Fatal Disseminated Cryptococcus gattii Infection in New Mexico

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Abstract

We report a case of fatal disseminated infection with Cryptococcus gattii in a patient from New Mexico. The patient had no history of recent travel to known C. gattii-endemic areas. Multilocus sequence typing revealed that the isolate belonged to the major molecular type VGII. Virulence studies in a mouse pulmonary model of infection demonstrated that the strain was less virulent than other C. gattii strains. This represents the first documented case of C. gattii likely acquired in New Mexico.

Introduction

Cryptococcus gattii was first isolated from a pediatric patient in the Congo [1], and environmentally from various species of Eucalyptus trees in Australia, where rural aboriginals have frequently been reported with infection [2]. It has since been reported from eucalyptus and other trees in tropical and subtropical regions including southern California, South America, parts of Africa and Southeast Asia [3,4]. Before 1999, C. gattii infections were only rarely reported from temperate climates of North America [5,6]; however, since 1999, an outbreak of C. gattii infections has been reported from British Columbia (BC), and more recently from the U.S. Pacific Northwest (Washington and Oregon) [7–9]. Although C. gattii was previously believed to be a tropical fungus, these outbreaks demonstrate a larger ecological niche. Investigations into the source of the outbreak in the temperate climate of Vancouver Island and the Pacific Northwest (PNW) provide evidence that decaying wood from tree hollows, soil, fresh and saltwater may all be sources of C. gattii [8–10].

C. neoformans and C. gattii are the only two major species of the genus Cryptococcus considered to be pathogenic in humans. Prior to the AIDS epidemic, cryptococcal infections were rare. Since the molecular characterization of C. neoformans and C. gattii and classification into separate species, ecological and clinical differences have been reported. C. gattii tends to be seen clinically in immunocompetent patients, although the spectrum of infection can involve immunocompromised patients as well, whereas C. neoformans is primarily an opportunistic pathogen. Both C. neoformans and C. gattii have a propensity to cause pulmonary and central nervous system (CNS) disease. In patients from Papua New Guinea and Australia, C. gattii is more likely than C. neoformans to cause cryptococcomas in the lung and brain, which may be mistaken for malignancies (as in this case) or abscesses [11,12]. Furthermore, whereas the outbreak strain identified in BC/PNW more commonly presents with a respiratory syndrome, non-outbreak strains appear to present more commonly with CNS infection [12,13].

The onset of cryptococcal infection is often subacute and nonspecific, with headache being the most common presenting symptom [14]. Compared to infections with C. neoformans, patients with C. gattii cerebral involvement were found to have more severe neurological sequelae such as hydrocephalus and focal CNS findings, including ataxia, hearing loss, altered mentation, papilledema, and higher intracranial pressures often requiring surgical procedures for management. Infections due to C. gattii follow a prolonged clinical course and are slower to respond to antifungal therapy; however mortality does not appear to be higher than C. neoformans infections [15,16].

We report the first documented case of C. gattii infection in New Mexico, from a patient without a recent history of travel to a known C. gattii-endemic area. Because the patient was immunocompetent and New Mexico is not currently known to be a C. gattii-endemic region, the infection went unrecognized until autopsy.

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Results

Clinical Presentation
The patient was a 56-year-old Hispanic man who was brought to the emergency room (ER) in late April 2010 for evaluation of a 2.5-month history of intermittent, progressively worsening headache. The patient was noted to have mild confusion. He reported no fever, chills, dyspnea, nausea, vomiting or diarrhea. He had returned home in February 2010 after release from a two-month incarceration in a state prison in Santa Rosa, NM. Upon entering his home, he found that his dogs had expired, and his house was extensively contaminated with dog feces. Several days after cleaning his house, he reported experiencing a headache which worsened over the next 2.5 months. In the ER, the patient was afebrile and his physical and neurological exam was unremarkable. Initial serum laboratory tests indicated mild leukocytosis (WBC 11.6×10^3/L, normal range 4–10.6), and hyponatremia (sodium 128 mmol/L, normal range 137–145). A chest radiograph showed a focal infiltrate or mass estimated to be 4×8 cm in the lingula as well as additional perilobar infiltrates, particularly in the right upper lobe. A computed tomography of the head without contrast revealed no evidence of focal lesions, and an opacified left maxillary sinus suggestive of sinusitis. The patient was begun on empiric ceftriaxone and azithromycin for possible community-acquired pneumonia, and admitted for further evaluation of headache and confusion.

