# Chronic pelvic pain due to *Mycobacterium parascrofulaceum* in an Iranian patient: first report of isolation and molecular characterization from Asia

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Herein we report a case of chronic pelvic pain (CPP) caused by a rare, recently characterized species, *M. parascrofulaceum*, from an Iranian middle aged woman.

## *CASE REPORT*

A 38 year old woman was admitted to the hospital because of CPP for over three months. There was no apparent evidence of immunodeficiency or HIV infection. In the initial evaluation the urine culture for bacteria was sterile. She was empirically started on antibiotic treatment for the presumed chlamydial or mycoplasmal infection but no improvement was observed. The patient returned to the hospital due to increasing lower abdominal pain. Examination of vaginal discharge confirmed the presence of acid-fast bacilli. The etiologic agent was assumed to be *M. tuberculosis* and the patient was put on antituberculosis therapy. Two months thereafter due to an aggregated condition the patient underwent hysterectomy.

Strain M79 was isolated from the removed uterus and confirmed by a combination of conventional and molecular tests including the sequence analyses of 16S rDNA, *hsp65*, *rpoB*, and ITS.[1-3] The GenBank accession numbers of the isolate determined in this work are as follow: GU121551, HM229794, HM229795 and HM229796 for the 16S rDNA, ITS, *hsp65*, *rpoB* genes respectively.

Conventional microbiological analysis of the isolate revealed a slowly growing yellow pigmented scotochromogenic mycobacterial species. It was positive for catalase and urease tests and negative for tellurite, nitrate, tween hydrolysis, niacin, arylsulfatase and iron uptake tests. It was susceptible to amikacin, clarithromycin, rifampicin, doxycycline, sulfamethoxazole, streptomycin, and imipenem.

The almost complete 16S rDNA gene sequence (1,426 bp) of the isolate showed a 99.58% similarity with *M. parascrofulaceum*. The signature nucleotide sequences of the isolate showed only a base pair difference at position 250 compared to that of *M. parascrofulaceum* type strain (Table 1). The ITS, *hsp65* and *rpoB* gene sequences of the isolate showed 98.71%, 99.39% and 100% similarities with those of the reference strain of *M. parascrofulaceum*, respectively.

In 2004, Turenne *et al.* introduced *M. parascrofulaceum* as a distinct species.[3] Later the organism was isolated from a few clinical samples.[4] However, to the best of our knowledge, there have been no reports from the rest of the world.

Genitourinary infection (GUI) due to non-tuberculous mycobacteria (NTM) is very rare and infrequently reported.[5] In the Iranian case herein reported *M. parascrofulaceum* was isolated from a female patient with no apparent immunodeficiency, although she was ill-famed in her community for being a woman with high-risk sexual behavior. Given that most NTM strains are resistant to traditional antituberculous agents, it is important to correctly differentiate genitourinary infections caused by NTM from genitourinary TB.[5] The clinical management of CPP of this Iranian patient was almost ineffective due misdiagnosis of the causative agent during the initial stages of her infection. This was why the practicing physician eventually resorted to surgical operation.

In conclusion, unless the causative organism is correctly identified noninvasive treatment of such complex cases is unlikely to occur.

***Table 1. Alignment of selected stretches of 16SrDNA gene of Iranian strain of M79 with those of closely related mycobacteria***

| **Strain** | **GenBank accession number** | **16S rDNA positions according to *E.coli* numbering system** | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | **128** | **129** | **129** | **134** | **183** | **183** | **183** | **183** | **183** | **183** | **156** | **193** | **193** | **190** | **191** | **250** | **264** |
| *M. parascrofulaceum* | AF337273 | G | C | A | G | G | A | C | T | T | G | C | C | C | G | G | A | T |
| *M. palustre* | AJ308603 | . | T | . | . | . | T | T | . | A | . | . | . | . | T | . | T | C |
| *M. kubicae* | AF133902 | . | T | G | A | . | . | T | G | A | A | T | T | . | A | . | T | C |
| *M. lentiflavium* | AF480583 | . | T | . | . | . | T | T | . | . | . | . | . | . | T | . | T | C |
| *M. simiae* | X52931 | | T | . | . | . | . | . | . | . | . | . | . | . | . | . | T | C |
| *M. scrofulaceum* | AF480604 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
| *M 79* | GU121551 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | T | . |

"." Indicates that the base pair was identical to that of type strain of *M. parascrofulaceum.*

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