proposed an alternative explanation: POA is primarily active against PanD but PanD is only essential if the bacteria are expressing a stringent response, the other genes associated with resistance in some way disrupt the stringent response and eliminate the sensitive phenotype. This suggests a critical role for the stringent response in the life cycle of \textit{M. tuberculosis} as compounds are being developed that target this pathway we suggest these compounds are particularly promising compounds for the treatment of tuberculosis.

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**IDENTIFICATION OF MUTATIONS OF RESISTANCE TO FLUOROQUINOLONES, AMINOGLYCOSIDES AND ETHAMBUTOL IN RIFAMPICIN-RESISTANT MYCOBACTERIUM TUBERCULOSIS**

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The aim of the study was to identify resistance mutations to second-line anti-tuberculosis drugs in patients with \textit{Mycobacterium tuberculosis} clinical samples resistant to rifampicin. Samples of biomaterial from 35 adult residents of the Tyumen region in West Siberia with established by GeneXpert system presence of rifampicin resistance have been reported as the causative agents of pulmonary and extrapulmonary diseases. To date, over 180 nontuberculous mycobacteria (NTM) species have been identified and almost 30 of these species have been reported as the causative agents of pulmonary and extrapulmonary diseases. \textit{Mycobacterium kansasii} is the sixth most frequently isolated NTM species across the world. The isolation rate of this pathogen, among other NTM, has been calculated at 5% in Europe and 4% globally. In Poland and Slovakia, the recovery of \textit{M. kansasii} from respiratory samples is particularly high, being 36% and 35%, respectively.

**6.5 MOLECULAR TYPING OF MYCOBACTERIUM KANSASII — A GLOBAL PERSPECTIVE**


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A total of 475 isolates recovered between 2000 and 2017 from as many patients with suspected \textit{M. kansasii} disease were analyzed. The isolates were collected from 19 countries.
tuberculosis (TB) remains an inglorious leader among infectious diseases in mortality, with its annual toll of 1.7 million lives worldwide. Pakistan ranks 5th among the world’s highest TB burden countries and is the 6th among countries with the highest burden of drug-resistant TB, including multi-drug resistant (MDR)-TB. However, very limited data are available on the genetic structure of strains circulating in Pakistan. The compactness of the drug resistant Mycobacterium tuberculosis population structure was apparent, as three major lineages, i.e. CAS1_DELHI, T1, and BEIJING comprised more than half (60.6%) of the isolates studied. Furthermore, the exceptionally low clustering rate suggests that recent transmission does not play an important role in the incidence of MDR-TB in Pakistan.

The molecular mechanisms by which Mycobacterium tuberculosis induces disease are complex and result from a long-lasting host-pathogen co-evolution that might have started already by its Mycobacterium canetti-like progenitors. Recent research has revealed numerous factors implicated in the pathogenesis of Mycobacterium tuberculosis, although the pathogen still holds many secrets of its successful strategy to circumvent host defences and persist in the host. As many pathogenicity factors relate to the exchange and secretion of biomolecules by Mycobacterium tuberculosis, special emphasis is given to secretion pathways that enable the Mycobacterium tuberculosis to circumvent immune defence mechanisms mounted by the host. These factors might represent new, alternative targets for development of combination therapies that would enhance immune defence mechanisms mounted by the host. These factors might represent new, alternative targets for development of combination therapies that would enhance the efficacy of the immune system in controlling Mycobacterium tuberculosis infections. Similarly, selected secretion systems may also represent important virulence factors in selected non-tuberculous mycobacteria. Here, recent insights into evolution of selected factors of Mycobacterium tuberculosis and selected other mycobacteria that are involved in host-pathogen interaction will be discussed.