European Science Foundation

Standing Committee for Life, Earth and Environmental Sciences (LESC)

ESF LESC EXPLORATORY WORKSHOP

The Last Biotic Frontier: Towards a Census of Canopy Life

Scientific Report

Royal Belgian Institute of Natural Sciences
Brussels, Belgium, 5-9 July 2005

Convened by:

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http://www.naturalsciences.be/cb/ants/meetings/esf_exploratory_workshop.htm

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With co-funding from

UNEP

GCP Global Canopy Programme

The IBISCA flight-intercept trap programme (FL) and focal taxa (Psocoptera, Diptera)

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Ordinal abundance patterns from 1,659 flight-intercept trap (FL) samples for all IBISCA focal taxa are briefly summarized. A total of 71, 721 specimens were captured in FL traps at six heights from the forest floor to the canopy, from September 2003 to October 2004. Coleoptera, Hymenoptera and Diptera represented 75% of the FL catch. Proportional representation of taxa was relatively constant between sites, but varied markedly between vertical heights. In particular, Coleoptera increased two-fold in abundance and proportional representation from the ground to the canopy. Focal Coleoptera families will be the most important taxa to analyse from FL samples. With respect to focal Psocoptera from FL traps, there was also a strong increase in abundance an species richness with increasing vertical height. For focal Diptera taxa across all IBISCA trapping programmes (N=190,461), we present a brief breakdown of progress on sample sorting, focal families to be sorted to morphospecies and results obtained so far. There were strong patterns of vertical stratification at the family-level for all Diptera and at the genus/species-level for Milichiidae (Diptera). Apparent canopy-dominant families include Dolichopodidae, Chloropidae, Milichiidae and Scatopsidae. Ground-dominant families include Cecidomyiidae, Drosophilidae, Phoridae, Sphaeroceridae. For Milichiidae, species composition is extremely unusual for a Neotropical assemblage, and canopy-level sampling has forced a re-evaluation of major sampling methods the are useful for collecting Milichiidae, and of the relative dominance of the genera *Phyllomyza* and *Pholeomyia* in the Neotropics.

The IBISCA sticky trap programme and focal taxa: Auchenorrhyncha and *Agrilus* (Hemiptera, Coleoptera)

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This contribution summarizes progress with the IBISCA sticky trap programme and presents preliminary results for two focal taxa: Auchenorrhyncha and *Agrilus* (Buprestidae). In total, the sticky trap programme surveyed 993 traps at 9 sites and yielded *ca*. 55,000 arthropods. Arthropod abundance/activity along the vertical transect follows a bimodal distribution and is significantly higher (and of similar magnitude) at the levels of soil/litter and upper canopy. Patterns of vertical stratification greatly differ among arthropod groups with different ecologies. Incident light measured below the traps appears to be a good predictor of the abundance/activity of arthropods collected per trap. About 15,000 homopterans (Auchenorrhyncha and Psylloidea) representing 446 morphospecies were collected with a variety of sampling methods during the IBISCA project. About 72% and 29% of this material was identified at the generic and species levels, respectively. Taxonomical studies are on-going. Stratification and faunal turnover is obvious at familial, subfamilial and specific levels. More species were collected in the understorey (where sampling effort was highest), but rarefaction curves were similar for the understorey and the upper canopy, with the mid-canopy being enriched from both habitats. Adults whose nymphs are fungal/root feeders are prevalent near the forest ground, whereas meristem-feeders dominate in the upper canopy. The distance (perhaps related to floristic composition) and the illumination of the sites

Interactions between organisms

Trophic interactions among tropical organisms

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Tropical insect herbivores, their host plants and their predators and parasitoids account for the vast majority of the earth's biodiversity. Studying trophic (feeding) interactions among these species in diverse tropical ecosystems creates special challenges, but has the potential to further our understanding of the processes structuring and maintaining patterns of diversity and abundance. I will briefly review approaches used to study plant-herbivore and herbivore-parasitoid interactions in tropical forests, and describe the use of food webs to quantify interactions across multiple trophic levels. Such studies allow us, for the first time, to make robust and testable predictions about the implications of adding or removing species from ecological communities. I will consider how IBISCA data might contribute to ongoing work on trophic interactions, and how data on tropical insects might in future be collected to maximise its value to the study of trophic interactions.

