

Prevalence of *Mycobacterium abscessus* among the Patients with Nontuberculous Mycobacteria

Saman Ayoubi, PhD^{1*}; Jafar Aghajani, PhD¹; Poopak Farnia, PhD²; Parissa Farnia, PhD¹; Jalaledin Ghanavi, MD¹; Ali Akbar Velayati, MD¹

¹Mycobacteriology Research Center (MRC), National Research Institute of Tuberculosis and Lung Disease (NRITLD), Shahid Beheshti University of Medical Sciences, Tehran, Iran

²Department of Biotechnology, School of Advanced Technology in Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: Considering the importance of the increasing incidence of non-tuberculous mycobacteria, especially *Mycobacterium abscessus* worldwide, we conducted a study to evaluate the incidence of these diseases in our area. The aim of this study was to evaluate the prevalence of *M. abscessus* in patients with non-tuberculous mycobacteria.

Methods: This descriptive study was performed on 18,083 samples isolated from patients with non-tuberculous mycobacteria during 2011-2017 at the Mycobacteriology Research Center (MRC), Tehran, Iran. To identify the *Mycobacterium* species, a 439 bp fragment of the IS6110 gene was first amplified using primers TB1 and TB2. Samples with a negative polymerase chain reaction (PCR) result were analyzed to investigate non-tuberculosis mycobacteria (NTM), especially *M. abscessus* using the RFLP method.

Results: Of the 18,083 samples, 5513 (30.49%, 95% CI, 12.95) strains of Complex Tuberculosis and 236 (1.31%, 95% CI, 1.84) strains of NTM were identified. The mean age of the patients with NTM was 18 years, and most of them were male. The most commonly identified species in this study were *M. abscessus* type I 32 (13.56%, 95% CI, 18.36) and *M. abscessus* type II 13 (5.51%, 95%CI, 20.04).

Conclusion: In this study, we observed a high prevalence of *Mycobacterium abscessus* type 1 in patients. As the treatment protocol for non-TB mycobacteria is different from *M. abscessus* complex, the diagnosis of these species as soon as possible will be significant for physicians.

Keywords: *Mycobacterium abscessus*, Nontuberculous mycobacteria, Polymerase chain reaction, Prevalence

Cite this article as: Ayoubi S, Aghajani H, Farnia P, Farnia P, Ghanavi J, Velayati AA. Prevalence of *Mycobacterium abscessus* among the patients with nontuberculous mycobacteria. Arch Iran Med. 2020;23(3):163-168.

Received: May 11, 2019, Accepted: September 25, 2019, ePublished: March 1, 2020

Introduction

The mycobacterium family has more than 160 species.¹ One of their most famous species is *Mycobacterium tuberculosis* the causative agent of tuberculosis.² The mycobacteria other than *M. tuberculosis* are usually classified as non-tuberculosis mycobacteria (NTM).^{3,4} This group of bacteria is present in all environmental sources such as water and soil, as well as dust particles in the air, and cause diseases in humans and animals as opportunistic bacteria.⁵⁻⁷ The transmission of these mycobacteria from humans to humans rarely happens. However, if this transmission occurs, these organisms can lead to serious complications.^{8,9} Atypical mycobacteria were classified by Runyon in 1950 based on their growth rate and pigment production.^{10,11} Accordingly, NTM are classified into 4 groups: groups 1 to 3 as fast-growing, and group 4 as slow-growing.¹²⁻¹⁴ These organisms are responsible for four distinct clinical conditions, including progressive pulmonary disease, superficial lymphadenitis, disseminated diseases, as well as skin and soft tissue infections.¹⁴⁻¹⁶ Lung diseases and other diseases caused by these mycobacteria are now known in many parts of

the world. Approximately 80% of patients with NTM infections are middle-aged or older women.^{17,18} NTM have been dramatically associated with pulmonary diseases in humans over the past 30 years.¹⁸⁻²⁰ *M. abscessus*, as one of the NTM, is a fast-growing bacterium which can increase respiratory diseases.²¹⁻²³ Evidence suggests the association between *M. abscessus* and respiratory infections in humans.²⁴⁻²⁶ Concerns about this issue are rising,²⁷ as in recent years, the role of *M. abscessus* has been identified in the development of respiratory infections, especially in patients with NTM.^{25,27,28} This topic is classified as an emerging disease, which is especially serious in immunodeficient patients.²⁵ For example, in patients with cystic fibrosis, infection with *M. abscessus* results in a high rate of mortality.^{13,29,30} Developing countries have long been researching the issue's sensitivity in terms of public health in this regard.^{31,32} Increased infection with NYM and the inability of health systems in developing countries to identify them have caused non-differentiation of *M. abscessus* in patients with NTM.^{8,14,33} The issue of *M. abscessus* in clinical specimens is a serious concern in advanced countries.^{31,34} However, less attention is paid

