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Nontuberculous mycobacterial infection in patients with bronchiectasis. A single-center study

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ABSTRACT

Background: Globally, bronchiectasis-related nontuberculous mycobacterial (NTM) disease is on the rise. The diagnosis of NTM infection is difficult and treatment varies according to NTM species. This study intended to detect the prevalence of NTM in patients with bronchiectasis. **Methods:** A total of 100 bronchoalveolar lavage (BAL) specimens were collected from patients with adult-onset bronchiectasis attending the chest medicine department, Mansoura University Hospitals (MUH), Egypt between December 2021 and November 2022. Clinical samples were processed to detect NTM isolates by phenotypic methods including microscopic examination, culture on Lowenstein Jensen (LJ) slants, and various biochemical reactions. Positive NTM specimens were further confirmed by multiplex polymerase chain reaction (PCR). **Results:** Out of 100 patients included in this study, seven cases were positive for NTM in their BAL by conventional methods. Of those, two were confirmed as *Mycobacterium kansasii* by multiplex PCR (29%; 2/7) and five (71.4%, 5/7) were unidentified NTM species. NTM infection was significantly associated with old age and immunocompromised status of the patients. **Conclusion:** Nontuberculous mycobacterial (NTM) lung disease is a common health problem in bronchiectasis and should be routinely examined particularly in old age and individuals with lower immune response.

Introduction

Nontuberculous mycobacteria (NTM), commonly referred to as opportunistic, environmental, or atypical mycobacteria, are pathogens other than *Mycobacterium leprae* and *Mycobacterium tuberculosis* complex. They have been isolated from soil, water, and shower aerosols, which are thought to be the natural sources of NTM infection [1]. Occasionally, NTM can infect humans or animals, causing a variety of pulmonary and extra-pulmonary infections [2]. Even though more

than 180 species have been identified to date, only a few of them have been linked to human illness, including rapidly growing NTM as *Mycobacterium abscessus*, *Mycobacterium chelonae*, and *Mycobacterium fortuitum*; and slow-growing NTM as *Mycobacterium avium* complex (MAC), *Mycobacterium kansasii* (*M. kansasii*), *Mycobacterium xenopi*, *Mycobacterium simiae*, *Mycobacterium malmoense* and *Mycobacterium szulgai* [3].

Both immunocompetent and immunocompromised individuals are affected by the increased prevalence of NTM lung disease [4]. Being common environmental organisms, genetic predisposition, immunological deficiencies, anatomic lung diseases, and humidity are among the risk factors that increase the rate of pulmonary NTM infection [5].

Bronchiectasis is a chronic lung disease associated with inflammation, structural lung damage, and decreased mucociliary clearance that is complicated by chronic airway infection, including NTM infection. Furthermore, some studies revealed that NTM might play a direct role in the anatomic change of the bronchi, defective airway clearance, and development of bronchiectasis. Regular screening of NTM in frequently exposed patients should be done to distinguish between active NTM infection and colonization [6].

Bronchiectasis can present either as a localized obstructive disease of a lung lobe or segment or as a diffuse disorder affecting the majority of the lungs. Diffuse bronchiectasis is more likely to be associated with numerous risk factors including cystic fibrosis, immunodeficiency, Aspergillus infection, and NTM infection. Clinical traits, radiographic findings, and microbiological testing all are required for the diagnosis of NTM [7].

Clinical presentation of NTM lung infection is similar to bronchiectasis including, excess sputum production, cough, dyspnea, and hemoptysis [8]. Pneumonic changes, multiple small nodules and cavities, tree-in-bud (TIB) abnormalities, and mosaic perfusion are the main radiographic findings favoring a diagnosis of NTM infection in bronchiectasis. Smear microscopy is a low-cost method for quickly identifying mycobacteria, but it is unable to distinguish between NTM and Mycobacteria tuberculosis [9]. A definitive diagnosis of NTM lung disease relies on the detection of mycobacterial growth in culture media, even though this procedure takes several weeks to produce results. Molecular methods based on nucleic acid amplification offer a potential more rapid and sensitive method for detection of NTM directly from respiratory specimens without the need for culture [10].

