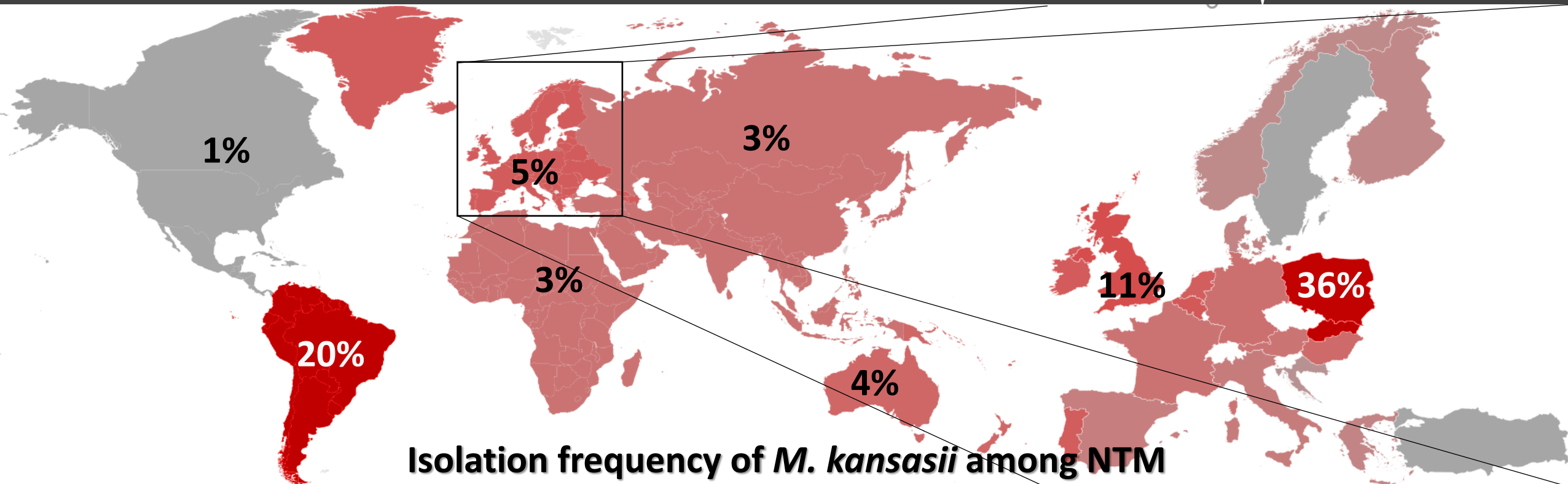


# Molecular typing of *Mycobacterium kansasii* clinical isolates from Europe

- *M. kansasii* is the 6<sup>th</sup> most frequently isolated non-tuberculous mycobacterial (NTM) species worldwide and one of the most virulent
- The genetic heterogeneity of *M. kansasii* is defined by the presence of seven genetic subtypes (I-VII)
- Types I and II are associated with disease, whereas types III-VII are commonly isolated from the environment and rarely cause disease

**VIRULENCE**

*M. kansasii*  
*M. abscessus*  
*M. intracellulare*  
*M. avium*  
*M. xenopii*  
*M. fortuitum*



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## PURPOSE OF THE STUDY:

- To analyze the distribution of *M. kansasii* subtypes among patients with and without NTM disease
- To determine the distribution of *M. kansasii* subtypes among clinical isolates in different European countries

