

## STUDIES OF NON-CODING RNA FROM *LEISHMANIA MAJOR*.

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One of the first activities of the *Leishmania* genome project was directed towards gene discovery. In that direction, cDNA libraries were sequenced to generate around 2,500 Expressed Sequence Tags (ESTs), 50% of them presented no match with other deposited sequences. We have used a sample of this population of clones to investigate the presence of small noncoding RNAs (ncRNAs) and their prospective role in the control of gene expression in *Leishmania*. We are currently investigating three of these putative ncRNAs genes (*ODD1*, *ODD2* and *ODD3*), whose secondary structure presents hairpin-like motif resembling those found in microRNAs. Conserved hairpin regions were used to search for candidate target mRNAs *in silico*. We have also generated constructs of each *ODD* gene to be overexpressed by *Leishmania major*. The phenotype of *L. major* transfectants was analyzed and the transcript levels of potential target genes were investigated. *ODD3* transfectants present impaired growth rate, altered morphology and noticeable ploidy changes. The level of transcript for a hypothetical protein, identified as a putative *ODD3* target gene, is modified in the *Leishmania* bearing the *ODD3* episome. Correlation between the targeted gene and *ODD3* phenotype is currently under investigation.

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