The patient’s prior medical history included hypertension, diabetes, and depression. His medication list included lisinopril, naproxen, hydrocodone/acetaminophen, and lorazepam. His family history was unremarkable. The patient had a one-year history of smoking but had quit in December 2009. He drank alcohol rarely and denied the use of recreational drugs. The patient was born and lived alone in the same house which was located in the South Valley area of Albuquerque, NM. In his home, he was reported to have burned firewood for heat. There was a chicken coop on his property where a relative raised chickens. He was employed as a sanitation truck driver. The patient rarely traveled, other than the recent incarceration in Santa Rosa, NM, and has never left the state of New Mexico. The patient did note a 30-pound weight loss during his two months of incarceration.

Further testing included HIV antibody ELISA, which was negative; CD4 T-cell count was 560 cells/mm^3. Magnetic resonance imaging of the brain revealed a sub-centimeter focus of restricted diffusion in the left global pallidus that was consistent with acute or sub-acute ischemic infarct, and a focus of abnormal increased T2 signal intensity in the sub-cortical white matter. A chest CT revealed the previously noted lingular mass, measuring 5.5×4.5 cm. Bilateral patchy multifocal nodular densities were identified in bilateral upper and lower lobes, some of which had a ground glass appearance. No significant adenopathy was identified. A PET-CT scan revealed a metabolically active mass in the lingula; clinically suspected to be a malignancy. During the course of the patient’s initial hospitalization of six days, the patient’s mental status, hyponatremia, and overall clinical status improved. Further evaluation of the patient’s initial hospitalization of six days, the patient’s mental status, hyponatremia, and overall clinical status improved.

A post-mortem examination was performed. Sections through the cerebral hemispheres demonstrated multiple, small vesicular lesions predominantly in the bilateral basal ganglia and also scattered throughout the bilateral white matter tracts (Figure 1A). No lesions were present in the cerebellum or brainstem. On histologic exam, sections from the bilateral basal ganglia showed multiple, cleared-out spaces containing numerous round yeast forms (Figure 1B).

In the lungs, a 7.5×5.0×4.0 cm, well-circumscribed yellow-tan mass was present in the lingula. Diffuse, bilateral, tan, ill-defined lesions were also present in all lobes of the lungs (Fig. 2A). Lung sections revealed occasional scattered, interstitial and intravascular clusters of encapsulated round yeasts morphologically consistent with Cryptococcus species (Figure 2B). Significant pulmonary edema with scattered acute inflammatory cells and macrophages were also present. Gomori methenamine silver (GMS) and mucicarmine stains of lung tissue revealed scattered yeasts.

Blood cultures collected on admission to the hospital as well as postmortem bacterial and fungal cultures of the lungs and heart blood grew Cryptococcus species, identified as C. gattii by the Fungus Testing Laboratory (University of Texas Health Science Center, San Antonio) on June 23, 2010.

Multilocus Sequence Typing (MLST) Identifies the VGIII Molecular Genotype
To delineate the relationship between the clinical isolate R4569 and isolates from the C. gattii emergence in the Pacific Northwest U.S. and British Columbia (PNW), MLST analysis, using the seven loci of the consensus MLST typing scheme was performed [17]. The isolate R4569 was genotyped as belonging to the major molecular type VGIII, which is different from the VGII major molecular type of the majority of the emerging isolates from the Pacific Northwest. To more accurately pinpoint the origin of isolate R4569, the phylogenetic relationships between a number of reference C. gattii isolates from the U.S. and neighboring Mexico were analyzed and a neighbor-joining dendrogram was constructed based on the seven concatenated MLST sequences (Figure 3, Table 1). The VGIII isolates investigated fell into three distinct clades, one containing isolates exclusively from Mexico, and two containing a mixture of Mexican and U.S. isolates. The New Mexico isolate (R4569) was more closely related to U.S. isolates and this grouping had a high bootstrap value.