19

20%

3%

4%

11%

36%

Isolation frequency of *M. kansasii* among NTM

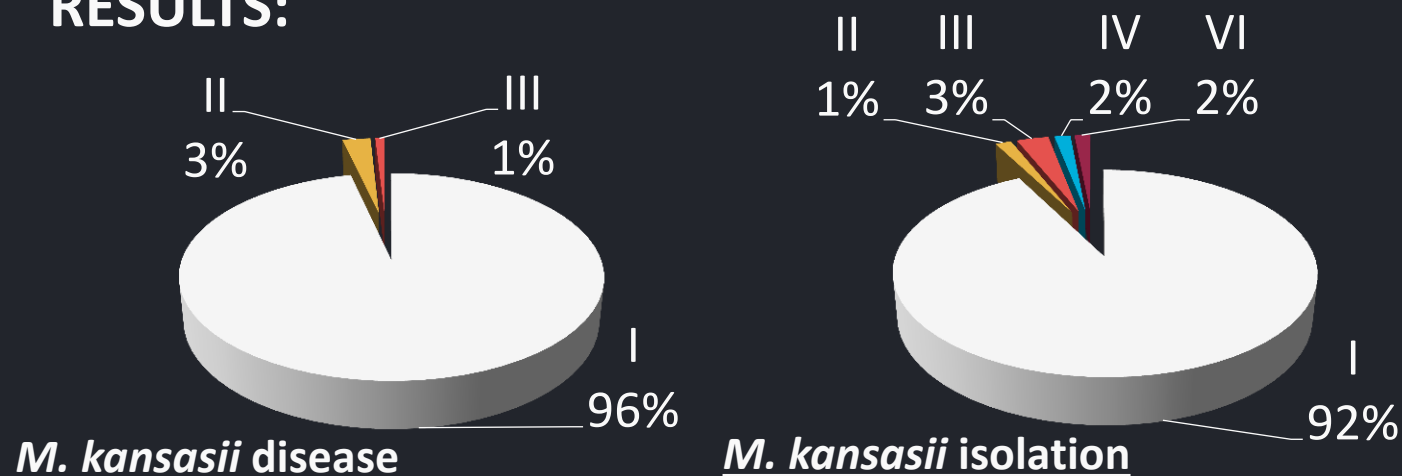
# Molecular typing of *Mycobacterium kansasii* clinical isolates from Europe

## MATERIALS AND METHODS:

- 279** isolates recovered between **2000-17** from **9** European countries, i.e.: (Bulgaria, Czech Republic, Estonia, Greece, Italy, Poland, Russia, Slovenia, the UK)
- PCR-REA-based genotyping:**  
*tuf* (Bakuła et. al., 2016)  
*hsp65* (Telenti et al., 1993)
- The patients were categorized as having *M. kansasii* disease following the ATS (2007) diagnostic criteria



## RESULTS:



<i>M. KANSASII</i> SUBTYPE DISTRIBUTION							
Country	I	II	III	IV	V	VI	TOTAL
Poland	140 (98.6%)	1 (0.7%)	0 (0%)	0 (0%)	1 (0.7%)	0 (0%)	142 (100%)
UK	45 (95.8%)	0 (0%)	1 (2.1%)	0 (0%)	0 (0%)	1 (2.1%)	47 (100%)
Slovenia	30 (90.9%)	3 (9.1%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	33 (100%)
Czech Republic	14 (82.3%)	0 (0%)	2 (11.8%)	1 (5.9%)	0 (0%)	0 (0%)	17 (100%)
Italy	8 (50%)	7 (43.8%)	1 (6.2%)	0 (0%)	0 (0%)	0 (0%)	16 (100%)
Russia	5 (55.6%)	4 (44.4%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	9 (100%)
Estonia	2 (28.6%)	0 (0%)	3 (42.8%)	0 (0%)	0 (0%)	2 (28.6%)	7 (100%)
Bulgaria	2 (50%)	0 (0%)	1 (25%)	0 (0%)	0 (0%)	1 (25%)	4 (100%)
Greece	4 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	4 (100%)
<b>TOTAL</b>	<b>250 (89.6%)</b>	<b>15 (5.4%)</b>	<b>8 (2.9%)</b>	<b>1 (0.35%)</b>	<b>1 (0.35%)</b>	<b>4 (1.4%)</b>	<b>279 (100%)</b>

