



Epidemiology of infections caused by Tuberculous and Non-Tuberculous Mycobacteria in the province of Pavia: a 12-year comparative analysis

¹M. Siciliano, ^{1,2}V. Monzillo, ¹J. Bagnarino, ¹G. Petazzoni, ¹F. Baldanti

¹U.O.C. Microbiologia e Virologia, Dipartimento Medicina Diagnostica, Fondazione IRCCS Policlinico San Matteo, Pavia

² Dipartimento di Medicina Interna e Terapia Medica, Università degli Studi di Pavia, Pavia

BACKGROUND-AIM

Mycobacteria pulmonary diseases cause significant morbidity and mortality to human health. Although tuberculosis (TB) remains a serious public health problem, the prevalence of lung diseases caused by Non-Tuberculous Mycobacteria (NTM) is increasing worldwide, affecting both immunocompetent and immunocompromised individuals. Pathologically, TB is characterized as necrotizing granulomatous inflammation of infected organs caused by inhalation of contaminated aerosols from patients with active pulmonary disease. NTM are environmental opportunistic pathogens causing pulmonary disease and skin infections in adults and cervical lymphadenitis in children. NTM human infections are mostly caused by *M. avium complex* (MAC), *M. abscessus complex*, *M. kansasii*, *M. xenopi* and *M. fortuitum*. NTM infections are difficult to treat because of different antibiotic resistance profiles and no standardized treatment protocols. Our study aims to illustrate the 12-year epidemiological changes of NTM and MTC infection in the province of Pavia.

METHODS

The study was performed on 794 biological samples positive for *Mycobacterium tuberculosis complex* (MTC) and NTMs from 2011 to 2022. All strains were isolated by using BACTEC MGIT™ 960 and identified with GenoType CM/NTM-DR and GeneXpert (MTC). The patients were considered incident in the year in which they became culture positive. We evaluated the distribution by age groups (0-18, 19-64, >65 years) and sex, paying special attention to the distribution of major NTMs species for the period considered.

RESULTS

Of the 794 samples considered, 437 were positive for MTC and 357 for NTM, among which the most frequent isolates were MAC (n=180; 61,5%), *M. abscessus complex* (n=26; 8,4%) *M. xenopi* (n=23; 7,4%), *M. fortuitum* (n=12; 3,9%), *M. chelonae* (n=11; 3,6%) and *M. kansasii* (n=8; 2,6%). A sharply increasing trend of NTMs has been observed over the years compared to MTCs, which have declined. MTC infections are more frequent in the age group of 19-64 years, while those sustained by NTMs are more widespread in over 65 year-patient. MTC is more frequent in male while NTMs are observed with a variable frequency over the years, with a higher incidence in women with lung disease.

