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Wild rodents as potential reservoirs of *Trypanosoma* spp. in Southeast Asia: a link towards human infections ?

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Abstract

The present study investigated the molecular prevalence of *Trypanosoma lewisi* and *Trypanosoma evansi* in wild rodents from Cambodia, Lao PDR and Thailand. Between 2008 and 2011, rodents were trapped in 10 localities and 584 of them were tested using three sets of primers: TRYP1 (amplifying ITS1 of ribosomal DNA of all trypanosomes), TBR (amplifying satellite genomic DNA of *Trypanozoon* parasites) and LEW (amplifying ITS1 of ribosomal DNA of *Trypanosoma lewisi*). Based on the size of the PCR products using TRYP1, 10% were positive for *Trypanosoma lewisi* and 2.6% positive for *Trypanozoon*. Results were confirmed by sequencing PCR products and by using more specific primers (LEW and TBR). The specificity of TRYP1 primers however failed as rodent DNA was amplified in some instances. Using LEW, the positive samples for *Trypanosoma lewisi* were confirmed both by PCR and sequencing. In Thailand, *T. lewisi* was found in *Rattus tanezumi, R exulans* and *Berylmys*; in Lao PDR, in *R. tanezumi* and *R. exulans* and in Cambodia in *R. tanezumi, R. exulans* and *R. norvegicus.* Using TBR, the positive samples for *Trypanozoon* were confirmed by sequencing; as *T. evansi* is the only species of the *Trypanozoon* sub-genus possibly present in Asian rodents. These results confirmed its presence in rodents from Thailand (*R. tanezumi*), Lao PDR (*R. tanezumi* and *R. nitidus*) and Cambodia (*R. tanezumi, Niviventer fulvescens* and *Maxomys surifer*). We tested how habitat structure affects the infection of common murine rodents, inhabiting human-dominated landscapes in South East Asia, by *Trypanosoma* species. For this, we used geo-reference data of rodents investigated for *Trypanosoma* infection and land covers developed for seven sites in Thailand, Cambodia and Lao PDR. Infection by *T. lewisi* was found in rodents living near human settlement and in areas with high cover of built-up habitat. Increased patchiness and high cover of rain-fed agriculture lands were the likely habitat explaining the infection of rodents by *T. evansi*. These results suggest a likely role of wild rodents as reservoir and possible source of atypical human infection by animal trypanosomes.

Keywords: *Trypanosoma evansi*, *Trypanosoma lewisi*, PCR, wild rodents, habitat, land covers, Southeast Asia, human settlement.