

Appendix from E. P. Economo and E. M. Sarnat, “Revisiting the Ants of Melanesia and the Taxon Cycle: Historical and Human-Mediated Invasions of a Tropical Archipelago”

(Am. Nat., vol. 180, no. 1, p. E1)

Supplemental Methods and Results of the Regression Analyses

The structure of the data set, aggregated from many individual collection efforts, presents some challenges to analysis. Fortunately, the size of the data set allows us to perform analyses under different assumptions. Here we provide both additional discussion of the data and methods and results from additional analyses supplementing those in the main text.

The data set consists of a set of species detections across samples collected by four different methods: hand, leaf litter sifting, malaise traps, and canopy fogging (a limited number of samples). It is well known that ant species vary in their detectability across these methods; for example, some leaf litter ants are cryptic and regularly collected only with leaf litter extraction. While species may differ in conspicuousness in collections independent of variation in actual abundance, we know of no reason why this would be biased by endemism class. All endemism classes reflect a phylogenetically diverse group of species with different body sizes, morphologies, colony sizes, and behaviors.

Methodology was not standardized across habitats in the full data set; for example, urban and agricultural areas lack leaf litter samples (due to an absence of leaf litter), while hand collections were taken in all habitats. One might reasonably argue that the presence of microenvironments such as leaf litter in the forest is a relevant ecological difference between a forest and a city, and thus including them does not introduce “bias.” A more conservative approach is to analyze only data collected with the method common to all habitats—hand samples. We performed the analysis both ways and compared results. In general, if the patterns differ across such variations, it would cast doubt on the generality of the conclusions (they did not).

The other main challenge is that the sampling was diffuse across many sites across the landscape but with low intensity at each site. Few if any individual localities have what could be considered a complete sample of the local community, which for ants requires concentrated and sustained sampling efforts. The multinomial logistic regression analysis models the relative probabilities of detecting species of a different class, not species richness or counts in each category, which are more sensitive to sampling effort. By modeling probabilities it accounts for noise introduced by low sample sizes. If only a single species was sampled, it will contribute less to the likelihood of the model (only one “trial” associated with a multinomial outcome) than a locality or sample where many species were sampled.

These relative probabilities reflect both the composition of species present across sites and their relative abundances, as more abundant species are more likely to be sampled. One limitation of the sampling design and multinomial logistic regression analysis is that for a species collected only in a single locality, it is difficult to know whether it is widespread and locally rare (and thus difficult to detect) or locally common but restricted to a small area within Fiji. Either case would be consistent with an “ecological decline” predicted by the taxon cycle, and differentiating them is not necessary for our analysis. However, this difference is biologically interesting and could be addressed by future work.

For analysis, the data can be aggregated by either sample or locality. The only difference is that in the former, if a species is detected in multiple samples in the same locality, it counts as multiple detection events. In the latter (by locality), multiple samples of the same species in the same locality are treated as a single detection. We performed the analyses both ways and compared results.

In total there were four permutations of data set used for multinomial logistic regression analysis: all methods by sample, all methods by locality, hand collections only by sample, hand collections only by locality. We presented the results in the main text for the “all methods by locality” model (figs. 2, 3). Equivalent figures for “all methods by sample” are presented in figure A1, “hand collections only by sample” in figure A2, and “hand collections only by locality” in figure A3.

The multinomial logistic regression fits a matrix of coefficients β in the equation,

$$\Pr(\text{obs}_i = \text{class}_j) = \frac{e^{X_i\beta_j}}{1 + \sum_c^j e^{X_i\beta_c}},$$

which gives the probability that the observed species is of endemism class j ; X_i are the predictor variables (including a constant term) for locality/sample i , and c indexes over the J endemism classes. As these are relative probabilities, one

endemism class is used as the reference category and all coefficients are set to zero. The fitted parameters for the other categories describe the change in probabilities relative to the reference category. We arbitrarily designated exotics as the reference category but confirmed that choice of reference category did not alter results. The fitted models were used to calculate a log likelihood of the data given the model, which were then used to calculate Akaike Information Criterion (AIC) for model selection. If two or more models were within a Δ AIC of 2, the simpler model was preferred. Fitted parameters and AIC values of all best models are presented in table A1. Note that the raw fitted probabilities do not account for the fact that there are different numbers of species in each endemism class. Even under a null hypothesis that species distribution is not related to endemism class, the categories would differ in probability. To account for this, the relative collection probabilities predicted by the multinomial regression model were divided by the total number of species in each class in the total fauna to give the average per-species collection probability of each endemism class. These corrected values are depicted in the figures and are the basis for all conclusions and interpretations.

