



Molecules meet macroecology—combining Species Distribution Models and phylogeographic studies

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Abstract

Combination of various techniques allows the identification of unique genetic lineages and/or taxa new to science via integrative taxonomy approaches. Next to molecular methods such as DNA ‘barcoding’ and phylogeographic analyses, Species Distribution Models may serve as compliment techniques allowing spatially explicit predictions of a species’ potential distribution even across millennia. They may facilitate the identification of possible recent and historical gene flow pathways. Herein, we highlight advantages of the combination of both molecular and macroecological approaches using the African miniature leaf litter frog *Arthroleptis xenodactyloides* as example.

Key words: *Arthroleptis xenodactyloides*, fundamental niche, integrative taxonomy, Last Glacial Maximum, realized niche

Introduction

In recent decades, an increasing amount of cryptic species has been indentified based on integrative taxonomy. Molecular genetics have provided the most successful advances, not only allowing for ‘barcoding’ approach for species delimitation, but above the ‘species level’ also for phylogenetic and below it for phylogeographic analyses. In recent years, it has been shown that information from macroecological modeling can be applied as supplement to other methods (e.g. molecular markers) for species delimitation (e.g. Raxworthy *et al.* 2007; Rissler & Apodaca 2007; Rödder *et al.* in press). Recent advances now allow for spatial predictions across millennia (Pearman *et al.* 2008) and testing of hypotheses across multiple time scales, thus creating a link to phylogeography. Our goal here is to emphasize that for the same phylogeographic question a combination of molecular markers and macroecological methods, each derived from different data types, may reveal complementary evidence.

In terms of macroecological methods, so called Species Distribution Models (SDMs) can be considered as a powerful tool. A SDM aims on the characterization of a species’ ecological niche and projects it into geographic space. The result is a map showing the potential distribution of the species under study. For this purpose, environmental information at species’ presence, which may comprise climate, land cover or other data, is obtained through GIS techniques. Subsequently, this information is compared to environmental conditions (commonly stored as raster data) elsewhere in a broader area under study (i.e. from where the target species is unknown). The resulted map shows the similarity of the characterized environmental envelope with the broader area which is interpreted as ‘likelihood’ of the species’ potential geographic distribution. This ‘likelihood’ can also be directly correlated with the maximum possible abundance of the target species at a given site (VanDerWal *et al.* 2009) making it valuable for spatial comparisons with gene flow patterns (Habel *et al.* in press-a). Furthermore, it has been demonstrated that when employing SDMs, hypotheses can be successfully generated on the potential existence and extent of refugial areas of species (e.g. Peterson & Nyári 2007; Waltari *et al.* 2007; Carnaval & Moritz 2008; Nogués-Bravo 2009). The other way around, SDMs may help to formulate hypotheses on historical extents of current refuges and possible