et al. First identification of autochthonous *Cryptococcus neoformans* var. *gattii* isolated from goats with predominantly severe pulmonary disease in Spain. *J Clin Microbiol.* 1998; 36: 458–461.
- McGill S, Malik R, Saul N et al. Cryptococcosis in domestic animals in Western Australia: A retrospective study from 1995 to 2006. *Med Mycol.* 2009; 47: 625–639.
- Sorrell TC, Chen SCA, Ruma P et al. Concordance of clinical and environmental isolates of *Cryptococcus neoformans* var. gattii by random amplification of polymorphic DNA analysis and PCR fingerprinting. J *Clin Microbiol.* 1996; 34: 1253–1260.

- Hagen F, Colom MF, Swinne D et al. Autochthonous and dormant Cryptococcus gattii infections in Europe. Emerg Infect Dis. 2012; 18: 1618– 1624.
- 11. Voelz K, May RC. Cryptococcal interactions with the host immune system. *Eukaryot Cell*. 2010; 9: 835–846.
- Meyer W. Cryptococcus gattii in the age of whole-genome sequencing. Mbio. 2015; 6: e01761–15.
- May RC, Stone NRH, Wiesner DL et al. *Cryptococcus*: From environmental saprophyte to global pathogen. *Nature Rev Microbiol*. 2016; 14: 106–117.
- Kwon-Chung KJ, Varma A. Do major species concepts support one, two or more species within *Cryptococcus neoformans? FEMS Yeast Res.* 2006; 6: 574–587.
- Kwon-Chung KJ. A new species of *Filobasidiella*, the sexual state of *Cryptococcus neoformans* B and C serotypes. *Mycologia*. 1976; 68: 943– 946.
- Cogliati M. Global molecular epidemiology of *Cryptococcus neoformans* and *Cryptococcus gattii*: An atlas of the molecular types. *Scientifica*. 2013; 2013: 675213.
- 17. Varma A, Kwonchung KJ. DNA probe for strain typing of *Cryptococcus* neoformans. J Clin Microbiol. 1992; 30: 2960–2967.
- Meyer W, Mitchell TG, Freedman EZ et al. Hybridization probes for conventional DNA-fingerprinting used as single primers in the polymerase chain-reaction to distinguish strains of *Cryptococcus neoformans. J Clin Microbiol.* 1993; 31: 2274–2280.
- Chen SCA, Brownlee AG, Sorrell TC et al. Identification by random amplification of polymorphic DNA of a common molecular type of *Cryptococcus neoformans* var. *neoformans* in patients with AIDS or other immunosuppressive conditions. J Infect Dis. 1996; 173: 754– 758.
- Meyer W, Castaneda A, Jackson S et al. Molecular typing of IberoAmerican Cryptococcus neoformans isolates. Emerg Infect Dis. 2003; 9: 189– 195.
- Boekhout T, Theelen B, Diaz M et al. Hybrid genotypes in the pathogenic yeast Cryptococcus neoformans. Microbiology. 2001; 147: 891–907.
- Litvintseva AP, Thakur R, Vilgalys R et al. Multilocus sequence typing reveals three genetic subpopulations of *Cryptococcus neoformans* var. *grubii* (serotype A), including a unique population in Botswana. *Genetics*. 2006; 172: 2223–2238.
- Meyer W, Aanensen DM, Boekhout T et al. Consensus multi-locus sequence typing scheme for *Cryptococcus neoformans* and *Cryptococcus gattii. Med Mycol.* 2009; 47: 561–570.
- Kidd SE, Hagen F, Tscharke RL et al. A rare genotype of *Cryptococcus gattii* caused the cryptococcosis outbreak on Vancouver Island (British Columbia, Canada). *PNAS USA*. 2004; 101: 17258–17263.
- Fraser JA, Giles SS, Wenink EC et al. Same-sex mating and the origin of the Vancouver Island *Cryptococcus gattii* outbreak. *Nature*. 2005; 437: 1360–1364.
- Hagen F, Illnait-Zaragozi MT, Bartlett KH et al. 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*. 2010; 54: 5139–5145.
- Hagen F, Khayhan K, Theelen B et al. Recognition of seven species in the Cryptococcus gattii/Cryptococcus neoformans species complex. Fungal Genet Biol. 2015; 78: 16–48.