In general, all permutations of the analysis exhibited similar general patterns consistent with the taxon cycle and our conclusions. There were some minor variations in the fitted models under different sampling schemes, which we briefly discuss here. First, when all methods are included in the model (figs. 2, A1), there is a U-shaped relationship for exotics and elevation, which is most prominent in the disturbed habitat category. This could reflect stronger elevational constraints on widespread natives than exotics, which could cause a U-shaped pattern in relative prominence. However, this pattern was not returned in the best model when using hand collections only (figs. A3, A4, although the full model, with a higher AIC, did show the same pattern. Thus, given the disagreement we do not make any conclusions about the validity of this pattern but note it in passing for future work. The second point of disagreement between the various models is whether there are significant differences between endemic allopecies and deep endemic categories. Differences were observed when malaise and leaf litter samples were included but not in the models which only included hand collections.

To cross-check our statistical methodology, we created 1,000 random permutations of the species-locality incidence matrix using a swapping algorithm (species and locality sums preserved) and performed the full multinomial regression model on each replicate. We found that 17 of 18 of the fitted coefficients for the actual data were outside the 95% null distributions for those coefficients, and all except two were over 2 standard deviations from the null mean. The average number of significant coefficients (based on a Wald test) in the null replicates was 1.012 (SD 1.3) out of 18 which is close to what would be expected under random expectation. For the observed data, 17 of 18 coefficients were significant in the Wald test.

For standardized samples (leaf litter and malaise trap), we can model absolute probabilities, as the detection of one species does not preclude the detection of other species in the sample. We could model these as counts of a Poisson process (Poisson regression), but these would not be directly comparable across classes, because there are different numbers of total species in each class. Rather, we treated each sample as a set of trials in which each species of a class was either present or absent. If every species has the same probability of detection in the samples, or if variability is not related to endemism class, then the expected number of detections should be proportional to the number of species in the class, and the binomial probabilities should not be significantly different. Coefficients and AIC values of the binomial logistic regression models are presented in table A2.

Additional Information on the Pheidole Phylogeny and Analysis

Our analysis of *Pheidole* builds upon two previous studies on the genus. First, Sarnat (2008) provided a taxonomic revision of the endemic spinescent Fijian *Pheidole roosevelti* group, describing their aberrant morphology and ecology in detail. Second, Sarnat and Moreau (2011) constructed a molecular phylogeny and found that the spinescent phenotype evolved independently from other similar phenotypes in the region. Their phylogeny is redrawn in figure A4 and shows the evolutionary relationships between different spinescent and nonspinescent lineages in the region. Note that this phylogeny is biased in sampling toward spinescent species, but most species in the region (and all extant *Pheidole* in the new world) are nonspinescent, and this is almost certainly the ancestral condition.

Our focus in this article is evaluating evidence for in situ evolutionary and ecological shifts predicted by the taxon cycle and hinted by the in situ evolution of spinescence. Thus, we focused our attention on the large endemic clade that includes the *P. roosevelti* group. There is one undescribed species from the neighboring Solomon Islands which would exclude *Pheidole vatu* and possibly *Pheidole* sp. FJ05 from this clade. While this could indicate either back colonization or multiple colonizations from Fiji, we are reluctant to make any conclusions about this pending further work using more markers and with greater taxon sampling in the source regions. With this caveat in mind, we reconstructed the ancestral state of the habitat and elevation scores of the clade treating the entire clade as derived from a single colonization event in Fiji.

In several cases, specimens identified as the same morphological species were not monophyletic in the best tree (fig.

A4), which could be due to either incomplete lineage sorting or problems with morphological species delineation. However, the topological uncertainties were relatively minor and toward the tips of the tree. To link the phylogeny to ecological data and reconstruct ancestral states, we required species to appear once on the tree. We took two approaches to this. First, using the dataset from Sarnat and Moreau (2011), we reran the maximum likelihood analysis in GARLI 0.951 using the same parameters as Sarnat and Moreau but under the constraint that morphological species are monophyletic. This is the tree depicted in the main text. Second, we reconstructed the ancestral states when varying species position across the alternatives, and confirmed that our conclusions are not sensitive to these variations. The tree branches were arbitrarily ultrametricized in Mesquite (Maddison 2006) before reconstructing with maximum squared-change parsimony for continuous characters (habitat and elevation mean) using the PDAP module (Midford et al. 2005).

