

## Case Report

# ***Mycobacterium kumamotonense* in the cervical region in an immunocompetent patient, clinical case report in Mexico**

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### Abstract

Non-tuberculous mycobacterial infection has increased significantly in recent years, especially in emerging countries. We present the case of a 25-year-old male patient, immunocompetent, with cervical lymphadenopathy, identifying *Mycobacterium kumamotonense*, a rare species in extrapulmonary forms and with a high drug resistance index.

**Key words:** Non-tuberculous mycobacteria; cervical lymphadenopathy; *Mycobacterium kumamotonense*.

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### Introduction

Non-tuberculous mycobacteria (MNT) are those unrelated to the *Mycobacterium tuberculosis* and *Mycobacterium leprae* complex. Approximately 170 species known to cause disease in humans are known [1]. These mycobacteria are part of the environment, being identified in soil, water, animals and food products [2]. The pulmonary form is the most frequent in adults, while cervical lymphadenopathies represent the most common extrapulmonary form in children. In patients with HIV / AIDS, disseminated tuberculosis is the main presentation form [1,3]. The incidence and prevalence of pathologies triggered by NTMs have been increasing especially in emerging countries, while in industrialized countries there is a rate that varies from 1 to 1.8 cases per 100,000 inhabitants [4]. The commonly involved agents are *Mycobacterium avium* complex, *Mycobacterium gordonae* and *Mycobacterium xenopi* [5]. Extrapulmonary forms predominate in the female gender with an average age of 50 years, and they are more frequent in skin and soft tissues, followed by disseminated disease and cervical lymphadenopathy [6].

In Mexico there are no epidemiological data or typification of the species involved. There are some case reports in patients with HIV / AIDS in whom *M. avium*, *M. kansasii*, *M. gordonae*, *M. fortuitum* and *M.*

*simiae* were isolated [7]. In previous studies of patients with cervical lymphadenopathy, MNT have been reported only in 6.6% of cases, identifying *M. intracellulare*, *M. gordonae* and *M. fortuitum* [3].

The *Mycobacterium terrae* complex (MTC) is the group of mycobacteria that has been linked as the causative agent of bone and joint infections. Among the main species identified in this complex are *Mycobacterium kumamotonense*, *M. sensuense*, *M. paraterrae*, *M. strain*, *M. engbaekii*, *M. longobardum*, *M. heraklionense*, *M. virginianense* and *M. arupense* [8].

In 2006, a new mycobacterial species, *M. kumamotonense*, was proposed, which has the insertion of 14 nucleotides, which is distinctive of the *M. terrae* complex in the 16S rRNA gene [9,10].

Here below is the report of a clinical case in which the presence of *M. kumamotonense* in an immunocompetent patient with no history of pulmonary pathology and HIV negative is identified.

### Clinical case

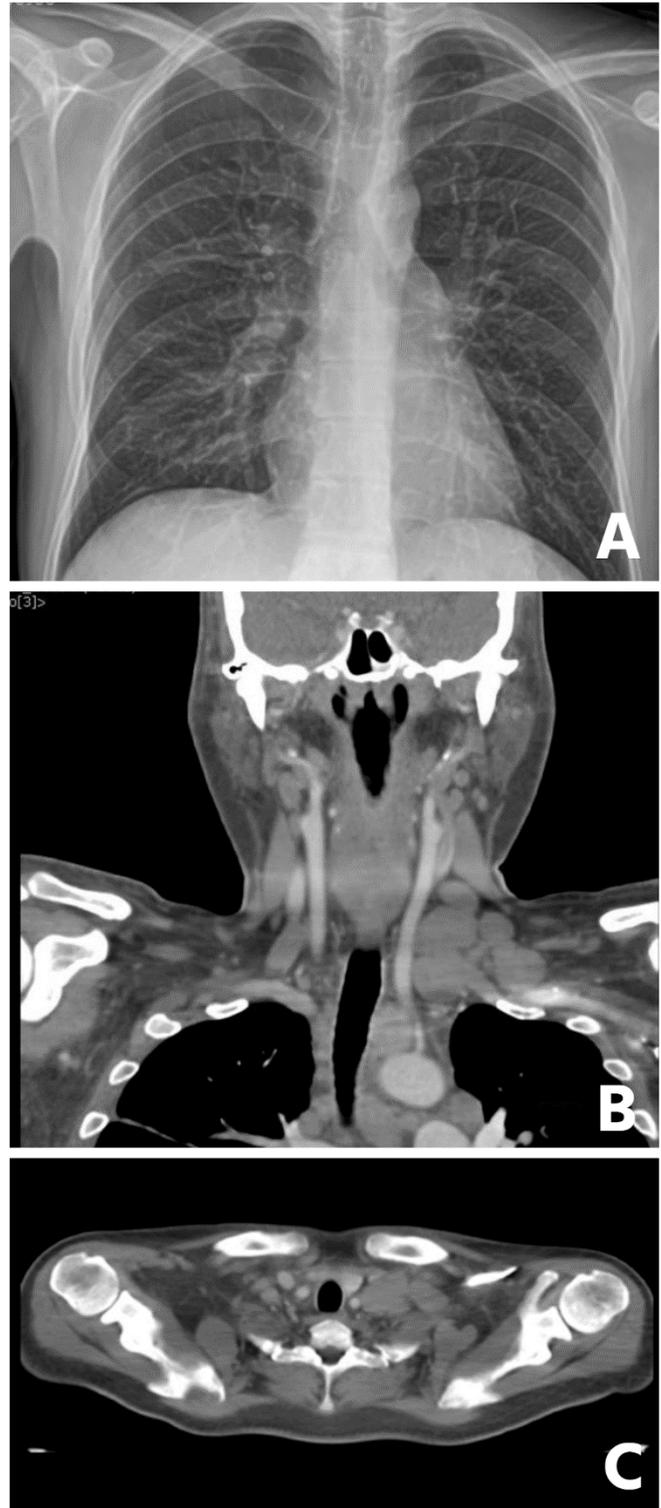
We present the case of a 25-year-old male patient, without a history of immunodeficiencies, who goes to a concentration hospital in Mexico City for presenting a 3-month clinical picture characterized by a fever of 38 ° C, loss 5 kg in weight, accompanied by cervical ganglion growth of approximately 3 cm in diameter,

