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POPULAR SCIENCE ABSTRACT

The group of non-tuberculous mycobacteria (NTM) consists of about 240 species that do not cause tuberculosis (TB) or leprosy. Although NTM are globally widely distributed, they are particularly well-adapted to human-engineered environments, such as drinking water distribution systems and plumbing in buildings. Furthermore, a growing number of studies have indicated that NTM are also found in various healthcare settings. NTM are for the most part opportunistic pathogens to humans and animals. The main clinical presentation of NTM infection is pulmonary disease. Other, less common, manifestations include lymphadenitis, skin and soft-tissue infections, and disseminated disease, particularly in patients with AIDS.

Nowadays, while the prevalence of tuberculosis is steadily decreasing in the developed world, the proportion of NTM infections is growing. The rise and expansion of NTM diseases is associated with the population and environmental changes, such as demographic shift to an older population, rising number of people suffering from various forms of immunosuppression, urban growth and global warming. Overall, the growing number of documented NTM cases along with people at higher risk has led to NTM being recognized as emerging public health threat, and NTM have gained a status of “the new uber-bugs”.

Disturbingly, the ecology of NTM remains a neglected area of research globally, while in Poland, the literature devoted to environmental sources of NTM is almost absent. The definite ecological niches, contagiousness, transmission routes and distribution in different geographic regions for most of the NTM remain unknown or only poorly understood.

This project was conceived with the aim of providing a systematic investigation into the ecology of NTM. This will be accomplished through extensive environmental sampling (of natural, household and hospital environments in Poland) and conventional culture-based methods, followed by novel molecular approaches such as culture-independent metagenomic analyses and high-throughput whole genome sequencing.

Among questions expected to be answered are: what are the natural reservoirs of NTM?; what is a relationship between those reservoirs and human disease?; whether all NTM have similar epidemiological potential?; whether any biotic or abiotic factor affects the abundance and distribution of NTM in the environment? What are the genetic basis of NTM drug resistance and virulence? This knowledge might be of utmost importance for engineering and implementation of new prophylactic strategies and will add considerably to the global strategy aimed at the eradication of NTM diseases.