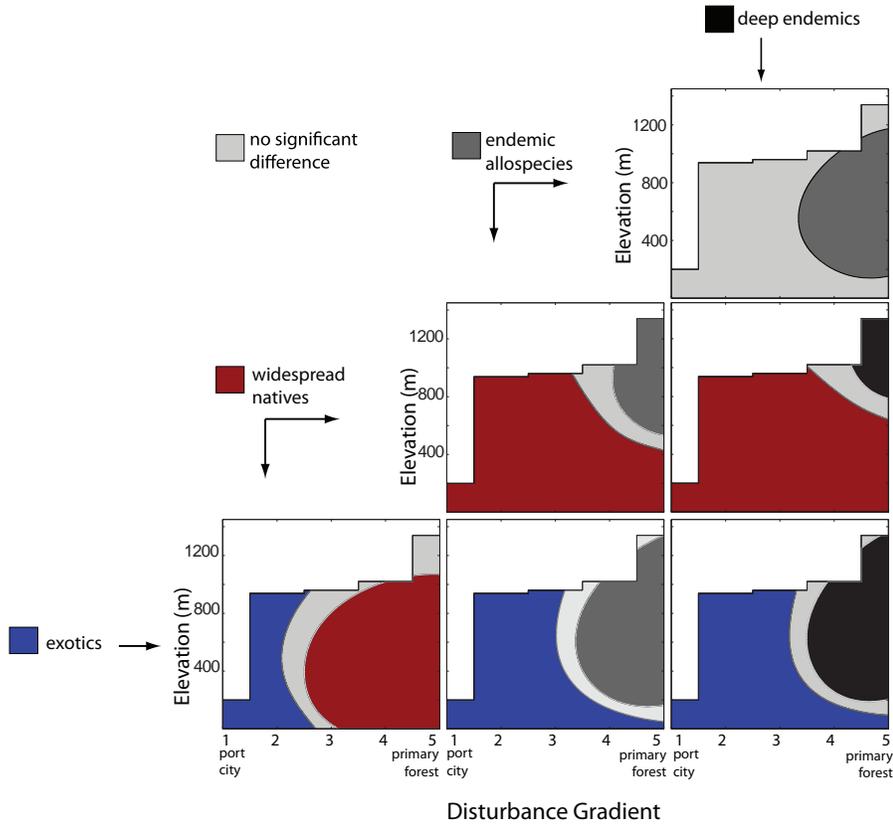
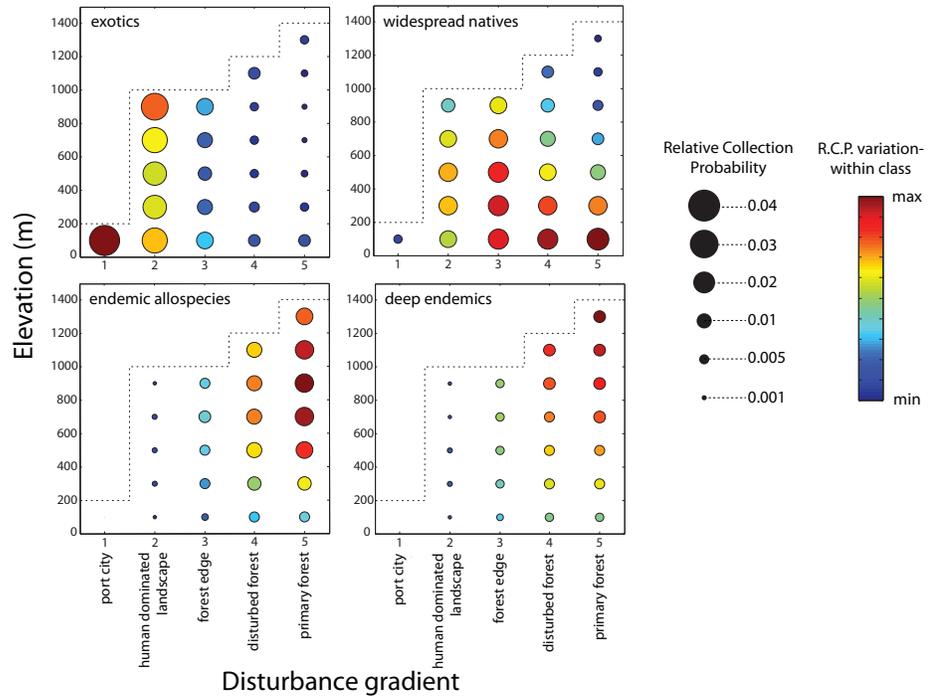


Figure A1: Multinomial logistic regression results for the “all methods by sample” data set equivalent in style to figures 2 and 3 in the main text.