- Kidd SE, Guo H, Bartlett KH et al. Comparative gene genealogies indicate that two clonal lineages of *Cryptococcus gattii* in British Columbia resemble strains from other geographical areas. *Eukaryot Cell*. 2005; 4: 1629–1638.
- Byrnes EJ, Bildfell RJ, Frank SA et al. 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.* 2009; 199: 1081–1086.
- Byrnes EJ, Li WJ, Ren P et al. A diverse population of *Cryptococcus* gattii molecular type VGIII in Southern Californian HIV/AIDS patients. *PLoS Path*. 2011; 7.

- MacDougall L, Kidd SE, Galanis E et al. Spread of *Cryptococcus gattii* in British Columbia, Canada, and detection in the Pacific Northwest, USA. *Emerg Infect Dis.* 2007; 13: 42–50.
- Springer DJ, Chaturvedi V. Projecting global occurrence of *Cryptococcus* gattii. Emerg Infect Dis. 2010; 16: 14–20.
- Phillips P, Galanis E, MacDougall L et al. Longitudinal clinical findings and outcome among patients with *Cryptococcus gattii* infection in British Columbia. *Clin Infect Dis.* 2015; 60: 1368–1376.
- Harris JR, Lockhart SR, Sondermeyer G et al. *Cryptococcus gattii* infections in multiple states outside the U.S. Pacific Northwest. *Emerg Infect Dis.* 2013, 19: 1620–1626.
- Overy DP, McBurney S, Muckle A et al. Cryptococcus gattii VGIIb-like variant in white-tailed deer, Nova Scotia, Canada. Emerg Infect Dis. 2016; 22: 1131–1133.
- Okamoto K, Hatakeyama S, Itoyama S et al. Cryptococcus gattii genotype VGIIa infection in man, Japan, 2007. Emerg Infect Dis. 2010; 16: 1155–1157.
- Kidd SE, Bach PJ, Hingston AO et al. Cryptococcus gattii dispersal mechanisms, British Columbia, Canada. Emerg Infect Dis. 2007; 13: 51–57.
- Harvell CD, Mitchell CE, Ward JR et al. Ecology—Climate warming and disease risks for terrestrial and marine biota. *Science*. 2002; 296: 2158–2162.
- Johannson KA, Huston SM, Mody CH et al. Cryptococcus gattii pneumonia. Can Med Assoc J. 2012; 184: 1387–1390.
- Lindberg J, Hagen F, Laursen A et al. Cryptococcus gattii risk for tourists visiting Vancouver Island, Canada. Emerg Infect Dis. 2007; 13: 178– 179.
- Hagen F, van Assen S, Luijckx GJ et al. Activated dormant Cryptococcus gattii infection in a Dutch tourist who visited Vancouver Island (Canada): A molecular epidemiological approach. Med Mycol. 2010; 48: 528–531.
- 42. Georgi A, Schneemann M, Tintelnot K et al. *Cryptococcus gattii* meningoencephalitis in an immunocompetent person 13 months after exposure. *Infection*. 2009; 37: 370–373.
- Levy R, Pitout J, Long P et al. Late presentation of *Cryptococcus gattii* meningitis in a traveller to Vancouver Island: A case report. *Can J Infect Dis Med Microbiol.* 2007; 18: 197–199.
- Kwon-Chung KJ, Bennett JE, Theodore TS. Cryptococcus bacillisporus sp. nov.: serotype B-C of Cryptococcus neoformans. Int J Syst Bacteriol. 1978; 28: 616–620.
- Peel MC, Finlayson BL, McMahon TA. Updated world map of the Köppen-Geiger climate classification. *Hydrol Earth Syst Sci.* 2007; 11: 1633–1644.
- Olson DM, Dinerstein E, Wikramanayake ED et al. Terrestrial ecoregions of the worlds: A new map of life on Earth. *Bioscience*. 2001; 51: 933–938.
- Curtis F. Contribution à l'étude de la saccharomycose humaine. Annales de l'Institut Pasteur. 1896; 10: 449–468.
- Vanbreuseghem R, Takashio M. An atypical strain of Cryptococcus neoformans (San Felice) Vuillemin 1894. II. Cryptococcus neoformans var. gattii var. nov. Ann Soc Belges Med Trop Parasitol Mycol. 1970; 50: 695–702.
- Gatti F, Eeckels R. An atypical strain of *Cryptococcus neoformans* (San Felice) Vuillemin 1894. I. Description of the disease and of the strain. *Ann Soc Belges Med Trop Parasitol Mycol.* 1970; 50: 689–693.
