

sDiv Workshop

*Species communities harboring the outcome of
plant diversification: museums and cradles
"CoMuCra"
January 6-11 2014*

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Workshop original summary:

Biodiversity is more than species numbers – it encompasses the evolutionary history of lineages and trait variation within lineages across millions of years. The outcome of this macroevolution is ultimately harboured within and among ephemeral local communities, connecting macroevolution to microecology. We identify the role of local communities as phylogenetic or functional museums - harboring ancient lineages or basal trait states within lineages - or inversely as phylogenetic or functional cradles. We then explain these differences and explore their conservation consequences.

Participants, applicant and post doc:

Andreas Prinzing (University of Rennes, France ; applicant) ; **Igor Bartish** (Academy of Sciences of the Czech Republic, Department of Genetic Ecology Institute of Botany, Czech Republic; participant); **Martin Braendle** (Philipps University Marburg Faculty of Biology, Animal Ecology, Germany; participant); **Matthew Helmus** (University of Chicago Department of Ecology and Evolution, USA ; participant); **Joaquín Hortal** (Museo Nacional de Ciencias Naturales Department of Biogeography and Global Change, Spain; participant); **Hervé Jactel** (INRA, Bordeaux, UMR Biodiversité Gènes et Ecosystèmes, France; participant); **Ingolf Kühn** (Helmholtz-Zentrum für Umweltforschung Department Biozönoseforschung, Germany; participant); **Daniel S. Moen** (CMAP, École Polytechnique, UMR7641, Paris, France; participant); **Wim Ozinga** (Alterra WUR / Radboud University Nijmegen, Team Vegetation, Forest and Landscape Ecology, Netherland; participant) **Sandrine Pavoine** (Museum national d'histoire naturelle, Paris, France; participant); **Ian Pearse** (Illinois Natural History Survey, USA; participant); **Oliver Purschke** (German Centre for Integrative Biodiversity Research, Leipzig, Germany; participant); **Cyrille Violle** (Centre d'Ecologie Fonctionnelle & Evolutive, Montpellier, France; participant); **Evan Weiher** (University of Wisconsin-Eau Claire Department of Biology, USA; participant); **Marten Winter** (German Centre for Integrative Biodiversity Research, Leipzig; Germany; participant); **Yguel Benjamin** (German Centre for Integrative Biodiversity Research, Leipzig; Germany; Post doc)

Focal areas of discussion:

Phylogenetic and functional diversity have been shown to be important community properties of communities. Indeed, evolutionary history and functional properties of species may impacts community assembly and ecosystem processes. Numerous measures of phylogenetic and functional diversity have already been developed. However, each of these phylogenetic and functional diversity metrics only accounts for a small amount of the

overall information of species phylogenetic or functional relatedness patterns within a community. For instance, existing methods do not identify whether a community is composed of both ancient lineages and of very recent lineages (hence operating as both museum and cradles of phylogenetic diversifications), or of intermediately related species. Most existing methods do not identify whether trait variation results from ancient trait divergences that have been conserved since or from recent trait divergence (functional museums and cradles).

During the workshop, different new methods were presented and discussed to more completely quantify and describe the evolutionary legacy represented in communities, both in terms of phylogenetic relatedness and in terms of trait evolution. Novelty and technical issues are discussed, as well as the way to use these different methods in order to infer the interaction between lineage evolution and community assembly.

Main results/conclusions/Workplan for the near future:

The workshop participants finally agreed on the novelty of the framework used in the new quantification of phylogenetic history of the species presented, its difference with diversity metrics and converged in the idea that its usefulness compared to existing metrics should now be demonstrate properly. The participants developed a new numerical approach to apply the new framework to describe species communities. The participants started elaborating a conceptual manuscript presenting the new framework of, and method for, quantifying phylogenetic history, its novelty and its relevance. Some technical issues concerning the measurement method of this new approach remained after the workshop but will be solved in the next month through collaboration between all the participants. In the case of the validation of this new method, the participants agreed that its application to many ecology issues could be promising.

In parallel to this conceptual paper, the participants worked on a research manuscript that will be developed using the functional cradle or museum measure presented in order to infer the interaction between lineage evolution and community assembly. More particularly we will work on the relationship between environmental gradient and functional cradle or museum status of plant communities.

Brief summary of presentations:

Andreas Prinzing presented the link between macroevolutionary pattern at global/regional scale and local process as community assembly in order to introduce the concepts of phylogenetic museum and cradle.

Igor Bartish presented one measure of phylogenetic museum and cradle and its application studying the relationship with habitat types of plant communities in Netherlands

Andreas Prinzing presented the concept of functional museum and cradle.

Sandrine Pavoine presented one measure of functional museum and cradle and its direct application on a dataset.

Joaquin Hortal presented one other measure of functional museum and cradle. He also presented its application in the context of separating alpha and beta functional diversity.

Marten Winter presented how diversity metrics could be or not use for conservation practices.

Martin Braendle and Oliver Purschke presented their work on the land use intensity on the phylogenetic relatedness between herbivores, and on the effect of phylogenetic relatedness between plants along successional stage.

Andreas Prinzing also presented in a seminar his work on the effect of the phylogenetic structure of communities on community assembly and ecosystem processes (e.g. effect on the species decline under environmental change, effect on trophic interactions, effect on functional diversity, effect on establishment of species in a new neighborhood)

General working atmosphere and feedback on sDiv-support:

From the feedback we received, the participants found the organization good and the atmosphere inspiring and liked the concept which emerged from our discussions.