fungal pathogens could be isolated from sputum by classic and molecular methods. After 4–5 days, his temperature was 40°C, a productive cough with dyspnea was noted, and his condition deteriorated. A chest radiograph showed progression of the infiltrates, and a computed tomography scan of the abdomen and chest showed infiltrates near the pleura, suggesting encapsulated fluid (Figure). An ultrasound-guided lung biopsy was performed, and mucoid material was aspirated. Microscopy and a culture from the aspirate showed a cryptococcal isolate. This isolate was further identified by internal transcribed spacer and D1/D2 sequencing, as well as amplified fragment-length polymorphism analysis (*2*). In addition, detailed genotyping was performed by using sequences of 7 genes (*IGS*, *CAP10*, *GPD1*, *LAC1*, *MPD1*, *PLB1*, and *TEF1*; GenBank accession nos. DQ861593–DQ861599) (*5*).

Extensive molecular research showed that this isolate belonged to the highly virulent AFLP genotype 6A (VGIIa) of *Cryptococcus gattii*, which is the major genotype involved in the Vancouver Island *C. gattii* outbreak (*1–4*). All 7 sequenced genes had a complete match with the sequence types specific for isolates involved in the Vancouver Island outbreak (*5*). Thus, we conclude that the pathogen was acquired during the patient's visit to Vancouver Island and imported to Denmark. The presence of 3 cryptococcal masses of more or less equal size suggests that the patient was exposed to a high concentration of infectious cells of *C. gattii*. The observed incubation time of 6 weeks is shorter than that was previously reported for infections related to the Vancouver Island outbreak (2–11 mo) (*4*). These observations, in combination with the absence of any known predisposing factor in this patient, such as smoking or treatment with corticosteroids, suggest that this specific AFLP6 genotype of *C. gattii* is highly virulent (*4*,*5*).

This case suggests a potential risk of tourists acquiring cryptococcosis while visiting Vancouver Island. Therefore, we recommend tourists and medical staff of healthcare centers worldwide be alert for symptoms of cryptococcosis after travel to Vancouver Island.

Jens Lindberg,* Ferry Hagen,† Alex Laursen,* Jørgen Stenderup,‡ and Teun Boekhout†§

*Skejby Hospital, Aarhus, Denmark; †CBS Fungal Biodiversity Center, Utrecht, the Netherlands; ‡Herning Hospital, Herning, Denmark; and §University Medical Centre, Utrecht, the Netherlands

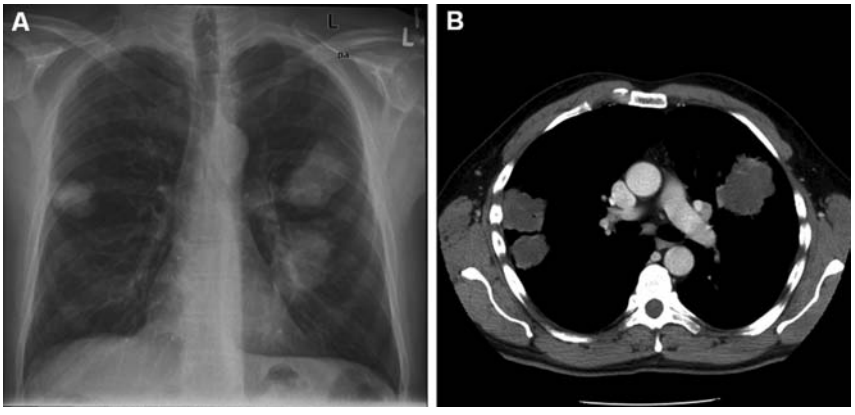

Figure. A) Chest radiograph and B) computed tomographic scan of the patient showing 3 nodular *Cryptococcus gattii* infiltrates near pleura.

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Address for correspondence: Jens Lindberg, Th. Nielsens Gade 31, DK-7400, Herning, Denmark; email: jens.lindberg@mail.dk

Clostridium difficile in Discharged Inpatients, Germany

To the Editor: Using discharge diagnoses from US hospitals in 2000–2003, McDonald et al. recently documented a dramatic increase in the rate of *Clostridium difficile*–associated disease (CDAD) (*1*). During the same period, a new strain of *C. difficile* was identified; this strain appears more virulent, at least in part because it produces higher levels of toxin (*2*).

