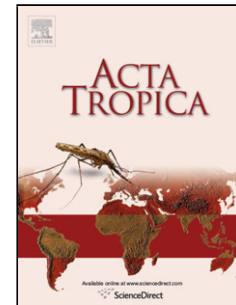


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The contribution of the DNA microarray technology to gene expression profiling in *Leishmania* spp.: a retrospective.

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ABSTRACT

The first genome project of any living organism excluding viruses, the gammaproteobacteria *Haemophilus influenzae*, was completed in 1995. Until the last decade, genome sequencing was very tedious because genome survey sequences (GSS) and/or expressed sequence tags (ESTs) belonging to plasmid, cosmid and artificial chromosome genome libraries had to be sequenced and assembled *in silico*. Nowadays, no genome is completely assembled actually, because gaps and unassembled contigs are always remaining. However, most represent the whole genome of the organism of origin from a practical point of view. The first genome sequencing projects of trypanosomatid parasites were completed in 2005 following those strategies, and belong to *Leishmania major*, *Trypanosoma cruzi* and *T. brucei*. The functional genomics era rapidly developed on the basis of the microarray technology and has been evolving. In the case of the genus *Leishmania*, substantial biological information about

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