

Molecular identification of *Leishmania martiniquensis* and *Leishmania siamensis*

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Leishmaniasis is a newly emerging disease in Thailand. Two new species called *Leishmania martiniquensis* and "*Leishmania siamensis*" have been reported as causative agents. Species typing in leishmaniasis is important in diagnostics, epidemiology, and clinical studies. In this study, two genetic markers, the internal transcribed spacer 1 region (ITS1) of the rRNA gene and the 3' untranslated region of the heat shock protein 70 (type I) gene (3'-UTR of *HSP70-I*), were used to identify the two species. PCR amplification of the 3'-UTR of *HSP70-I* could be used to differentiate between *L. martiniquensis* (480-2 bp), *L. siamensis* (672-4 bp) and other *Leishmania* species. These results were confirmed by sequencing of the PCR products. PCR amplification of ITS1 produced products that could not be reliably distinguished based on their size alone, but when sequenced confirmed their identity. Phylogenetic analysis of the ITS1-rRNA and the 3'-UTR of *HSP70-I* sequences showed that *L. martiniquensis* and *L. siamensis* were grouped into the *Leishmania enriettii* complex. We conclude that the 3'-UTR of *HSP70-I* is a suitable target for PCR-based identification of both parasites. The technique is simple to perform and can be implemented in all settings where PCR is available.