- Sorrell TC. Cryptococcus neoformans variety gattii. Med Mycol. 2001; 39: 155–168.
- Kwon-Chung KJ, Bennett JE. High prevalence of *Cryptococcus neoformans* var. *gattii* in tropical and sub-tropical regions. *Zentralbl Bakteriol Mikrobiol Hyg A*. 1984; 257: 213–218.
- Chowdhary A, Randhawa HS, Boekhout T et al. Temperate climate niche for *Cryptococcus gattii* in Northern Europe. *Emerg Infect Dis.* 2012; 18: 172–174.
- Randhawa HS, Kowshik T, Sinha KP et al. Distribution of *Cryptococcus gattii* and *Crytococcus neoformans* in decayed trunk wood of *Syzygium cumini* trees in north-western India. *Med Mycol.* 2006; 44: 623–630.
- 54. Costa S, Lazera MD, Santos WRA et al. 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. 2009; 104: 662–664.

- Davel G, Abrantes R, Brudny M et al. 1st environmental isolation of Cryptococcus neoformans var. gattii in Argentina. Rev Argent Microbiol. 2003; 35: 110–112.
- Fortes ST, Lazera MS, Nishikawa MM et al. First isolation of *Crypto-coccus neoformans* var. *gattii* from a native jungle tree in the Brazilian Amazon rainforest. *Mycoses*. 2001; 44: 137–140.
- Lazera MS, Cavalcanti MAS, Londero AT et al. Possible primary ecological niche of *Cryptococcus neoformans. Med Mycol.* 2000; 38: 379–383.
- Lazera MS, Cavalcanti MAS, Trilles L et al. *Cryptococcus neoformans* var. *gattii*—Evidence for a natural habitat related to decaying wood in a pottery tree hollow. *Med Mycol.* 1998; 36: 119–122.
- Mazza M, Refojo N, Eugenia Bosco-Borgeat M et al. Cryptococcus gattii in urban trees from cities in north-eastern Argentina. Mycoses. 2013; 56: 646–650.
- Refojo N, Perrotta D, Brudny M et al. Isolation of *Cryptococcus neo-formans* and *Cryptococcus gattii* from trunk hollows of living trees in Buenos Aires City, Argentina. *Med Mycol.* 2009; 47: 177–184.
- Vilcins I, Krockenberger M, Agus H et al. Environmental sampling for *Cryptococcus neoformans* var. gattii from the Blue Mountains National Park, Sydney, Australia. Med Mycol. 2002; 40: 53–60.
- Chen Y, Litvintseva AP, Frazzitta AE et al. Comparative analyses of clinical and environmental populations of *Cryptococcus neoformans* in Botswana. *Mol Ecol.* 2015; 24: 3559–3571.
- Chowdhary A, Prakash A, Randhawa HS et al. First environmental isolation of *Cryptococcus gattii*, genotype AFLP5, from India and a global review. *Mycoses*. 2013; 56: 222–228.
- Colom MF, Hagen F, Gonzalez A et al. *Ceratonia siliqua* (carob) trees as natural habitat and source of infection by *Cryptococcus gattii* in the Mediterranean environment. *Med Mycol.* 2012; 50: 67–73.
- 65. Gugnani HC, Mitchell TG, Litvintseva AP et al. Isolation of *Cryptococcus gattii* and *Cryptococcus neoformans* var. *grubii* from the flowers and bark of *Eucalyptus* trees in India. *Med Mycol*. 2005; 43: 565–569.
- Kangogo M, Bader O, Boga H et al. Molecular types of *Cryptococcus gattii/Cryptococcus neoformans* species complex from clinical and environmental sources in Nairobi, Kenya. *Mycoses*. 2015; 58: 665–670.
- Randhawa HS, Kowshik T, Khan ZU. Decayed wood of Syzygium cumini and Ficus religiosa living trees in Delhi/New Delhi metropolitan area as natural habitat of Cryptococcus neoformans. Med Mycol. 2003; 41: 199–209.
- Randhawa HS, Prakash A, Hagen F et al. First environmental isolation of *Cryptococcus gattii*, molecular type VGIII/AFLP5, from decayed wood inside trunk hollow of a *Manikara hexandra* tree in Delhi, India. *Mycoses*. 2012; 55: 247–248.
