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LETTER

Non-tuberculous mycobacteria in sputum cultures in Suriname

Dear Editor,

The NTM-NET Collaborative Study highlights the worldwide presence of non-tuberculous mycobacteria (NTM).[1] NTM are increasingly recognised as important opportunistic pathogens that can cause TB-like pulmonary disease.[2] Suriname, in South America, is a lower middle-income country (with a population of 542 000 in 2012)[3] and was not included in this study because NTM data were unavailable.[1] We seek to bridge this gap by reporting on NTM in Suriname.

TB is a notifiable disease in Suriname and all patients treated for TB are registered with the National Tuberculosis Programme (NTP), which maintains the national TB register. Prior to 2012, when the Xpert® MTB/RIF (Cepheid, Sunnyvale, CA, USA) test was introduced to Suriname for TB diagnostics, diagnosis of TB was made based on WHO criteria.[4] While assessing the incidence of TB in Suriname, we noted the presence of NTM in patients treated for TB.

From 2010 to 2011, a total number of 9004 samples consisting of sputum and other bodily fluids were sent to the Central Laboratory of the Bureau of Public Health for evaluation, and 668 (7.4%) samples yielded growth in culture. Of these, 379 were sent for identification via CAREC (Caribbean Epidemiology Center, Port of Spain, Trinidad and Tobago) to the University of Massachusetts, Amherst, MA, USA, to identify the isolate by DNA sequencing of the partial *hsp65* gene. These samples included sputum (358 samples), tracheal fluid (10 samples), gastric lavage (7 samples), pus (two samples [lymph node aspirates]) and one urine sample; the origin of one sample was unknown. Forty-eight individuals had multiple positive culture samples sent for identification. In 191 (50%) of the 379 isolates, *Mycobacterium tuberculosis* was cultured, whereas in 161 (42%) of the isolates, 180 instances of NTM growth were detected (from 47 different NTM species). The most frequently cultured NTM species were *M. fortuitum* (48 samples), *M. gordonae* (31 samples), *M. abscessus* (9 samples) and *M. senegalense* (8 samples). Twenty-seven (8%) isolates were bacteria such as *Nocardia* and *Rothia* species, or could not be identified. The gastric aspirates showed growth of *M. tuberculosis* in 3 samples, growth of NTM in 3 samples, and 1 sample could not be classified. The urine sample yielded growth of *M. flavescens*. Pus samples and the unclassified sample showed growth of *M. tuberculosis*. Samples of eight patients yielded growth of both an NTM and *M. tuberculosis*. *M. avium* complex (MAC) species were cultured in nine sputum samples from seven patients (of whom two were HIV-positive). *M. abscessus* was cultured in nine sputum samples from eight patients. One patient, whose HIV status was unknown, had two sputum samples submitted over an interval of 2 months. Both sputum samples yielded growth of *M. abscessus*. Sputum of one patient, whose HIV status was also unknown, yielded growth of *M. kansasii*. The identified NTM are listed in the Table, which shows 47 different NTM species cultured in sputum samples from 148 patients treated for suspected TB.

These positive cultures were obtained while awaiting the identification results from the supranational reference laboratories and may have been presumed to be *M. tuberculosis*. This delay in identification results may have led to overtreatment, as these results were only available months after patients had completed their TB treatment. None of the patients received any additional NTM treatment after the results were obtained. Since the introduction of the Xpert in 2012, the possibility of TB overdiagnosis and overtreatment has diminished. However, cases of NTM disease are likely to be missed. *M. fortuitum* (27%) and *M. gordonae* (17%) were the most frequently cultured NTM, which is similar to the distribution of NTM species observed in neighbouring French Guyana.[5] Both *M. fortuitum* and *M. gordonae* can cause pulmonary disease, but their isolation most frequently represents temporary colonisation of the airways.[1,6,7] Also, these mycobacteria could be present in water.[8,9] Analysis of quality control data in the laboratory showed no NTM contamination of equipment or water (data not shown). Nevertheless, we were also able to identify several potential pathogens, namely *M. abscessus, M. kansasii* and MAC—the latter two species are associated with HIV. In 2011, the estimated HIV prevalence in the adult population (15–49 years) of Suriname was estimated to be between 0.7% and 1.5%.[10]

