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Short Communication

Tuberculosis-Like Peritonitis Due to an Atypical *Mycobacterium* Infection in a Japanese Woman

Hirokazu Kimura*, Masakazu Yoshizumi, Misa Iijima[1], Toshio Tsukagoshi[1], Toshinobu Nishimura[1], Masahiko Kato, Yukio Morita, Ryota Tanaka[1], Kunihisa Kozawa, Masahiro Fujita, Masaru Kojima[1] and Hisanori Minakami[2]

Gunma Prefectural Institute of Public Health and Environmental Sciences, Gunma 371-0052; [1]Gunma Prefectural Cancer Center, Gunma 373-8550; and [2]Department of Obstetrics, Hokkaido University Graduate School of Medicine, Sapporo 060-8638, Japan

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SUMMARY: It is not known whether atypical *Mycobacterium* (AM) causes peritonitis in humans. We described a case of tuberculosis-like peritonitis caused by an AM. Genetic analysis of the biopsy specimens suggested an AM infection. Thus, we concluded that peritonitis in humans can be caused by some AM species as well as by *Mycobacterium tuberculosis* complex.

Bacteria included in the *Mycobacterium tuberculosis* complex (*M. tuberculosis*, *M. bovis*, *M. africanum*, and *M. microti*) and most atypical mycobacteria can cause various diseases such as lung disease, arthritis, and lymphadenitis in humans (1). *M. tuberculosis* complex also causes tuberculous peritonitis, which often mimics peritonitis carcinomatosa (2,3). Although atypical mycobacteria can cause systemic infection, including peritonitis in immunocompromised patients (4), it is not known whether it can cause peritonitis in humans.

We present the case of a 38-year-old Japanese woman suspected of having tuberculous peritonitis after undergoing exploratory laparotomy. Culture methods were not helpful in identifying the microorganism responsible for the disease, but a genetic analysis of the biopsy specimens of this patient suggested atypical *Mycobacterium* (AM) as a causative agent.

A 38-year-old Japanese woman presented with a 3-month history of abdominal pain and increased abdominal girth with weight loss (5 kg). Pyrexia, cough, or leg edema was not seen in this patient. HIV antibody was negative. Ultrasonography and enhanced CT revealed marked ascites and thickening of the omentum with swollen mesenteric lymphonodes; however, no mass lesions were detected in the lung, liver, pancreas, kidneys, or ovaries. Endoscopic examinations did not reveal any malignancy in the alimentary tract. Neither malignant cells nor bacteria were isolated from the ascites collected by paracentesis. Middlebrook 7H9 broth or Middlebrook 7H10 agar medium (Oxoid, Hampshire, England) used in this study failed to grow acid-fast bacterium. The intradermal tuberculin test was positive (skin induration, 25 mm), but a microscopic examination revealed that the sputum was negative for acid-fast bacteria.

An exploratory laparotomy that was performed 3 weeks later revealed multiple small implants (diameter, approximately 5 to 10 mm) in the peritoneal cavity and the surface of the ovaries. Biopsy specimens were obtained from the small nodules. Epithelioid cell granulomas with a central area of caseous necrosis (Fig. 1) were seen in these specimens during the microscopic examination; however, no acid-fast bacteria were detected after Ziehl-Neelsen staining. We amplified *rpoB* (RNA polymerase β subunit gene) of the *Mycobacterium* spp. (5) by using DNA extracted from the biopsy specimens. The purified amplicons were sequenced by the direct sequencing method (5). The DNA sequences were aligned (306 nucleotides), and homology analysis of sequenced *rpoB* was performed by using BLAST (basic local alignment search tool; see http://www.ncbi.nih.gov/BLAST/) (6). A homology of over 90% was observed between our strain and 5 strains of AM spp. (*M. cookii* [GenBank accession no. AY544904], 91%; *M. aichience* [AY544882], 90%; *M. intermedium* [AY544929], 90%; *M. shimoidei* [AF057486], 90%; and *M. terrae* [AF057488], 90%), while the observed homology between the *M. tuberculosis* complex and our strain ranged from less than 85 to 90%. The homology observed among the strains of the *M. tuberculosis* complex was 100%. Phylogenetic analysis was performed using the neighbor-joining method (N-J method) (7). As shown in Fig. 2, *rpoB* from our samples was located in the same cluster of some species of AM in the phylogenetic tree. These results suggested that the *rpoB* was derived from AM spp. but not from the *M. tuberculosis* complex. The patient was treated

