

## Worldwide typing of *Mycobacterium kansasii* clinical isolates

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**Background:** To date, over 180 nontuberculous mycobacteria (NTM) species have been identified [1] and almost 30 of these species have been reported as the cause of pulmonary and extrapulmonary diseases [2]. *Mycobacterium kansasii* is the sixth most frequently isolated NTM species across the world. The isolation rate of this pathogen, among other NTM, is 5% in Europe and 4% globally. It is particularly high in Poland (36%) and Slovakia (35%) [3].

The genetic heterogeneity of *M. kansasii* is defined by the presence of seven genetic subtypes [4]. Most of the disease-related strains belong to type I and II, while the others (III-VII) have usually been linked to environmental sources. Therefore, subtyping of *M. kansasii* isolates from human samples is considered helpful for clinical diagnosis.

The aim of this study was to determine the global distribution of *M. kansasii* subtypes among clinical isolates.

**Materials/methods:** A total of 475 isolates recovered between 2000 and 2017 from as many patients with suspected *M. kansasii* disease were analyzed. The isolates were collected from 19 countries across 4 continents (**Table 1**). For the PCR restriction-enzyme analysis (PCR-REA) subtyping, protocols described by Telenti et al. (*hsp65* gene) [5] and Bakula et al. (*tuf* gene) [6] were used. The patients were categorized as having *M. kansasii* disease following the American Thoracic Society 2007 diagnostic criteria [7].

**Results:** The vast majority of isolates (392; 82.5%) presented patterns characteristic for subtype I. Forty-three (9%) exhibited the subtype II pattern. There were 19 (4%), 2 (0.4%), 2 (0.4%) and 13 (2.7%) isolates of type III, IV, V, and VI, respectively. Four (0.8%) isolates gave inconsistent results (mixed type - I/II). The isolates of type I, II, III and VI were isolated from both disease-associated and non-disease associated cases. Of two type IV isolates, one was obtained from a non-disease associated case, and one from a patient with unknown status. For two type V isolates, data concerning *M. kansasii* disease was unavailable.

The highest frequency of *M. kansasii* type I isolates was observed for Poland (140/142; 98.6%), and the lowest for Estonia (2/7; 28.6%) (Table 1).

**Conclusions:** This study demonstrated that subtype I represented the vast majority of *M. kansasii* clinical isolates and it has been isolated from both disease-related and non-disease-related cases. Therefore, the currently available subtyping schemes do not permit differentiation between isolates that did and did not cause definite disease. Furthermore, the genetic diversity of the *M. kansasii* population shows important regional variation.

**TABLE 1.** Worldwide *M. kansasii* subtypes distribution.

Country	<i>M. kansasii</i> subtype							TOTAL
	I	I/II	II	III	IV	V	VI	
Australia	15 (62.5%)	0 (0%)	2 (8.3%)	1 (4.2%)	0 (0%)	0 (0%)	6 (25%)	24 (100%)
Bulgaria	2 (50%)	0 (0%)	0 (0%)	1 (25%)	0 (0%)	0 (0%)	1 (25%)	4 (100%)
Chile	13 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	13 (100%)
Czech Republic	14 (82.3%)	0 (0%)	0 (0%)	2 (11.8%)	1 (5.9%)	0 (0%)	0 (0%)	17 (100%)
Denmark	18 (56.3%)	0 (0%)	13 (40.6%)	0 (0%)	0 (0%)	0 (0%)	1 (3.1%)	32 (100%)
Estonia	2 (28.6%)	0 (0%)	0 (0%)	3 (42.8%)	0 (0%)	0 (0%)	2 (28.6%)	7 (100%)
France	10 (90.9%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (9.1%)	11 (100%)
Germany	51 (68.9%)	1 (1.3%) <sup>a</sup>	9 (12.3%)	10 (13.5%)	1 (1.3%)	1 (1.3%)	1 (1.3%)	74 (100%)
Greece	4 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	4 (100%)
Italy	8 (50%)	0 (0%)	7 (43.8%)	1 (6.2%)	0 (0%)	0 (0%)	0 (0%)	16 (100%)
Japan	9 (90%)	0 (0%)	1 (10%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	10 (100%)
Lithuania	3 (60%)	0 (0%)	1 (20%)	0 (0%)	0 (0%)	0 (0%)	1 (20%)	5 (100%)
Poland	140 (98.6%)	0 (0%)	1 (0.7%)	0 (0%)	0 (0%)	1 (0.7%)	0 (0%)	142 (100%)
Russia	5 (55.6%)	0 (0%)	4 (44.4%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	9 (100%)
Slovenia	30 (90.9%)	0 (0%)	3 (9.1%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	33 (100%)
South Korea	17 (85%)	3 (15%) <sup>b</sup>	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	20 (100%)
Sweden	5 (71.4%)	0 (0%)	2 (28.6)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	7 (100%)
Switzerland	1 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)
the UK	45 (97.8%)	0 (0%)	0 (0%)	1 (2.2%)	0 (0%)	0 (0%)	0 (0%)	46 (100%)
<b>TOTAL</b>	<b>392 (82.5%)</b>	<b>4 (0.8%)</b>	<b>43 (9%)</b>	<b>19 (4%)</b>	<b>2 (0.4%)</b>	<b>2 (0.4%)</b>	<b>13 (2.7%)</b>	<b>475 (100%)</b>

<sup>a</sup> PCR-REA *tuf*: type I; PCR=REA *hsp65*: type II

<sup>b</sup> PCR-REA *tuf*: type I; PCR=REA *hsp65*: BstEII - II / HaeIII - I

PCR-REA *tuf*: type II; PCR=REA *hsp65*: BstEII - II / HaeIII - I BstEII - II / HaeIII - I

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