- 69. Nawange SR, Shakya K, Naidu J et al. Decayed wood inside hollow trunks of living trees of *Tamarindus indica*, *Syzygium cumini* and *Mangifera indica* as natural habitat of *Cryptococcus neoformans* and their serotypes in Jabalpur City of Central India. J Mycol Med. 2006; 16: 63–71.
- Hagen F, Chowdhary A, Prakash A et al. Molecular characterization of *Cryptococcus gattii* genotype AFLP6/VGII isolated from woody debris of divi-divi (*Caesalpinia coriaria*), Bonaire, Dutch Caribbean. *Rev Iberoam Micol.* 2014; 31: 193–196.
- Granados DP, Castaneda E. Isolation and characterization of *Crypto-coccus neoformans* varieties recovered from natural sources in Bogota, Colombia, and study of ecological conditions in the area. *Microb Ecol.* 2005; 49: 282–290.
- Barbosa GG, Trilles L, Wanke B et al. Cryptococcus gattii VGI and Cryptococcus neoformans VNI associated with wood decay in Ficus hollow trees in Rio de Janeiro, Brazil. Br Microbiol Res J. 2013; 3: 106–115.
- Cogliati M, D'Amicis R, Zani A et al. Environmental distribution of *Cryptococcus neoformans* and *C. gattii* around the Mediterranean basin. *FEMS Yeast Res.* 2016; 16: fow045.
- 74. Bartlett KH, Duncan C, Bach P et al. Microbe hunting: A curious case of *Cryptococcus. Korean J Environ Health Sci.* 2005; 31: 199–206.

- Callejas A, Ordonez N, Rodriguez MC et al. First isolation of *Cryptococcus neoformans* var. *gattii*, serotype C, from the environment in Colombia. *Med Mycol.* 1998; 36: 341–344.
- Diaz MR, Boekhout T, Theelen B et al. Molecular sequence analyses of the intergenic spacer (IGS) associated with rDNA of the two varieties of the pathogenic yeast, *Cryptococcus neoformans. Syst Appl Microbiol.* 2000; 23: 535–545.
- 77. Ellis DH, Pfeiffer TJ. Natural habitat of *Cryptococcus neoformans* var. *gattii. J Clin Microbiol.* 1990; 28: 1642–1644.
- DeBess E, Lockhart SR, Iqbal N et al. Isolation of *Cryptococcus gattii* from Oregon soil and tree bark, 2010-2011. *BMC Microbiol.* 2014; 14: 323.
- Halliday CL, Bui T, Krockenberger M et al. Presence of alpha and a mating types in environmental and clinical collections of *Cryptococcus neoformans* var. *gattii* strains from Australia. *J Clin Microbiol.* 1999; 37: 2920–2926.
- Kumar CPG, Prabu D, Mitani H et al. Environmental isolation of Cryptococcus neoformans and Cryptococcus gattii from living trees in Guindy National Park, Chennai, South India. Mycoses. 2010; 53: 262– 264.
- Mahmoud YAG. First environmental isolation of *Cryptococcus neoformans* var. *neoformans* and var. *gattii* from the Gharbia Governorate, Egypt. *Mycopathologia*. 1999; 148: 83–86.
- Montenegro H, Paula CR. Environmental isolation of Cryptococcus neoformans var. gattii and C. neoformans var. neoformans in the city of Sao Paulo, Brazil. Med Mycol. 2000; 38: 385–390.
- Pfeiffer TJ, Ellis DH. Environmental isolation of Cryptococcus neoformans var. gattii from Eucalyptus tereticornis. J Med Vet Mycol. 1992; 30: 407–408.
- Mseddi F, Sellami A, Jarboui MA et al. First environmental isolations of *Cryptococcus neoformans* and *Cryptococcus gattii* in Tunisia and review of published studies on environmental isolations in Africa. *Mycopathologia.* 2011; 171: 355–360.
- 85. Escandon P, Sanchez A, Martinez M et al. 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.* 2006; 6: 625–635.
- Firacative C, Torres G, Rodriguez MC et al. First environmental isolation of *Cryptococcus gattii* serotype B, from Cucuta, Colombia. *Biomedica*. 2011; 31: 118–123.
- 87. Kidd SE, Chow Y, Mak S et al. 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*. 2007; 73: 1433–1443.
- Randhawa HS, Kowshik T, Chowdhary A et al. The expanding host tree species spectrum of *Cryptococcus gattii* and *Cryptococcus neoformans* and their isolations from surrounding soil in India. *Med Mycol.* 2008; 46: 823–833.