*Corresponding Author: Saman Ayoubi, PhD; Mycobacteriology Research Center (MRC), National Research Institute of Tuberculosis and Lung Disease (NRITLD), Shahid Beheshti University of Medical Sciences, Tehran, Iran. Tel: +989119439234; Fax:+982126109680; Email: s.ayoubi@theaasm.org

to developing countries due to technical and practical limitations.³⁵⁻³⁸ *M. abscessus* is one of the most important known mycobacteria among non-tuberculosis. It is considered to be the most common non-tuberculosis mycobacterium in the United States, Asia, and most of Europe.^{25,28,34} However, Iran as a developing country, is less concerned with this issue and limited activities are being undertaken against it. Differences in the diagnostic methods of this bacterium compared to other non-tuberculosis bacteria have made its timely diagnosis significant for both physicians and the community. The aim of this study was to determine the prevalence of *M. abscessus* in non-tuberculosis clinical specimens.

Materials and Methods

This descriptive study was performed on 18083 samples isolated from patients during 2011-2017 at the Mycobacteriology Research Center (MRC), Tehran, Iran. Initial isolation of *Mycobacterium* strains was performed by Petrof method and Johnson culture media. In the next step, DNA of *Mycobacterium* was extracted from the sputum samples of patients using the Kiagen kit (QiAamp DNA) according to the manufacturer's instructions. To identify the *Mycobacterium* species, a 228-bp fragment from IS6110 gene was amplified using specific primers. The polymerase chain reaction (PCR) mixture with a final volume of 50 mL contained 33.5 μ L distilled water, 2.5 μ L X10 buffer, 4 μ L primer, 1 μ L dNTP mix, 2.5 μ L MgCl₂, 2 μ L DNA template, and 0.5 μ L Taq DNA polymerase enzyme. The PCR reaction in the thermal cycler machine was as follows; The first cycle was 95°C for 10 minutes for initial denaturation, consisting of 35 cycles, 93°C for 20 seconds, 65°C for 1 minute, 72°C for 20 seconds continued, with the final cycle performed for 5 minutes at 72°C for final elongation. In the next step, PCR products were loaded onto 1.5% agarose gel containing iodide bromide (Figure 1, Table 1).

The samples, which were IS6110 positive, were considered as a complex of tuberculosis. The samples with a PCR result of IS6110 negative were analyzed using the PCR-RFLP method to investigate NTM using gene hsp65. Duplication of this gene was performed using Nested PCR. In the first stage, a pair of specific primers were used. Then, the PCR mix was used with a final volume of 50 μ L containing 4 picomoles of special primers, 1.5 mM MgCl₂, 0.5 units of Taq polymerase enzyme, 1 mM dNTP, 1.5 mM X10 buffer, and 1% of DMSO. The PCR reaction

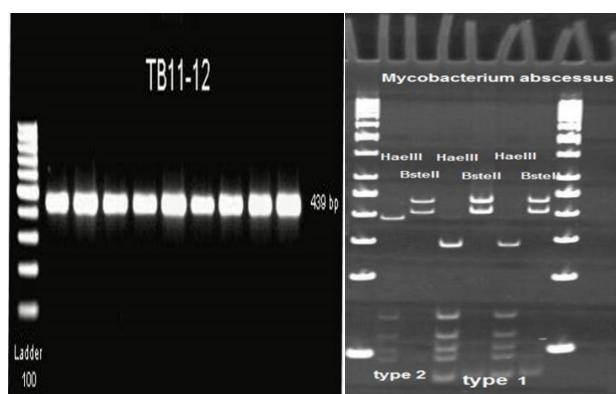


Figure 1. *Mycobacterium abscessus*, Hsp, 65kd, PCR Product: 439 bp, Digest with BstEII & HaeIII.

occurred in the thermal cycler machine consisting of 30 cycles at an annealing temperature of 60°C. The second stage was performed using a pair of specific primers. PCR reaction was used with 50 μ L final volume containing 8 picomoles of a specific primer, 1.5 mM MgCl₂, 1 unit of Taq polymerase enzyme, 0.2 mM dNTP, 1 mM of X10 buffer, and 2% of DMSO. The reaction temperature conditions were as follows: The first cycle was 95°C for 5 min for initial denaturation, which continued with 30 cycles of 94°C for 30 seconds, 56°C for 1 minute, and 72°C for 40 seconds, with the final cycle completed at 72°C for 10 minutes. Finally, the proliferated fragment of PCR was electrophoresed on 1.5% agarose with a band of 439 bp observed. The fragments amplified by two restriction enzymes Hae III and BstE II were digested according to the manufacturer's instructions. Digestive products were electrophoresed on 8% acrylamide gel with the digested genetic model compared with the standard strain genetic model. SPSS version 20.0 software was used to analyze the data where the frequency of percentages was calculated.