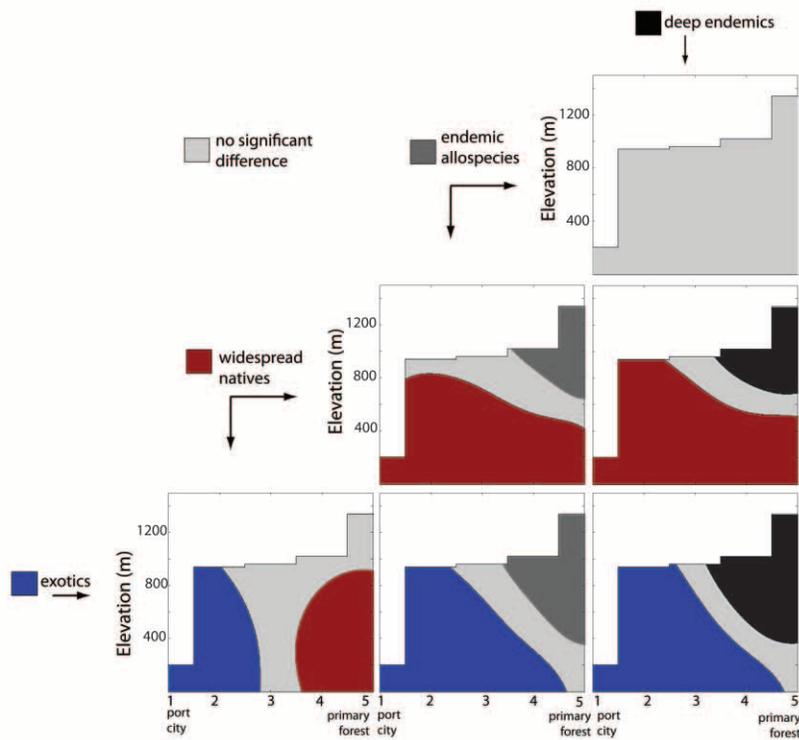
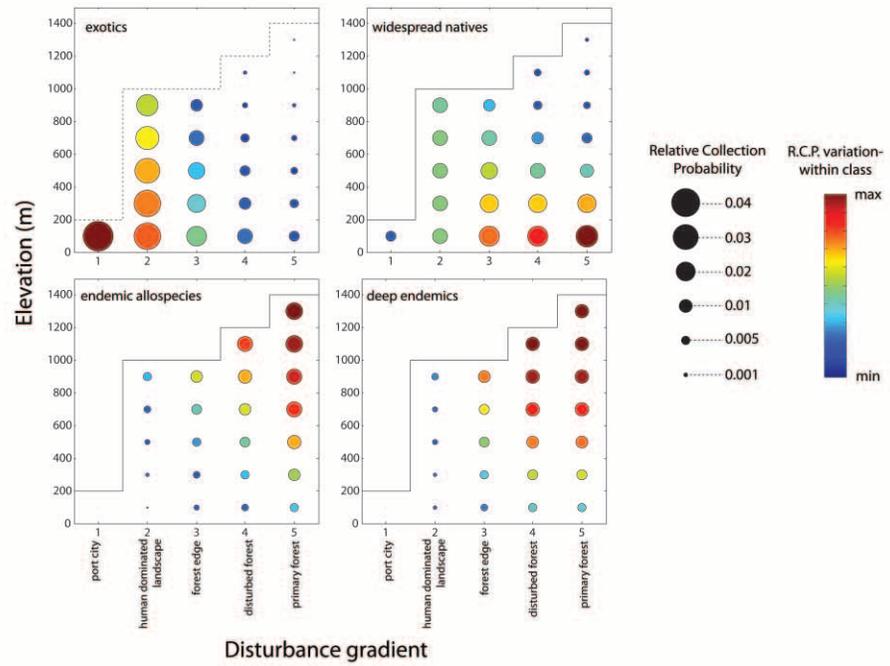


Figure A2: Multinomial logistic regression results for the “hand collection by sample” data set, equivalent in style to figures 2 and 3 in the main text.