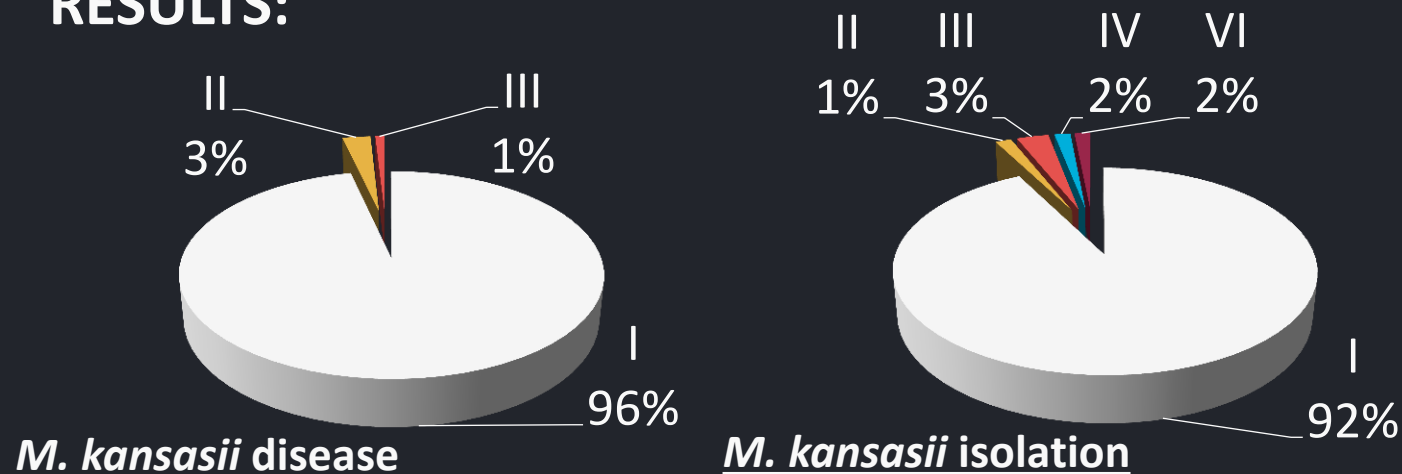
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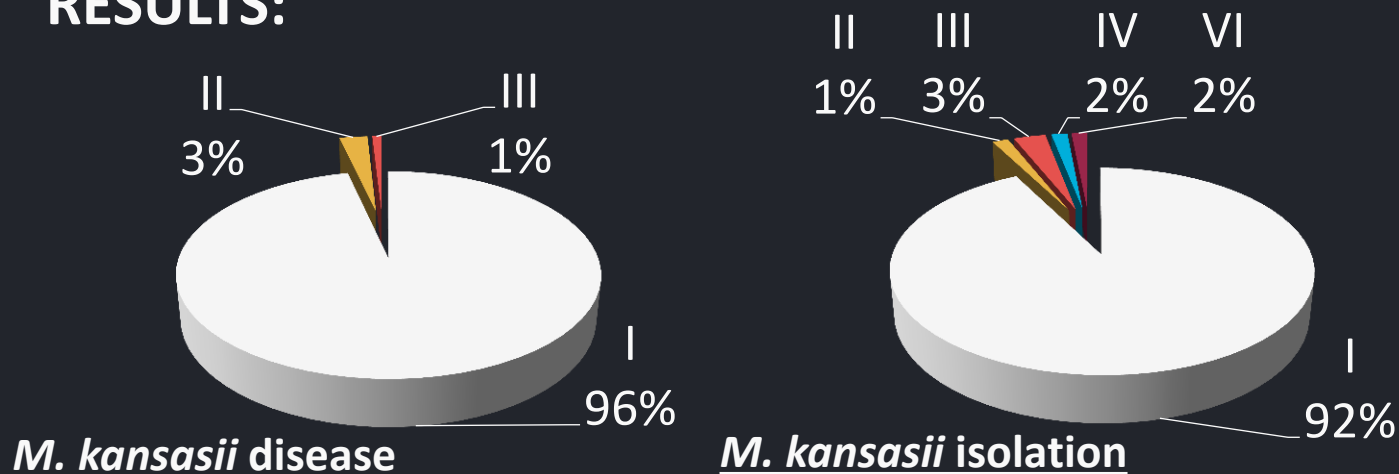
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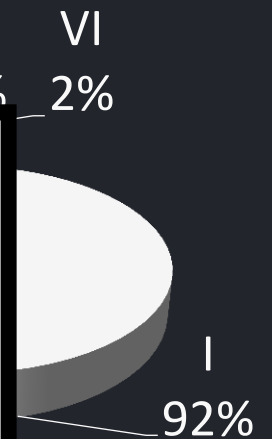
## MATERIALS AND METHODS:

## RESULTS:

- **279** isolates from **9** European countries: Czech Republic, Poland, Russia
- **PCR-REA-based**
  - tuf* (Bak)
  - hsp65* (Tele)
- The patients *M. kansasii* (2007) diagnosed

## CONCLUSIONS:

- Subtypes I, II, and III were identified in both disease-related and isolation (non-disease) cases
- Subtype I accounted for nearly 90% (250/279) of *M. kansasii* isolates
- Subtyping does not permit differentiation between isolates of clinical relevance and those representing isolation
- The genetic diversity of the European *M. kansasii* population shows regional variation