Results

A total of 18083 patients with mycobacteria [Complex Tuberculosis strains (5513/18083; 30.49%, 95% CI, 12.95) and NTM strains (236/18083; 1.31%, 95% CI, 1.84)] were examined for the incidence of *M. abscessus* in the MRC from 2011 to 2017 (Tables 1 and 2). The mean age of patients referring to this center was 2 to 40 years. The male/female ratio for *M. abscessus* was 56% to 53% (24 males/ 21 females) (Tables 3 and 4).

Of the 18083 patients referring to the MRC, 236 (236/18083; 1.31%, 95% CI, 1.84) had NTM and 5513

Table 1. Digest with BstEII & HaeIII

Rapidly Growing	<i>Mycobacterium abscessus</i>			
	HSP65	Gene		
Non-pigmented	BstEII pattern	95% CI	Haell pattern	95% CI
<i>Mycobacterium abscessus</i> type 1	235 / 210 / 0	0.26	145 / 70 / 60 / 55	0.61
<i>Mycobacterium abscessus</i> type 2	235 / 210 / 0	0.26	200 / 70 / 60 / 50	1.02

(5513/18 083; 30.49%, 95% CI, 12.95) had complex tuberculosis. According to our study, out of 236 people with NTM, 45 (45/236; 19.07%) were infected with *M. abscessus*. Of the 236 specimens infected with NTM of all patients (18 083) referring to the MRC, only 45 (45/236; 19.07%) cases had *M. abscessus*; of this number, 5.51% (13/236; 5.51%, 95% CI, 20.04) of subjects had *M. abscessus* type 2 and 13.56% (32/236; 13.56%, 95% CI, 18.36) harbored *M. abscessus* type I (Table 3). Statistical data in this study revealed that *M. abscessus* type I (32/236; 13.56%, 95% CI, 18.36) had the highest frequency in comparison with *M. abscessus* type II (13/236; 5.51%, 95% CI, 20.04) among NTM (236/18083; 1.31%) (Table 3). According to these findings, *M. abscessus* type I could play an important role in the severity of pulmonary disease in these individuals.

Also, the study of the prevalence of *M. abscessus* in terms of gender in the patients referring to the MRC suggested that the incidence of *M. abscessus* type I was higher in both men and women as compared to *M. abscessus* type II. It was also found that the incidence of *M. abscessus* type I (14/32; 43.75%) was higher in women than men (13/32; 40.63%) referring to the MRC (Table 4). It was also observed that the incidence of *M. abscessus* type II was higher in men (10/13; 76.93%) than women (5/13; 38.47%) (Table 4).

Finally, according to the results, *M. abscessus* type I in women and *M. abscessus* type I in men were the most frequent among all samples. In general, it can be concluded that *M. abscessus* type I has a higher incidence among women and men referring to the MRC compared to *M. abscessus* type II (Table 3).

Table 2. Frequency of Different Species Isolated from Patients Referring to Masih Daneshvari Hospital

Isolated Species of <i>Mycobacteria</i>	Total Number of Patients (n = 18083)	95% CI
NTM	(236/18083; 1.31%)	1.84
Complex tuberculosis	(5513/18083; 30.49%)	12.95
Total number	18083	-

Table 3. Frequency of *Mycobacterium abscessus* in Patients with Non-tuberculosis Mycobacteria

NTM Species	Total Number of NTM (n = 236)	95% CI
<i>Mycobacterium abscessus</i> 1	(32/236; 13.56%)	18.36
<i>Mycobacterium abscessus</i> 2	(13/236; 5.51%)	20.04
Total number of <i>Mycobacterium abscessus</i>	(45/236; 19.07%)	-

Table 4. Prevalence of *Mycobacterium abscessus* in Terms of Gender

Gender (n = 45)	<i>Mycobacterium abscessus</i>	<i>Mycobacterium abscessus</i>
	Type 1 (n = 32)	Type 2 (n = 13)
Female (n = 21)	14/32; 43.75%	5/13; 38.47%
Male (n = 24)	13/32; 40.63%	10/13; 76.93%

