

53<sup>rd</sup>  
**ATBC**  
2016

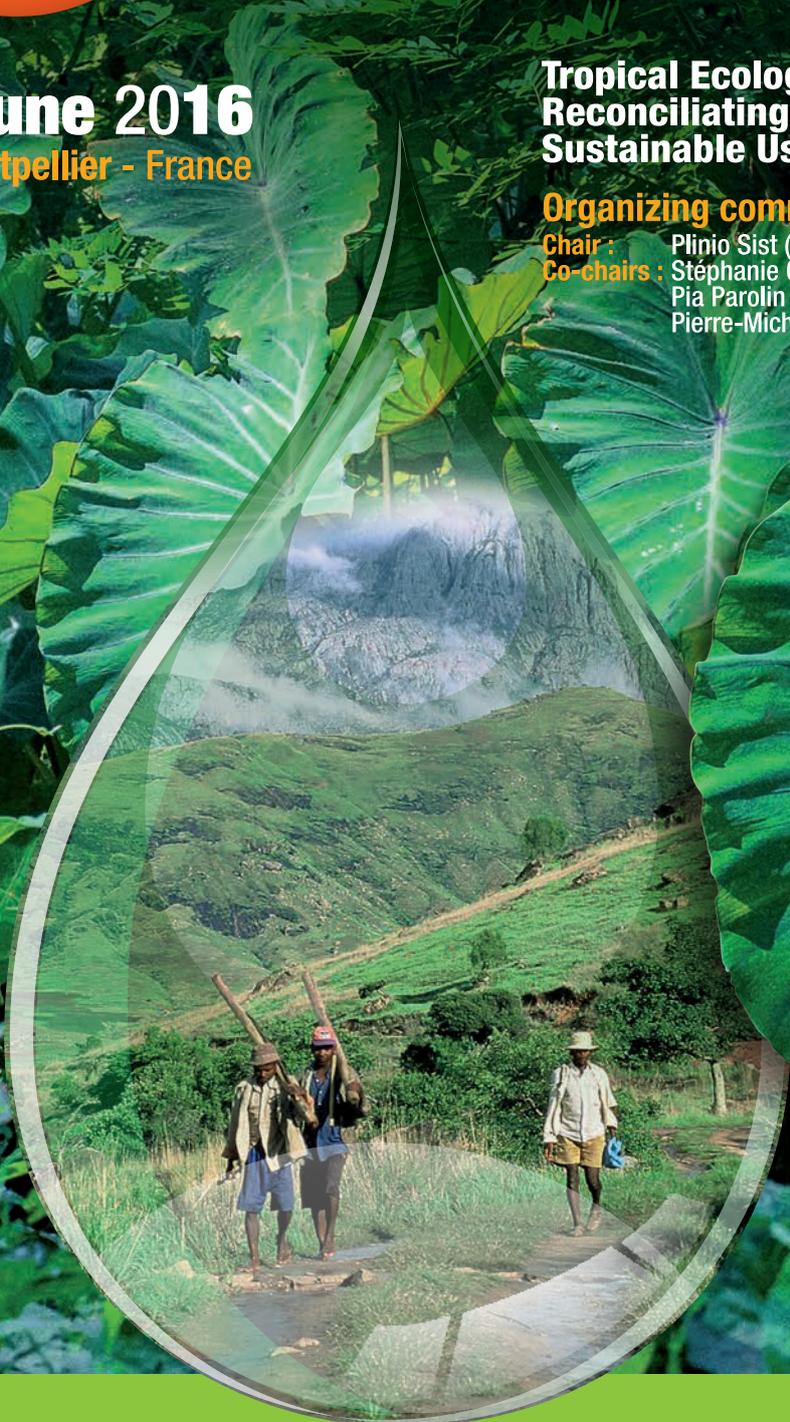
# Annual Meeting of the Association for Tropical Biology and Conservation

**19-23 June 2016**  
Le Corum, Montpellier - France

**Tropical Ecology and Society  
Reconciling Conservation and  
Sustainable Use of Biodiversity**

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**PROGRAM  
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ABSTRACTS**

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## O20-03 – S20 Free session: Plant-microbial interactions

Tuesday 21 June / 16:00-17:30 – Sully I

### Microbes drive decomposition and carbon cycling in a rainforest epiphyte microcosm

JULIAN DONALD, SAM BONNETT, PETE MAXFIELD, M.D. FARNON ELLWOOD

University of the West of England, Biological, Biomedical and Analytical Sciences, BS16 1QY, Bristol, UK

**Background:** Suspended soils, such as those in epiphytes, form important components of the discrete, often limited nutrient pools of tropical forests. The bird's nest fern (*Asplenium nidus*) is a natural microcosm, which has been used to reveal patterns and processes in canopy invertebrate diversity and rainfall nutrient enrichment. However, little is known of the microbial communities associated with these canopy epiphytes, with almost no information on microbial community composition, or its role in decomposition and nutrient cycling. This is largely due to the difficult nature of working in rainforest canopies, and to the sensitivity of soils to manipulation.