- Springer DJ, Billmyre RB, Filler EE et al. *Cryptococcus gattii* VGIII isolates causing infections in HIV/AIDS patients in southern California: Identification of the local environmental source as arboreal. *PLoS Path*. 2014; 10: e1004285.
- Arguero Licea B, Garza Garza D, Flores Urbieta V et al. Isolation and characterization of *Cryptococcus neoformans* var. *gattii* from samples of *Eucalyptus camaldulensis* in Mexico city. *Rev Iberoam Micol.* 1999; 16: 40–42.
- Krockenberger MB, Canfield PJ, Malik R. *Cryptococcus neoformans* in the koala (*Phascolarctos cinereus*): Colonization by *C. n.* var. *gattii* and investigation of environmental sources. *Med Mycol.* 2002; 40: 263– 272.
- Chakrabarti A, Jatana M, Kumar P et al. Isolation of *Cryptococcus* neoformans var. gattii from *Eucalyptus camaldulensis* in India. J Clin Microbiol. 1997; 35: 3340–3342.
- Escandon P, Sanchez A, Firacative C et al. Isolation of *Cryptococcus gattii* molecular type VGIII, from *Corymbia ficifolia* detritus in Colombia. *Med Mycol.* 2010; 48: 675–678.

- Loperena-Alvarez Y, Ren P, Li X et al. Genotypic characterization of environmental isolates of *Cryptococcus gattii* from Puerto Rico. *Mycopathologia*. 2010; 170: 279–285.
- Escandon P, Quintero E, Granados D et al. Isolation of *Cryptococcus* gattii serotype B from detritus of *Eucalyptus* trees in Colombia. *Biomed*ica. 2005; 25: 390–397.
- Romeo O, Scordino F, Criseo G. Environmental isolation of *Cryptococcus gattii* serotype B, VGI/MAT alpha strains in southern Italy. *Mycopathologia*. 2011; 171: 423–430.
- Linares C, Colom MF, Torreblanca M et al. Environmental sampling of *Ceratonia siliqua* (carob) trees in Spain reveals the presence of the rare *Cryptococcus gattii* genotype AFLP7/VGIV. *Rev Iberoam Micol.* 2015; 32: 269–272.
- Montagna MT, Viviani MA, Pulito A et al. *Cryptococcus neoformans* var. *gattii* in Italy. Note 2. Environment investigation related to an autochtonous clinical case in Apulia. *J Mycol Med*. 1997; 7: 93–96.
- Brito-Santos F, Barbosa GG, Trilles L et al. Environmental isolation of *Cryptococcus gattii* VGII from indoor dust from typical wooden houses in the deep Amazonas of the Rio Negro Basin. *PLoS One.* 2015; 10: e0115866.
- Kidd SE, Sorrell TC, Meyer W. Isolation of two molecular types of *Cryptococcus neoformans* var. *gattii* from insect frass. *Med Mycol.* 2003; 41: 171–176.
- 101. Lazera MS, Wanke B, Nishikawa MM. Isolation of both varieties of *Cryptococcus neoformans* from saprophytic sources in the city of Rio De Janeiro, Brazil. J Med Vet Mycol. 1993; 31: 449–454.
- Gezuele E, Calegari L, Sanabria D et al. Isolation in Uruguay of Cryptococcus neoformans var. gattii from a nest of the wasp Polybia occidentalis. Rev Iberoam Micol. 1993; 10: 5–6.
- 103. Mak S, Klinkenberg B, Bartlett K et al. Ecological niche modeling of *Cryptococcus gattii* in British Columbia, Canada. *Environ Health Perspect*. 2010; 118: 653–658.
- Uejio CK, Mak S, Manangan A et al. Climatic influences on *Cryptoccoccus gattii* populations, Vancouver Island, Canada, 2002–2004. *Emerg Infect Dis.* 2015; 21: 1989–1996.
- 105. Bartlett KH, Cheng P, Duncan C et al. A decade of experience: *Cryptococcus gattii* in British Columbia. *Mycopathologia*. 2012; 173: 311–319.
- 106. Galanis E, MacDougall L, Kidd S et al. Epidemiology of Cryptococcus gattii, British Columbia, Canada, 1999–2007. Emerg Infect Dis. 2010; 16: 251–257.
