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18 **Number of words in Abstract:** 96

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20 **Running title:** NTM spectrum: conventional vs. 16S sequencing

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23 **SUMMARY**

24 Non-tuberculous mycobacterial isolates from gold miners were speciated using standard  
25 biochemical testing (SBT) and 16s rDNA sequencing. Of 237 isolates tested, SBT identified  
26 126 compared with all 237 identified by sequencing. Of 111 isolates unspciated by SBT but  
27 identified by sequencing, 38 (34.2%) were identified as *Mycobacterium gordonae* and 8  
28 (7.2%) were new species. Of 126 isolates speciated by both methods, 37 were discordant,  
29 with 14/17 *M. gordonae* isolates incorrectly identified as *M. scrofulaceum* using SBT. The  
30 majority of these were the potentially pathogenic strain D *M gordonae*: sequencing is  
31 preferable where available to guide treatment.

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34 Identifying non-tuberculous mycobacteria (NTM) is important, especially where HIV is  
35 prevalent; to distinguish potential pathogens. In South African gold mines, use of liquid  
36 mycobacterial culture media has increased both the yield of positive cultures and the  
37 proportion of NTM isolated [1].

38

39 Conventionally, NTM are speciated using standard biochemical testing (SBT). 16S ribosomal  
40 ribonucleic acid (rRNA) gene sequence determination (16S rDNA sequencing) provides  
41 faster, accurate speciation and can identify new species [2].

42

43 We compared the spectrum of NTM identified by SBT versus sequencing in a gold-mining  
44 population and linked a subgroup of isolates to clinical data. This is the one of the larger  
45 clinical studies of NTM reported.

46

## 47 **METHODS**

48 This work was part of a sub-study [1] of “Thibela TB”, a cluster-randomised trial of  
49 community-wide isoniazid preventive therapy (IPT). At pre-IPT screening and follow-up  
50 visits, [1] and at routine mine health facilities (restricted to those without prior tuberculosis),  
51 we recruited individuals with suspected tuberculosis, between July 2006 and December 2007.  
52 Participants gave one sputum specimen; all isolates with results from both SBT and  
53 sequencing were included.

54

55 Following decontamination, specimens were cultured using both BACTEC MGIT 960  
56 system (BD Diagnostics, Sparks MD) and Löwenstein-Jensen media [1]. *Mycobacterium*  
57 *tuberculosis* complex was distinguished from NTM by detection of MPB64 antigen (Capilia  
58 TB, Japan). Phenotypic identification was based on growth rate at 25<sup>0</sup>C, 37<sup>0</sup>C, 42<sup>0</sup>C, 45<sup>0</sup>C

59 and with p-nitrobenzoic acid; pigmentation and colony morphology in light and dark  
60 conditions at 37<sup>0</sup>C. SBT included Tween hydrolysis; nitrate reduction and the catalase test.  
61 For sequencing, heat-killed culture lysates were subjected to 5'-16s rDNA amplification;  
62 sequenced [2] and referred to the RIDOM and NCBI GenBank sequence databases for  
63 identification [3,4]. GyrB genes of heat killed lysates were sequenced to confirm the absence  
64 of *M. tuberculosis*, identify other members of MTB complex and confirm *M. kansasii*  
65 identification.

66  
67 Where SBT and sequencing results were discrepant, sequencing was repeated. SBT was  
68 repeated for isolates identified as *M. scrofulaceum* using SBT and *M. gordonae* using  
69 sequencing. For a subgroup with discrepant identification, because of uncertainty regarding  
70 pathogenicity, routine clinical data were collected retrospectively using a standardised case  
71 report form.

## 73 RESULTS

74 237 isolates were included. Dominant species identified using SBT included *M. kansasii*  
75 (51 isolates), *M. avium* complex (47) and *M. scrofulaceum* (17); and using sequencing,  
76 *M. gordonae* (62), *M. kansasii/M. gastri* (53), *M. avium complex* (38) and *M.*  
77 *parascrofulaceum* (20). 28/237 isolates (11.8%) contained mixed NTM species on  
78 sequencing but none had mixed NTM/MTB. 111 isolates were not identifiable by SBT, but  
79 sequenced as follows: *M. gordonae* (38 isolates), *M. fortuitum* (17), *M. parascrofulaceum*  
80 (10), *M. avium complex* (7), *M. kansasii/M. gastri* (5), other NTM species (22), new  
81 mycobacterial species (8) or non-mycobacterial species (4).

