



POSTER PRESENTATION

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Molecular characterization of a Tax-2C protein variant identified in Brazilian subjects infected by HTLV-2C

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Although the etiologic difference in pathogenic properties of HTLV-1 and HTLV-2 still remains unclear, it has been suggested that it could be attributed to the differential structure and activities of their transactivating Tax proteins. Tax-1 and Tax-2, although having 85% amino acid (aa) similarity, present phenotypic differences consistent with a more robust transformation capacity of Tax-1. Interestingly, the HTLV-2C Brazilian variant present in Amerindians and in IDU from urban areas is genotypically close to HTLV-2A but Tax-2C possesses an additional 25aa in the C-terminal region similar to that of Tax-2B. We have already demonstrated that Tax-1 and Tax-2B have several common domains, but present differential cellular distribution. To add some information concerning the structure and site domains present in Tax-2C we conducted the present study. We have obtained the Tax-2C sequence from 25 different HTLV-2C subjects and analyzed the amino acid homology between Tax-2B and Tax-2C variants. We found that they differ for amino acid substitutions in eleven different positions that may affect cellular localization or post-translational modification. Studies on phenotypic properties and cellular localization of Tax-2C are in progress. Support: MCT/CNPq # 303545/2012-7, CAPES, IAL # 49D/2010), Brazil.

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