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Preliminary transcriptional evaluation of CXCL10 as a biomarker to identify latent tuberculosis infection

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Tuberculosis (TB) remains a pressing global health concern, particularly due to the difficulty in distinguishing latent TB infection (LTBI) from active TB (ATB) and contact exposure. This study aimed to evaluate the transcriptional performance of CXCL10 as a potential biomarker to differentiate these TB states. CXCL10, also known as IP-10, is an interferon-gamma-inducible chemokine involved in immune cell trafficking and granuloma formation, making it a promising candidate in TB diagnostics. A selected cohort of 21 LTBI cases, 11 ATB cases, and 11 TB contactss was recruited following clinical examination, Tuberculin Skin Test (TST)/Mantoux testing. Peripheral blood samples were collected, total RNA was extracted using the phenol-chloroform method and reverse transcribed into cDNA using the Promega Reverse Transcriptase Kit. Quantitative PCR (qPCR) was conducted using B2M primers for internal validation and CXCL10 primers to assess gene expression differences among the groups. Gene expression normalization was performed using ΔCT values calculated as $CT_{B2M} - CT_{CXCL10}$. Negative ΔCT values were interpreted as relative downregulation of CXCL10. The average CT values for CXCL10 expression were 18.23±9.37 in LTBI, 22.96±1.96 in ATB, and 21.34±7.52 in contact. However, statistical analyses using both one-way ANOVA ($p = 0.4452$) and the non-parametric Kruskal–Wallis H-test ($p = 0.3180$) revealed no statistically significant differences in normalized CXCL10 expression between the study groups. These findings suggest that CXCL10 alone may not sufficiently discriminate between TB disease statuses within the limits of this study. While the observed transcriptional trends are biologically plausible, especially the tendency for higher CXCL10 expression in LTBI cases, they were not statistically conclusive. The limited sample size may have reduced the power to detect true differences. Hence, further investigations using larger and more diverse populations are recommended to determine the potential role of CXCL10 in transcriptional TB diagnostics.

Keywords: *Gene expression, latent infection, biomarker, qPCR, tuberculosis*

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