

RNA Expression Analysis of Mycobacterial Methyltransferases Genes in Different Resistant Strains of Mycobacterium Tuberculosis

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Abstract : Background: The global health issue of tuberculosis (TB) still affects patients in every country. TB control may not be as effective as it should be, especially when resistant strains are involved. In this regard, mycobacterial MTases play a major role in tuberculosis, but the mechanisms underlying their function have yet to be fully deciphered. Methods: Five resistant isolates of M.tb were accumulated. As a reference strain, M.tb H37Rv (ATCC 27249) was used. For this analysis, seven putative mycobacterial MTase genes (Rv0645c, Rv1694, Rv2966c, Rv3919c, Rv2756c, Rv1988, and Rv3263), as well as Rv1392 as SAM synthase, were selected. Comparing mutations and expression levels of MTases in different strains was accomplished by PCR-sequencing and qRT-PCR. The relative expression levels of these genes were calculated using the $2^{-\Delta\Delta Ct}$ method. Results: The Rv3919c gene (T to G in codon 341) and Rv1392 gene (G to A in codon 97) were the only mutations found in the INHR strain. In all sensitive and resistant isolates, Rv0645c, Rv3263, Rv2756c, and Rv2966c were overexpressed. However, the expression of Rv1988 and Rv3919c decreased in the sensitive strains, whereas the expression of Rv1694 increased. There was also a decreased expression of Rv1392 in the INHR isolate. Conclusion: The presence of mycobacterial MTases as well as resistance to antibiotics were found to be correlated in M.tb strains. Undoubtedly, there are some MTases that are associated with the virulence process. It is necessary to conduct additional studies to fully explore the impact of mycobacterial MTases within specific strains of M.tb to develop novel diagnostic and treatment strategies.

Keywords : mycobacterium tuberculosis, drug resistance, methyltransferases, s-adenosylmethionine

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