

5th Congress
ITALIAN SOCIETY FOR
EVOLUTIONARY BIOLOGY
Trento, 28-31 August 2013

**PROGRAM,
BOOK OF ABSTRACTS,
AUTHOR INDEX.**

EDITED BY LINO OMETTO AND OMAR ROTA-STABELLI



V congress of the Italian Society for Evolutionary Biology. Trento, 28-31 August 2013

Effects of climate on fine-scale spatial genetic structure in four alpine keystone species

Elena Mosca¹, Erica A. Di Pierro¹, Katharina Budde², David B. Neale³, Santiago C. González-Martínez²

¹Research and Innovation Centre, Fondazione Edmund Mach, Via Mach 1, 38010 San Michele all'Adige (TN), Italy.

²INIA, Forest Research Centre, Carretera de La Coruña km 7.5, 28040 Madrid, Spain.

³University of California at Davis, Department of Plant Sciences, 95616 Davis CA, United States of America.

Contact: elena.mosca@fmach.it

Genetic responses to environmental changes can take place at different spatial scales. While the effect of climate on the wide-range distribution of genetic diversity has been the focus of several recent studies, studies of genetic responses to climate at local scales are relatively scarce. Fine-scale spatial genetic structure (SGS) was investigated in four Alpine conifers (4 to 8 natural populations per species) in the Eastern Italian Alps. SNP assays were used to characterize SGS in *Abies alba* and *Picea abies* (384 SNPs), *Larix decidua* (528 SNPs) and *Pinus cembra* (768 SNPs). Significant SGS was found for 11 out of 25 populations tested, varying from Sp of 0.0018 in *P. cembra* to 0.0035 in *Larix decidua*. Several linear models were constructed to associate SGS with climate variables. Once corrected by confounding effects (e.g. differences of SGS across species due, for instance, to dispersal capability), the best model identified April minimum temperature and spring precipitation as the most relevant climatic variables associated with differences in SGS across populations. To study the potential effect of winter temperature in relation to plant physiology, two ecological indexes related to vegetation growth (chilling-degree-day, CDD, and freezing-degree-day, FDD) were also tested for association to SGS. A significant association was found between SGS and CDD across species. This study provides new insights on the expected genetic responses of four coniferous species to climate change at local scales, suggesting that climate change, through altering SGS, could also have relevant impacts in plant microevolution.

Mean phylogenetic surprise: a unit of measure for describing changes across biological communities

Saverio Vicario¹, Bachir Balech²

¹Istituto di Tecnologie Biomediche, Consiglio Nazionale delle Ricerche, Italy.

²Istituto di Biomebrane e Bioenergetica, Consiglio Nazionale delle Ricerche, Italy.

Contact: saverio.vicario@gmail.com

The availability of NGS technology increased the amount of communities described by environmental sequencing, while the large effort of the biodiversity scientific community mobilized and exposed very large data sets on the presence of organisms in public repository as the Global Biodiversity information facility or Sistema Ambiente 2010 in Italy. These two sources of check lists and species abundance data could be used to build knowledge on how communities are organized and how they correlate with abiotic factors. But, no real consensus exists on how to compare communities both with scalar (Jost, 2006) or phylogenetic indices (McCoy and Matsen, 2013). Generally, phylogenetic indices are expected to be more insightful. In fact, the presence of a given organism within a community depends on its ecological attributes built through the history of evolutionary adaptations and innovations of its lineage. So related organisms are likely to stay in a given community for shared reasons. This consideration makes clear that the correct level of taxonomic classification to study the correlation between abiotic factor and communities is not always at species level. This strategy of including the contribution of higher level classification decreases the effect of low counts (McCoy and Matsen, 2013). Until now, all phylogenetic approaches are within the frame of index based approach where no clear statistical framework links the index to the phenomenon of interest, making difficult to include replicates within the experimental design and in general to interpret the results. In this work, we show the phylogenetic entropy of degree one, a family member of diversity indices, proposed as by Chao et al. (2010), is indeed a true measure of information, that describes the mean surprise of an observer, sampling organisms and classifying them using a given rooted phylogenetic tree. This measure is used to build a formal measure of beta diversity that takes into account phylogenetic structure of communities that is measuring the decrease of surprise from the marginal to the conditional distribution of observation. This phylogenetic beta diversity measure is used to produce an ANOVA-like procedure which uses a phylogenetic tree of all organisms found in all sampled communities and highlight the contribution of each branch of the phylogeny and each group of communities present in the experimental design to the diversification across groups. This framework allows to include replicates (technical or biological) within the pipeline of analysis given that each groups could be represented by several sample communities. The proposed metric is numerically validated as information measure by testing different required properties of information metrics. Precision, accuracy and power of the procedure was tested using simulation of community with log normal distribution of abundance in which each group of community differs in the abundance of a given clade. Results are compared with Shannon based beta diversity estimates. An example use case is used to illustrate the web implementation of the procedure. The figure shows how the method correlates abundances of the leaf in the different groups with branch contribution to beta diversity in the phylogeny.