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Poster presentation

Comparative analysis of HTLV-1 and HTLV-2 post-translational modifications of Tax proteins in relation to their intracellular localization and activation of gene expression

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The functional analysis of regulatory proteins Tax-1 and Tax-2 can provide useful information to further understand the difference in pathogenicity between HTLV-1 and HTLV-2.

Tax-1 molecules phosphorylated at serine residues 300 and 301, ubiquitinated or sumoylated at lysine residues 280 and 284 and acetylated at lysine 346 have been identified. These modifications control Tax-1 intracellular localization, the formation of Tax-1 nuclear bodies and sequential steps in Tax-1-mediated activation of the NF-κB pathway, a critical event thought to be involved in HTLV-1 transforming capacity [1].

By comparing internally tagged Tax-1 and Tax-2B, we demonstrated that Tax-2B activates gene expression via the NF-κB pathway, is present in nuclear bodies and in the cytoplasm and is modified by ubiquitination and sumoylation similarly to its homologue Tax-1 [2].

In the present study, we constructed a series of Tax-2B mutants with substitutions of specific lysine residues by arginines. The post-translational modifications, subcellular localization and capacity to activate gene expression of these Tax-2B mutants will be compared to those obtained for the corresponding mutants of Tax-1.

References

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