The non-specific symptoms, lack of routine screening and few numbers of studies that examined NTM in depth make underestimation of the isolation rate of NTM in bronchiectasis, which may be higher

than expected. In the current study, the prevalence of NTM infection in a well-defined group of individuals with adult-onset bronchiectasis will be investigated, and the clinical correlation will be also assessed.

Subjects and methods

Study design

One hundred adult patients with confirmed bronchiectasis were enrolled in this prospective cohort study during the period from December 2021 to November 2022. Patient were recruited from chest medicine department, Mansoura University Hospital (MUH), Egypt. Patients diagnosed as mycobacterial tuberculosis were excluded. Each participant was subjected to history taking including demographic data (age, sex, and residence), underlying medical conditions, and smoking habit.

Samples collection and processing

Following the recommendations of the American Thoracic Society (ATS), bronchoscopy was used to obtain bronchoalveolar lavage (BAL) samples [11]. The specimens were delivered right away to the Microbiology Diagnostics and Infection Control Unit (MDICU), Medical Microbiology and Immunology Department, Mansoura college of Medicine, Egypt. In the event of a delay, samples were stored at 4 °C.

After samples were centrifuged for 15 minutes at 3000 rpm, sediments were utilized for both Ziehl-Neelsen staining (Egyptian Diagnostic Media (EDM), and culture on Lowenstein Jensen (LJ) media slants (Accumix, India). All culture plates were incubated aerobically at 37°C and inspected weekly for 4-6 weeks. Dry, rough, raised, irregular colonies of NTM were identified [2].

For pigment production cultures were exposed to light for 1h and then re-incubated again for 24-48h; NTM cultures that produced yellow to orange pigment during exposure to light only and no pigment production in the dark were considered photochromogens; while those that produced yellow, orange or red colonies during incubation in the dark were named scotochromogens. Cultures that produce no pigments either during incubation in the dark or light were considered non-photochromogens [12].

The isolated NTM were distinguished using biochemical reactions such as urea hydrolysis tests, catalase tests, and nitrate reduction tests purchased from Mast Group Ltd., Merseyside, UK; growth in

the presence of 5% NaCl in LJ medium (FIPCO, Egypt), and growth on MacConkey's agar without crystal violet (Liofilchem, Italy) [13].

Molecular identification of NTM by multiplex polymerase chain reaction (PCR)

Colonies of NTM on LJ medium slants were verified by multiplex PCR based on identification of the 16S rRNA, and internal transcribed spacer (ITS) using the following primers obtained from (Enzynomics, South Korea) (**Table 1**). NTM colonies were suspended in 1.0 ml of the TE buffer, boiled for 15 minutes at 95°C, and then frozen for 30 min at -20°C. The mixture was centrifuged to create pellet and then kept at -80°C to facilitate further DNA amplification [14].

The thermal cycler conditions used for DNA amplification were initial denaturation at 95°C for 15 min, 30 cycles of denaturation at 95°C for 1min, primer annealing at 62°C for 1 min, extension at 72°C for 60 sec, and finally elongation at 72°C for 10 min. After operating at 100 V for 1 hour, amplicons were seen on a 1.5 % agarose gel containing Ethidium bromide (Sigma, USA). The 100 bp DNA marker (Promega, USA) was used to estimate the length of the PCR products [15].

Ethical approval

The Ethical Committee of the Faculty of Medicine, Mansoura University examined and approved this work (R.21.06.1549). All of the participants in this study gave written informed consent.

Data analysis

The Statistical Package of Social Science (SPSS) program version 24 (SPSS Inc., Chicago, IL, USA) was used. The qualitative data were described in terms of numbers and percentages. The mean \pm SD (standard deviation) was used to represent continuous variables. The Chi-square test, Fisher exact test, and independent t-test were used to compare distinct variables. When $p \leq 0.05$, the results were deemed significant.

Table 1. Primers used in the study and amplicon size.