Fatal Disseminated C. gattii in NM
R4569 is Less Virulent in Mice than Other Known C. gattii Strains

To assess the virulence potential of the R4569 isolate in an animal model, BALB/c mice were intranasally infected with $1 \times 10^5$ CFU of R4569. Separate cohorts of mice were also infected with C. gattii strains R265 and R272, reference strains for VGIIa and VGIIb molecular subtypes respectively, associated with the Vancouver Island outbreak [18], as well as the C. neoformans reference strain H99 [19]. All mice infected with C. gattii strain R265 and C. neoformans strain H99 succumbed to infection with median survival times of 27 days and 23.5 days, respectively (Figure 4a) similar to previous studies [20,21]. Survival rates for mice infected with C. gattii strains R272 and R4569 were significantly greater (87.5% and 100% survival, $p<0.05$) than mice infected with R265 or H99 (Figure 4a). The survival rate of mice challenged with C. gattii R272 strain was similar to earlier survival analysis using this strain [21] (Wormley lab, unpublished observations). Nonetheless, no mice infected with strain R4569 appeared ill by day 50 post-infection; however, fungal burden determination from the lungs and brain of mice at the termination of the experiment revealed the presence of numerous viable yeasts in mice infected with strain R272 or R4569 (Figure 4a). Significantly fewer CFUs were cultured from the lungs and brains of mice infected with strain R4569 than those infected with strain R272. Furthermore, histological examination revealed greater inflammation in the lungs of mice infected with strain R272 compared to strain R4569 (Figure 4b). Many yeast cells of strain R4569 were confined within activated “foamy” macrophages, that are indicative of increased intracellular killing of cryptococci by macrophages and thus control of fungal replication (Figure 4b, arrows) [22,23]. Altogether these results suggest that strain R4569 is less virulent than the VGII reference isolates in a mouse model of pulmonary infection or, alternatively, an enhanced capacity of mice to limit the growth of R4569 yeast.

Discussion

Our findings represent the first documented case of C. gattii infection believed to have been acquired in New Mexico. The
source of \( C. \text{gattii} \) infection in this patient remains unknown. The patient had no travel history to a known endemic region, and while \( C. \text{gattii} \) infection in domestic animals has been documented, these have been reported in animals residing in areas endemic to \( C. \text{gattii} \) \[8,24\]. New Mexico is an arid region covered mostly by mountains, plains, and desert, with little annual rainfall and relatively low humidity. Since 2002, there has been an increase in precipitation around the Albuquerque area, which was highest between 2004 and 2008 compared to the 30-year normal averages. In addition, the annual temperature has also been above average, with a median temperature of 58 degrees Fahrenheit \[25\]. New Mexico has regions similar to those in Mexico known to harbor \( C. \text{gattii} \) \[26–29\], whereas the foothills of the Rocky Mountains, which run through Albuquerque, may represent a more temperate climate niche. Environmental sampling in the Pacific Northwest demonstrated that \( C. \text{gattii} \) has established ecological niches in trees other than \textit{Eucalyptus}, including species of fir, maple, alder, cedar, spruce, pine and oak trees \[10,24\]. In another environmental surveillance study, certain species of cacti in Puerto Rico were also found to harbor \( C. \text{gattii} \) \[4,30\]. Both of these sources could potentially serve as an ecological niche for \( C. \text{gattii} \) in New Mexico. Further environmental surveillance of the patient’s residential area was not conducted (as resources to pursue this are not available).

In general, cryptococcal disease appears to be rare in New Mexico. Between 2003 and 2007, we estimate there were at least one to two confirmed cases of cryptococcal disease in the Albuquerque area, which is home to the four largest hospitals in New Mexico. Starting in 2008, the number of confirmed cases increased with three cases in 2008, eight cases in 2009 and at least five cases to date in 2010. The autopsy report of this patient led to the diagnosis of disseminated \( C. \text{gattii} \) infection. However, due to the initial clinical impression of lung malignancy, the patient’s immunocompetent status and lack of a travel history did not heighten clinical awareness of a cryptococcal infection in time to initiate antifungal therapy. Because the clinical presentation was most suggestive of a lung mass or malignancy, and the actual diagnosis is infrequently seen in this area, further testing for invasive fungal infection was not performed. The patient had widely disseminated infection with extensive inflammation, and likely succumbed to overwhelming systemic infection and sepsis, rather than elevated intracranial pressure with brainstem herniation, based on post-mortem findings. To date, \( C. \text{gattii} \) infections in the United States have been reported in Washington, Oregon, California, and North Carolina, in which all patients had some geographical exposure to endemic regions. \[7,8,31,32\] The case reported here is similar to another case report of a 44-year-old immunocompetent man in Japan with \( C. \text{gattii} \) CNS disease who had no history of recent overseas travel \[33\]. Although this strain was VGIIa, similarities to this case include the endemic nature of the infection, and clinically, the mass lesion was also initially suspected to be a tumor. Cases such as these, in which immunocompetent patients who lack geographical risk factors living in non-endemic areas are acquiring \( C. \text{gattii} \) infections, suggest that there might be a broader distribution of the pathogen than is currently recognized.