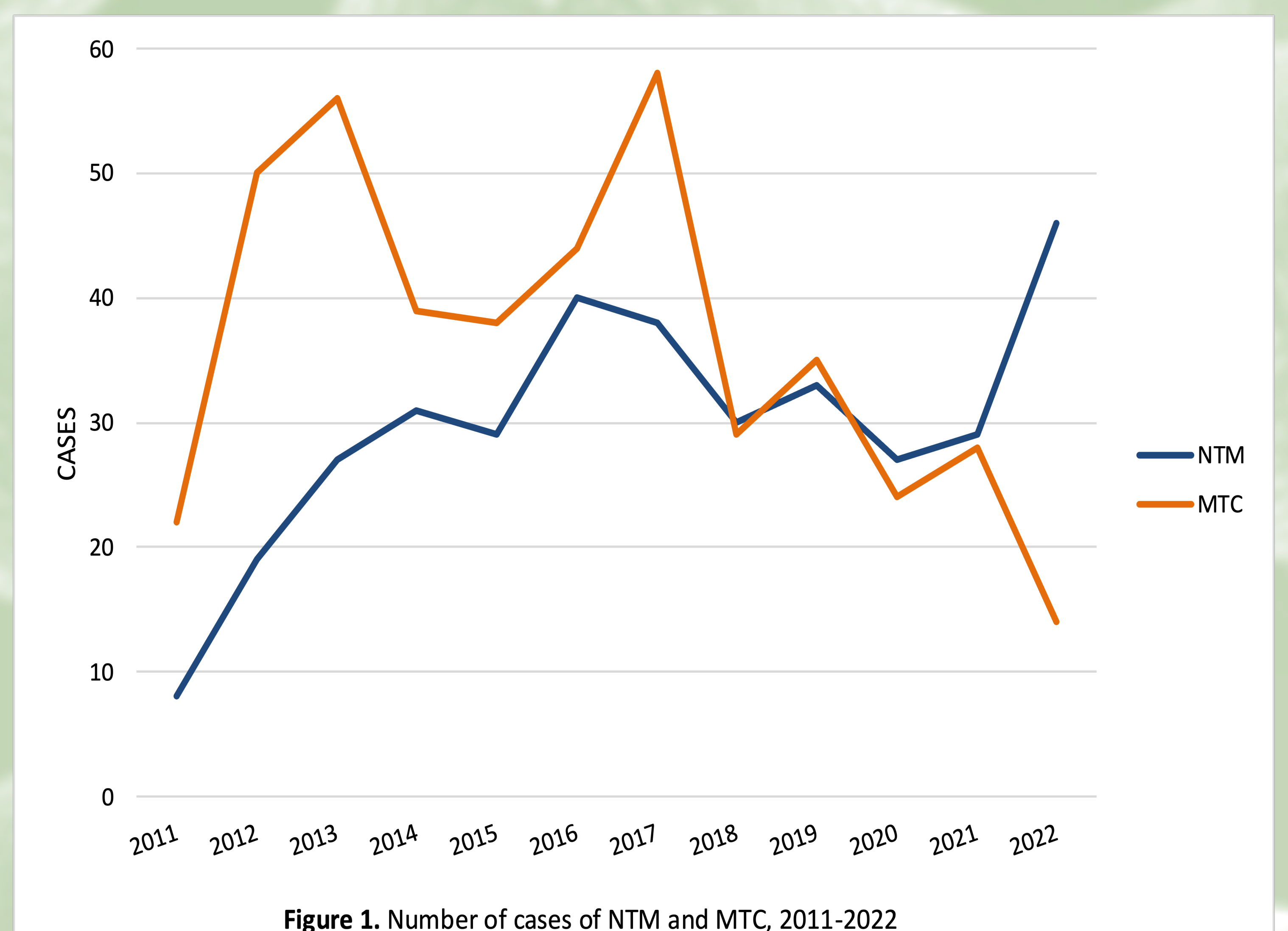


Figure 1. Number of cases of NTM and MTC, 2011-2022

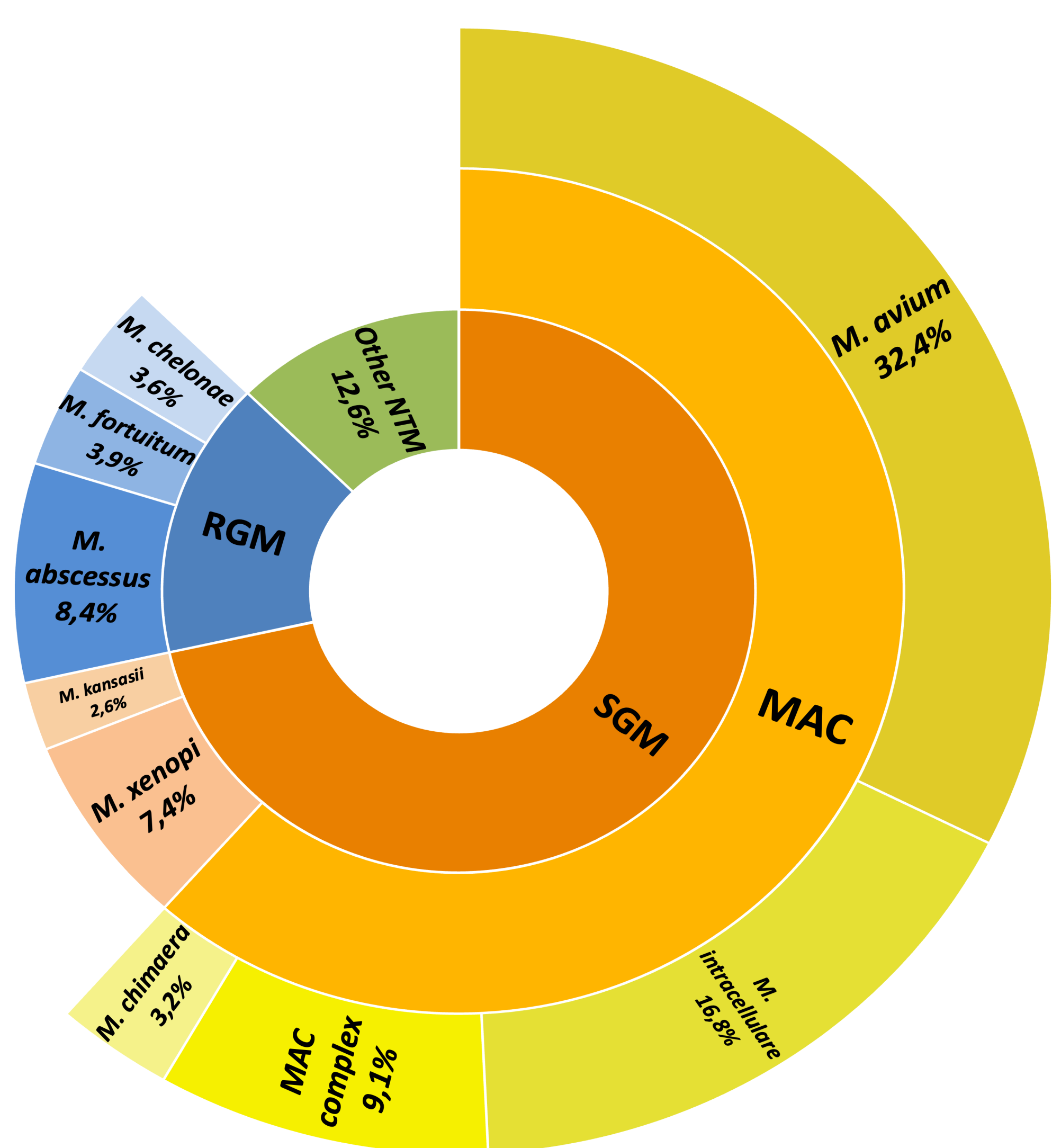


Figure 2. Species distribution among NTM isolates. RGM: Rapid growing mycobacteria, SGM: Slow growing

