

Supporting Information

1. Calculation of sampling completeness across geography and clade.

One challenge to working with relatively poorly known taxa is the possible influence of unknown and unsampled taxa. While there are 1159 described *Pheidole* species and subspecies globally, there are many more yet to be described. Moreover, the distribution of this sampling completeness is not random. Tropical faunas may be less documented than temperate faunas, and different bioregions have received different amounts of attention from researchers. For example, it is likely that New World *Pheidole* species are much better documented than the Old World *Pheidole*, due to a major monograph pursued by Wilson that described a large number of species³⁰.

We devised a method to account for this potential bias that, while coarse and imperfect, should address the big picture of whether our overall sampling reflects the distribution of overall *Pheidole* richness. Over the last years, our project has sought material from *Pheidole* faunas around the world, both described and undescribed. We made a vigorous effort to identify all the taxa we included in the phylogenetic study. We are thus quite confident that the morphospecies on our tree reflect undescribed, rather than unidentified, taxa. For the purposes of this calculation, we made the *assumption* that

the fraction of described species (FD) within each clade/region on our tree reflects the true fraction of undescribed species in the region. For example, on our tree there is a higher fraction of morphospecies from the Australia-New Guinea clade (undescribed: 93, described: 21, $FD \sim 0.18$) compared to the New World clade (described: 143, undescribed: 34, $FD \sim 0.80$). From the GABI data, we know the number of described species occurring in each region (and thus clade, given the tight correspondence between region and clade), which we call ND. Using the number described from each region and the estimated fraction described we can calculate the estimated total richness in the region/clade ($ER=ND/FD$). For example, for Australia-New Guinea there are 112 described taxa, while in the New World there are 649 described taxa. Using the FD from our sampling, we estimate there to be $ER \sim 608$ species in the Australia-New Guinea clade ($ER_{AUSNG}=ND_{AUSNG}/FD_{AUSNG}=93/0.18=608$) and 803 species in the New World clade ($ER_{NEWORLD}=ND_{NEWORLD}/FD_{NEWORLD}=649/0.39=803$). From this we can compare the sampling representation of taxa on our tree to the estimated distribution of richness in *Pheidole* (Table S2).

We performed the calculation two ways, first by estimating sampling fraction for each clade, and second by estimating sampling fraction for the tropical and extratropical species of each hemisphere (since this latitudinal distinction is important for our analysis). Using clades, we estimated there to be ~ 2175 *Pheidole* species globally using the clade-wise calculation with about 55% of them described. Our sampling of different clades broadly matched the estimated proportion of total *Pheidole* richness in those

clades (Table S2). Using latitude and hemisphere, we estimated 2127 species globally (54% described). We detected a degree of oversampling of New World temperate taxa on our tree (11% actual vs. 6% estimated) and undersampling of Old World temperate taxa (3.3% actual vs. 12% estimated). Overall, we estimated global fraction of temperate species to be 19%, which was reasonably close to the fraction on our tree (14%).

For the BAMM, BiSSE, HiSSE, and GeoSSE analyses, we chose to explore a range of global sampling fractions (i.e. the fraction of total *Pheidole* species that are on the tree) that broadly encompass the estimated value, and evaluate whether our conclusions are stable within that range. We chose a range of 1500, 2000, 2500 total *Pheidole* species representing the minimum and maximum plausible *Pheidole* richness, and set sampling fraction accordingly at 0.3, 0.22, or 0.18, which we denote L, M, H, respectively. This range enclosed our estimated values (2127 or 2179).

Overall, the distribution across clades and latitudes of our sampling intensity was reasonably similar to the estimated richnesses for *Pheidole* (Table S2). Thus, for the most part we did not use clade-specific sampling correction factors. However, the oversampling of taxa on our tree in the Nearctic region relative to the Neotropical region is of some concern, particularly as we performed analyses on the New World data alone. The latter was performed because the New World is less broken up by biogeographic barriers than the Old World and most likely to clearly reflect diversification-latitude correlations (if they exist). Thus, we performed additional analyses of all methods to account for differential sampling of the tropics and extratropics, which we denote M*.