Discussion

Non-tuberculosis *Mycobacterium* species are rapidly expanding, though the level of their infectivity is limited to humans. *M. abscessus* is a fast-growing species and the most important mycobacteria known among non-tuberculosis types.³⁹ It is considered to be the most common non-tuberculosis mycobacterium in the United States, Asia, and most of Europe.⁴⁰ The increasing prevalence and high rates of proliferation of this bacterium have caused a sensitivity in developed countries, while Iran as a developing country is less concerned with this issue, and limited activities have been undertaken.²⁹ The diagnosis principle in this bacterium is more important than other NTM for its timely diagnosis for physicians and the community.²⁵ The study showed that in Iran, the prevalence of non-tuberculous mycobacteria has been neglected; so, the incidence of *M. abscessus* diseases may grow in Iran. In 2010, Esther et al in the United States investigated the association between *M. abscessus* infection and lung function decline in cystic fibrosis patients.⁴¹ They examined 1216 patients with cystic fibrosis over 8 years in the presence of mycobacteria abscesses. They found that infection with *M. abscessus* is very common in cystic fibrosis patients and reduces their lung function.⁴¹ In another study by Van Ingen et al in the Netherlands, the clinical relevance of *M. abscessus* was studied in 95 patients. They looked at patients' clinical data from their clinical records from 1999 to 2005 where *M. abscessus* was isolated from clinical specimens using the *rpoB* sequencing. They observed that a quarter of patients with pulmonary disease were infected with *M. abscessus*.⁴² Also, in another study by Benwill and Wallace in the United States, diagnosis and treatment of *M. abscessus* were evaluated in patients. They concluded that *M. abscessus* survival was improved in patients with non-tuberculous contamination.⁴³ In another study by Griffith in Texas, the clinical features of pulmonary patients (n = 80) caused by fast-growing mycobacterium were studied. They observed that the highest incidence rate was related to *M. abscessus* type I species.⁴⁴ All of these studies suggest that *M. abscessus* is highly prevalent in patients infected with NTM, yet many countries ignore the spread of this bacterium. The results of our studies were consistent with the findings of other studies. The results of our study revealed that *M. abscessus* (45/236; 19.07%) was the most common among the isolated NTM (236/18083; 1.31%). Other studies have shown that among *M. abscessus* isolated from NTM (236/18083; 1.31%), *M. abscessus* type I and II were isolated. Specifically, the results indicated that *M. abscessus* type I (32/236; 13.56%, 95% CI, 18.36) is more abundant than *M. abscessus* type II (13/236; 5.51%, 95% CI, 20.04). Also, by examining the prevalence of *M. abscessus* based on gender in patients referring to the MRC, *M. abscessus* type I was found to be more prevalent in men and women than *M. abscessus* type II. The results of this study are consistent with the results of the studies by

Velayati et al and Henkle et al who examined the prevalence of NTM in environmental and clinical samples. These results indicate that NTM are expanding.^{25,45} Further studies have indicated that *M. abscessus* type I (Female, 14/32, 43.75%; male, 13/32, 40.63%) is more common in women than men. It was also found that *M. abscessus* type II (Male, 10/13, 76.93%; Female, 5/13, 38.47%) is more common in men than women. These results suggest that *M. abscessus* should be considered seriously, so as to prevent the prevalence of many pulmonary diseases. Based on different sources, the incidence of *M. abscessus* in non-tuberculosis was very low, with quantitative studies testing this matter. Through this study, we were able to take a positive step in this direction and to determine that *M. abscessus* (45/236; 19.07%) in non-tuberculosis (236/18083; 1.31%) can play a very important role in the development of various pulmonary diseases.

Our study yielded important information about the prevalence of NTM. In this study, we observed a high incidence of *M. abscessus* among patients. It can be stated that since the samples used in this study were lung and sputum specimens, if it were possible to take samples from other tissues, or soil etc., those results would be similar to other findings.^{4,6,7,10,14,16,18} Another reason for the differences in our study with similar studies in the United States, Asia, and most European regions is that the patients studied here, unlike most provincial studies, were from all over Iran who were referred to the tuberculosis center of the country.^{40,46,47} Therefore, the study conducted in this regard is more general and indicates the abundance of NTM throughout Iran.^{4,25,34} Various reports show that the prevalence of NTM, especially *M. abscessus*, is high in parts of America, Asia, and most European regions.⁴⁷⁻⁵² Considering the similarity of this mycobacterium to *M. tuberculosis*, molecular methods for differentiating *M. abscessus* from *M. tuberculosis* are more accurate, faster, and more sensitive than current tests.⁵³⁻⁵⁵ As stated earlier, the results revealed that *M. abscessus* type I has a higher frequency compared to *M. abscessus* type II. *M. abscessus*, as well as other fast-growing mycobacteria, are often found in water resources and soils.⁵⁶⁻⁵⁸ Observation of non-tuberculosis mycobacteria has increased due to changes in behavior and for unknown reasons, with the growth and dispersal of NTM in the environment.^{4,18,59,60} Boiling water is a simple method for people living in Asia which may protect them against lung colonization. Based on this protocol, NTM with *M. tuberculosis* complex (5513/18083; 30.49%, 95% CI, 12.95), which are more prevalent than NTM (236/18083; 1.31%, 95%CI, 1.84), have been different in this study. Therefore, timely diagnosis will have significant implications for physicians. The treatment of NTM varies depending on the species. However, a cure for this mycobacterium has never been easy, as it requires the use of several drugs within 24 months. In addition, they have significant side effects, some of which are often

not curable. The laboratory, with timely and accurate diagnosis of NTM, can take an effective step in treatment of pulmonary diseases and guide the physician in choosing the appropriate treatment protocol.

