

**SYMPOSIUM 16: DNA BARCODES AND BEYOND: DEVELOPING AND UTILIZING
COMMUNITY-WIDE DNA SEQUENCE DATA TO UNDERSTAND ECOLOGY AND EVOLUTION OF
TROPICAL BIODIVERSITY**

Bonito, 20th June 2012 (Wednesday)

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The global revolution in high throughput DNA sequencing proposes many challenges and opportunities for tropical biologists. The low cost and feasibility of generating genome scale data now makes it practical to consider sequencing genomes for any given species and, as a result, entire communities. What kinds of questions can be answered using molecular genetic data from entire communities and how will this change our understanding of the ecological and evolutionary mechanisms that give rise to and maintain tropical diversity? How does incorporating evolutionary information about phylogenetic relatedness of species within a community improve our understanding of tropical diversity? How will molecular data help us to understand extremely complex networks of food webs and ecological interactions found in tropical ecosystems? We propose to bring together a group of early career and established ecologists and evolutionary biologists working at the interface of the lab and field who are using molecular genetic data from *entire species assemblages* to address questions regarding to origin and maintenance of tropical biodiversity. The proposed symposium is clearly in strong agreement with the theme of this year's ATBC meeting "Ecology, Evolution, and Sustainable use of Tropical Biodiversity" as it will directly address both ecological and evolutionary questions within a single symposium, make connections between the two, and offer insight into conservation issues facing tropical biodiversity. We have contacted 10 speakers who have accepted our invitation. This group is working with plants, animals, fungi and several talks will explore interactions between groups. These researchers are working in Central American, South American, African, and Asian tropics.

TALKS (Room Kadiwéu 1, 09h00-12h30)

09h00-09h15 (S16.OC.01) **Plant DNA barcodes and community phylogenies: how highly-resolved evolutionary relationships aid the understanding of community assembly.**

John Kress

09h15-09h30 (S16.P.13) **Niche partitioning and habitat definition in a neotropical forest: a new detection approach.** *Flávia Regina Capellotto Costa*

09h30-09h45 (S16.P.03) **Phylogenetic turnover in tropical tree communities - testing evolutionary and ecological hypotheses on species assembly rules at contrasting spatial scales.** *Olivier Hardy*

09h45-10h00 (S16.OC.04) **eDNA metabarcoding: high throughput taxa identification.**

Pierre Taberlet

10h00-10h15 (S16.OC.05) **Spatial structure of the plant community at Nouragues, French Guiana: preliminary insights from a metabarcoding survey.** *Jerome Chave*

10h15-10h30 (S16.OC.06) **Below ground tropical tree species and phylogenetic diversity accessed through DNA barcoding and massively parallel sequencing.** *Andy Jones*

Coffee Break

11h00-11h15 (S16.P.02) **Fern phylogenetic differentiation in a tropical forest: the role of life forms structuring community.** *Sara Mortara*

11h15-11h30 (S16.P.08) **Testing the role of ecology and life history in structuring genetic variation across a landscape: a comparative ecophylogeographic approach.** *Andrea Paz*

11h30-11h45 (S16.P.09) **Phylogenetic diversity in rock outcrop plant communities in Southeastern Brazil.** *Sara Lucía Colmenares Trejos*

11h45-12h00 (S16.P.10) **Spider trait evolution: unraveling the role of habitat structure, spatial scale and phylogeny.** *Thiago Gonçalves Souza*

12h00-12h15 (S16.P.11) **What do arthropods tell us about niche evolution in the neotropics?** *Jérôme Murienne*

12h15-12h30 (S16.P.12) **Untangling phylogenetic and geographic effects on host plant ranges of phytophagous insects.** *Leonardo Ré Jorge*

POSTERS (Karuha Space, 15h30-16h30)

S16.P.04. **DNA barcodes for the identification of the heavily logged Amazonian timber species, *Manilkara huberi*, and related *Manilkara* species.** *Vânia Cristina Rennó Azevedo*

S16.P.06. **Discriminating the effects of phylogenetic hypothesis, tree resolution, and clade age estimates on phylogenetic signal measurements.** *Guilherme Dubal dos Santos Seger*

S16.P.07. **Drivers of the ecological and evolutionary structure of tree communities in southern Brazil.** *Eduardo L. Hettwer Giehl*

S16.P.08. **Does functional or taxonomic diversity best predict ecosystem functioning in the Brazilian Amazon?** *Hannah Griffiths*

S16.P.09. **Functional and phylogenetic turnover of tree assemblages on fine spatial scale in Atlantic forests.** *Igor Silva*

S16.P.10. **The interspecific abundance-body size relationship in Neotropical butterflies (Nymphalidae: Ithomiini).** *Geoffrey Gallice*

S16.P.11. **Spatial distribution of Scarabaeinae related to vegetation structure.** *Wallace Beiroz*

S16.P.12. **Structure and composition of the edaphic arthropod community and its bioindicators in different land use systems.** *Ananza Mara Rabello*



- S16.P.14. **Integrating metacommunity processes with biogeography in the study of latitudinal gradients.** *Thiago Gonçalves Souza*
- S16.P.15. **Distribution patterns of floristic composition in relation to soil gradient in the Central Amazon, Amazonas, Brazil.** *Fernanda Souza*
- S16.P.16. **Fine-scale environmental variation drives harvestmen (Opiliones) diversity patterns.** *Tiago Nascimento Bernabé*
- S16.P.17. **Spatial patterns on functional diversity of African mammals.** *Marcos de Souza Lima Figueiredo*
- S16.P.18. **Species richness vs. phylogenetic diversity: assessing the conservation needs of the *Didymopanax* group of *Scheffera* (Araliaceae).** *Pedro Fiaschi*