First, we set state-specific sampling fractions to be different for extratropical and tropical taxa. For global *Pheidole*, we calculated the extratropics to be slightly undersampled on our tree (tropics=0.22, extratropics=0.16), and for New World *Pheidole* the reverse was true (tropics=0.185, extratropics=0.35), using our estimated total richness (2127). We used these values to set the state-specific sampling fraction in the BiSSE/HiSSE/GeoSSE analysis (AB

	Taxa on tree	Estimated fraction described	Current described richness	Estimated richness (described / fraction described)	Fraction of total taxa on tree	Target fraction of total richness (estimated fraction of total richness)
By Clade						
New World	177	0.81	649	803	0.39	0.38
Africa-Asia	124	0.60	356	597	0.28	0.28
Australia-New Guinea	114	0.18	112	608	0.25	0.29
Madagascar	34	0.29	35	119	0.08	0.06
Total	449	0.55	1138	2126		
By Latitude/Hemisphere						
New World tropical	129	0.73	512	695	0.29	0.32
New World extratropical	48	1.00	137	137	0.11	0.06
Old World tropical	257	0.39	424	1089	0.57	0.50
Old World extratropical	15	0.33	86	258	0.03	0.12
Total				2179		

range was set to middle of the two). Second, we performed an additional set of analyses on 10 trees where the number of Nearctic taxa had been reduced by randomly pruning taxa from the tree to lower the number from 48 to 27. The latter adjusts the fraction of Nearctic species to be consistent with the estimated fraction using our calculation. We also ran BAMM on these trees using the M assumption for the global sampling fraction.

2. GeoSSE methods, analysis, and discussion

The GeoSSE model (Goldberg *et al.*, 2011) implements trait-dependent diversification in a geographic context, where lineages can occur in one of two areas (A or B) or both (AB). As this method does not allow for hidden-state null models to be compared with trait-dependent models (such as HiSSE), we did not consider it as part of our main results. However, since it explicitly deals with geographic dynamics, we present an analysis here for comparison. In the model, extinction and speciation rates may be different for the different geographic states A and B (controlled by rate parameters s_A , s_B , x_A , x_B), and dispersal (transition from A→AB and B→AB, with rates d_A and d_B respectively). An additional speciation process (with rate, s_{AB}) splits AB into two species localized to the two different areas. Geography-dependent diversification (such as with latitude) can be inferred by comparing models in which the parameters are free to differ among the two areas or constrained to be equal.

The candidate model set included a full model where all three rates are different across the two areas, or that one or more rates are constrained to be equal (e.g., one or more of, $s_A=s_B$, $x_A=x_B$, $d_A=d_B$), which makes a total of ($2^3=8$ models). In initial testing, we found that the between-area speciation rate (s_{AB}) generally converged toward zero and never improved the model fit, so to reduce model space we set it to zero ($s_{AB}=0$) for subsequent analyses. To ensure we converge on the global model, we first fitted the full model using 20 total parameter values including the values suggested by

starting.point.geosse()), and 19 parameter sets consisting of uniform random numbers between 0 and 1. For the rest of the models, we used the suggested starting point, the full model ML parameters, and 18 random parameter sets as starting points. To estimate and visualize uncertainty in model parameters for representative results, we ran mcmc Bayesian inference on the full model using a chain of 10000 generations, using the ML parameter values as the starting point.

