

## Phylogenetic Symposium 2016 - Evolution meets Ecology Leipzig, Bibliotheca Albertina

### Concluding Remarks

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The Phylogenetic Symposium #58 in Leipzig, held at Bibliotheca Albertina, continued the tradition of bringing together a limited number of persons from student to emeritus to discuss a focused topic in evolutionary biology. A balanced selection of speakers covering plant, animal, theory or modeling perspectives were arranged in four sessions: "Big data or case studies?"; "Drivers of diversification"; "Global change – evo/eco approaches"; and "Genomic data in evolution and ecology". The program was set to evaluate recent achievements in evolutionary ecology and biodiversity research, to explore the new possibilities due to great increase of the efficiency in genomic data production for connecting evolutionary and ecological questions, and to pinpoint and discuss the problems arising from the vast amount of data.

In the first talk, Erika Edwards, by asking the question "Are we ready for an automated natural history?", argued that despite having the tools and in part also the data to address the big questions, such large data sets carry the dangers of over-simplification or over-parameterization, so that the outcome is often problematic. She beautifully argued that it is often much more promising to carefully select specific models to address specific questions. Indirectly, she made the point that the classic model systems, *E. coli*, *Caenorhabditis*, *Drosophila*, zebrafish or mice, are now being extended by several new systems for which new data are progressively accumulated. Erika laid out the red thread through this symposium, in that most following speakers addressed their research question with their selected model systems: *Viburnum*, Neogene mammals, hummingbirds, Paelearctic trees, mountain systems, *Wolbachia*, the poplar tree system.

The more theoretically oriented talks of Susanne Fritz and Alexandre Antonelli exemplified problems arising from large-scale macro-eco-evo approaches, and stressed the necessity to produce the data in the selected models that are needed to adequately address the question by a more data-based modeling. Christian Lexer took the argument further by reminding us that the theoretical framework to address evolutionary questions is fully developed and we need to adapt them for the amount of data that are now possible. He outlined, how we can bridge the macro- and micro-evolutionary perspectives by taking subsamples of our data sets, e.g. by pruning the tips of a large-scale phylogeny, or by picking (poplar) taxa representing snapshots in the speciation continuum.

While big data in genomic context were a frequent focus, Susanne Renner reminded us by sharing new insights from her model system to study the regulation of leaf-out using temperate climate trees in various botanical gardens, that simple but clever experiments (using transparent and non-transparent plastic-bags to cover branches of botanical garden trees) can sometimes give more answers than large-scale approaches.

I should not forget to mention that the many outstanding posters also added nicely to the issues discussed in this symposium and conclude with a big Thank you to the organizers Alexandra Muellner-Riehl and Martin Schlegel and their team.