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Expression profile of toll-like receptors mrnas in latently infected and non-infected school: Age children and adolescents

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Background: About one-third of the global population is considered to be latently infected with tuberculosis (TB) causing bacteria, *Mycobacterium tuberculosis*. Only 10% progress to active disease, while the majority contain the infection. Latently infected individuals are considered as reservoirs for continuous new TB infections.

Objective: The aim of this study is to measure the mean fold change in mRNA gene expression of Toll-like receptors (TLRs) during latent TB infection as a diagnostic biomarker tool for detection of TB progression.

Methodology: Quantitative real-time PCR (qRT-PCR) was used to measure the expression of selected TLRs (TLR-1, TLR-2, TLR-4, TLR-6 and TLR-9) in a total of 64 cDNA samples, retrieved from AHRI biorepository and collected from 32 tuberculin skin test (TST) positive and 32 TST negative, using convenient sampling, apparently healthy school children and adolescents, aged between 11 and 20 years. Specific primers and fluorescent labeled probes were used to span exon-intron junctions to prevent amplification of genomic DNA. Human acidic ribosomal protein (HuPO) was used as an internal control. A comparative CT method was used to describe fold change in the relative expression of TLR genes. Data were analyzed using Graph-Pad Prism 7.01 for Windows and a p-value of less than 0.05 was considered statistically significant. This study was approved by the AHRI/ALERT Ethics Review Committee (AAERC), AAU-CHS IRB and the National Research Ethics Review Committee (NRERC).

Result: An increased mean fold change in the relative expression of TLR-2 and TLR-6 mRNA was observed in TST positives relative to TST negatives ($p < 0.05$), whereas a slight fold decrease was observed for TLR-1 gene. A strong positive linear correlation ($r = 0.7$) was also observed between intra-compartment receptor, TLR-9 and surface receptors, TLR-1, TLR-2, TLR-4, and TLR-6 expression in latently infected tuberculosis relative to non-infected. A similar comparison was done between different age groups and both sexes; however, no apparent difference was observed in the fold change expression of TLRs.

Conclusion: Overall, an increased mean fold change in the mRNA expression of TLRs was observed in latently infected individuals relative to non-latently infected individuals, possibly showing a role for TLRs during latent tuberculosis infection, thereby maintaining and continuously stimulating immune responses through TLRs signaling pathways.

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