The findings of this retrospective study shows the presence of NTM in patients suspected of having TB in Suriname, which highlights the possible overdiagnosis and overtreatment of TB prior to the introduction of Xpert. Our study has some limitations, however. Not all sputum culture results from the central laboratory could be matched to patients treated for TB according to the NTP register, probably due to registration

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Table NTM detected in 161 lysates from 148 Surinamese patients in 2010 and 2011

Group	Species
M. avium complex	*M. avium* (*n* = 4)
	M. intracellulare (*n* = 2)
	M. chimaera (*n* = 2)
	M. timonense (*n* = 1)
Other slow growers	*M. gordonae* (*n* = 31)
	M. terrae (*n* = 5)
	M. kumamotonense (*n* = 3)
	M. asiaticum (*n* = 1)
	M. arupense (*n* = 1)
	M. hibernae (*n* = 1)
	M. sherrisii (*n* = 1)
	M. saskatchewanense (*n* = 1)
	M. shimoidei (*n* = 1)
	M. kansasii (*n* = 1)
	M. gastri (*n* = 1)
M. fortuitum group	*M. fortuitum* (*n* = 48)
	M. senegalense (*n* = 8)
	M. conceptionense (*n* = 3)
	M. houstonense (*n* = 1)
M. chelonae-abscessus group	*M. abscessus* (*n* = 9)
	M. chelonae (*n* = 2)
	M. bolletii (*n* = 2)
Other rapid growers	*M. phocaicum* (*n* = 4)
	M. lacticola (*n* = 4)
	M. engbaekii (*n* = 3)
	M. novocastrense (*n* = 3)
	M. mucogenicum (*n* = 3)
	M. austroafricanum (*n* = 1)
	M. flavescens (*n* = 1)
	M. boenickei (*n* = 1)
	M. aichiense (*n* = 1)
	M. obuense (*n* = 1)
	M. brumae (*n* = 1)
	M. hassiacum (*n* = 1)
Uncharacterised NTM species	*M. senuense* (*n* = 6)
	M. vanbaalenii (*n* = 2)
	M. chlorophenolicum (*n* = 1)
	M. sp. 2000-301223 (*n* = 8)
	M. sp. Asan 3 (*n* = 2)
	M. sp. GN10803 (*n* = 1)
	M. sp. 2000-301020 (*n* = 1)
	M. sp.Bejaia (*n* = 1)
	M. sp. JLS (*n* = 1)
	M. sp. JDM601 (*n* = 1)
	M. sp. 6PY1 (*n* = 1)
	M. sp. M05 (*n* = 1)
	M. sp. IEC35 (*n* = 1)

NTM = non-tuberculous mycobacteria.

disparities between the NTP databases and the laboratory. Due to this mismatch, we could not reliably identify cases of overtreatment. To address this mismatch, we recommend setting up one central database to include all clinical and laboratory data for patients. A key limitation of the current study is that we do not have access to clinical data to investigate the clinical significance of NTM isolation in the affected patients. Another limitation is that not all positive cultures were sent to the supranational reference laboratories; this may have biased the NTM species distribution we observed in this study. Our dated culture results constitute another limitation. As far as we know NTM culture results are not available from 2012 onwards, so the contemporary presence of NTM could not be evaluated.

In summary, NTM were isolated frequently from clinical samples of presumptive TB cases in Suriname. The *M. fortuitum* complex species were most frequently isolated, while the most notorious NTM pathogens, MAC and *M. abscessus*, were less frequently cultured. The clinical significance of NTM isolation in patients from Suriname warrants follow-up and investigation to determine the impact on a patient's health.

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