The IBISCA social insects programme: ants

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Distribution of termites from the ground to the canopy of a Panamanian rainforest

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Termites are inhabitants of warm temperate or tropical ecosystems. Numerous studies focusing on fallen logs, leaf litter or humus have established their importance as decomposers at ground level, but almost no attention has been paid to their presence in the upper strata of tropical forests. Within the framework of the IBISCA project in the San Lorenzo Protected Area (Panama), we conducted the first systematic sampling campaign to evaluate the diversity and richness of a termite fauna, from the ground to the canopy. Dead wood or termite-built covered runways were examined on a total of 125 trees along two transects, whereas quadrats provided samples of the ground fauna at the same sites, for comparative purposes. Canopy collections (here defined as higher than 10 m above ground) yielded 63 occurrences (colony samples) representing 10 termite species, whereas 29 species were recorded in 243 occurrences from the ground. Five species were recorded in both habitats. Species accumulation curves revealed that the inventory of canopy species was near completion, whereas ground species were still accumulating in a logarithmic pattern. Remarkable components of the canopy fauna include several drywood species (Kalotermitidae), forming small colonies within dead branches or stumps. By contrast, soil feeders were exclusively found in ground samples, where they were abundant (19 species, 110 occurrences). Wood feeders displayed a similar species richness at both levels, although most species showed a clear preference for either ground or canopy. Further data still to be analyzed include: 5 ground transects (> 350 series) in other sites of the same forest, to evaluate Beta-diversity; 27 series of additional hand-collected canopy samples; 78 series of non-flying termites collected by standardized sampling methods (Berlese, Winkler, pitfalls, etc.); and > 370 samples of flying termites (alates) collected by light or flight interception traps, yet to be identified. Put

The taxonomic impediment comprises two components, one spatial and one temporal. The first of these is that the majority of the world's biodiversity is confined to the tropics, while most taxonomic capacity is found in the "developed" world. The second is that taxonomic capacity is decreasing, while the need for taxonomic information is increasing. This taxonomic impediment has stimulated ongoing discussions and initiatives to ameliorate the problem, such as digitizing museum collections, DNA "bar coding" of species, biodiversity megadatabases. How will these initiatives help when taxonomic capacity is so limited and knowledge of fauna and flora so incomplete for most of the biodiverse tropical countries. Will we have to wait until all species are described? What are the ways forward and are there any shortcuts? This paper gives an overview of possible strategies and tools to reduce the problems arising from the taxonomic impediment

Working with parataxonomists
O. Missa

Parataxonomists are typically local people with no formal education in biology, who stand "at the side" of professional taxonomists and biologists and help them in the acquisition of biological information. In the past, the parataxonomist's role has often been limited to helping biologists collect samples in the field. More recently, however, parataxonomist activities have expanded to include sorting (at a variety of levels from families to morpho-species), databasing, preparing specimen and even digital imaging. Given the proper training and feedback there are few repetitive tasks that parataxonomists could not perform reliably for professional biologists. Although involving parataxonomists in a biodiversity inventory can be very productive, it is also paved with potential pitfalls. A strategy must therefore be put in place to guarantee that data quality is high and remains constant throughout a project. I conclude this short talk by presenting my own personal views on how to involve parataxonomists with maximum efficiency in a project like IBISCA.

The IBISCA database
M. Leponce & Y. Basset

The IBISCA database currently contents more than 50,000 records including 400,000 specimens classified into 2,189 taxa (species or higher level). Taxa already identified up to species level are principally: Coleoptera (Anthribidae, Carabidae, Cerambycidae, Chrysomelidae, Curculionidae, Scarabaeidae, Scydmaenidae), Hemiptera (Achilidae, Cicadellidae, Cixiidae, Delphacidae, Derbidae, Flatidae, Issidae, Membracidae, Psyllidae), Hymenoptera (Apidae, Formicidae), Isoptera and Lepidoptera (Arctiidae, Geometridae, Pyralidae).

Characterizing community diversity in species rich systems – statistical pitfalls, remedies, and insights from a phylogenetic perspective.
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Assessing species diversity of rich communities is a difficult task due to the numerous sources of biases that can occur when collecting data and when analyzing them. I will overview the common pitfalls and discuss some remedies, essentially from a statistical point of view (which estimators to choose). Some links between diversity coefficients and neutral community models will be mentioned. I will show the potential interest of partitioning diversity coefficients into alpha and beta components (within versus among sites, sampling units, local habitats,…) for inferential purposes. I will also illustrate the potential insights that can be obtained by integrating phylogenetic information into the analysis of community structure. Finally, I will try to demonstrate that all this can be overviewed in 15 minutes.

Meta data and multivariate analyses of large datasets
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