In conclusion, the results of NTM suggested that despite the misconceptions of some physicians, NTM, such as *M. abscessus*, could be dangerous. As observed in this study, the spread of NTM, especially *M. abscessus*, was very common in Iran and was a causative agent in patients referring to the MRC. Therefore, it is crucial that they are recognized properly, which will prevent the administration of misleading and rapid acting treatments.

Authors' Contribution

SA: wrote the paper, analyzed the data. JA: collected the data. PoF: collected the data, performed the experiments. PaF: wrote the paper, performed the experiments, conceived the experiments, collected the data, and analyzed the data. JG and AAV: collected the data, performed the experiments, conceived the experiments.

Conflict of Interest Disclosures

None.

Ethical Statement

The study was approved by Shahid Beheshti University of Medical Sciences, Tehran, Iran (Ethical Approval: IR.SBMU.NRITLD.REC.1396.362).

Funding Sources

The funding source of this study was from Mycobacteriology Research Center (MRC), National Research Institute of Tuberculosis and Lung Disease (NRITLD), Shahid Beheshti University of Medical Sciences, Tehran, Iran.

References

1. Lim JM, Kim JH, Yang HJ. Management of infections with rapidly growing mycobacteria after unexpected complications of skin and subcutaneous surgical procedures. Arch Plast Surg. 2012;39(1):18. doi: 10.5999/aps.2012.39.1.18.
2. Tortoli E. Impact of genotypic studies on mycobacterial taxonomy: the new mycobacteria of the 1990s. Clin Microbiol Rev. 2003;16(2):319-54. doi: 10.1128/CMR.16.2.319-354.2003.
3. OFFICIAL T. Diagnosis and treatment of disease caused by nontuberculous mycobacteria. Am Rev Respir Dis. 1990;142:940-53. doi: 10.1164/ajrccm/142.4.940.
4. Velayati AA, Rahideh S, Nezhad ZD, Farnia P, Mirsaeidi M. Nontuberculous mycobacteria in Middle East: current situation and future challenges. Int J Mycobacteriol. 2015;4(1):7-17. doi: 10.1016/j.ijmyco.2014.12.005.
5. Wallace Jr R. Diagnosis and treatment of disease caused by nontuberculous mycobacteria. Am J Respir Crit Care Med. 1997;156:s1-s25. doi: 10.1164/ajrccm.156.2.
6. Khaledi A, Bahador A, Esmaeili D, Tafazoli A, Ghazvini K, Mansury D. Prevalence of nontuberculous mycobacteria isolated from environmental samples in Iran: A meta-analysis. J Res Med Sci. 2016;21. doi: 10.4103/1735-1995.187306.
7. Mertaniasih NM, Kusumaningrum D, Koendhori EB, Kusmiati T, Dewi DNSS. Nontuberculous mycobacterial species and *Mycobacterium tuberculosis* complex coinfection in patients with pulmonary tuberculosis in Dr. Soetomo Hospital, Surabaya, Indonesia. Int J Mycobacteriol. 2017;6(1):9. doi: 10.4103/2212-5531.201894.
8. Farivar TN, Johari P, Moien AA, Shahri MH, Naderi M, Oskouie H. Assessment of prevalence of non-tuberculous mycobacteria

