Sujet de thèse:  
Using insular macroevolutionary data to investigate the role of ecological opportunity in driving evolutionary radiations

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Publications récentes des directeurs de thèse avec leurs anciens doctorants:  

Descriptif du sujet de thèse et méthodes envisagées:  
Evolutionary diversification is the fundamental process by which all species on earth have been generated. At any defined spatial scale, we find that some lineages have diversified more than others. Although there exist a wide variety of case-specific explanations for differences in diversification rate per unit area, our ability to identify general tenets or conclusions of broad taxonomic and geographic scope have so far been limited, principally due to the difficulty in inferring the spatial scale in which speciation has occurred across multiple lineages.

Organisms endemic to oceanic islands provide significant advantages in inferring the spatial scale of speciation. The isolation of islands and their long-standing boundaries allow in situ speciation (within the island) to be readily distinguished from immigration from outside sources (unlike continental settings). The opportunity afforded by such island lineages has already been exploited in a landmark paper (Kisel & Barraclough, 2010), using phylogenetic and population genetic data from multiple lineages that vary in their dispersal ability (flowering plants, birds, bats, mammals, lizards, butterflies and snails) to investigate the spatial scale of speciation. This study drew two main conclusions, that: (1) the probability of speciation occurring within a given region increases with the size of the region; and (2), this pattern is driven by the strength of intra-specific gene flow, since area required for speciation is positively correlated with the geographic separation required for neutral genetic differentiation. Nonetheless, the authors acknowledge that the strength of gene flow is simply one correlating factor, and that others might be involved.

Another factor potentially determining the probability of speciation within a given region is 'ecological opportunity' (Kisel & Barraclough, 2010). Using external calibrations from Magallon et al. (2015). Trait data will be quantified for each radiation considered, using the extensive phylogenetic studies show that lineages with low dispersal capacity (e.g. animal-dispersed plants, or landsnails) have usually accumulated more species within a given area and with greater ecological disparity than have lineages with higher dispersal capacity (e.g. wind-dispersed plants or birds). It is predicted that the lower the dispersal capacity of a group, the greater the ecological opportunity experienced by colonists of new environments, due to the absence of other members of its group. Recent years have seen a significant increase in the number of insular molecular phylogenetic studies. Since all such published data is publically available, the time is now ripe for an insular macroevolutionary study using taxa of varying dispersal ability to investigate the role of ecological differences between lineages in driving evolutionary diversification. Specifically, do poor dispersers have an intrinsically higher potential for radiation per unit area than good dispersers? If so, what is the role of ecological opportunity in this observation?

The MNHN is an especially suitable academic environment in which to base such a study; compared with other institutions worldwide, there are specialists in an unusually wide variety of insular taxa, and collections providing an abundant source of trait data. This project is focussed on an insular region familiar to both supervisors ' the Mascarene archipelago, Indian Ocean. Focussing on a taxon common to both supervisors (plant lineages that are animal- vs. wind-dispersed), the student will combine phylogenetic, geographic and trait data (published and from collections) from lineages that differ in their dispersal capacity (herein 'focal groups') in order to calculate rates of island colonisation, sympatric species accumulation, and trait evolution. Specific hypotheses suitable for testing, implying an important role for ecological opportunity include:

1) The rate at which focal groups colonise islands is negatively correlated with the rate at which each colonising lineage accumulates sympatric species through inter-island colonisation;  
2) The rate at which focal groups colonise islands is negatively correlated with the rate of in situ trait evolution.

Beginning with a solid taxonomic foundation (multi-volume ‘Flora of the Mascarenes’), relaxed clock methods will be used to reconstruct ultrametric trees for a wide range of published Mascarene flowering plant datasets including grasses, herbs and trees, using external calibrations from Magallon et al. (2015). Trait data will be quantified for each radiation considered, using the extensive Mascarene collections in the MNHN herbarium. Colonisation history and trait evolution will be quantified objectively, using geobiographic and ancestral state reconstruction methods, respectively.

Stratégie de publication:  
The PhD will form at least 3 publications. The first paper will focus on the historical biogeography and timing of colonisation events in all the plant lineages considered in this study (suitable for Mol. Phy. Evo., J Biogeo.). A second paper will combine the phylogenetic data from the first paper with data and analyses of trait evolution, investigating the role of morphological evolution in insular radiations (suitable for BMC Evol Biol, Proc B, Evolution). The third paper will combine all elements to respond to the core hypotheses (suitable for Am Nat, Evolution). Note that the main paper inspiring this project was the work of a PhD student (Kisel being a European PhD, supervisor: Barraclough). Given the availability of the data and a motivated student, we are therefore confident of obtaining solid publications within 3 years.

Récurrence possible du sujet si échecs:  
This project has negligible risk concerning data availability. All molecular data is published and fully available. Abundant MNHN collections ensure the availability of traits for measurement. In the event that some plant phylogenies lack sufficient resolution to resolve inter-island colonisation, BW has abundant well resolved phylogenies on animals with different dispersal capacities (birds & landsnails) that can be used to fill the gap. The absence of a predicted correlation (or opposing correlation) is certainly possible. However, little is understood about the spatial scale of radiation and so although the target journal may be influenced, we are
confident that regardless of results, a strong publication will be generated.

**Faisabilité sur 3 ans (échéancier):**

Despite being novel and addressing important topics, the subject poses no risk in its feasibility. All the material is already published or available on site (MNHN collections) and the methods involved (in phylogenetics and systematics) are well developed and tested.

First year: Literature search. Reconstruction of dated molecular phylogenies and biogeographic histories. Writing of biogeographic article.
Second year: Acquisition & analysis of trait data. Analyses of all data combined. Writing of article concerning trait evolution.
Third year: Writing of article that combines all elements to respond to core hypotheses. Thesis writing & submission.

**Profil du candidat recherché:**

Proven competences (internship M2) in molecular phylogenetics (phylogenetic reconstruction, dating, biogeographic & ancestral state reconstruction), or in morphometrics (comparative analyses of trait data), or in testing correlations between different eco-evolutionary variables.

First-hand knowledge or interest in one or more of the plant groups studied would be a bonus.