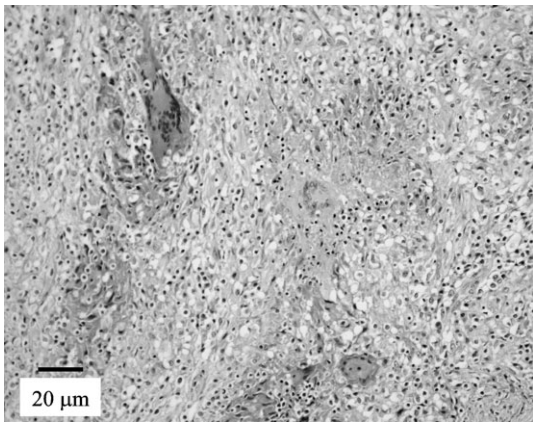

Fig. 1. Epithelioid cell granulomas with a central area of caseous necrosis. Note the Langerhans' giant cells. Hematoxylin-Eosin stain, Bar, 20 μm.

*Corresponding author: Mailing address: Gunma Prefectural Institute of Public Health and Environmental Sciences, 378 Kamioki-machi, Maebashi-shi, Gunma 371-0052, Japan. Tel: +81-27-232-4881, Fax: +81-27-234-8438, E-mail: kimura-hi@pref.gunma.jp

