

tions, 3) low levels of platelets ($<100 \times 10^9/L$) and 4) increased capillary permeability (5). Our patient fulfilled all 4 criteria. Few cases of reported DHF fulfill criterion 3 due to the short duration of severe thrombocytopenia in mild clinical forms (8). Increased vascular permeability was shown in our patient by the peritoneal and bilateral pleural effusions.

The probability of diagnosing dengue fever in Europe increases with travel to dengue-endemic areas, in view of the increase of DHF numbers (2006–2007) and several outbreaks around the world, even during the non-dengue season (9). Frequent travelers are more at risk for DHF. In a recent European publication, 17% of patients with imported dengue fever exhibited a secondary immune response, thus having a higher risk of developing DHF in the future (6). Serologic tests confirm dengue infection only if a 4-fold increase in titers in consecutive serum samples occurs, as in our case.

In dengue-endemic areas, despite the higher disease incidence, many cases still fail to meet WHO criteria (9). A comprehensive revision of dengue and DHF series (8) shows differences in applying WHO criteria for diagnosis, and sometimes the correlation was poor between criteria-fulfilling cases and severity of disease. Some reports (6,8) suggest that WHO criteria should be reviewed and perhaps new parameters should be established to define severe dengue disease.

Although our patient was not infected in Europe, lessons from the recently described chikungunya outbreak in Italy indicate the possibility of new arbovirus outbreaks in previously non-disease-endemic areas due to the increasingly established presence of vectors like *Ae. albopictus* (10).

Dengue virus infection should therefore be considered in the differential diagnosis of fever in returning travelers. DHF diagnosis, although unusual, could become more frequent in the future.

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**María Jesús Pinazo Delgado,*††
José Muñoz Gutierrez,*††
Ljiljana Betica Radic,§
Tomislav Maretic,¶
Sime Zekan,¶
Tatjana Avšič-Županc,#
Ethel Sequeira Aymar,**
Antoni Trilla,*††
and Joaquim Gascon
Brustenga*††**

*Barcelona International Health Research Center, Barcelona, Spain; †August Pi Sunyer Biomedical Research Institute, Barcelona; ‡University of Barcelona Hospital Clinic, Barcelona; §General Hospital, Dubrovnik, Croatia; ¶University Hospital for Infectious Diseases Dr. Fran Mihaljevic, Zagreb, Croatia; #Institute of Microbiology and Immunology, Ljubljana, Slovenia; and **Centro de Atención Primaria del Sector del Eixample (CAPSE), Barcelona

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Address for correspondence: María Jesús Pinazo Delgado, Villarroel St 170, 08036 Barcelona, Spain; email: mpinazo@clinic.ub.es

Mycobacterium setense Infection in Humans

To the Editor: A 66-year-old man had a bone graft for treatment of an oroantral fistula in March 2007 in Marseille, France. The surgery consisted of a bilateral maxillary sinus filling with a parietal osseous graft to close the fistula (position 24–25). Painful edema of the hemiface and mild fever developed in the patient in July 2007. Computed tomography showed areas of hypodensity in the osseous graft in the left maxillary sinus consistent with osteolysis. Microscopic examination of a bone biopsy specimen after gram staining did not reveal any organisms but this specimen did grow *Enterobacter cloacae* and colonies of a gram-positive bacillus after a 2-day inoculation on 5% blood agar incubated at 37°C in an atmosphere of 5% CO₂. Tentative identification of this catalase-positive, oxidase-negative gram-positive rod (isolate 74023791) by an API Coryne

strip (API bioMérieux, La Balme-les Grottes, France) remained inconclusive. Isolate 74023791 exhibited acid fastness and was further identified by comparing its 16S rDNA (1) and heat shock protein 65 (hsp65) (2) sequences with those in the GenBank database and its RNA polymerase subunit B (*rpoB*) sequences (3) with those of *Mycobacterium* spp. in our local *rpoB* database.