Primer	Sequence (5'-3')	Target NTM	Amplicon size (bp)	Reference
16S rRNA	TGAGATACGGCCAGACTCCT CTCTAGACGCGTCCTGTGCAT	Pan-mycobacterial species	688	15
ITS	CAACAGCAAATGATTGCCAG CACATTTTCGATGAACGCCG	<i>Mycobacterium avium</i> complex	169	
ITS	ATCCCAACAAGTGGGGTGC CGCTACCCGTAGGGCAACG	<i>Mycobacterium kansasii</i>	218	
16S rRNA	CCTTTCTAAGGAGCACCATTT CGAGCGAGGCTATGTTTAGAT	<i>Mycobacterium abscessus</i>	271	

Results

One hundred clinically diagnosed adult bronchiectasis patients were included in this study. Their age ranges from 32 to 77 years with a mean age of 52.11 \pm 10.99. The study results showed a male preponderance with 54 (54.0%) patients, while 46 (46.0%) were females. About 52% of the studied patients were from urban residences whilst 48% were from rural areas. Sixty-six patients (66.0%) were non-smokers, 22% were active smokers and 12% were ex-smokers. Among the studied patients, 55% of the patients were immunocompromised including diabetes mellitus (DM), rheumatoid arthritis, systemic lupus erythematosus, and cancer, whereas 72.0% were on prolonged antibiotic therapy (**Table 2**).

The overall prevalence of NTM amongst studied patients was 7% (n= 7/100) by phenotypic methods. DNA amplification of isolated NTM using multiplex PCR showed that *Mycobacterium kansasii* represented (28.6%, 2/7), while other species of isolated NTM represented (71.4%, 5/7) as described in **figures (1, 2)** and **table (3)**.

Patients with positive NTM disease had higher mean age (60.00 \pm 7.59) in comparison to negative NTM patients (51.51 \pm 11.0) (**Figure 3**); furthermore, there was a significant correlation between NTM infection and older age (P value 0.048). In addition, the NTM infection was significantly correlated with the immune status of the patients (P value 0.016) as all NTM positive cases suffered from weak immunity; 3 cases had DM, 3 cases had solid organ malignancy and 1 patient had bronchogenic carcinoma. However, there was no discernible difference in terms of gender, place of residence, smoking, body mass index (BMI), or prolonged antibiotic therapy between positive NTM infection and negative cases (P values were 0.700, 0.707, 0.479, 0.885, and 0.402 respectively) (**Table 4**).

Table 2. Demographic data and characteristics of the 100 studied patients.

111	n (%)
Age (Years)	
Mean \pm SD	52.11 \pm 10.99
Min-Max	32-77
Age categories	
< 40 y	21 (21.0%)
40-60 y	54 (54.0%)
>60 y	25 (25.0%)
Sex	
Male	54 (54.0%)
Female	46 (46.0%)
Residence	
Urban	52 (52.0%)
Rural	48 (48.0%)
Smoking	
Non smoker	66 (66.0%)
Smoker	22 (22.0%)
Ex- smoker	12 (12.0%)
BMI*	
Underweight	31 (31.0%)
Normal	39 (39.0%)
Obese	30 (30.0%)
Immune status	
Immunocompromised	55 (55.0%)
Immunocompetent	45 (45.0%)
Long term antibiotics	
Yes	72 (72.0%)
No	28 (28.0%)

*BMI: Body mass index

Table 3. Culture, biochemical reactions, and PCR results of the isolated NTM species (n= 7).

Isolated NTM species	Culture results	Pigment production	Biochemical reactions				PCR results
			Urease test	Catalase test	Growth in the presence of 5% NaCl	Growth in MacConkey's agar without crystal violet	
NTM 1	>7 days	Non-photochromogens	-	+	-	-	Other NTM
NTM 2	>7 days	Non-photochromogens	-	-	-	-	Other NTM
NTM 3	<7 days	Non-photochromogens	-	+	-	-	Other NTM
NTM 4	>7 days	Photochromogens	+	+	-	-	<i>M.kansasii</i>
NTM 5	>7 days	Non-photochromogens	+	-	-	-	Other NTM
NTM 6	>7 days	Non-photochromogens	+	+	-	-	Other NTM
NTM 7	>7 days	Photochromogens	+	+	-	-	<i>M.kansasii</i>

Table 4. Association between NTM infection and patients' characteristics.