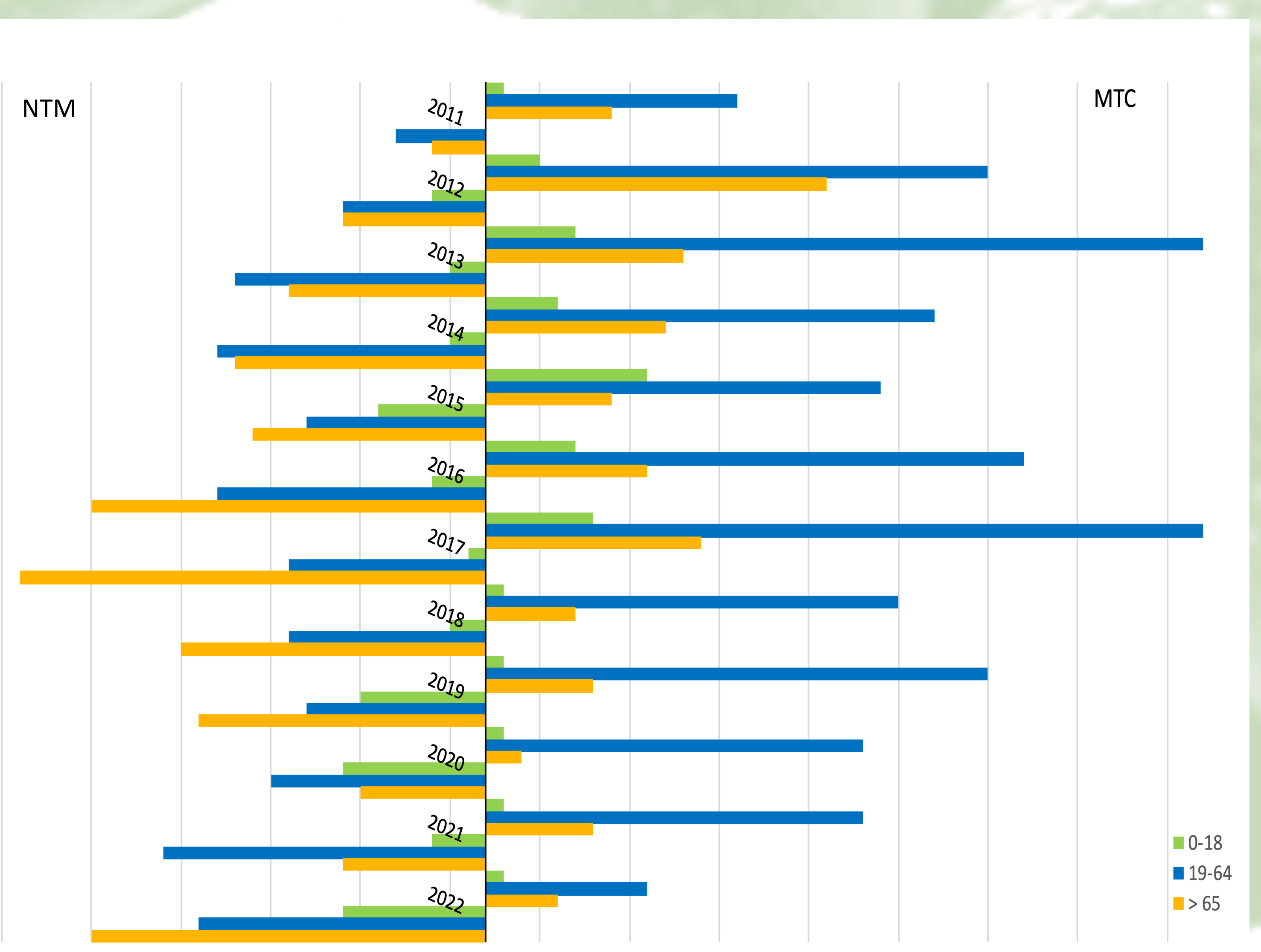


Figure 3. Age distribution of patients with NTM and MTC disease during 2011-2022

CONCLUSION

In conclusion, our epidemiological analysis is in line with literature data and confirmed the substantial increase in the number of NTMs. The change in epidemiology could reflect the development of microbiological methods which have allowed the isolation and identification of NTM and an increasing numbers of population aging with lung diseases such BPCO and bronchiectasis. To be diagnosed with NTM disease, patients should meet all clinical and microbiologic criteria, but the decision to start treatment is complex, requiring careful individualized analysis of risks and benefits.