The non-VGII genotype of this \( C. \text{gattii} \) isolate indicates it does not represent the migration of the PNW outbreak strains southward to New Mexico. Because of the lack of a clonal relationship to isolates from Mexico, it also does not likely represent the recent migration of \( C. \text{gattii} \) isolates northward from Mexico. Rather, this isolate likely represents the emergence of a clonal genotype that, based on geography of the common isolates has probably persisted in the U.S. for quite some time.
literature review [24] reported that VGIII isolates of \textit{C. gattii} are most common in South America but they are also found in North America, Central America, Australasia and Southeast Asia. It was also recently reported that the majority of \textit{C. gattii} isolates from HIV+ patients in California are VGIII [31]. Isolates of the genotype VGIII have not been infrequently found in the U.S. in association with eucalyptus trees [34]. Subtype VGIII isolates had not been reported from the PNW emergence until a single isolate was reported from Washington in 2009 [18,32]. Subsequently, human and veterinary isolates were reported from Washington, Oregon, and California, dating back to as early as 1992 [35]. It will be important to monitor further for the emergence of this genotype in other parts of the southwestern U.S.

\textit{C. gattii} causes granulomatous pulmonary and disseminated disease in mouse inhalation models of infection, irrespective of the mouse strain used. In terms of genotypic variation in virulence, VGIIa isolates from the U.S. and from the Vancouver outbreak are more virulent in mice than VGIII isolates from either region [36–39]. Our results suggest that the VGIII isolate R4569 is less virulent than either of the VGII strains tested. The morbidity observed in mice given an experimental infection with the VGIII isolate R4569 is similar to the morbidity observed in mice experimentally infected with other VGIII clinical isolates. Of the \textit{C. gattii} cases reported to the CDC between 2004 and 2010, 50% were molecular type VGIIa, 10% were VGIIb, and only 3% were VGIII [40]. While the relationship of mouse virulence to human disease is unclear, it has been demonstrated that \textit{C. gattii} infections are immunologically similar in mice and infected humans with respect to cytokine profiles [37,41]. \textit{C. gattii} replicates intracellularly within macrophages. It has been demonstrated that intracellular replication rate within murine macrophages \textit{in vitro} is correlated with \textit{in vivo} virulence in mice [38,42,43]. VGIIa isolates replicate more quickly in macrophages \textit{in vitro} and are more virulent \textit{in vivo} than VGIIb isolates. Furthermore, intracellular replication rate in murine macrophages correlates very highly with the intracellular replication rate in human macrophages, suggesting there might be a correlation between genotype and human virulence and disease [43]. Additional studies comparing the intracellular growth rate of \textit{C. gattii} R4569 and other isolates within murine and human macrophages will be needed to support this hypothesis. The major clinical point from these in vivo studies is that despite strain R4569 being less virulent in this mouse infection model is that it is still highly capable of causing severe morbidity and mortality, particularly in the absence of timely diagnosis and therapy.