Patients characteristics	Positive NTM cases (n=7)	Negative NTM cases (n=93)	Test of significance	P value
Age (Years) Mean \pm SD	60.00 \pm 7.59	51.51 \pm 11.0	t=1.99	0.048*
Sex Male Female	3 (42.9%) 4 (57.1%)	51 (54.8%) 42 (45.2%)	FET	0.700
Residence Urban Rural	3 (42.9%) 4 (57.1%)	49 (52.7%) 44 (47.3%)	FET	0.707
Smoking Non smoker Smoker Ex- smoker	4 (57.1%) 1 (14.3%) 2 (28.6%)	62 (66.7%) 21 (22.6%) 10 (10.8%)	MC	0.479
BMI Underweight Normal Obese	3 (42.9%) 2 (28.6%) 2 (28.6%)	28 (30.1%) 37 (39.8%) 28 (30.1%)	MC	0.885
Immune status Immunocompromised Immunocompetent	7 (100%) 0 (0%)	48 (51.6%) 45 (48.4%)	FET	0.016*
Long term antibiotics Yes No	6 (85.7%) 1 (14.3%)	66 (71.0%) 27 (29.0%)	$\chi^2=0.702$	0.402

t: Independent t test; FET: Fisher exact test; MC: monte carlo test; χ^2 :Chi square test; *significant $p \leq 0.05$

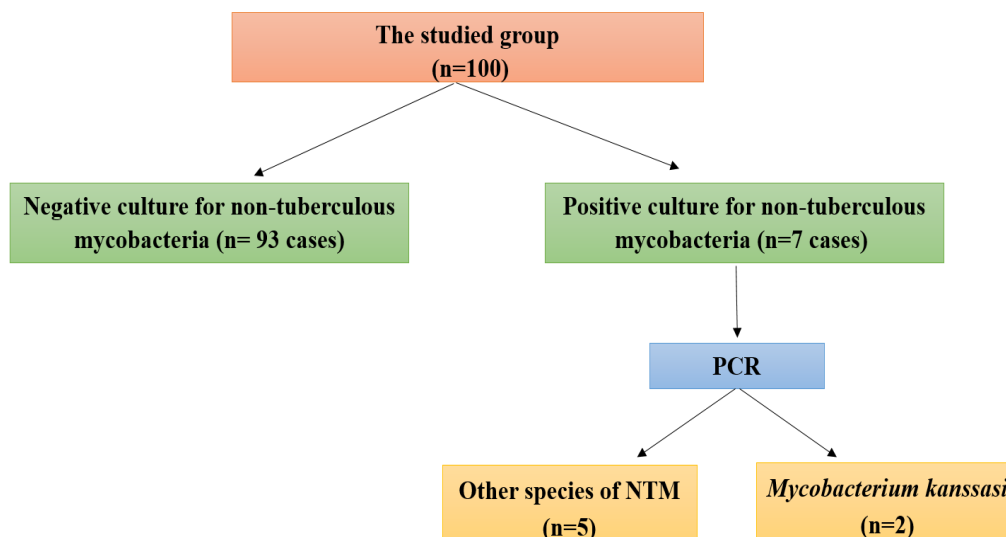
Figure 1. Flow chart describes the study

Figure 2. Gel electrophoresis of amplified DNA products of Nontuberculous Mycobacteria (NTM) by multiplex polymerase chain reaction (PCR). Lane 1 M: DNA Ladder (1000 bp); Lanes 4 and 7: positive *Mycobacterium kansasii* (218bp); Lanes 2, 3, 5, 6, 8-13: negative result for NTM; Lane 14: Negative control.