**Method:** The Eden Project in Cornwall is a unique botanic collection, providing a 'half-way house' between laboratory experiments and in-situ field work. Eden's rainforest biome is highly suited to modelling rainforest processes, in this case canopy soil function. In this study, <sup>13</sup>C-labelled maize litter was added to the soil of twenty bird's nest ferns which were then suspended at 10 metres in two replicate tree crowns. This was achieved through the development of an innovative canopy platform and irrigation system. The standardised soils were sampled prior to litter addition and installation; and again after intervals of 3 and 6 months. Soil microbial activity was analysed using extracellular enzyme assays. Microbial composition, biomass and carbon uptake were determined using Phospholipid Fatty Acid Analysis (PLFA) and Isotope-ratio mass spectrometry (IRMS).

**Results:** Suspended soils within the ferns exhibited significant levels of hydrolase and oxidative enzyme activity. PLFA analysis revealed that fern soils had a microbial biomass and community composition comparable to the soil on the ground below. Whilst enzyme activity and biomass decreased over time, IRMS analysis revealed that soil microbial carbon sequestration increased over time.

**Discussion:** These results show that the suspended soils of bird's nest ferns support functioning microbial communities that actively decompose and assimilate carbon. Microbial community biomass and enzyme activity decreased over time, likely as a response to the drier conditions associated with the canopy environment, but carbon sequestration was unaffected. Given the ubiquity of epiphytes, their associated suspended soil and microbial communities, such microcosms should be considered integral elements of the carbon cycle of tropical forests.

## O20-04 – S20 Free session: Plant-microbial interactions

Tuesday 21 June / 16:00-17:30 – Sully I

### Ectomycorrhizal fungal biodiversity from New Caledonian rainforests on ultramafic soils

FABIAN CARRICONDE<sup>1</sup>, MONIQUE GARDES<sup>2</sup>, JEAN-MICHEL BELLANGER<sup>3</sup>, KELLY LETELLIER<sup>1</sup>, SARAH GIGANTE<sup>1</sup>, VÉRONIQUE GOURMELON<sup>1</sup>, STÉPHANE MCCOY<sup>4</sup>, JULIE GOXE<sup>4</sup>, JENNIFER READ<sup>5</sup>, LAURENT MAGGIA<sup>6</sup>

<sup>1</sup>Institut Agronomique néo-Calédonien (IAC), Axe 2 "Diversités biologique et fonctionnelle des écosystèmes terrestres", 98800, Nouméa, New Caledonia

<sup>2</sup>Université de Toulouse-CNRS, UMR 5174 EDB, 31062, Toulouse, France

<sup>3</sup>INSERM, UMR5175, 34293, Montpellier, France

<sup>4</sup>Vale Nouvelle-Calédonie, Direction de l'Environnement et des Relations Communautaires, 98846, Nouméa, New Caledonia

<sup>5</sup>Monash University, School of Biological Sciences, 3800, Melbourne, Australia

<sup>6</sup>Institut Agronomique néo-Calédonien (IAC)-Cirad, Axe 2 "Diversités biologique et fonctionnelle des écosystèmes terrestres"-UMR AGAP, 98800, Nouméa, New Caledonia

**Background:** Ectomycorrhizal (ECM) fungi play key roles in ecosystems functioning, such as in plant community dynamic. However, very few studies have been undertaken in the tropics. New Caledonia is an archipelago located in the South West Pacific and is well-recognized for its exceptional biodiversity, especially due to its geographical isolation and the presence of ultramafic soils. In this study, we present the first large molecular study on ECM fungal communities in New Caledonian rainforests from ultramafic soils.

**Method:** We collected ECM root tips and fruit bodies from three sites located in the South of the main island. In each site, sampling was performed in two monodominant rainforests, with an upper canopy dominated by *Nothofagus aequilateralis* (Nothofagaceae) or *Arillastrum gummiferum* (Myrtaceae). Adjacent mixed rainforests were also studied. These formations might represent different successional stages of forest dynamic. Fungi were identified by sequencing the internal transcribed spacer (ITS) of the nuclear ribosomal genes, and host plant were identified as well using the same genomic region.

**Results:** Out of the 587 ECM root tips and 2372 fruit bodies, 312 OTUs, belonging to at least 29 lineages, were delineated. The community was largely dominated by the *Cortinariaceae* lineage in the above- and below-ground communities. Furthermore, community structure analyses strongly suggested host preferences.

**Discussion - conclusion:** This work increases our knowledge of ECM fungal biodiversity in the tropics, particularly in terms of diversity and dynamic. Indeed, the species diversity seems to be similar to the diversity observed in other tropical and temperate forests and most of the molecular species delineated might be unique to New Caledonia. We could also hypothesise that some fungal groups play major roles in the community dynamic as inoculum sources. Additionally, in the context of land disturbance, the results obtained will permit to develop biological indicators for further conservation and ecological restoration programs of New Caledonian ultramafic ecosystems.