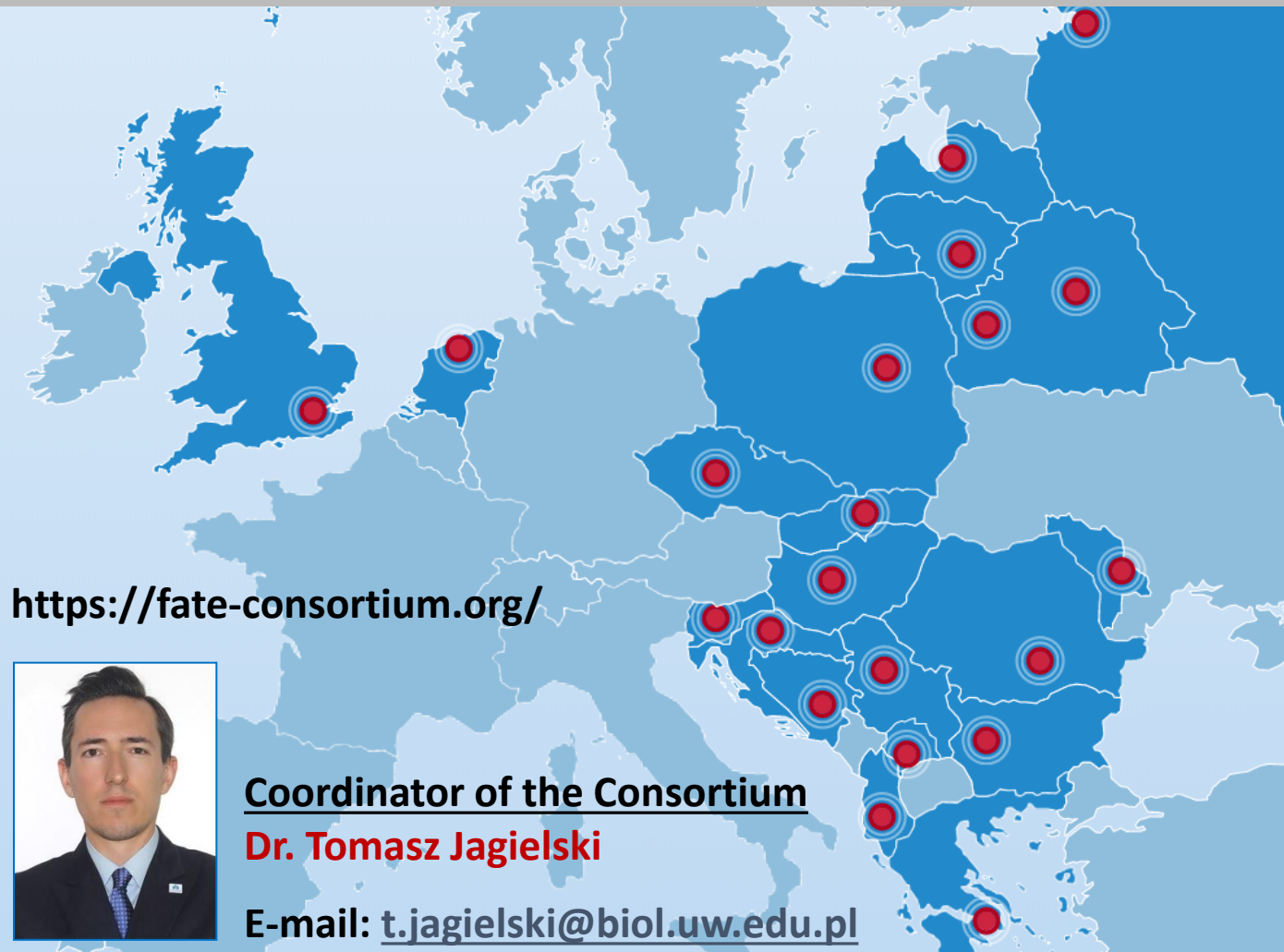
VI	TOTAL
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## FIGHT AGAINST TUBERCULOSIS IN CENTRAL & EASTERN EUROPE

International Research Consortium on Tuberculosis and Other Mycobacterial Diseases



<https://fate-consortium.org/>



**Coordinator of the Consortium**  
**Dr. Tomasz Jagielski**

E-mail: [t.jagielski@biol.uw.edu.pl](mailto:t.jagielski@biol.uw.edu.pl)

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