Estimated Mycobacterium Tuberculosis Transmission Rate among Iranian Population

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Background & Objectives: Population structure of infectious disease is often characterized by genetic markers. In the case, mycobacterium tuberculosis vastly investigated to understand its dynamic population structure and transmission rate among effective population. Although a number of attempts have been motivated by mycobacterium tuberculosis data include IS6110 or MIRU output, but we aimed to use spoligotyping result and RTI, RTIn-1 and TMI indices to calculate transmission rate in Iranian population.

Methods: One hundred two *M.tuberculosis* isolates were subjected to spoligotyping according to standard protocol and then analyzed by RTI, RTIn-1 and TMI indices, also it completed by simpson's index.

Results: 77.2% of strains were isolated from Iranian and the remaining was isolated from immigrants (22.8%) that referred to our centre for diagnosis and treatment. About RTI, RTIn-1 and TMI indices that might between zero up to one hundred which means no diversity to infinite respectively, thus we calculate 0.75, 0.65 for RTI, RTIn-1 respectively and 0.15 for TMI also 0.19 for simpson's index. According to estimated indices 0.75, 0.65 for RTI, RTIn-1 are pretty high volume estimate among Iranian population also more accurate data than estimated result in Iran before because of mathematical support for these methods.

Conclusion: In spite of RTI, RTIn-1 that are close enough to true estimate, TMI is in need of estimation of genetic marker mutation and even more complicate the number of mutation in each level of research so this index is not accepted. Beside low rate of simpson's index show high quality of experiment. Overall, new transmission indices provide more accurate and reliable way to follow up transmission rate among Iranian population.

Keywords: *Mycobacterium tuberculosis*; Transmission Rate; Iran