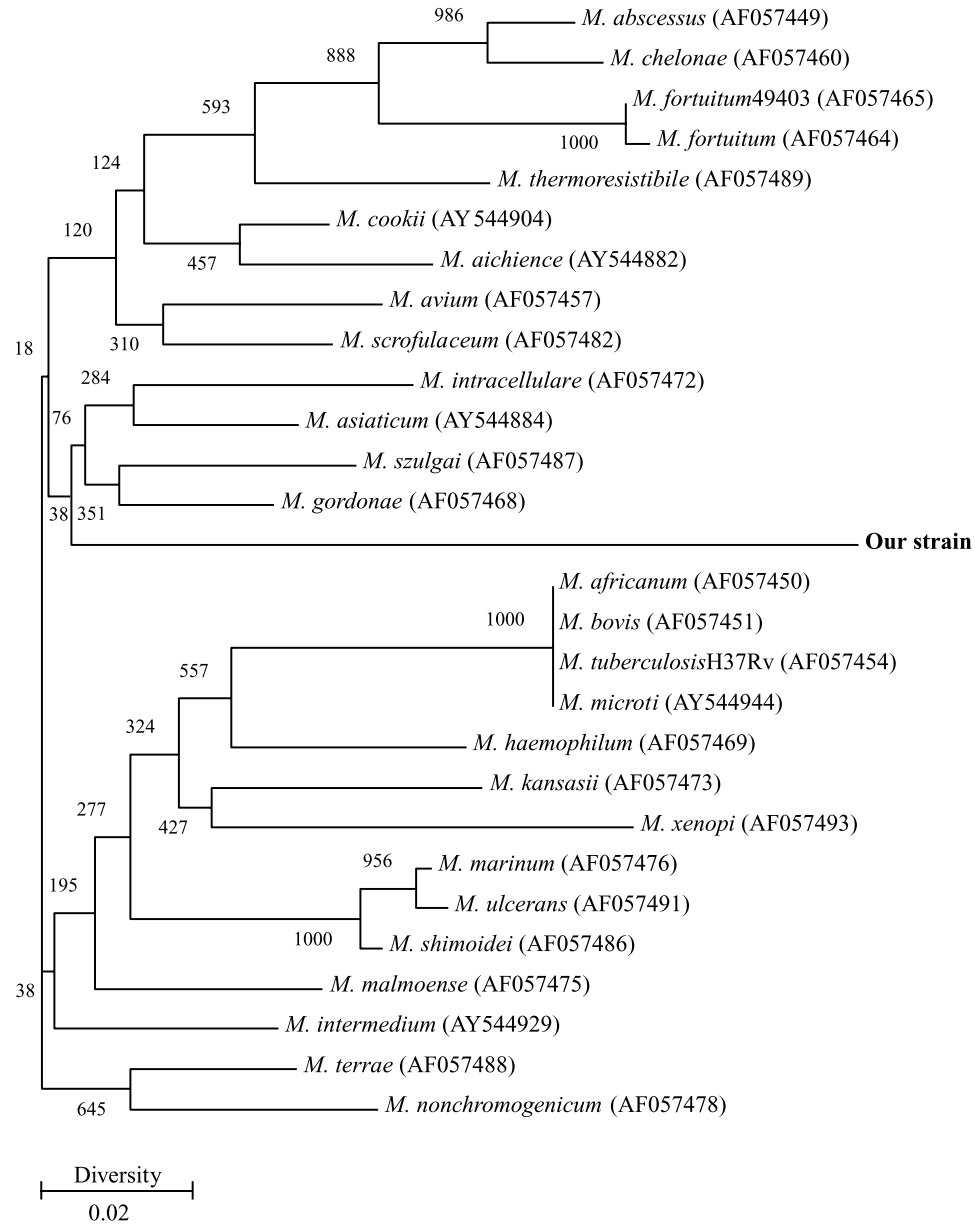

Fig. 2. Phylogenetic tree based on *rpoB* nucleotide sequences in various strains of *Mycobacterium*. A phylogenetic tree of *rpoB* of various *Mycobacterium* strains. The distance was calculated by using Kimura's two parameter method, and the tree was plotted by using the neighbor-joining method. The numbers at each branch indicate bootstrap values for the clusters supported by that branch. The numbers in parentheses are the GenBank accession numbers.

with a 2-month course of isoniazid, rifampicin, pyrazinamide, and ethambutol and a 4-month course of isoniazid and rifampicin. Following this treatment, her clinical symptoms completely resolved.

In this case, an exploratory laparotomy was performed and the pathological findings of the resected specimens strongly suggested a *Mycobacterium* infection; additionally, no malignant cells were observed in these specimens. However, the culture methods employed in this study did not prove to be useful in identifying the pathogen. A genetic analysis of the *rpoB* gene indicated that the causative agent was an AM. In general, AM primarily causes lung diseases in humans (1). However, systemic AM infections, including peritonitis, occur in AIDS patients (8). Immunologically, our patient appeared normal. Thus, some AM can cause systemic infections such as peritonitis in humans.

The sequences of *rpoB* are either genus- or species-specific for *Mycobacterium* (5). In addition, it is suggested that analysis of the 16S ribosomal RNA gene may be useful to confirm AM (9), although we did not perform an analysis of the gene in this study. It has been reported that the similarity of *rpoB* among the strains of the *Mycobacterium* genus was more than 85%, and that within the species it was very high, i.e., 99-100% (5). In our study, the homology of *rpoB* between the *M. tuberculosis* complex (*M. tuberculosis*, *M. bovis*, *M. africanum*, and *M. microti*) and that isolated from the patient was approximately 85%, and the genetic diversity was approximately 10% (Fig. 2). Thus, the possibility of *M. tuberculosis* complex being the causative agent was excluded. A homology of over 90% between the strain detected from the patient and 5 strains of AM spp. reasonably supports the fact that the causative agent was an AM rather than the *M. tuberculosis* complex, although it was possible that another pathogen was involved.

The incidence of another disease –tuberculous peritonitis– has been reported, although it is relatively rare (10). Stout et al. reported a case of peritonitis mimicking ovarian cancer in a young woman; in this case, the causative agent was *M. bovis* (3). Simsek et al. have reported patients with tuberculous peritonitis caused by the *M. tuberculosis* complex (2). However, to the best of our knowledge, no case of peritonitis caused by AM has been reported to date. In conclusion, tuberculosis-like peritonitis may have been caused by some species of AM and *M. tuberculosis* complex, although this would be a rare occurrence.

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