### Table 1. Isolates used for comparison in this study.

| Isolate | State | CAP59 | GPD1 | LAC1 | PLB1 | SOD1 | URA5 | IGS1     | Source | Subtype | Reference |
|---------|-------|-------|------|------|------|------|------|---------|--------|---------|-----------|
| B7415   | CA    | 18    | 3    | 3    | 6    | 40   | 19   | 1       | alpaca  | VGIII   | 29        |
| B8964   | CA    | 18    | 3    | 3    | 6    | 40   | 19   | 1       | human   | VGIII   | This study |
| B8212   | WA    | 18    | 3    | 3    | 6    | 40   | 19   | 1       | human   | VGIII   | 29        |
| B8516   | OR    | 18    | 3    | 3    | 6    | 40   | 19   | 1       | cat     | VGIII   | This study |
| R4569   | NM    | 18    | 3    | 3    | 20   | 28   | 25   | 1       | human   | VGIII   | This study |
| B7495   | CA    | 18    | 3    | 32   | 20   | 40   | 23   | 1       | human   | VGIII   | 29        |
| B8260   | WA    | 29    | 9    | 2    | 4    | 28   | 19   | 18      | cat     | VGIII   | 29        |
| WM 1826 | Mexico | 18    | 3    | 3    | 6    | 40   | 19   | 1       | human   | VGIII   | 43        |
| B8262   | CA    | 18    | 3    | 3    | 34   | 38   | 19   | 1       | human   | VGIII   | 29        |
| WM 1815 | Mexico | 18    | 3    | 22   | 6    | 28   | 19   | 1       | human   | VGIII   | 43        |
| WM 1819 | Mexico | 18    | 3    | 32   | 20   | 40   | 23   | 1       | human   | VGIII   | 43        |
| WM 1814 | Mexico | 29    | 7    | 2    | 4    | 28   | 21   | 5       | human   | VGIII   | 43        |
| WM 1823 | Mexico | 29    | 7    | 2    | 4    | 28   | 21   | 5       | human   | VGIII   | 43        |
| WM 1618 | Mexico | 18    | 3    | 22   | 6    | 28   | 19   | 1       | human   | VGIII   | 43        |
| WM 1635 | Mexico | 18    | 3    | 22   | 21   | 32   | 19   | 1       | human   | VGIII   | 43        |
| WM 1620 | Mexico | 18    | 3    | 20   | 17   | 28   | 29   | 23      | human   | VGIII   | 43        |
| WM 1824 | Mexico | 18    | 3    | 20   | 17   | 32   | 29   | 1       | human   | VGIII   | 43        |
| WM 1631 | Mexico | 18    | 3    | 22   | 17   | 32   | 19   | 23      | human   | VGIII   | 43        |
| WM 1811 | Mexico | 35    | 3    | 22   | 20   | 41   | 28   | 5       | human   | VGIII   | 43        |
| WM 1812 | Mexico | 35    | 3    | 22   | 20   | 41   | 28   | 5       | human   | VGIII   | 43        |
| B6253   | CA    | 16    | 15   | 5    | 5    | 45   | 12   | 3       | dolphin | VGII    | 44        |
| B8263   | CA    | 16    | 5    | 5    | 5    | 32   | 12   | 3       | human   | VGII    | 29        |
| B8551   | OR    | 16    | 14   | 5    | 5    | 32   | 12   | 3       | human   | VGII    | This study |
| B7394   | WA    | 2     | 6    | 4    | 2    | 15   | 2    | 10      | cat     | VGIIb   | 29        |
| B7395   | WA    | 1     | 1    | 4    | 1    | 14   | 7    | 4       | dog     | VGIIa   | 29        |
| B7432   | OR    | 6     | 6    | 4    | 1    | 15   | 2    | 15      | human   | VGIIc   | 29        |

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Based on the few previous reports [18,32,35,38] there may be a low level of C. gattii infection in the U.S. due to VGIII isolates that may be unrecognized outside of HIV+ patients. However, the underlying level of infection due to C. gattii is currently unknown because many of the cases of cryptococcosis in the U.S. are diagnosed using an antigen test and most cases outside of the Pacific Northwest are assumed to be caused by C. neoformans. The heterogeneity of the VGIII isolates in this study, as compared to the almost exclusively clonal nature of the current VGII PNW emergence isolates, would be consistent with a long-term presence in the U.S. and a possibly unrecognized, long term, low level, endemicity. It is also interesting to note that among HIV+ patients in California in the 1990’s almost all of the infections due to C. gattii were caused by isolates of the VGIII genotype [31,44], where globally VGIII isolates were more often found in the non-immunocompromised patient population [45,46]. We therefore support speciation of Cryptococcus clinical isolates due to the implications for public health and for understanding the epidemiological distribution of this fungal pathogen. In addition, there is epidemiological evidence that there are substantive differences in the clinical presentation of C. gattii and the course of disease compared to C. neoformans [13].

