

Nearly One Third of Drug Resistant *Mycobacterium tuberculosis* Strains reported in Sri Lanka Belong to Beijing Lineage; A Preliminary Investigation

06 Nov.

MHS27

Tharaka D Liyanage¹, Dushantha Madegedara², Dhammika N. Magana-Arachchi^{1(*)}

¹National Institute of Fundamental Studies, Kandy, Sri Lanka, ²General Teaching Hospital, Kandy, Sri Lanka

(*)E.mail :dhammika.ma@nifs.ac.lk

Mycobacterium tuberculosis (MTB), the causative bacterium of Tuberculosis (TB), has seven lineages, wherein; Beijing Lineage (BL) is predilected with Drug Resistance (DR) elsewhere. Herein, we intended to study the association of DR and BL in Sri Lanka; as such information is limited in the country. 77 MTB isolates obtained from pulmonary TB patients diagnosed from Kandy and Welisara (Period; Feb 2018-May 2019) were tested for drug susceptibility using proportion method and Mycobacterial Growth Indicator Tube. DNA was extracted from isolates with resistance to at least one drug. A multiplex PCR was conducted using primers targeting Rv0627c, a gene with single nucleotide polymorphism unique to BL. Reaction mixture, contained 0.33mM dNTP, 0.33 μ M primers; Fw-GTCACTGAACGTGGCCGGCTC, R1-TCGGTCACCGTTT TTGTAGGT GACCGTC, 0.13 μ M R2-AGCAACCTCGCAATCTGACC, 1xPCR buffer, 2.25mM MgCl₂ and 0.8U Taq-DNA polymerase. Thermo-cycle program was set at 95C-1min denaturation, 35 cycles (denaturation at 95C-10s, annealing at 66C-30s, and elongation at 72C-30s), final extension at 72C-3 min. A confirmed Beijing strain and H37Rv were used as positive and negative controls. Accordingly, one Extensively-Drug Resistant (XDR), two Multi-Drug Resistant, four resistant to RIF and EMB, one resistant to INH and EMB and eight mono-resistant isolates (two INH, four EMB, two RIF) were identified (16/77;20.77%), amongst which one INH-resistant, one RIF-resistant, one EMB-resistant, one isolate resistant to RIF and EMB and another XDR-TB isolate belonged to BL (5/18;27.77%). Accordingly, approximately one third of the drug resistant TB strains belonged to BL and it is significant that XDR-TB is from Beijing, which should be further studied through molecular methods.

Keywords: Beijing lineage, Tuberculosis