- in archival acid-fast bacilli positive smear slides by TaqMan real-time PCR assay. *N Am J Med Sci.* 2012;4(5):231. doi: 10.4103/1947-2714.95907.
9. Velayati AA, Farnia P, Hoffner S. Drug-resistant *Mycobacterium tuberculosis*: Epidemiology and role of morphological alterations. *J Glob Antimicrob Resist.* 2018;12:192-6. doi: 10.1016/j.jgar.2017.10.006.
 10. Dailloux M, Laurain C, Weber M, Hartemann P. Water and nontuberculous mycobacteria. *Water Research.* 1999;33(10):2219-28. doi: 10.1016/S0043-1354.
 11. Muthusami JC, Vyas FL, Mukundan U, Jesudason MR, Govil S, Jesudason S. *Mycobacterium fortuitum*: an iatrogenic cause of soft tissue infection in surgery. *ANZ J Surg.* 2004;74(8):662-6. doi: 10.1111/j.1445-1433.2004.03018.
 12. He W, Soll CE, Chavadi SS, Zhang G, Warren JD, Quadri LE. Cooperation between a coenzyme A-independent stand-alone initiation module and an iterative type I polyketide synthase during synthesis of mycobacterial phenolic glycolipids. *J Am Chem Soc.* 2009;131(46):16744-50. doi: 10.1021/ja904792q.
 13. Farnia P, Ghanavi J, Saif S, Farnia P, Velayati AA. Association of interferon- γ receptor-1 gene polymorphism with nontuberculous mycobacterial lung infection among Iranian patients with pulmonary disease. *Am J Trop Med Hyg.* 2017;97(1):57-61. doi: 10.4269/ajtmh.16-0905.
 14. Varahram M, Farnia P, Saif S, Marashian M, Farnia P, Ghanavi J, et al. Identification of different subtypes of rapid growing atypical *Mycobacterium* from water and soil sources: Using PCR-RFLP using hsp65 and rRNA 16S-23S genes. *Int J Mycobacteriol.* 2016;5:S212-S3. doi: 10.1016/j.ijmyco.2016.09.057.
 15. Hanak V, Kalra S, Aksamit TR, Hartman TE, Tazelaar HD, Ryu JH. Hot tub lung: presenting features and clinical course of 21 patients. *Respir Med.* 2006;100(4):610-5. doi: 10.1016/j.rmed.2005.08.005.
 16. Rahideh S, Derakhshanezhad Z, Farnia P, Mozafari M, Seif S, Malekshahian D, et al. Review and meta analysis of nontuberculous mycobacteria in the Middle East. *Int J Mycobacteriol.* 2015;4:149. doi: 10.1016/j.ijmyco.2014.07.002.
 17. Shamsi M, Zolfaghari MR, Farnia P. Evaluation of p2x7 and IFN- γ gene polymorphisms in patients with pulmonary tuberculosis using PCR-RFLP method. *Int J Mycobacteriol.* 2015;4:130. doi: 10.1016/j.ijmyco.2014.11.015.
 18. Nasiri MJ, Farnia P. Prevalence of rapidly growing mycobacteria (RGM) in Iran: Systematic review and meta-analysis. *Int J Mycobacteriol.* 2015;4:145. doi: 10.1016/j.ijmyco.2014.11.010.
 19. Joob B, Wiwanitkit V. Drug resistance pattern of *Mycobacterium abscessus*: Change of pattern in 20-year period after the first report of human pulmonary infection in Thailand. *BBRJ.* 2019; 3(2):92. doi: 10.4103/bbrj.bbrj_35_19.
 20. Malekshahian D, Farnia P, Velayati AA. Rapid identification of environmental NTM species using molecular genotyping. *Int J Mycobacteriol.* 2015;4:107. doi: 10.1016/j.ijmyco.2014.11.016.
 21. Gondil VS, Chhibber S. Exploring potential of phage therapy for tuberculosis using model organism. *BBRJ.* 2018; 2(1):9. doi: 10.4103/bbrj.bbrj_93_17.
 22. Mirsaeidi M, Farnia P, Sadikot R, Hsueh P-R, Aliberti S. Nontuberculous mycobacteria: epidemiologic, mycobacteriologic, and clinical aspects. *Biomed Res Int.* 2015;2015. doi: 10.1155/2015/523697.
 23. Velayati AA, Farnia P, Mozafari M, Mirsaeidi M. Nontuberculous mycobacteria isolation from clinical and environmental samples in Iran: twenty years of surveillance. *Biomed Res Int.* 2015;2015. doi: 10.1155/2015/254285.
 24. Cassidy PM, Hedberg K, Saulson A, McNelly E, Winthrop KL. Nontuberculous mycobacterial disease prevalence and risk factors: a changing epidemiology. *Clin Infect Dis.* 2009;49(12):e124-e9. doi: 10.1086/648443.