- Datta K, Bartlett KH, Marr KA. Cryptococcus gattii: Emergence in Western North America, exploitation of a novel ecological niche. Interdiscip Perspect Infect Dis. 2009; 2009: 1–8.
- Ellis D, Pfeiffer T. The ecology of Cryptococcus neoformans. Eur J Epidemiol. 1992; 8: 321–325.
- 109. Hagen F, Boekhout T. The search for the natural habitat of *Cryptococcus* gattii. Mycopathologia. 2010; 170: 209–211.
- Ngamskulrungroj P, Meyer W. Melanin production at 37°C is linked to the high virulent *Cryptococcus gattii* Vancouver Island outbreak genotype VGIIa. *Aust Mycol.* 2009; 28: 9–15.
- 111. Clarke A, Rothery P. Scaling of body temperature in mammals and birds. *Funct Ecol.* 2007; 22: 58–67.
- 112. Pfeiffer T, Ellis D. Environmental isolation of *Cryptococcus neoformans* gattii from California. J Infect Dis. 1991; 163: 929–930.
- 113. Bartlett K, Byrnes EJ, Duncan C et al. The emergence of *Cryptococcus gattii* infections on Vancouver Island and expansion in the Pacific Northwest. In: Heitman J, Kozel TR, Kwon-Chung J, Perfect JR, Casadevall A, eds. *Cryptococcus: From Human Pathogen to Model Yeast*. Washington, DC: ASM Press; 2011: 313–323.
- 114. Meidinger DV, Pojar J. *Ecosystems of British Columbia*. Minnesota: Research Branch, Ministry of Forests; 1991.
- Stephen C, Lester S, Black W et al. Multispecies outbreak of cryptococcosis on southern Vancouver Island, British Columbia. *Can Vet J.* 2002; 43: 792–794.
- 116. Morera N, Juan-Salles C, Torres JM et al. *Cryptococcus gattii* infection in a Spanish pet ferret (*Mustela putorius furo*) and asymptomatic carriage

in ferrets and humans from its environment. *Med Mycol.* 2011; 49: 779–784.

- 117. Duncan C, Bartlett KH, Lester S et al. Surveillance for *Cryptococcus* gattii in horses of Vancouver Island, British Columbia, Canada. Med Mycol. 2011; 49: 734–738.
- 118. Krockenberger MB, Canfield PJ, Malik R. *Cryptococcus neoformans* var. *gattii* in the koala (*Phascolarctos cinereus*): A review of 43 cases of cryptococcosis. *Med Mycol.* 2003; 41: 225–234.
- 119. Lester SJ, Malik R, Bartlett KH et al. Cryptococcosis: Update and emergence of *Cryptococcus gattii*. Vet Clin Pathol. 2011; 40: 4–17.
- Duncan C, Schwantje H, Stephen C et al. *Cryptococcus gattii* in wildlife of Vancouver Island, British Columbia, Canada. J Wildl Dis. 2006; 42: 175–178.
- 121. Sorrell TC, Ellis DH. Ecology of Cryptococcus neoformans. Rev Iberoam Micol. 1997; 14: 42–43.
- 122. Wang YL, Casadevall A. Decreased susceptibility of melanized *Cryptococcus neoformans* to UV light. *Appl Environ Microbiol.* 1994; 60: 3864–3866.

- 123. Mitchell TG, Litvintseva AP. Typing species of *Cryptococcus* and epidemiology of cryptococcosis. In: Ashbee HR, Bignell EM, eds. *Pathogenic Yeasts*. London: Springer; 2010: 179.
- 124. Cooney CM. Climate change and infectious disease: Is the future here? *Environ Health Perspect*. 2011; 119: 394–397.
- Duncan CG, Stephen C, Campbell J. Evaluation of risk factors for Cryptococcus gattii infection in dogs and cats. J Am Vet Med Assoc. 2006; 228: 377–382.
- 126. Brandt ME, Park BJ. Think fungus prevention and control of fungal infections. *Emerg Infect Dis.* 2013; 19: 1688– 1689.
- Nucci M, Varon AG, Garnica M et al. Increased incidence of invasive fusariosis with cutaneous portal of entry, Brazil. *Emerg Infect Dis.* 2013; 19: 1567–1572.
- Das R, McNary J, Fitzsimmons K et al. Occupational coccidioidomycosis in California outbreak investigation, respirator recommendations, and surveillance findings. J Occup Environ Med. 2012; 54: 564– 571.