82 Among 126 isolates successfully speciated by both methods, 38 (30%) were discordant on  
83 initial testing (table 1). Among 17 isolates identified as *M. scrofulaceum* using SBT, most  
84 (14/17) were identified as *M. gordonae* by sequencing.

85

86 Figure 1 shows a portion of the 16S rRNA sequence of *M. scrofulaceum* and *M. gordonae*  
87 strains (positions 392 to 446), indicating one of the few major differences between these  
88 species. Differences are visible at positions 411 to 427, including a three base-pair  
89 insertion/deletion. Only two minor variations within *M. gordonae* strains are observed  
90 among these 10 isolates at position 412 (TC or CC) and position 426 (GC or AT). The  
91 sequences of 14 isolates, biochemically identified as *M. scrofulaceum*, are identifiable as *M.*  
92 *gordonae* strains by sequencing. In 9/13 strains (one was not re-sequenced fully), TC  
93 replaces CC in position 412.

94

95 On repeat SBT, successful for 11/14 isolates originally identified as *M. scrofulaceum*, 10  
96 were *M. gordonae* and one retained the initial identification of *M. scrofulaceum*. Among 38  
97 isolates for which SBT and sequencing were discordant, repeat sequencing produced the  
98 same result for 28; one isolate initially identified as *M. szulgai* was identified as *M.*  
99 *parascrofulaceum* on repeat sequencing; the remaining nine isolates had poor and  
100 uninterpretable results.

101

102 Clinical data were available for 8/10 *M. gordonae* strain D isolates, identified by SBT as *M.*  
103 *scrofulaceum*. Six individuals were recruited at Thibela TB study sites and two at routine  
104 health services. 3/8 had a history of previous tuberculosis; all were smear negative; 2/8  
105 reported cough, with one additionally reporting weight loss. An HIV test result was recorded  
106 for 1/8, who was HIV negative. 3/8 had cavitation on chest radiograph, only one of whom

107 had previous tuberculosis. 1/8 (HIV negative with chest cavitation and no prior tuberculosis)  
108 was given standard tuberculosis treatment.

109

## 110 **DISCUSSION**

111 *M. gordonae* identified in sputum is generally considered to be non-pathogenic and has  
112 frequently been isolated from tap water, whereas *M. scrofulaceum* is considered to cause  
113 disease [5]. In nine of our *M. gordonae* isolates, a polymorphism (TC replacing CC at  
114 position 412) was shown that is associated with *M. gordonae rpoB* cluster D, which may be  
115 more pathogenic than other strains [6]. We note that *M. gordonae* can be pathogenic in the  
116 immunocompromised [7, 8] and may be causing disease in some individuals in this  
117 population, although relatively low numbers make it difficult to be certain. Accurate  
118 distinction between species is therefore important in populations with high HIV prevalence,  
119 such as this.

120

121 The dominant NTM species were *M. kansasii*, *M. gordonae*, *M. parascrofulaceum* and  
122 members of *M. avium* and *M. fortuitum* complexes. *M. kansasii* is known to be prevalent  
123 among miners [9]. In previous studies of NTM in miners, SBT was used to identify species  
124 mostly cultured on LJ [9, 10]; our data suggest that some *M. gordonae* strains could have  
125 been misidentified by SBT as *M. scrofulaceum*, some being associated with features of  
126 disease. The importance of this observation lies in the perceived pathogenicity of these two  
127 organisms and in our understanding of NTM species distribution in this population.

128

## 129 **CONCLUSIONS**

130 Some *M. gordonae* strains can be misclassified by SBT as *M. scrofulaceum*.

131 Misidentification of NTM may lead to suboptimal clinical management, particularly in



132 settings with HIV prevalence. Sequencing should be used where available to accurately  
133 identify NTM and where SBT is used, the possibility of misidentification should be  
134 considered.

