Use of DNA barcoding for Brazilian earthworm biodiversity assessment: untangling taxonomy for conservation*

Elodie Da Silva[*1], Samuel James[2], Márcio Da Rosa[3], Marie Bartz[4], David Stanton[5], Eliza Busch[6], Guilherme Schuhli[1], Luis Cunha[5], Dilmar Baretta[7], Thibaud Decaens[8], Peter Kille[5], and George Brown[†1]

[1]Embrapa Forestry – Brazil
[2]University of Iowa – Brazil
[3]Universidade do Estado de Santa Catarina – Brazil
[4]Positivo University – Brazil
[5]Cardiff University – United Kingdom
[6]Federal University of Paraná – Brazil
[7]Universidade do Estado de Santa Catarina-CEO – Brazil
[8]Centre d'Ecologie Fonctionnelle et Evolutive (CEFE) – Campus CNRS, UMR 5175 – 1919 route de Mende;34293;Montpellier Cedex 5, France

Abstract

Worldwide, soils and their biodiversity are threatened by land use changes and management practices that can have profound effects on soil organisms that perform important ecosystem services. However, our ability to adequately assess biodiversity in soils is greatly hindered by taxonomic impediment. The present research work addresses these issues/limitations, by focusing on DNA barcoding of Brazilian earthworms, a major soil ecosystem engineer.

Around 850 specimens from 175 sites (mainly in S Brazil) were DNA barcoded, to delimit molecular operational taxonomic units (MOTUs), and MOTU number and composition were used to estimate species richness. In total, barcodes have been generated for approx. 232 MOTUs with $> 10\text{-}14\%$ genetic distances, most of them representing species new to science. In S and SE Brazil, approximately 75 species-level lineages of *Glossoscolex* and 29 of *Fimoscolex* were found, most of which belonged to undescribed species. They were found mostly in forested sites and some different species were also found in tree plantations (*Araucaria* and *Eucaliptus*) and pastures. While the barcode sequence itself is not sufficient for robust phylogenetic tree generation, it allowed the detection of cryptic species as the native species *Urobenus brasiliensis* with $> 12\%$ of genetic distance. Furthermore, *DNA barcoding* has helped to separate individuals with more complicated taxonomy such as for the Ocnerodrilidae family recently sampled in Southern Bahia.

The *DNA barcoding* has been shown to be very effective for Brazilian earthworms, allowing

---

*Corresponding author:
†Speaker

species-level identification of adults, juveniles and cocoons. It is a valuable tool for preliminary species delineation (MOTUs) and therefore the estimation of earthworm biodiversity. While there are still restrictions to the extensive use of barcodes for identifying species, we still expect that a comprehensive database can be a powerful taxonomic tool that merits further development and will help identify species, their distribution ranges and intraspecific diversity, which ultimately can be used to assess biodiversity in areas under pressure for development or conservation in Brazil.