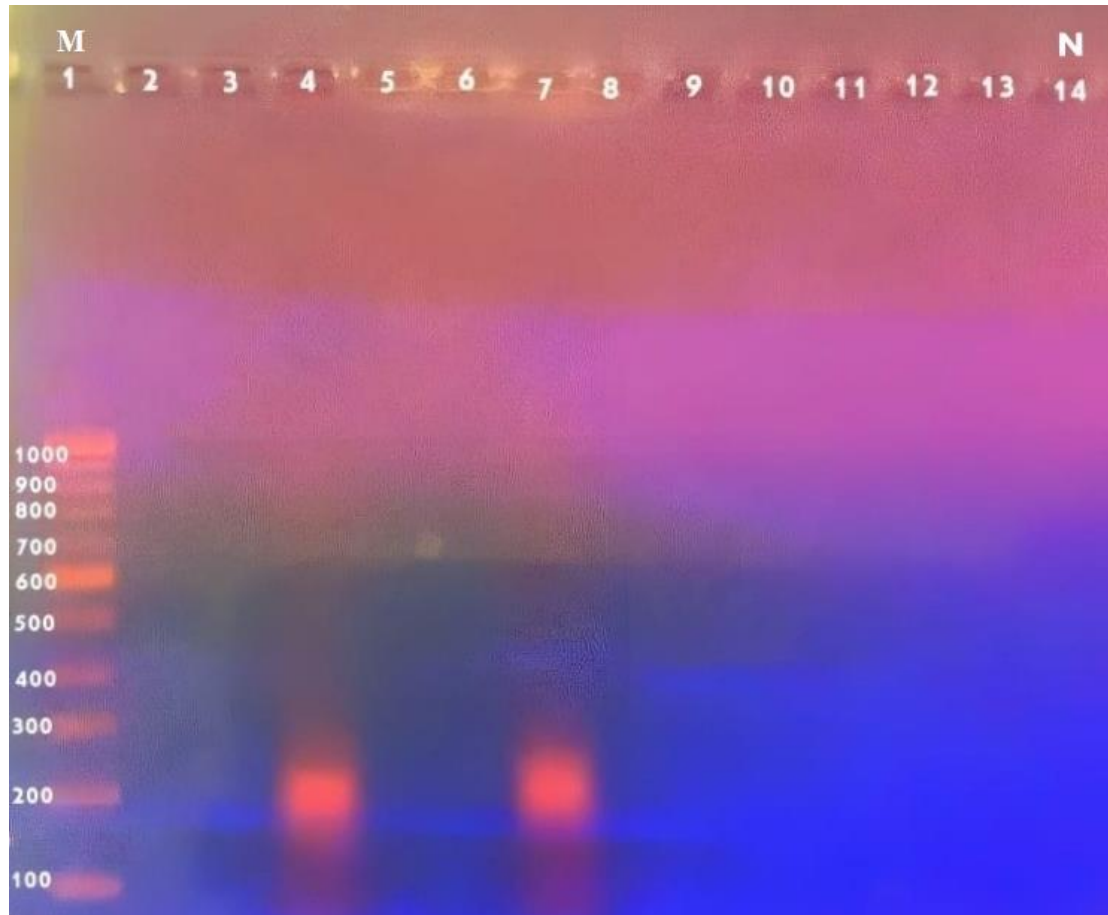
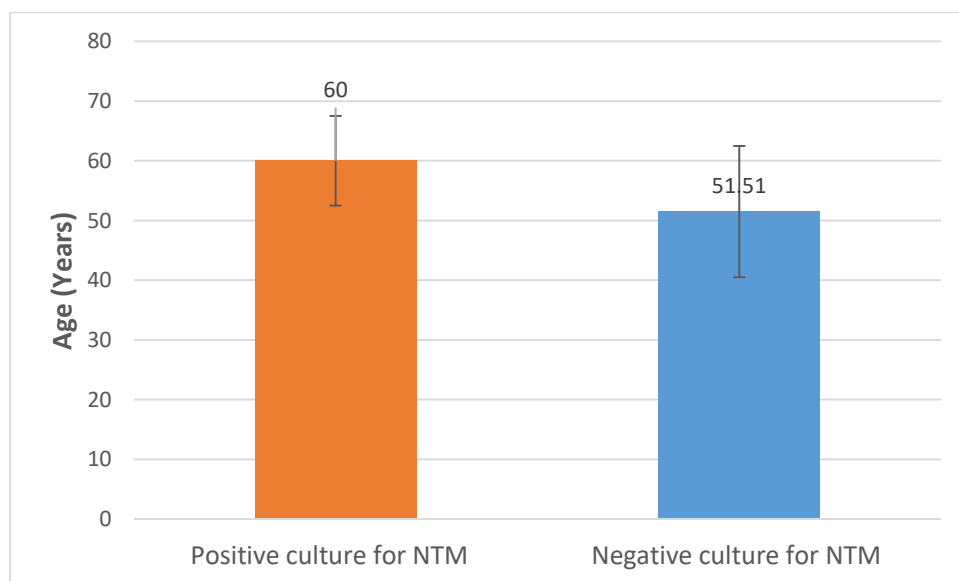


Figure 3. Age distribution between positive and negative NTM cases.



