

STEROL METABOLISM OF *LEISHMANIA (VIANNIA) BRAZILIENSIS*:
CLONING A POTENTIAL STEROL-24-METHYLTRANSFERASE CODING
GENE

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Leishmaniasis is an endemic disease in 88 tropical and subtropical countries, affecting about 12 million people in the world. *L. (V.) braziliensis* is one of the etiological agents of leishmaniasis and it is the most important species in Brazil. Unfortunately, drugs commonly used in leishmaniasis treatment are very toxic. Therefore, the aim of this work is to investigate the sterol metabolism of *L. (V.) braziliensis* using genomic data, searching for potential new targets for developing of alternative drugs. We have identified several genes in *L. (V.) braziliensis* which can be implicated in the sterol pathway by sequence similarity searching using public databanks (GenBank, EMBL and SangerCentre) and genomic sequencing data from the strain MHOMBR75M2903, provided by GSS performed in our laboratory. Among these we were able to identify a unique genomic sequence similar to the enzyme sterol-24-methyltransferase (EC 2.1.1.41), which plays an essential role in trypanosomatid sterol biosynthesis and is absent in humans. After cloning, using the *pBad/TOPO*[®]ThioFusion kit (Invitrogen), and sequencing the construct, a structural conserved methyltransferase 11 domain was identified. A high level of similarity was also observed between this sequence and other sterol-24-methyltransferases from *L. donovani* and plants.

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