 25. Velayati AA, Farnia P, Mozafari M, Malekshahian D, Seif S, Rahideh S, et al. Molecular epidemiology of nontuberculous mycobacteria isolates from clinical and environmental sources of a metropolitan city. *PloS one.* 2014;9(12):e114428. doi: 10.1371/journal.pone.0114428.
 26. Mozafari M, Farnia P, Nezhad ZD, Rahideh S, Seif S, Malekshahian D, et al. WITHDRAWN: Meta analysis of NTM (from environmental and clinical samples) in the last 20 years in Iran. *Int J Mycobacteriol.* 2014. doi: 10.1016/j.ijmyco.2014.07.001.
 27. Donfack VF, Ngando L, Pefura EW, Che DS, Ateba G, Bigna JJ, Foe JL, Kuaban C, Eyangoh S. Comparative study of LoopampTM *Mycobacterium tuberculosis* Complex Kit for Rapid Detection of *Mycobacterium tuberculosis* complex in cameroon. *BBRJ.* 2018;1;2(1):46. doi: 10.4103/bbrj.bbrj_86_17.
 28. Tabarsi P, Baghaei P, Farnia P, Mansouri N, Chitsaz E, Sheikholeslam F, et al. Nontuberculous mycobacteria among patients who are suspected for multidrug-resistant tuberculosis—need for earlier identification of nontuberculous mycobacteria. *Am J Med Sci.* 2009;337(3):182-4. doi: 10.1097/maj.0b013e318185d32f.
 29. Kumar A, Singh AK, Upadhyay V, Pandey J. Epidemiology of multi-drug-resistant tuberculosis in Northern India. *BBRJ.* 2018; 2(2):112. doi: 10.4103/bbrj.bbrj_26_18.
 30. Mansouri D, Mahdaviani S, Khalilzadeh S, Mohajerani S, Hasanzad M, Sadr S, et al. IL-2-inducible T-cell kinase deficiency with pulmonary manifestations due to disseminated Epstein-Barr virus infection. *Int Arch Allergy Immunol.* 2012;158(4):418-22. doi: 10.1159/000333472.
 31. Ruas R, Abreu I, Nuak J, Ramos A, Carvalho T, Ribeiro M, et al. Nontuberculous mycobacteria in a tertiary Hospital in Portugal: A clinical review. *Int J Mycobacteriol.* 2017;6(4):344. doi: 10.4103/ijmy.ijmy_177_17.
 32. Tortone CA, Zumárraga MJ, Gioffr AK, Oriani DS. Utilization of molecular and conventional methods for the identification of nontuberculous mycobacteria isolated from different water sources. *Int J Mycobacteriol.* 2018;7(1):53. doi: 10.4103/ijmy.ijmy_192_17.
 33. Merza MA, Farnia P, Tabarsi P, Khazampour M, Masjedi MR, Velayati AA. Anti-tuberculosis drug resistance and associated risk factors in a tertiary level TB center in Iran: a retrospective analysis. *J Infect Dev Ctries.* 2011;5(07):511-9. doi: 10.3855/jidc.1259.
 34. Farnia P, Mohammadi F, Masjedi MR, Varnerot A, Zarifi AZ, Tabatabaei J, et al. Evaluation of tuberculosis transmission in Tehran: using RFLP and spoligotyping methods. *J Infect.* 2004;49(2):94-101. doi: 10.1016/j.jinf.2003.11.015.
 35. Farnia P, Mohammadi F, Zarifi Z, Tabatabaei D, Ganavi J, Ghazisaeedi K, et al. Improving sensitivity of direct microscopy for detection of acid-fast bacilli in sputum: use of chitin in mucus digestion. *J Clin Microbiol.* 2002;40(2):508-11. doi: 10.1128/jcm.40.2.508-511.2002.
 36. Mohammadi S, Esfahani BN, Moghim S, Mirkhendi H, Zanihani FR, Safaei HG, et al. Optimal DNA Isolation method for detection of nontuberculous mycobacteria by polymerase chain reaction. *Adv Biomed Res.* 2017;6:133. doi: 10.4103/2277-9175.217216.
 37. Kiani A, Razavi F, Mortaz E, Emami H, Ghazali S, Anbardan AD, Mehravar H, Abedini A. The prevalence of latent tuberculosis infection among Iranian sarcoidosis patients. *BBRJ.* 2018;2(4):247. doi: 10.4103/bbrj.bbrj_115_18.
 38. Velayati AA, Farnia P, Masjedi MR. The totally drug resistant tuberculosis (TDR-TB). *Int J Clin Exp Med.* 2013;6(4):307.
 39. Maurya AK, Nag VL, Kant S, Sharma A, Gadepalli RS, Kushwaha RA. Recent methods for diagnosis of nontuberculous