Antimicrobial susceptibility testing using E-test (AB Biodisk, Bruz, France) indicated that isolate 74023791 was susceptible to ciprofloxacin with an MIC of 0.047 µg/mL and resistant to amoxicillin (MIC >256 µg/mL), ceftriaxone (MIC >256 µg/mL), erythromycin (MIC >256 µg/mL), clarithromycin (MIC >256 µg/mL), and rifampin (MIC >32 µg/mL). Disk testing and reference broth dilution method (4) showed that isolate 74023791 was susceptible to imipenem after a 3-day incubation. However, E-test showed heterogeneous resistance with colonies exhibiting an MIC >256 µg/mL. The same observations were made for *Mycobacterium setense* type strain CIP109395T (Collection de l'Institut Pasteur, Paris, France) (5). Daily treatment with 2 g imipenem and 1.5 g ciprofloxacin was prescribed for 1 month before the imipenem E-test and broth dilution results were available, and was followed by 1.5 g/day ciprofloxacin for 3 months, resulting in a favorable clinical and radiologic evaluation at 5-month follow-up.

Phylogenetic analyses indicated that isolate 74023791 belonged to the *M. fortuitum* group, along with *M. porcinum* and *M. conceptionense*, and was most closely related to *M. setense*, a recently described species of this group (5) (Figure). Isolate 74023791 shared 100% 16S rDNA (GenBank accession no. EU371507), 99.5% hsp65 (accession no. EU371508), and 99.0% *rpoB* (accession no. EU371509) sequence similarity with *M. setense* (accession nos. EF138818 and EU371504, EF138819 and EU371505, and EF414447 and EU371506, respectively). Because the 99% *rpoB* sequence similarity of the patient's isolate was above the 97% *rpoB* sequence similarity cut-off value used to identify rapidly growing mycobacteria (3), isolate 74023791 was therefore identified as *M. setense*.

M. setense, in association with an *E. cloacae* strain susceptible to antimicrobial drug therapy, was an agent of infection in our patient. It is noteworthy that *M. setense* and the closely-related species *M. conceptionense* were isolated from patients with post-traumatic osteitis (5,6); *M. porcinum* was isolated from 7/46 cases of osteomyelitis and additional cases of postsurgical infection, respectively (7); *M. fortuitum* osteomyelitis has also been reported (8). These data emphasize the role of *M. fortuitum* group organisms in posttraumatic and postsurgical osteitis.

In a later interview, the patient disclosed that he rinsed his mouth with well water during the weeks after receiving the bone graft. We initially suspected that the water was the source of *M. setense*, as previously suspected for *M. conceptionense* (6) and reported for *M. porcinum* (7). However, neither *M. setense* nor *M. setense* DNA were detected in the well water in October 2007.

Initially, *M. setense* was reported to be susceptible to imipenem by the disk diffusion method, which is not the reference method (5). In this report, the disk and reference broth dilution methods showed that both clinical and reference *M. setense* strains were initially susceptible to imipenem but the E-test disclosed that both strains exhibited heterogeneous resistance to imipenem; colonies exhibited an MIC >256 µg/mL. This result was unexpected because the E-test showed that related species *M. fortuitum* CIP104534T, *M. conceptionense*, CIP 108544T and *M. porcinum* CIP105392T were susceptible to imipenem (6). Likewise, the modified broth dilution method showed that the MIC for imipenem was ≤4 µg/ml for *M. fortuitum* (9). However, when a broth dilution method was used, the MIC for imipenem ranged from 0.5 µg/mL to 8 µg/mL in 42 *M. porcinum* strains (7). Together, these data challenge the susceptibility to imipenem in organisms of the *M. fortuitum* group.