To our knowledge, this strain has not been identified in Germany. However, to address this emerging threat, we conducted a similar analy-

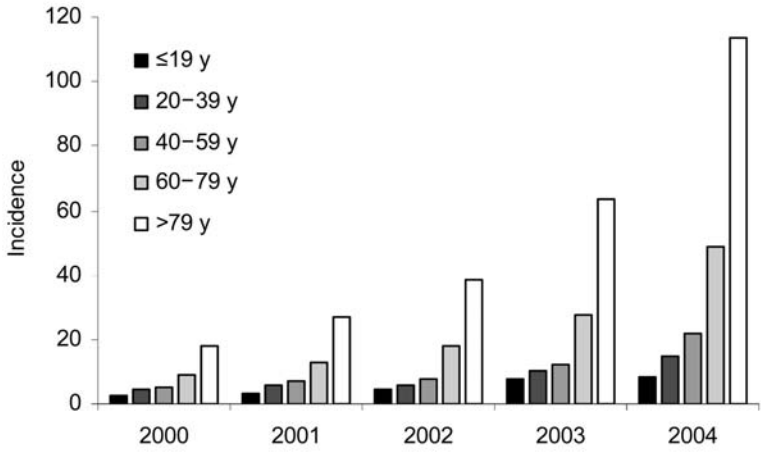

Figure. Incidence of *Clostridium difficile*–associated disease per 100,000 inpatients upon discharge from hospitals in Germany.

sis of discharge data to compare findings from the United States with data from Germany. We therefore determined the absolute number of inpatient discharges from all hospitals in Germany with the number of discharge diagnoses of CDAD reported in the national Statistische Bundesamt for the years 2000–2004. We then calculated the incidence of CDAD as a discharge diagnosis for each year and stratified our results by age groups (Figure).

Our results confirm the observations from the United States. The effect of *C. difficile* on illness of patients in hospitals in Germany has escalated dramatically. This is true especially for patients ≥60 years of age. This trend indicates the need for increased awareness of this pathogen and a concerted effort to control CDAD by reducing unnecessary antimicrobial drug use and implementing currently recommended infection control measures. It also highlights the need to develop more rapid and accurate diagnostic tools and more effective prevention and treatment strategies.

Ralf-Peter Vonberg,*
Frank Schwab,†
and Petra Gastmeier*

*Medical School Hannover, Hannover, Germany; and †Charité – University Medicine Berlin, Berlin, Germany.

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Address for correspondence: Ralf-Peter Vonberg, Institute for Medical Microbiology and Hospital Epidemiology, Medical School Hannover, Carl-Neuberg-Str. 1, D-30625 Hannover, Germany; email: vonberg.ralf@mh-hannover.de

Human Bocavirus in Febrile Children, the Netherlands

To the Editor: Human bocavirus (HBoV) is a recently discovered virus of the family *Parvoviridae*, genus *Bocavirus*, which appears to cause widespread respiratory tract infections (RTI) in children. In selected groups of children with RTI, detection rates have varied from 2.8% to 11.3% (*1–9*). However, the exact prevalence and pathogenic effects of this virus remain to be established.

During a prospective cohort study to evaluate the prognosis of fever at a general practice after-hours service in Rotterdam, nasopharyngeal swabs were collected from febrile children and tested for respiratory viruses, including HBoV. We report the incidence and clinical features of HBoV infection in these children.

From June 1, 2005, through January 16, 2006, all children 3 months to 6 years of age whose parents contacted the after-hours service because of fever, as reported by parents and not further defined, were eligible for inclusion in the study. Children were excluded when the parents could not communicate in Dutch (n = 77) and if the child had already been included within the past 2 weeks (n = 11). A research nurse visited the child at home within 24 hours of inclusion. The child was physically examined, and a nasopharyngeal swab and a blood sample for C-reactive protein measurement were collected. The parents subsequently recorded the child's symptoms in a diary for 7 days. The Central Committee on Research Involving Human Subjects, the Netherlands, approved this study.

Nucleic acids were isolated on a MagnaPure isolation station (Roche Applied Science, Penzberg, Germany) and subsequently analyzed by real-time assays. Detection of HBoV was performed by using a primers set and a