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Article

Cord factor producer *Mycobacterium abscessus* subsp. *bolletii* in asymptomatic immunocompetent host sputa samples

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We report a case of *Mycobacterium abscessus* subsp. *bolletii* colonization *in* upper respiratory tract of an immunocompetent patient, who was misdiagnosed as tuberculosis by Acid Fast Bacilli (AFB) and cord factor formation observed directly from the sputa culture in liquid medium. This fact reflected a significant impact on the individual case's life and showed the importance to identify the mycobacteria isolated from clinical sample at species level, and to determine the true implication of nontuberculous mycobacteria (NTM) detected in clinical samples.

Keywords: Nontuberculous mycobacteria. Tuberculosis. Diagnosis. Microscopy. Molecular diagnosis.

INTRODUCTION

Microscopic cord factor aggregation is a phenotypic characteristic of *Mycobacterium tuberculosis*, firstly reported by Robert Koch in 1882, and associated with virulence since 1947 by Middlebrook and colleagues (1974). It is composed by tight bundles formed by parallel alignments of bacilli, which are historically considered a distinct trait, and used as a practical criterion for rapid and presumptive identification of *M. tuberculosis* isolates in clinical laboratories (Carter, Ratkiewicz, 1998).

The cord factor aggregation has been related to intracellular replication and granuloma formation by *M. tuberculosis* (Yamagami *et al.*, 2001). In other mycobacteria, the occurrence of cord factor aggregation was demonstrated in some nontuberculous mycobacteria (NTM) distantly related to *M. tuberculosis,* which includes *Mycobacterium marinum* and *Mycobacterium Abscessus* Complex (Julián *et al.*, 2010). Likewise, cord producers *M. abscessus* Complex tend to harbor drug resistance (Rüger *et al.*, 2014) with severe lung disease (Sanguinetti *et al.*, 2001).

NTM form a large group within the *Mycobacterium* spp., and show wide environmental distribution. More than 100 species are found in soil, potable water, food, and animals. Inside the NTM group, the rapidly growing mycobacteria (RGM), which are able to produce mature colonies on agar plates within 5 to 7 days, have been considered important human pathogens in the last decades (Pang et *al.*, 2015).

The pathogenicity of NTM species, whether in man or in animals, ranges from an innocuous colonization to a wide kind of human diseases, mainly pulmonary and soft tissue infections. The detection of NTM, in clinical specimens, can have no clinical significance. The determination of their clinical significance in such specimens is sometimes not easy to interpret, and requires specific criteria to make the distinction between

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colonization and disease (mycobacteriosis). Also, the identification of the NTM, at species level, is laborious and sometimes inconclusive.

The increase of NTM caused diseases and the laboratory challenges for presumptive differentiation of NTM bacillus motivated us to write this case report. This case study aimed to alert the microbiologist about the importance of the correct identification of the *Mycobacterium* species and its impact for the health and life of the patients.

CASE PRESENTATION

Due to traveling requirements, an asymptomatic 23-year-old female was assisted by a primary care physician. A chest X-ray done at the time did not reveal thoracic alterations.However, the acid-fast staining microscopy of expectorated sputa showed the presence of acid-fast bacilli (AFB) in two independent samples (+ and ++ in the acid-fast staining microscopy by Ziehl Neelsen, Z-N). At that time, tuberculosis therapy was started, according to the World Health Organization recommendation (WHO, 2016; Brasil, 2011). In parallel, two new sputa samples cultures were required. The cultures of samples were carried out on BD BACTEC MGIT System (Mycobacteria Growth Indicator Tube) (BD Difco™ BBL™, USA). After 5 days of cultures incubation, it was observed AFB growth, which were subcultured in Lowenstein-Jensen medium. After the same time of incubation at 35 °C in normal atmosphere, smooth white colonies were observed.

Until mycobacterial identification, a gradually smooth to rough reversion in the colony morphotype was observed in bacillus subcultures in Lowentein-Jensen medium. These colonies morphology changes occurred by the predominance of smooth white colonies on the first culture, and the progressive predominance of rough colonies in the last ones. The Z-N from the Middlebrook 7H9 medium, added of 0.2 % glycerol (SIGMA – Aldrich St Louis Mo, USA) and supplemented with OADC(BD Difco™ BBL™, USA), showed acid-fast cord factor aggregates after subsequent culture. Identification at the species level was performed by PCR-restriction fragment length polymorphism analysis (PRA) of a 441 bp *hsp65* fragment. Interpretations of PRA-*hsp65* patterns in PRA site were characteristic of *Mycobacterium abscessus* subsp. *bolletii* (BstEII, 235/210/0; HaeIII, 200/70/60) (http://app.chuv.ch/prasite/index.html).

