

sDiv sabbatical report, Douglas Chesters

Overview

Sabbatical took place July and August of 2019. Main project is 'Phylogenetic diversity of insects under plant diversity gradients', which will be discussed below. Second project is a collaboration with PhD student Li Yi, Andreas Schuldt and Tesfaye Wubet on microbial communities associated with herbivores in a tree diversity gradient; we furthered discussion on the aims of this project, and currently arranging a stay of Li Yi in Tesfaye's lab during 2020. A third project with more uncertainty, at early stages of data optimization and design; regards metabarcoding honey bee hives in apiaries of Yunnan.

Participants:

Helge Bruelheide, Robert Paxton, Andreas Schuldt, Michael Staab, Marten Winter, Tesfaye Wubet, Chaodong Zhu.

Project background and aims:

Studies on phylogenetic diversity (PD) and drivers of PD in insects are sparse, due to factors such as high species diversity, limited genetic data and incomplete molecular phylogenies. But emerging evidence has found plant diversity drives insect PD in an (evolutionary-) depth dependent manner. This study will build on recent work on phylogenetic integration of species-rich insect data, and aims to construct phylogenies for insect communities occurring in several plant diversity experiments, particularly BEF-China. With these phylogenies produced, measurements of PD will be possible for various functional groups, and the contribution of plant diversity and other plot variables to assembly of insect communities should be illuminated.

Progress, status and further plans:

Analysis framework is implemented. Framework is currently tested on two datasets, with preliminary results given below. Currently refining major issues based on preliminary suggestions, and arranging further datasets. Next stages will finalization of a robust insect phylogeny, refining hypotheses, and statistical analysis.

Method summary

Insect observation data from several plant diversity experiments was obtained. For BEF-China (china.befdata.biow.uni-leipzig.de), we used ant observations from the comparative study plots (dataset 432), and associated plot metadata (datasets 144 and 205). From Cedar Creek we used arthropod sweep net samples from the main plots conducted between 1996-2006; dataset e120 from portal.itsernet.edu. Phylogenies used in analyses were a genus level phylogeny of ants and a 1400 species phylogeny of insects constructed from transcriptome and mitogenome sequence data. Reference sequence data was downloaded

from the BOLD API. Taxa observed in plot level data were sought in the DNA barcode reference library. Firstly, a list of genera and species from the plot data was compiled. Then for each genus, if all the plot-level species were represented in the reference library, then only the DNA barcodes of these species were retrieved, in cases where a plot species was not represented in the reference library, a barcode was assigned from a randomly selected (non-plot) congener. Next, phylogenies were constructed for the plot-level taxa, using the DNA barcode data. Due to limited phylogenetic information content in DNA barcodes, topological constraints were applied during phylogenetic inference. The inference was conducted using Raxml. Phylogenetic diversity indices were calculated for plot data in R.

Preliminary results

BEF-China comparative study plots, ants; Of 91,152 Formicidae barcodes on BOLD, 88,716 were COI - 5prime and had complete species label, and 3,080 when filtered at the species level. The BEF-China CSP's contained 56 ant species, of which 14 were found in the BOLD database, 35 were substituted for a congener, and 7 were of genera totally absent in bold and thus ignored. For phylogenetic inference, 23 relational constraints were inferred from the backbone tree and 570/745 plot-level species could be assigned to at least one constraint. For taxon constraints, of 32 inferred monophyls on the backbone tree, 14 could be applied to taxa on the plot data, and all members were applied to at least one monophyly. Taxonomic likelihood was calculated for genera and tribe ranks on the Maximum likelihood of the constrained and an unconstrained tree search. The constrained tree (TL = -204.498921) was a significant improvement over an unconstrained tree (TL = -217.447152; SD = 4.59, $p < 0.01$ in SH test). Phylogenetic diversity and derived indices were calculated as a function of plant species richness and functional diversity (not shown).

Cedar Creek main plots; Totally this dataset comprised 266 species and 221 genera over 172 plots. After retrieving barcodes from BOLD and NCBI for members of the genera in this dataset, processing and filtering at the species level, 2,681 representative remained. 38 relational constraints were applied from the backbone inset tree, to 799 of 2,403 plot taxa. 322 taxon constrained were inferred for the backbone tree of which 92 could be applied to the plot species, most plot species had at least on constraint (2,380/2,403) calculated from genus, family, order, taxonomic likelihood of the constrained tree (-1870.899186) was significantly better than when unconstrained (-1960.961515; SD: 20.424841, $p < 0.01$, SH test). Phylogenetic diversity of insects under varying plant species richness and functional diversity was calculated.