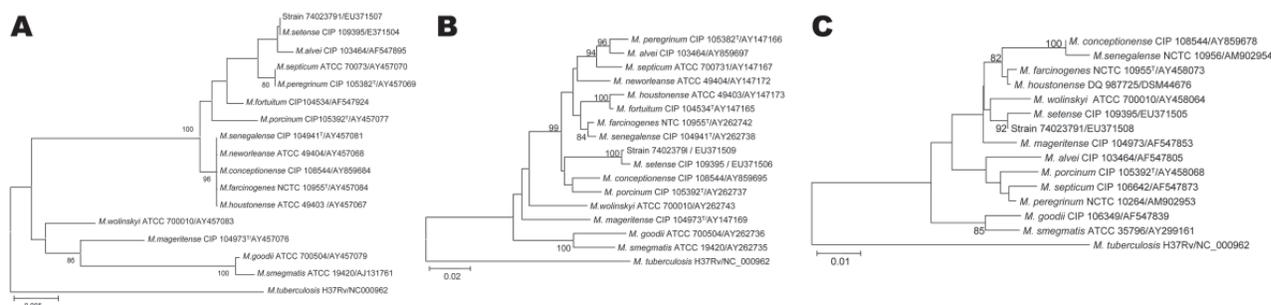


Figure. Phylogenetic position of isolate 74023791 and 16 rapidly growing *Mycobacterium* species based on A) 16S rDNA, B) partial RNA polymerase subunit B, and C) partial heat shock protein 65 sequences analyzed by using the neighbor-joining method and Kimura 2-parameter distance correction model. The support of each branch, as determined from 1,000 bootstrap samples, is indicated by the value at each node when ≥80% (as a percentage). *M. tuberculosis* was used as the outgroup species. Scale bars represent differences in nucleotide sequences.

M. setense is an emerging organism of the *M. fortuitum* group that must be added to the growing list of rapidly growing mycobacteria isolated from humans. The initial gram-positive rod appearance of *M. setense* may delay its accurate identification. Determination of antimicrobial drug susceptibility needs to be conducted by the reference broth dilution method. Further reports are warranted to characterize the role of *M. setense* in infection.

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**Alexandre Toro,*
Toidi Adekambi,†
François Cheynet,‡
Pierre-Edouard Fournier,*
and Michel Drancourt***

*Université de la Méditerranée, Marseille, France; †Centers for Disease Control and Prevention, Atlanta, Georgia, USA; and ‡Assistance Publique Hôpitaux de Marseille, Marseille, France

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Address for correspondence: Michel Drancourt, Unité des Rickettsies, Faculté de Médecine, Université de la Méditerranée, 27 Blvd Jean Moulin, 13385 Marseille CEDEX 5, France; email: michel.drancourt@medecine.univ-mrs.fr

Human Bocavirus in Tonsillar Lymphocytes

To the Editor: We read with great interest the recent report by Longtin and colleagues (1) describing human bocavirus (HBoV) infection among Canadian children with acute respiratory tract illnesses (ARI). The authors identified HBoV by PCR in nasopharyngeal aspirates from 13.8% of young children hospitalized with ARI, an infection rate well within the range reported by other studies on children (2). However, these authors also detected an unexpectedly high rate of HBoV for their control group (43%), >3 times the rate for ARI case-patients.

In contrast, several similar studies did not detect HBoV in asymptomatic children. Kesebir et al. detected HBoV in 23 (5.2%) of 425 young children with ARI but in none of 96 children during routine well-child visits (3). Maggi et al. detected HBoV in 9 (4.5%) of 200 infants with ARI but in none of 30 healthy infants or 21 preadolescent healthy children without signs of ARI or history of asthma or wheezing (4). Finally, Allander et al. detected HBoV in 5 (19%) of 259 young children with acute expiratory wheezing but in none of 64 children who had not had respiratory symptoms during the preceding 4 weeks (5). In a recent study, we detected HBoV by PCR in 44 (12%) of 369 Thai children ≤4 years of age hospitalized with pneumonia but in only 2 (2%) of 85 asymptomatic age and temporally matched controls (6).

The inexplicably high rate of HBoV infection for patient controls reported by Longtin et al. (1) may reflect a unique feature of the children selected. The 100 controls were children without concomitant respiratory symptoms or fever at admission who were hospitalized during the study period for elective surgery, primarily of the ear, nose, and throat (71%). Most surgeries consisted of myringotomies, adenoidectomies, and tonsillectomies. The authors reported that these surgeries were more frequently performed on children found to be PCR positive for HBoV than on children negative for HBoV (84% vs. 61%). One possible explanation is that HBoV infection may directly induce inflammation of tonsillar tissues or facilitate bacterial superinfection prompting surgical intervention. Another possibility is that inflammation of mucosal lymphoid tissues enhances HBoV replication by recruitment of immune cells permissive for HBoV infection or by latent virus reactivation. Persistent infections and dependence on rapidly dividing cells are common features of the related parvoviruses, for example, human erythrovirus B19 (7). The presence of