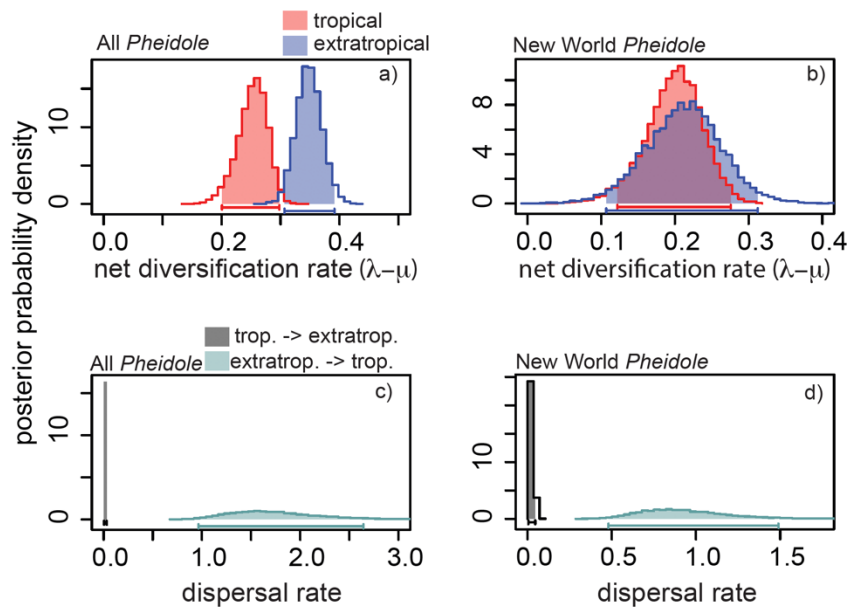


Figure S2 | Posterior probability distributions of *Pheidole* macroevolutionary rate parameters inferred with the GeoSSE model. Net diversification rate (a, b) and dispersal rate (c, d) inferred from the (a,c) global *Pheidole* phylogeny and (b,d) new world *Pheidole* only. The global analysis presented assumed used the M sampling fraction while the New World analysis assumed M*, which corrects for potential latitudinal sampling bias (see text for results using other assumptions).

As with the BAMM and BiSSE/HiSSE analyses, we repeated the inference with different values of sampling fraction (L, M, H). Since the New World is less broken up by

biogeographic barriers, we also performed the same analyses on the New World *Pheidole* clade with the Old World lineage removed. Since we detected possible oversampling of Nearctic species we performed an additional analysis (M*) with state-specific sampling fraction that accounts for this difference. Finally, we performed the analyses with the M global sampling fraction on the 10 trees where Nearctic species have been culled, using either all *Pheidole* or only New World taxa. Again, if our conclusions about net diversification differences or dispersal rate differences are sensitive to these uncertainties in sampling fraction, we will consider them not to be robust. The above analyses were performed with the *diversitree* package (FitzJohn, 2012) in R.

For the global *Pheidole*, GeoSSE inferred a slightly elevated net diversification rate for *extratropical* lineages (1.2x-1.6x of net diversification rate in the top models, Fig. 4). This result was robust to uncertainty in the global sampling fraction (e.g. L, M, H). When the New World *Pheidole* are considered alone, net diversification rate is also slightly elevated by a similar degree. However, when uneven latitudinal sampling fractions in the New World are accounted for—either by altering the sampling fraction parameter in GeoSSE or by culling species from the tree—the difference in net diversification rate disappears (Fig. 4) and net diversification is not different than zero.

The main difference between the GeoSSE results and the BiSSE/HiSSE results was that strong differences in dispersal rate were statistically supported in all of the GeoSSE analyses, with extratropical lineages transitioning to the tropics more easily than the reverse. This discrepancy probably has to do with the different ways geographic states

are coded (e.g. binary A/B in BiSSE/HiSSE or A/AB/B in GeoSSE), in GeoSSE a species that has any part of its range crossing the boundary of the tropics, it is coded as present in both states (AB), whereas when coded as a binary trait the center of the range must pass outside of the tropics to change the state from tropical to extratropical. Thus these represent different types of evolutionary change and we find the binary state to be more relevant to the question at hand.