Discussion

Nontuberculous mycobacteria (NTM) are becoming an increasing public health issue that could develop serious infections in both immunocompetent and immunocompromised individuals [16]. Due to their ubiquitous existence in soil and water, humans frequently are exposed. The majority of NTM species are not pathogenic; however, some are able to cause human disease. About 80-90% of all NTM infections appear as pulmonary manifestations [17].

Though normally sterile, the lower respiratory tract in individuals with bronchiectasis can easily become colonized with fungi and NTM, which have a substantial impact on the disease's pathogenesis [18]. It is challenging to make a clinical diagnosis of NTM infection in people with pre-existing lung illness, such as bronchiectasis [19].

About 60% of people with adult-onset bronchiectasis have a history of NTM infection, according to the United States Bronchiectasis Research Registry [20]. Because screening for NTM in respiratory secretions is not routinely required, reporting is not always done, and it can be difficult to distinguish between colonization and active disease, the actual estimates of NTM prevalence in bronchiectasis are unknown. However, a number of variables, such as improvements in diagnostic methods and a growing awareness of NTM infection, have led to an increase in the rates of NTM isolation in recent years [21].

In the present investigation, 100 patients with adult-onset bronchiectasis, including 54 men and 46 women, with a mean age of (52.11± 10.99) years, were assessed for the clinical incidence of NTM infection. The infection rate of NTM infection among the studied patients was 7%. Although this percentage seems low, it was in line with another study conducted in Egypt in which only three NTM were isolated from 40 patients with an infection rate of 7.5% [22]. In addition, our results were similar to another study from Spain where they isolated NTM from sputa of 218 bronchiectasis patients with an infection rate of 8.3 % [23]. In addition, our results were consistent with other researchers from the UK who isolated seven NTM from 80 adult patients with bronchiectasis with a prevalence rate of 8.8 % [24].

In contrast to this study, **Palwatwichai et al.** reported a lower incidence of NTM in

bronchiectasis patients (6%) [25]. Additionally, **Pieters et al.** from Netherland, **Sharif et al.** from Pakistan, and **Dhar et al.** from India found a lower prevalence of NTM disease amongst patients with bronchiectasis (5 %, 2.3%, and 0.6%) respectively [26-28]. In addition, several cohort studies from France [29], McDonnell et al., from the UK, **Guan et al.** from China, **King et al.** from Australia, and **Dimakou et al.** from Greece stated low NTM infection rates in bronchiectasis (4 %, 3.9 %, 3.5 %, 2 %, and 0.9 %) respectively [30-33].

Previous studies from the USA, Taiwan, Korea, and Japan found higher incidence rates of NTM pulmonary disease in patients with bronchiectasis, with isolation rates of 50%, 36.5%, 25%, and 17.7%, respectively [34-37]. Similarly, another study from New Zealand described an increased rate of NTM infection with an isolation rate of 10.5% [38]; also, **Faverio et al.** from Italy found a higher rate of NTM infection (12%) [39]. A meta-analysis including 14 studies from multiple geographical regions found that the global prevalence of NTM in adults with bronchiectasis from 2006 to 2021 was 10% [40].

Patients with bronchiectasis are likely predisposed to NTM colonization and subsequent infection because structural abnormalities in the airways impair mucociliary clearance and increase mucus production [41].

There is a difference in the proportions of NTM infection among people with bronchiectasis according to geographical distribution [42]. Based on the American Thoracic Society (ATS) guidelines, 10% to 30% of bronchiectasis patients have NTM lung disease [43]. In a meta-analysis conducted by **Zhu et al.** there was a significant heterogeneity among the included studies, they stated that the highest frequency of NTM in bronchiectasis was in the United States 50%; while lower percentages were described in other regions, such as 9.5% from 8 studies in Asia, 5.4% from 9 studies in Europe, 5.6% from 2 studies in Australia, and 7.5% from 1 study in Africa with overall prevalence of 7.7% [44].

Uncertain ecological factors, such as climate, environmental exposure [45], sample size, collection techniques (sputum versus bronchoalveolar lavage fluid), and detection methods, may all play a role in this geographic heterogeneity [46].