As no clinical symptoms and lung impairment was correlated with NTM disease, and no immunocompromised background such as HIV/AIDS or a primary immunodeficiency was detected in the patient, the tuberculosis treatment was suspended. No treatment for NTM was introduced and the patient has been clinically followed by the clinician.

The patient signed the informed consent form for the publication of this clinical case, and reported that the main impact on her personal life was the interruption of an international scholarship, scheduled at that time, due to the misdiagnosis of tuberculosis.In addition, as consequence of the anti-tuberculosis therapy, the patient suffered from adverse effects. The study was approved by the Ethics Committee (COPEP) of the State University of Maringá, Brazil, according to Portaria Nº 004/ 2013, under opinion nº 1.937.

DISCUSSION

This report raises the question of preliminary identification of *M. tuberculo*sis by the presence of cord factor aggregation, which is widely used in low income clinical laboratories. This come to reinforce the need for the correct and rapid identification of the acid fast bacilli (AFB), detected in clinical samples, at species level.

All mycobacteria species have an unusual cell wall structure, in which outside the plasma membrane, a non-fluid hydrophobic fatty acid layer supports a fluid monolayer rich in glycolipids as trehalose 6,6-dimycolate – TDM (cord factor). This cell wall composition plays a role in the prevention of bacterial desiccation, and TDM seems to be an important antigen for the immune modulation in M. *tuberculosis* infections (Harland *et al*., 2008).

The smooth to rough colony morphotype reversion, observed in *M. abscessus* subsp. *bolletii* isolated from the sputa samples in this case, is a recognized change that occurs in NTM cell wall composition, which leads to increase in the bacilli virulence and survival

into macrophages (Julián *et al*., 2010).This colony morphotype variation occurs due to a defect in the cell wall glycopeptidelipid (GPL) production that has been observed in *M. abscessus* Complex, including *M. abscessus* subsp. *bolletii* (Howard et al., 2006; Medjahed, Reyrat, 2009). Such change of *M. abscessus* colony phenotype was recently, related to mutations in the *gpl* gene, which codify GPL, leading to a defective GPL production, as demonstrated in *M. abscessus,* as well as in *M. abscessus* subsp. *bolletii* clinical isolates (Kim *et al*., 2013).

According to Howard *et al.* (2006) the location of GPL in the outer most portion of the cell wall in *M. abscessus* smooth phenotype colony can prevent the interaction of TDM molecules from contiguous bacteria necessary for cording formation.This explains the observation of cording formation in *M. abscessus* subsp. *bolletii* detected after subcultures of sputa from the individual case in this study.

The cording factor formation in *M. abscessus* Complex was observed previously, which involves glycolipid trehalose 6,6'-dimycolate (TDM), and is associated with the virulence of bacterial variants to persist and cause invasive disease(Howard *et al*., 2006).

We can argue here that the false tuberculosis diagnosis was first indicated by AFB smear (++). Also, it is important to emphasize that the *M. abscessus* subsp. *bolletii* detection does not prompt to a disease, which can create diagnostic errors and lead to unnecessary and wrong treatment, as occurred with the patient case. The determination of clinical significance of NTM isolated in sputum as a disease-causing or as part of transient microbiota is not always easy, and requires specific criteria (Li *et al*., 2017). It is important to emphasize that, in the present case, the *M. absessus* subsp. *bolletii* was isolated in two primary sputa samples and in another requested by the laboratory for case confirmation.

Diseases caused by NTM are associated with the natural resistance to many antibacterial drugs, which leads to disappointing clinical results from currently available therapy. This notorious situation is not different with *M. abscessus* Complex, as it is one of the most chemotherapeutic resistant NTMs, responsible for poor treatment outcomes (van Ingen, Kujiper, 2014).

The present case report raises the question of how important it is to carry out diagnosis assays for identification of mycobacteria at species level, in clinical specimens, as soon as possible, to introduce the correct treatment and confirm the NTM susceptibility by drug susceptibility testing.

CONCLUSION

The present study draws attention to the importance of identifying the mycobacteria species in clinical sample and determine the true implication of NTM detected as the causative agent of the disease.Furthermore, the treatment for tuberculosis differs from those for diseases caused by NTM. A misdiagnosis can have serious consequences for the mental and social health of the patient.

