
Genotypic identification of *Orientia tsutsugamushi* strains causing scrub typhus disease in southern Sri Lanka

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Scrub typhus (ST) is a febrile illness in human caused by intracellular bacterium *Orientia tsutsugamushi* (OT). OT is transmitted to humans via a chigger bite leaving an eschar at the bite site. High genotypic diversity of OT is a major obstacle in developing diagnostics and vaccines. Little is known regarding OT genotypes in Sri Lanka (SL). Present study determined the OT genotypes in Southern Province, SL. A total of 13 eschars, 4 peripheral blood cell samples (PBCs) and 5 blood clots (BCs) were collected from 22 clinically suspected ST patients between 2018 and 2020. Specimens were stored in RNAlater at -80 °C prior to analysis and DNA was extracted with DNeasy Blood and Tissue DNA extraction kit (Qiagen). Partial *tsa56* gene locus (483bp) was amplified by nested Polymerase Chain Reaction (PCR), and sequenced. A phylogenetic tree was constructed using maximum likelihood method in MEGAX10.1 (nucleotide substitution; Tamura nei model, 1000 Bootstrap Trials). OT genotypes of Karp related (54.5 %), Kato (18.2%), Taiwan Gilliam variant clade of Gilliam/Kawasaki (22.7%) and TA763 (4.5%) were identified. This is the first to report TA763 genotype in SL showing 0.009 nucleic acid divergence from prototype TA763. Residue conservation analysis showed amino acid substitutions Q168P, N170D in variable domain (VD)II, V218A in VDIII and Q223R at spacer VDIII are conserved within the Karp strains of this study. Substitutions K236R, F238L at spacer VDIII are also notable in TA763 detected in SL. These domains have been shown to elicit immune responses via CD4 T-cell receptor epitopes.

Keywords: Scrub typhus, *Orientia tsutsugamushi*, TA763, Sri Lanka

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