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181 **Figure Legend:**

182 Figure 1: 16S rRNA sequence alignment of *M. gordonae* and *M. scrofulaceum*. Sequences of  
183 *Mycobacterium* type strains are shown in row 1-12. *M. scrofulaceum* type strain sequences  
184 (ATCC 19981 and DSM 43992) are shown in row 1-2, while row 3-12 show *M. gordonae*  
185 type strain sequences (ATCC 14470, DSM 44160, agha3, Tropicalis, NIPHL050404TB,  
186 M138, M120, M223, Tropicalis-2 and Tropicalis-3). Rows 13-15 are examples of clinical  
187 isolates from our study that were identified as *M. scrofulaceum* on initial standard  
188 biochemical testing and *M. gordonae* on sequencing. Two of these clinical isolates (rows 14-  
189 15) show TC instead of a CC at position 412.

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192 **Tables**

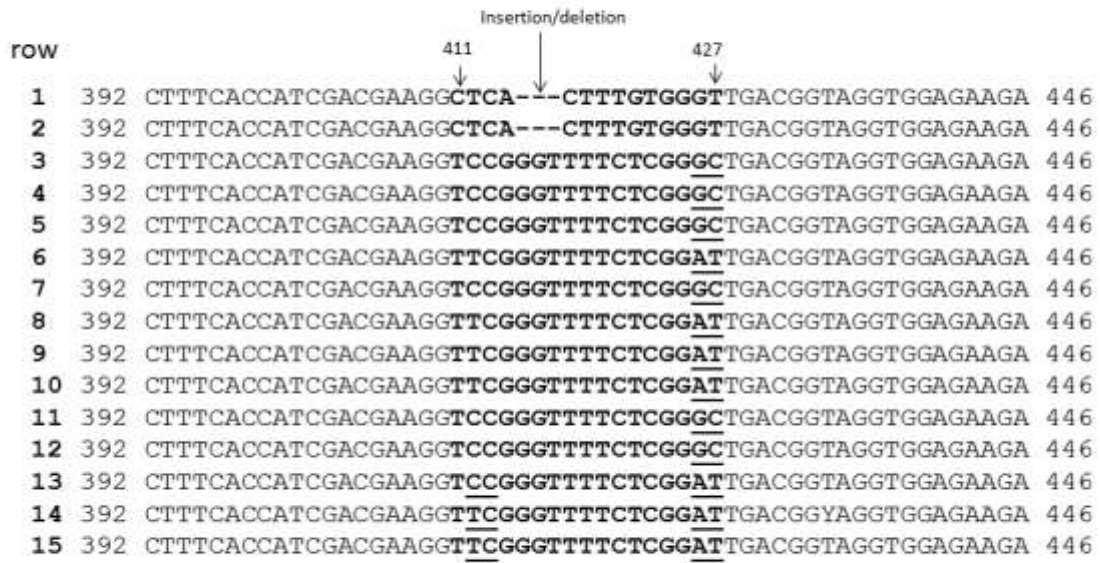
193 Table 1: Identification of non-tuberculous mycobacteria using standard biochemical testing  
 194 and 16S rDNA sequencing: discordant results on initial testing

<b>Standard biochemical testing</b>	<b>n</b>	<b>16S rDNA sequencing</b>	<b>N</b>
<i>M. scrofulaceum</i>	17	<i>M. gordonae</i>	14
		<i>M. szulgai</i>	2
		<i>M. fortuitum</i>	1
<i>M. avium</i> complex	16	<i>M. parascrofulaceum</i>	9
		<i>M. paraffinicum</i>	3
		<i>M. fortuitum</i>	1
		<i>M. kyorinense</i>	1
		<i>M. palustre</i>	1
		New mycobacterial species	1
<i>M. kansasii</i>	3	<i>M. gordonae</i>	1
		<i>M. parascrofulaceum</i>	1
		<i>M. szulgai</i>	1
<i>M. gordonae</i>	1	<i>M. asiaticum</i>	1
<i>M. flavescens</i>	1	<i>M. gordonae</i>	1
Total	38	Total	38

195

196

Figure 1:



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