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Correspondence

Mycobacterium heraklionense as an emerging cause of tenosynovitis



Microbiology Immunology

KEYWORDS

Gene sequencing; Mycobacterium heraklionense; Tenosynovitis

Dear Editor,

Mycobacterium heraklionense was recently identified as a novel species within the Mycobacterium terrae complex.¹ We reported here three recent cases of *M. heraklionense*associated tenosynovitis in immunocompetent men.

The first case was diagnosed in a 31-year-old male who was injured with a palm thorn that penetrated into the proximal interphalangeal joint of his right index finger. In the following weeks, arthritis appeared on this finger. He took non-steroidal anti-inflammatory drugs, which relieved his pain. One year after his initial injury, arthritis persisted, and magnetic resonance imaging confirmed arthritis with collection of the dorsal side of the hand, and joint effusion. He underwent synovectomy. Histopathology revealed subacute and chronic synovitis. He was treated with clarithromycin and rifabutin for six weeks with marked improvement, but was subsequently lost to follow-up.

In the second case, a 52-year-old male developed inflammation of his left third finger in the weeks following an injury with a broken plant pot. Tenosynovitis was diagnosed. He received three weeks of corticosteroids, and two cortisone injections in the affected finger with only temporary symptomatic improvement. Seven months after the onset of symptoms, as his finger was more inflammatory with clinical signs of infection, he underwent synovectomy. He completed six months therapy with clarithromycin (switch for azithromycin due to gastrointestinal side effects) and rifabutin (switch for rifampin because of stockout of rifabutin) with clinical resolution.

In the third case, two months after hitting a nail that fell on the ground into his right hand, a 58-year-old male developed severe swelling of the second and fifth fingers, and wrist. He received corticosteroid therapies with partial efficiency. Ten months after initial injury, ultrasound showed extensive tenosynovitis of the carpal tunnel flexor tendons and of the fifth finger. He underwent urgent synovectomy. Histology showed fibrin deposit and rare polynuclear neutrophils. The patient was treated with clarithromycin, ethambutol and rifampin for severe months with complete resolution.

In the three cases, mycobacterial culture of perioperative specimens grew a slowly-growing mycobacterium in 16–24 days. Species was not identified by commercialized molecular methods (GenoType CM and AS, Hain LifeScience). Sequencing of the 16S rRNA gene showed that the three isolates were closely related to *M. heraklionense* (Fig. 1).

Five additional cases of *M. heraklionense* tenosynovitis have been described.^{2–4} Most patients were immunocompetent, and reported prior trauma to the affected area, suggesting that inoculation was the infection mechanism. Duration of symptoms until diagnosis varied from two to ten months. All cases involved the hand with histopathologic findings of inflammation and granuloma, and growth of the organism from operative materials after prolonged incubation time. Species identification required gene sequencing. Of note, more than one debridement procedure was needed. Synovectomy associated with prolonged antibiotherapy reached a positive outcome in 4 of 5 patients.^{2–4} *M. heraklionense* was also retrospectively involved in 10 additional cases of tenosynovitis between 1986 and 2014 in the USA.⁵

In conclusion, our report provides further evidence that *M. heraklionense* is an emerging cause of tenosynovitis. Identification is challenging and relies on gene sequencing.

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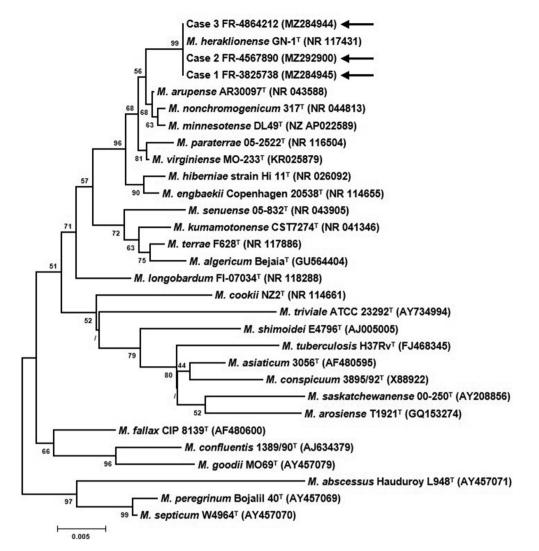


Figure 1. Evolutionary relationships of Mycobacterium taxa based on the 16S rRNA gene. The phylogeny presented is based on the alignment of approximately 1397 bp-length 16S rRNA gene. The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 0.22078491 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. The tree is not rooted and drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method and are in the units of the number of base substitutions per site. The analysis included 30 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 1363 positions in the final dataset. Evolutionary analyses were conducted in MEGA6. Arrows indicate the 16S rRNA gene sequences clustered within the branch of *M. heraklionense*. T, type strain./, bootstrap values below 50%.

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