

Non-tuberculous mycobacteria in children: A 7-year multicentre retrospective laboratory analysis

To the Editor: Data on the prevalence of non-tuberculous mycobacteria (NTM) remain fragmented, with information primarily available from only a few countries.^[1] In cases of paediatric community-acquired infections, NTM is often considered a less likely diagnosis unless there are targeted efforts to raise awareness. Within the hospital setting, an NTM aetiology is frequently overlooked until the patient fails to respond to broad-spectrum antibiotics or tuberculosis treatment.^[1] Additionally, unlike *Mycobacterium tuberculosis*, NTM is not classified as a notifiable disease, and the paucibacillary nature of infections in paediatric populations may contribute to the under-reporting of the NTM burden in this age group.^[2] The current study analysed culture data from children aged ≤12 years, sourced from two tertiary academic hospital laboratories and one regional tuberculosis laboratory, to assess the frequency and types of NTM in the paediatric population of the Western Cape Province of South Africa (SA).

NTM data were collected between 1 January 2016 and 31 December 2022 from the National Health Laboratory Service (NHLS) laboratory information system (TrakCare, Australia). NTM were identified from mycobacterial growth indicator tube cultures using the GenoType Mycobacterium common

mycobacteria (CM) and additional species (AS) line probe assays (LPAs) (Bruker, USA).

A total of 3 758 LPAs were screened to identify 186 paediatric NTM cultures (162 patients), representing 4.9% of all cases. The sample types included sputum ($n=96$), gastric aspirates ($n=53$) and bronchial alveolar lavages ($n=10$), which accounted for 85% of the total samples. In comparison, 15% were extrapulmonary samples ($n=6$ fluid aspirates, $n=6$ superficial swabs, $n=5$ cerebrospinal fluids, $n=5$ tissues, $n=3$ fine needle aspirates, $n=1$ blood culture, $n=1$ urine). From the cohort of 133 patients with sputum and gastric aspirate samples, only 3 (2.2%) children had NTM confirmed with a second sample, collected at least 1 week apart. Males made up 50.8% of the cases. The predominant NTM identified were mycobacterium species unidentified to the species level (76/186, 40.8%), followed by *Mycobacterium intracellulare* (48/186, 25.8%), and *M. abscessus* (14/186, 7.5%) (Fig. 1). Toddlers aged 1 day to 3 years showed a higher prevalence of *M. abscessus* (14 cases compared with 0 in other age groups). In addition, *M. intracellulare* was less common in the toddler group ($n=20/109$), with an odds ratio of 0.23 (95% confidence interval 0.14 - 0.37), compared with early adolescents aged 10 - 12 years ($n=15/30$).

NTM among paediatric patients in SA remain rare. The current NTM prevalence of 4.9% aligns with the SA literature, which reports a 6% yield of NTM among children investigated for pulmonary tuberculosis as part of a tuberculosis vaccine surveillance programme.^[3] Owing to the ubiquitous nature of NTM, their microbiological presence should be confirmed with a second independent sputum sample.^[4] The limited number of repeat samples (2.2%) for confirmation in the current study may reflect clinical judgement regarding potential contamination, a lack of awareness of the diagnostic criteria, or challenges in obtaining a second sample due to patient loss to follow-up or difficulties in collecting sputum from children.^[5] The study data suggest a higher likelihood of infection with the *M. avium* complex in older children, as observed in published adult data,^[6] while there was a trend toward *M. abscessus* infection in younger children. We detected 15% of the samples to be from an extrapulmonary site. The presentation of disseminated NTM disease in previously healthy children is uncommon, and should raise suspicion and further investigation for an underlying immunological defect, such as Mendelian susceptibility to mycobacterial disease.^[7] Finally, we acknowledge that this study did not include data on NTM

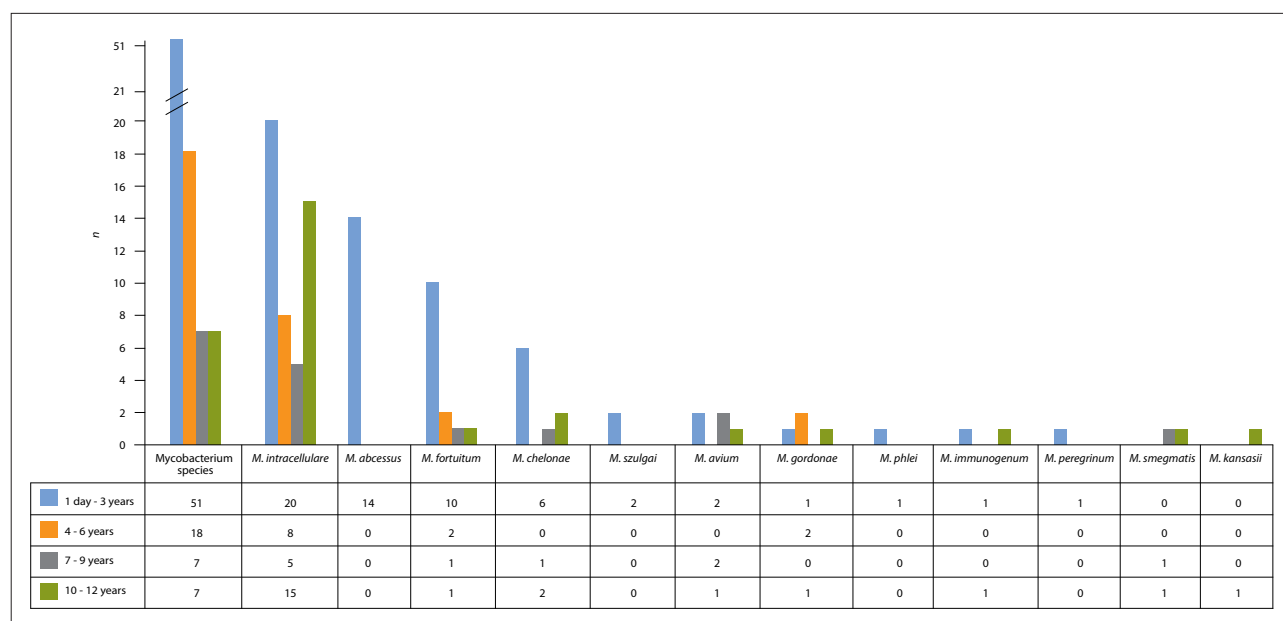


Fig. 1. Prevalence of non-tuberculous mycobacteria in the paediatric population by age in Western Cape Province, South Africa, 2016 - 2022. Non-tuberculous mycobacteria were identified from cultures using the GenoType Mycobacterium common mycobacteria and additional species line probe assays at the National Health Laboratory Service laboratories (Groote Schuur Hospital, Tygerberg Hospital and Green Point Tuberculosis Laboratory). 'Mycobacterium species' are those that were not classified to the species level.

treatment, outcomes, or clinical factors. Diagnosing NTM respiratory disease requires a thorough radiological, clinical and microbiological assessment.^[4] Therefore, laboratory reports alone are insufficient to differentiate between a true NTM infection and a harmless bystander during colonisation.

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Data availability. Data analysed in support of this study can be obtained from the corresponding author (CO) upon reasonable request. Institutional approval from the NHLS for access is required.

Ethical approval. This study received ethical approval with a waiver of informed consent from the Human Research Ethics Committee of Stellenbosch University (ref. no. S22/10/191). Institutional approval was granted by the NHLS (ref. no. PR 2232714).

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