Title:

Predicting tropical flowering co-occurrence using phylogenetic, trait, and species interactions

Co-flowering increases with pollinator niche overlap in a tropical community

Authors:

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Abstract:

Keywords:

Introduction

Explaining the co-occurrence of related species in diverse assemblages is a persistent aim of community ecology (Colwell, Fine, Brown). The balance between differences in species mean fitness and niche overlap lead to observed patterns of presence within local assemblages (Chesson, Adler, Kraft). In tropical plant assemblages, the observed co-occurrence of many congeneric species has suggested that co-occurrence may be related to niche-based (Swenson, Cavender-Bares), non-equilibrium (Jetz), or neutral processes (Hubble). Analysis of species communities tend to focus on species occupancy as the primary window into mechanisms of co-occurrence. Fewer studies have evaluated the importance of species interactions as mediating patterns of co-occurrence at local and regional levels. This is largely because gathering data on species interactions is time-consuming and labor-intensive. Here we analyze a multi-year dataset of co-flowering and pollinator overlap among related Gesneriaceae species in a diverse cloud-forest assemblage. Combining data on floral morphology, evolutionary relatedness, and observed pollinator visitation, we can test a diverse set of candidate models to assess seasonal flowering communities.

For flowering plants, interactions with pollinators can yield insight into the potential roles of competition and facilitation in maintaining co-occurrence. Competition among closely related species should lead to low co-flowering, thereby reducing heterospecific pollen transfer and potentially negative impacts of hybridization. Alternatively, co-flowering among related species could lead to pollinator facilitation, in which the local abundance of resources attracts many pollinators, leading to increased fitness for all species. Evidence …

The complex interplay between phylogenetic relatedness, morphological diversity, and species interactions complicates quantitative analysis of species co-occurrence. We follow the general philosophy of phylogenetic generalized linear mixed models presented in (Ives & Helmus, 2011; Rafferty & Ives, 2013). Our quantitative approach, 1) estimates co-flowering intensity based on models of phylogeny, trait, and interaction co-variance, 2) estimates both the strength and uncertainty of co-flowering, 3) generates testable predictions for model comparison. This final point is crucial in assessing the model fit, given the high risk of overfitting due to the highly variable nature of flowering timing. By withholding data from model fitting, we can assess the predictive power of candidate models.

Methods

* Data Collection
  + Transects
  + Cameras
  + Traits
  + Phylogeny
* Pollinator overlap and relatedness
  + Detection probabilities?
  + Pagels Lambda
  + Niche Overlap
* Predictive Models of co-flowering
  + Training-testing split
  + Baseline model
    - We have intentionally left out elevation and julian day as a predictor of co-flowering. The models of covariance outlined below describe the correlation in intensity of flowering among sampling periods. If we use elevation or julian day, for example as a proxy of environmental conditions, the phylogenetic and trait co-variance will be captured by the variation in response to date or location. In practice, it is not possible to differentiate the phylogenetic effect of the timing of flowering, versus the phylogenetic effect on co-occurrence leading to different flowering times. Both parameterizations represent changes among sampling periods.
  + Models of Covariance for phylogenetic and trait distance
    - Attraction
    - Repulsion
  + Model evaluation
* Results
* Figure 1
  + Conceptual: Co-flowering competition and facilitation with raw data, flowchart to show how data comes together
* Figure 2
  + Pollinator niche overlap matrix
* Figure 3
  + Discrepancy in covariance models and observed data
* Figure 4
  + Discrepancy in covariance models and predicted data