The conventional phenotypic techniques, such as Ziehl-Neelsen (ZN) staining, and various biochemical reactions cannot speciate NTM species; additionally, they are time-consuming and complicated. Molecular techniques may help to differentiate and identify various NTM species from cultures [47]. Herein, multiplex PCR was done to confirm the diagnosis of NTM. Amongst the seven identified NTM isolates by phenotypic methods, 2 (29%) were confirmed as *M. kansasii* by multiplex PCR, while 5 (71%) were non-specific other types of NTM species. In contrast to our findings, a prior study by **Darwish et al.** found that Mycobacterium avium complex (MAC) was the most prevalent NTM (66.6%) and *M. kansasii* represented only (33.4%) [22]. Furthermore, according to **Kwak et al.** *M. avium*, *M. intracellulare*, and *M. abscessus* were the most frequently isolated NTM from bronchiectasis [48]. Additionally, *M. abscessus* and MAC were shown to be the two most common NTM subspecies in bronchiectasis, according to **Chu et al.** [49]. While in a prior study, MAC was the most common NTM in bronchiectasis [39]. Furthermore, **Wickremasinghe et al.** discovered that in 72% of sputum samples from patients with bronchiectasis, MAC was the main NTM species identified [50].

Another study revealed that *M. simiae* (33%), *Mycobacterium avium-intracellulare* (MAI) (25%), *M. fortuitum* (15%), and *M. abscessus* (10.5%) were the most predominant NTM species in bronchiectasis [21].

The bulk of our NTM-infected patients in this study were over sixty years old. This was in line with findings by **Park et al.**, **Máiz et al.** and **Metersky** and his colleague, and **Izumi et al.**, who discovered that older bronchiectasis patients had a much-increased likelihood of developing NTM disease [18,23,51,52]. This may be owing to impaired pulmonary function and weak immune response in elderly patients.

In this study, there was no correlation between the increased risk of NTM in bronchiectasis and gender, residence, smoking, socioeconomic position, or BMI. This finding was in line with the results of a study by **Zhu et al.** which found that gender, body mass index (BMI), and smoking behaviors were not risk factors for NTM pulmonary illness in bronchiectasis [44]. Our findings, however, were different from those of a prior study that found that individuals with low BMI had a considerably higher incidence of NTM isolation

[53]. In addition, contrary to our outcomes, earlier research revealed that females were more likely to have NTM pulmonary disease [19,54].

A previous study demonstrated that women over the age of 50 years are more likely than younger women to have NTM infections; this finding may be related to the menopausal state and a decline in estrogen, which has a protective effect against NTM. In addition, menopause causes a decrease in macrophage colony-stimulating factor serum levels [55].

Studies showed a relationship between the prevalence of NTM lung disorders and a lower socioeconomic level [56]. Unexpectedly, patients with high socioeconomic status who had never smoked before were found to have an elevated risk of NTM development, according to **Shteinberg et al.** [21]. However, these results could be deceiving and overestimated as the increased detection rate in high socio-economic status may be owing to intensive follow-up and increased health consciousness in those patients. In the present study, we did not find any association between the socioeconomic status of our patients and the incidence of NTM infection.

Patients with immunocompromised illnesses had a significantly greater rate of NTM infection, however, there was no significant association between increased NTM infection rates in bronchiectasis and prolonged antibiotic use. The increased incidence of NTM in immunocompromised patients was also validated by **Chai et al.** [57].

Conclusion

Adult patients with bronchiectasis are at risk for NTM-pulmonary diseases. Co-infection worsens the disease progression and increases exacerbations. The physicians should be aware of this and include NTM screening in routine bronchiectasis diagnostic workup.

Authors' contributions

Marwa Elmongi was responsible for designing the study protocol, writing the manuscript, and collecting and processing studied samples. Mohammed F. Elkenawy was responsible for supervision of the study. Tamer A. Elhadidy Rasha was responsible for collecting studied samples and clinical data of the patient. Rasha M. Elnagar was responsible for study protocol, data

analysis, writing the manuscript and final revision of the manuscript.

Conflict of interest

None declared.

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Availability of data and material

Will be available on reasonable request.

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