As infections due to C. gattii increase both in the United States and worldwide, epidemiologic surveillance will play an important role in identifying new ecological niches or reservoirs for this emerging fungal pathogen. Since not all clinical and reference laboratories are equipped to differentiate between C. gattii and C. neoformans, a heightened clinical awareness of the disease will be required to prompt further identification and genotyping to track the distribution of C. gattii.

Materials and Methods

Approvals and Ethics Statement

The authorized representative of the patient in this manuscript has given written informed consent (as outlined in the PLoS
consent form) to publication of their case details. These animal experiments were approved by The University of Texas at San Antonio Institutional Animal Care and Use Committee (IACUC), approved protocol number MU021-11/1A2, and mice were handled according to IACUC guidelines. An IRB waiver was approved protocol number MU021-11/1A2.

Microbiologic Identification

Fungal identification was performed at the Fungus Testing Laboratory (University of Texas Health Science Center, San Antonio) using canavanine-glycine-bromthymol blue (CGB) agar and 

Multilocus Sequence Typing

The isolate was subtyped using The ISHAM consensus multilocus sequence typing (MLST) scheme [17]. The URA5, IGS, PLB1, SOD1, GPD1, PFL1, and CAP59 gene fragments were amplified as described by Meyer and colleagues [17]. Briefly, isolates were grown on YPD plus 0.5% NaCl and DNA was isolated using the UltraClean DNA Isolation Kit as described by the manufacturer (MO BIO Laboratories, Carlsbad, CA). Gene fragments were amplified and sequenced in both directions using the primers of Meyer et al [17]. Allele and sequence types were assigned according to the C. gattii MLST database at mlst.mycologylab.org. The compiled sequences were compared to C. gattii sequences collected during the U.S. PNW surveillance (SRL) or during a previous surveillance in Mexico [W. Meyer, unpublished data]. Phylogenetic relationships, the neighbor-joining tree and bootstrap values were calculated using the Mega 4.1 software package [47]. All generated allele and sequence types of the seven genetic loci studied herein are accessible at the C. gattii MLST database at mlst.mycologylab.org.

Mouse Pulmonary Model of Infection

Female BALB/c (H-2b) mice, four to six weeks of age (National Cancer Institute/Charles River Laboratories), were used throughout these studies. Mice were housed at The University of Texas at San Antonio Small Animal Laboratory vivarium and handled according to guidelines approved by the Institutional Animal Care and Use Committee.

Pulmonary cryptococcal infections were initiated by nasal inhalation as previously described [48]. Briefly, BALB/c mice (eight per group) were anesthetized with 2% isoflurane using a rodent anesthesia device (Eagle Eye Anesthesia, Jacksonville, FL) and then given an inoculum of 1 x 10^5 colony forming units (CFU) of C. neoformans strain H99 or C. gattii strains R265 (VGIIa), R272 (VGIIb), or R4569 (isolate from this case) in 50 μl of sterile PBS introduced directly into the nares. The strains R265 and R272 were provided by Joseph Heitman (Duke University Medical Center, Durham, NC). The inocula used for nasal inhalation were verified by quantitative culture on yeast peptone dextrose (YPD) agar. The mice were fed ad libitum and monitored by inspection twice daily. Mice were either euthanized when moribund or at day 50 post-inoculation. For histopathology (three mice per group), lungs were transcardially perfused with PBS then inflated with 10% formalin via an intratracheal catheter. Lungs were tied off, dissected, and stored in formalin until paraffin embedding, sectioned, and stained by hematoxylin and eosin (Histology Laboratory at The University of Texas Health Science Center at San Antonio). For colony-forming unit (CFU) determination in surviving mice (four to five mice per group), lung tissues were excised using aseptic technique, homogenized in 1 ml of sterile PBS, and cultured by 1:10 dilutions on YPD agar supplemented with chloramphenicol (Mediatech, Inc., Herndon, VA). CFUs were enumerated following incubation at 30°C for 48 h.

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Author Contributions

Conceived and designed the experiments: SH FW S. Lockhart JH CF WM. Performed the experiments: SH FW S. Lockhart JH CF WM. Analyzed the data: SH FW S. Lockhart JH CF WM. Contributed reagents/materials/analysis tools: SH FW S. Lockhart JH CF WM AF BW. Wrote the paper: CW S. Lee TS NK WG JG-W LM S. Lockhart JH CF WM. Performed autopsy and histologic analyses: JG-W LM.

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