- mycobacteria infections: Relevance in clinical practice. *BBRJ*. 2017; 1(1):14. doi: 10.4103/bbrj.bbrj_18_17.
40. Maes R. Tuberculosis serology is useful in rural areas. *BBRJ*. 201; 1(2):85. doi: 10.4103/bbrj.bbrj_82_17.
 41. Esther CR Jr, Esserman DA, Gilligan P, Kerr A, Noone PG. Chronic *Mycobacterium abscessus* infection and lung function decline in cystic fibrosis. *J Cyst Fibros*. 2010;9(2):117-23. doi: 10.1016/j.jcf.2009.12.001.
 42. van Ingen J, de Zwaan R, Dekhuijzen RP, Boeree MJ, van Soolingen D. Clinical relevance of *Mycobacterium chelonae-abscessus* group isolation in 95 patients. *J Infect*. 2009;59(5):324-31. doi: 10.1016/j.jinf.2009.08.016.
 43. Benwill JL, Wallace Jr RJ. *Mycobacterium abscessus*: challenges in diagnosis and treatment. *CURR OPIN INFECT DIS*. 2014;27(6):506-10. doi: 10.1097/QCO.0000000000000104.
 44. Griffith DE. Nontuberculous mycobacterial lung disease. *CURR OPIN INFECT DIS*. 2010;23(2):185-90. doi: 10.1097/QCO.0b013e328336ead6.
 45. Henkle E, Hedberg K, Schafer S, Novosad S, Winthrop KL. Population-based incidence of pulmonary nontuberculous mycobacterial disease in Oregon 2007 to 2012. *Ann Am Thorac Soc*. 2015;12(5):642-7. doi: 10.1513/AnnalsATS.201412-559OC.
 46. Wu J, Zhang Y, Li J, Lin S, Wang L, Jiang Y, et al. Increase in nontuberculous mycobacteria isolated in Shanghai, China: results from a population-based study. *PLoS One*. 2014;9(10):e109736. doi: 10.1371/journal.pone.0109736.
 47. Koh W-J, Kwon OJ, Jeon K, Kim TS, Lee KS, Park YK, et al. Clinical significance of nontuberculous mycobacteria isolated from respiratory specimens in Korea. *Chest*. 2006;129(2):341-8. doi: 10.1378/chest.129.2.341.
 48. Joob B, Wiwanitkit V. Common and different lipidomes for lung cancer and tuberculosis: a comparative lipidomics analysis. *BBRJ*. 2019 Oct 1;3(4):233. doi:10.4103/bbrj.bbrj_36_19.
 49. Marras TK, Mendelson D, Marchand-Austin A, May K, Jamieson FB. Pulmonary nontuberculous mycobacterial disease, Ontario, Canada, 1998–2010. *Emerg Infect Dis*. 2013;19(11):1889. doi: 10.3201/eid1911.130737.
 50. Thomson RM, Carter R, Tolson C, Coulter C, Huygens F, Hargreaves M. Factors associated with the isolation of nontuberculous mycobacteria (NTM) from a large municipal water system in Brisbane, Australia. *BMC Microbiol*. 2013;13(1):89. doi: 10.1186/1471-2180-13-89.
 51. Garima K, Varma-Basil M, Pathak R, Kumar S, Narang A, Rawat KS, et al. Are we overlooking infections owing to non-tuberculous mycobacteria during routine conventional laboratory investigations?. *Int J Mycobacteriol*. 2012;1(4):207-11. doi: 10.1016/j.ijmyco.2012.10.005.
 52. Kim H, Lee S, Kim B, Kook Y. Allele-specific duplex polymerase chain reaction to differentiate *Mycobacterium abscessus* subspecies and to detect highly clarithromycin-resistant isolates. *Indian J Med Microbiol*. 2016;34(3):369. doi: 10.4103/0255-0857.188355.
 53. Kim B-J, Kim G-N, Kim B-R, Shim T-S, Kook Y-H, Kim B-J. Phylogenetic analysis of *Mycobacterium massiliense* strains having recombinant rpoB gene laterally transferred from *Mycobacterium abscessus*. *PloS One*. 2017;12(6):e0179237. doi: 10.1371/journal.pone.0179237.
 54. Caskey S, Moore JE, Rendall JC. In vitro activity of seven hospital biocides against *Mycobacterium abscessus*: Implications for patients with cystic fibrosis. *Int J Mycobacteriol*. 2018;7(1):45. doi: 10.4103/ijmy.ijmy_197_17.
 55. Set R, Shastri J. Laboratory aspects of clinically significant rapidly growing mycobacteria. *Indian J Med Microbiol*. 2011;29(4):343. doi: 10.4103/0255-0857.90157.
 56. Petrini B. *Mycobacterium abscessus*: an emerging rapid-growing potential pathogen. *APMIS*. 2006;114(5):319-28. doi: 10.1111/j.1600-0463.2006.apm_390.x.
 57. Trovato A, Baldan R, Costa D, Simonetti TM, Cirillo DM, Tortoli E. Molecular typing of *Mycobacterium abscessus* isolated from cystic fibrosis patients. *Int J Mycobacteriol*. 2017;6(2):138. doi: 10.4103/ijmy.ijmy_33_17.
 58. Ridell M. *Mycobacterium abscessus*: An environmental mycobacteria being a human pathogen. *Int J Mycobacteriol*. 2015;4:41. doi: 10.1016/j.ijmyco.2014.10.027.
 59. Sharma S, Baweja UK, Mehta Y, Sarma S. *Mycobacterium abscessus* bacteraemia in an immunocompetent patient following a coronary artery bypass graft. *J Cardiovasc Dis Res*. 2011;2(1):80-2. doi: 10.4103/0975-3583.78604.
 60. Joao I, Cristovao P, Antunes L, Nunes B, Jordao L. Identification of nontuberculous mycobacteria by partial gene sequencing and public databases. *Int J Mycobacteriol*. 2014;3(2):144-51. doi: 10.1016/j.ijmyco.2014.04.001.

 © 2020 The Author(s). This is an open-access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.