CONFLICT OF INTERESTS

None to declare

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REFERENCES

Brasil, Ministério da Saúde. Manual de recomendações para o controle da tuberculose no Brasil. 1ª edição. Ministério da Saúde. Brasília. 2011. Available at: http://bvsms.saude.gov.br/bvs/publicacoes/manual_recomendacoes_controle_tuberculose_brasil.pdf.

Carter YSMC, Ratkiewicz IN. Cord formation in BACTEC medium is a reliable, rapid method for presumptive identification of *Mycobacterium tuberculosis* complex. J Clin Microbiol. 1998;36(9):2769–71.

Harland CW, Rabuka D, Bertozzi CR, Parthasarathy R. The *Mycobacterium tuberculosis* virulence factor trehalose dimycolate imparts desiccation resistance to model mycobacterial membranes. Biophys J. 2008;94(12):4718–24. doi:10.1529/biophysj.107.125542.

Howard ST, Rhoades E, Recht J, Pang X, Alsup A, Kolter R, et al. Spontaneous reversion of *Mycobacterium abscessus* from a smooth to a rough morphotype is associated with reduced expression of glycopeptidolipid and reacquisition of

an invasive phenotype. Microbiology. 2006;152(Pt. 6):1581–90. doi:10.1099/mic.0.28625-0.

Li G, Pang H, Guo Q, Huang M, Tan Y, Li C, Wei J, Xia Y, Jiang Y, Zhao X, Liu H, Zhao LL, Liu Z, Xu D, WanK. Antimicrobial susceptibility and MIC distribution of 41 drugs against clinical isolates from China and references strains of nontuberculous mycobacteria. Int J Antimicrob Agents. 2017;49(3):364-374.doi: 10.1016/j.ijantimicag.2016.10.024.

Julián E, Roldán M, Sánchez-Chardi A, Astola O, Agustí G, Luquin M. Microscopic cords, a virulence-related characteristic of *Mycobacterium tuberculosis*, are also present in nonpathogenic mycobacteria. J Bacteriol. 2010;192(7):1751–60. doi:10.1128/JB.01485-09.

Kim Byoung-Jun, Kim B-R, Lee S-Y, Kook Y-H, Kim Bum-Joon. Rough colony morphology of *Mycobacterium massiliense* Type II genotype is due to the deletion of glycopeptidolipid locus within its genome. BMC Genomics. 2013;14:890. doi:10.1186/1471-2164-14-890.

Medjahed H, Reyrat J-M. Construction of *Mycobacterium abscessus* defined glycopeptidolipid mutants: comparison of genetic tools. Appl Environ Microbiol. 2009;75(5):1331–8. doi:10.1128/AEM.01914-08.

Middlebrook BYG, Dubos RENJ, Pierce C. Virulence and morphological characteristics of mammalian tubercle bacilli. J Exp Med. 1947;86(2):175–184. doi: 10.1084/jem.86.2.175

Pang H, Li G, Wan L, Jiang Y, Liu H, Zhao X, et al. In vitro drug susceptibility of 40 international reference rapidly growing mycobacteria to 20 antimicrobial agents. Int J Clin Exp Med. 2015;8(9):15423-31.

Rüger K, Hampel A, Billig S, Rücker N, Suerbaum S, Bange FC. Characterization of rough and smooth morphotypes of *Mycobacterium abscessus* isolates from clinical specimens. J Clin Microbiol. 2014;52(1):244–50. doi:10.1128/JCM.01249-13.

Sanguinetti M, Ardito F, Fiscarelli E, Sorda MLA, Argenio PD, Ricciotti G, et al. Fatal pulmonary infection due to multidrug-resistant *Mycobacterium abscessus* in a patient with cystic fibrosis. J Clin Microbiol. 2001;39(2):816–9. doi: 10.1128/JCM.39.2.816-819.2001

Van Ingen J, Kuijper EJ. Drug susceptibility testing of nontuberculous mycobacteria. Future Microbiol. 2014;9(9):1095-110.doi: 10.2217/fmb.14.60.

Yamagami H, Matsumoto T, Fujiwara N, Arakawa T, Kaneda K, Yano I, et al.Trehalose 6,6′-dimycolate (cord factor) of *Mycobacterium tuberculosis* induces foreign-body- and hypersensitivity-type granulomas in mice. Infect Immun. 2001;69(2):810–5. doi:10.1128/IAI.69.2.810-815.2001.

World Health Organization. World health statistics 2016: monitoring health for the SDGs, sustainable development goals. World Health Organization. 2018.

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