hard, non-painful, asthenia and adynamia. HIV Elisa test was performed and reported negative and imaging studies, in which chest image was found without lung involvement data. The neck CAT (Computed axial tomography) scanned multiple enlarged cervical ganglion chains (Figure 1). Excisional biopsy of lymphadenopathy was performed finding granulomatous reaction and caseous necrosis in the histopathological study (Figure 2). Ziehl-Neelsen staining was performed identifying the presence of acid-alcohol resistant bacilli. In order to confirm the diagnosis of tuberculosis, culture was carried out in a liquid medium for the detection of *M. tuberculosis* with the diagnostic Becton Dickinson kit, Sparks, MD, USA, observing positive growth at 32 days. Subsequently, DNA was extracted with a phenol chloroform method and PCR technique was performed to amplify a 440 bp fragment corresponding to the hsp65 fragment using primers TB11: 5'-ACCAACGATGGTGTCCAT-3' and TB12: 5'-CTGTGCGAACCGCATAACCCT-3'. This procedure was performed using ABI PRISM\_3130xl Genetic Analyzer (Applied Biosystems, Foster City, CA, USA). The phylogenetic analysis was carried out with MEGA v.6.0 software (distance Neighbor Joining method) using the database for MNT species reported by Escamilla-Escobar [11], including the sequences with ID: KX077601 (strain study), KF432567, KF432807, AB239920, AJ307656, AF547879, GU564405, FJ268582, JN571203, JN571202, KF432509, KT185529 obtained from GenBank.

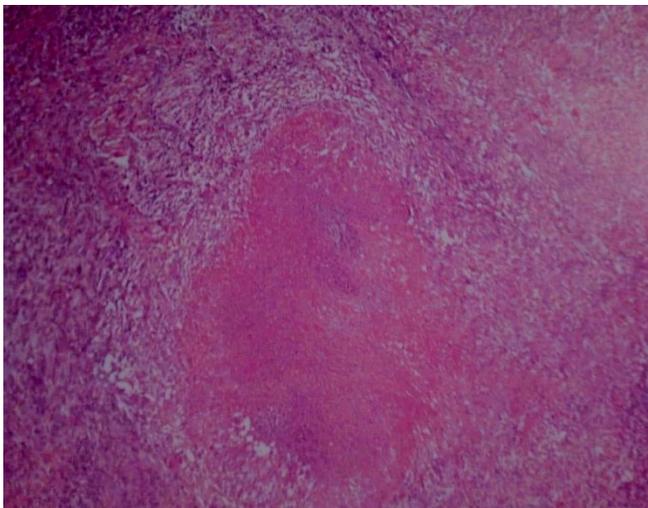
In the results of the protein PCR thermal shock restriction analysis, 65 genes were consistent with those of *Mycobacterium kumamotoense*. The phylogenetic

tree was made based on the sequences of the hsp65 gene under the method of the nearest neighbor (Figure 3).

**Figure 1.** A. Homogeneous calcified image, 1 cm in diameter, in the right hilar region. B. Node conglomerate in left supraclavicular space and paratracheal region which compress the carotid. C. Displaced carotid by node conglomerate.



**Figure 2.** Histological section of cervical lymph node showing chronic granulomatous inflammation with the presence of caseous necrosis with HE staining. 10X.





the other hand, mass spectrometry has also been used, although one of its main limitations is the lack of standardization in the preparation of samples for the specific identification of these species [10].

The most commonly used methods are probes, which identify the most common subtypes of mycobacteria. The identification of mycobacteria by the PCR-RFLP (Restriction fragment length polymorphism) method of *hsp65* has been shown to have advantages over conventional methods for being fast, lower cost and highly specific with results in 48 hrs. It has been reported that the *hsp65* gene is present in all mycobacteria, is more variable than the 16S rRNA gene sequence and is therefore potentially useful for the identification of genetically related species. In our case, a culture medium specific for *M. tuberculosis* was used for the identification of *M. kumamotoense*. Once identified, the *hsp65* gene was amplified, which showed 100% identity with *M. kumamotoense*, so, within the various methods proposed, we agree with what is reported in the literature in which PCR is the most accurate method and accessible for the correct identification of the multiple subtypes of mycobacteria [16].

Although NTMs are usually related to nosocomial infections, there is little evidence of the person-to-person spread of this type of pathogens and the range of diseases that can lead is wide, so the rapid and accurate identification of mycobacteria to the Species level is essential to facilitate early treatment of mycobacteriosis [17,18].

## Conclusions

It is important to note that health personnel do not suspect the presence of MNT in immunocompetent patients with extrapulmonary disease and much less to the isolation of *M. kumamotoense*, a species little studied and unfortunately resistant to first-line medications, causing a chronic disease in the most cases.

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