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### ► To cite this version:

Thibaud Decaëns, David Porco, Samuel W. James, George Brown, Lise Dupont, et al.. Dissecting tropical earthworm biodiversity patterns in tropical rainforests through the use of DNA barcoding. 5. Encontro Latino-Americano de Ecologia e Taxonomia de Oligoquetas (ELAETAO5), Jun 2015, Curitiba, Brazil. 1 p. hal-02741959

**HAL Id: hal-02741959**

**<https://hal.inrae.fr/hal-02741959>**

Submitted on 3 Jun 2020

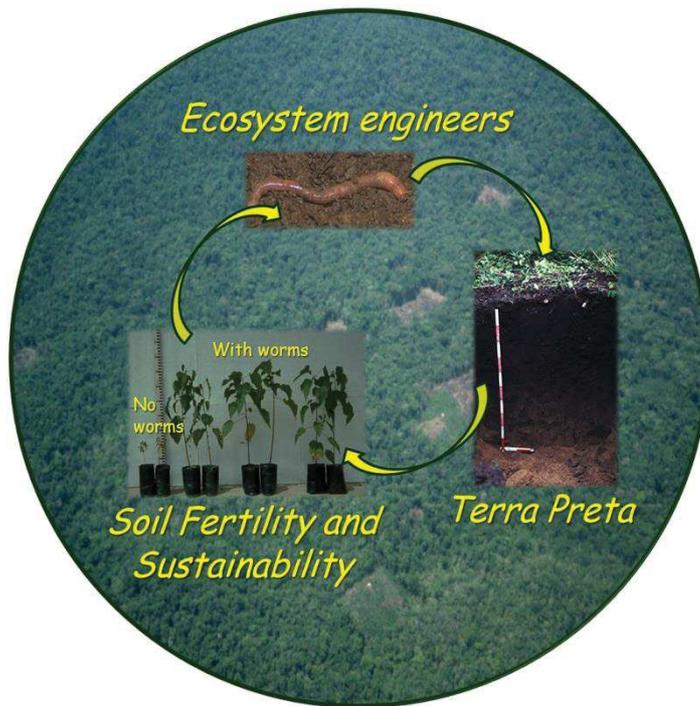
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# ELAETAO

08 e 09 de junho de 2015



## SIMPÓSIO ENGENHEIROS EDÁFICOS, FERTILIDADE DO SOLO E TERRA PRETA DE ÍNDIO (TPI)

10 e 11 de junho de 2015

APOIO:





## Dissecting tropical earthworm biodiversity patterns in tropical rainforests through the use of DNA barcoding

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**Abstract** - Despite representing a key component of terrestrial biota, soil invertebrates in tropical rainforests have been poorly studied from both a taxonomic and an ecological perspective. Earthworms in particular comprise about 6000 described species, a number thought to represent less than half of the actual biodiversity of this group. Earthworm taxonomy is particularly weakly resolved in the tropics, resulting in difficulties for species identifications, and a critical lack of ecological studies on earthworm communities. DNA barcoding has been proposed as a useful approach to counter this problem through allowing automated species identifications or the use of molecular species proxy that are expected to facilitate and increase the pace of ecological studies in poorly studied tropical regions. During the past years, we conducted several projects in South America and Central Africa with the aim of describing diversity patterns of earthworm communities at different scales. In French Guyana and Gabon, we collected thousands earthworms in different localities representing the main ecosystems of the region. Specimens were DNA barcoded to delimit molecular operational taxonomic units (MOTUs), and we used MOTU number and composition to estimate species richness and describe community structure in the different habitats/localities. We found unexpectedly high levels of local species diversity (e.g. 48 MOTUs found in the Nouragues site) and species turnover ( $\beta$  diversity ranging from 60% to 90% depending on geographical distance between sites). The taxonomic spectrum of local communities suggested the importance of long-term diversification processes and current ecological factors for the structuring of local communities. In a few sites MOTUs were described using a selection of relevant traits to explore community functional structure. Combined with the use of community phylogenetic tools, this approach was an interesting way to explore in more details the assembly rules that were responsible for the observed community patterns.