O4-01 – S4 *Termites, earthworms and tropical soils: their diversity and conservation*
Monday 20 June 20 / 11:00-15:30 – Sully I

DNA barcode for earthworm taxonomy, biodiversity assessment and conservation of Brazilian species

ELODIE DA SILVA[1], SAMUEL WOOSTER JAMES[2], MARCIO GONCALVES DA ROSA[3], GUILHERME SCHÜHLI[1], MARIE LUISE CAROLINA MARIE[4], THIBAUD DECAENS[5], GEORGE GARDNER BROWN[1]
[1]EMBRAPA FLORESTAS, SOIL ECOLOGY, 834111-000, COLOMBO, BRAZIL
[2]University Of Iowa, Biology, 52242, Iowa City, USA
[3]Universidade Do Estado De Santa Catarina, Soil, 88035-001, Lages, Brazil
[4]Universidade Positivo, Environmental Mana, 81280-330, Curitiba, Brazil
[5]Universite De Montpellier, Cefe Umr 5175 Cnrs, 34293, Montpellier, France

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 soil ecosystem services. Therefore, it is important to adequately assess populations and biodiversity of soil animals such as earthworms, so that they can be used as bioindicators of sustainable management practices and of environmental quality.
However, our ability to perform this task is greatly hindered by a taxonomic impediment, including the small number of specialists in the tropics, the inability to identify most cocoons, incomplete and/or juvenile worms, the existence of many small and difficult-to-identify species and the absence of easily internet-accessible information on tropical earthworm ecology and taxonomy. These limitations are especially problematic in Brazil, home to about 10% of the world's biodiversity and where rapid land-use changes and management practices are threatening a biodiversity that we are not even fully aware of yet, due to the vast number of still undescribed species. The present research work addresses these issues/limitations, focusing on a major soil ecosystem engineer: the earthworms.
The Cytochrome Oxidase I (COI) barcode region has been shown to be very effective for earthworms, allowing species-level identification of adults, juveniles and cocoons. While the Barcode sequence itself is not sufficient for robust phylogenetic tree generation, it is a valuable tool for preliminary species delineation, detection of cryptic species, and estimation of biodiversity.
At present, there are barcodes for ~600 earthworms from 175 sites, mainly in Southern Brazil. In total, we estimate that barcodes have been generated for approx. 175 species, most of them new to science, with > 14-15% genetic distances. In S and SE Brazil, approximately 56 species-level lineages of Glossoscolex and Fimoscolex were found, most of which belonged to undescribed species. The neighbor joining tree of these sequences shows geographical structure within each genus, sometimes on very small spatial scales. Barcoding has helped to separate morphologically similar species, species with more complicated taxonomy and show geographic variation within species.
While there are still restrictions to the extensive use of barcodes for identifying of Brazilian species, we still expect that a comprehensive database can be a powerful taxonomic tool that merits further development.

O4-02 – S4 *Termites, earthworms and tropical soils: their diversity and conservation*
Monday 20 June 20 / 11:00-15:30 – Sully I

Diversity and structure of tropical earthworm communities as revealed by DNA barcoding

THIBAUD DECAËNS[1], DAVID PORCO[1], SAMUEL W. JAMES[2], ELODIE DA SILVA[3], LISE DUPONT[4], EMMANUEL LAPIED[5], RODOLPHE ROUGERIE[6], VIRGINIE ROY[4]
[1]University of Montpellier, UMR CEFE, 34293, Montpellier, France
[2]University of Iowa, Department of Biology, IA 52242, Iowa City, USA
[3]EMBRAPA, Florestas, 83411, Curitiba, Brazil
[4]University of Créteil, UMR IEES, 94010, Créteil, France
[5]Norwegian University of Life Sciences, NBIO, 1431, As, Norway(6) MNHN, UMR ISYEB, 75005, Paris, France

Despite being recognized as important actors of soil functioning, earthworms have been poorly considered from a taxonomic perspective. As a consequence, the nearly 6000 species currently recognized worldwide probably represent at best half the actual biodiversity of the group. This taxonomic deficit is particularly critical in the tropics, resulting in difficult species identifications and a lack of ecological studies on earthworm communities.
Earthworm communities were sampled in eight study sites of French Guiana (grants from CNRS-Nouagues and Labex CEBA). In each site, a rapid screening of communities was achieved in a selection of habitats using a standardized protocol based on the systematic harvesting of specimens in all types of microhabitats available in a 1 ha area. DNA barcodes (COI gene) obtained for a selection of specimens were used to delimit molecular operational taxonomic units (MOTUs), the number and composition of which was further used to describe community diversity and structure at different spatial scales.
DNA barcodes produced for 2826 specimens clustered into 166 MOTUs, resulting in a great improvement of our knowledge of regional diversity, as compared to the 22 species that were reported for French Guiana in a recent checklist. Beta-diversity among sites was high, with up to 70% of the MOTUs only found in a single study site. As a consequence, the number of species accumulates steadily with the number of study sites sampled, and a rough estimates suggests that at least 400 species could be found in French Guiana. This region of Amazonian forests could therefore represent one of the richest hotspots for earthworm diversity, and additional research is critically needed to progress toward documenting the actual number of species in this region.
At a local scale, assemblages seem to be dominated by specialist species, with only a small fraction of generalists able to colonize a broad range of habitats or microhabitats. The number of species co-existing in a given habitat never exceeded 15 MOTUs, suggesting that interspecific competition may drive niche saturation during the process of community assembly. The ongoing development of a functional trait database will allow combining functional, phylogenetic and taxonomic diversity approaches in order to disentangle the relative contribution of habitat filters, biotic interactions and neutral processes in the structuring of earthworm communities in the rainforest of French Guiana.