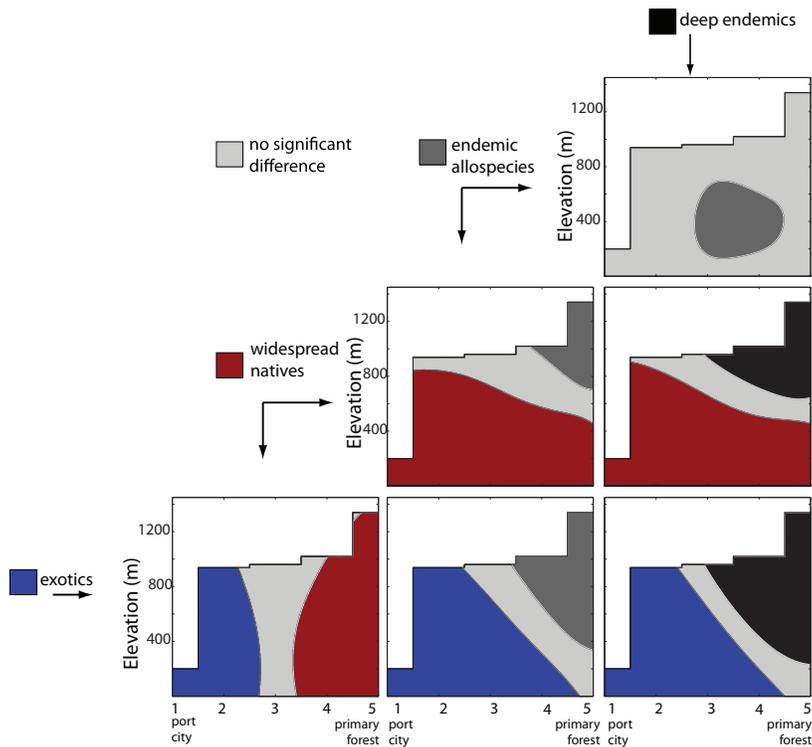
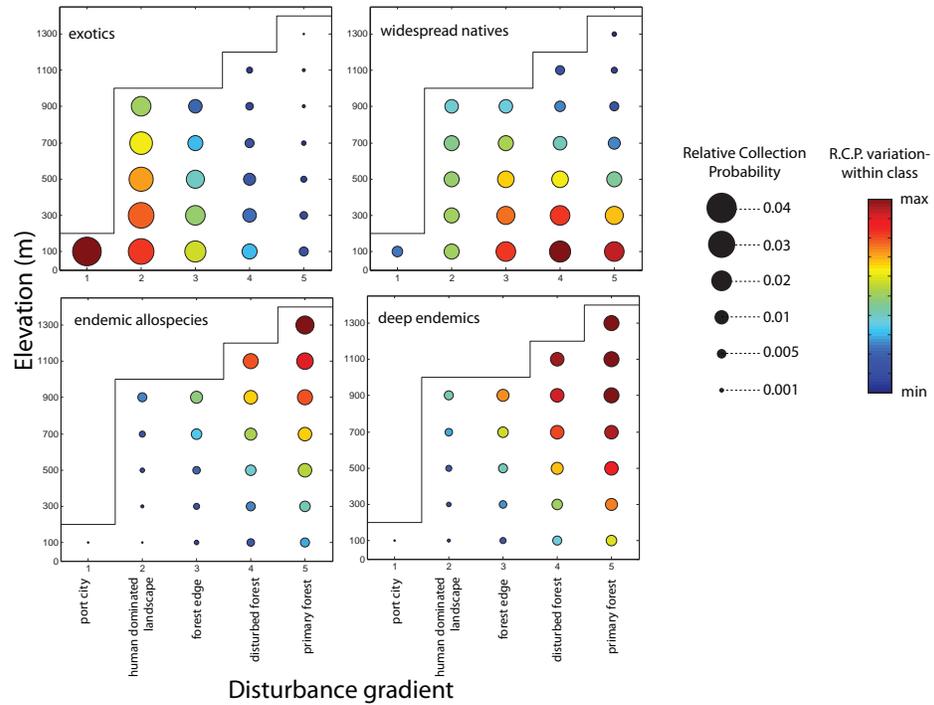


Figure A3: Multinomial logistic regression results for the “hand collection by locality” data set, equivalent in style to figures 2 and 3 in the main text.

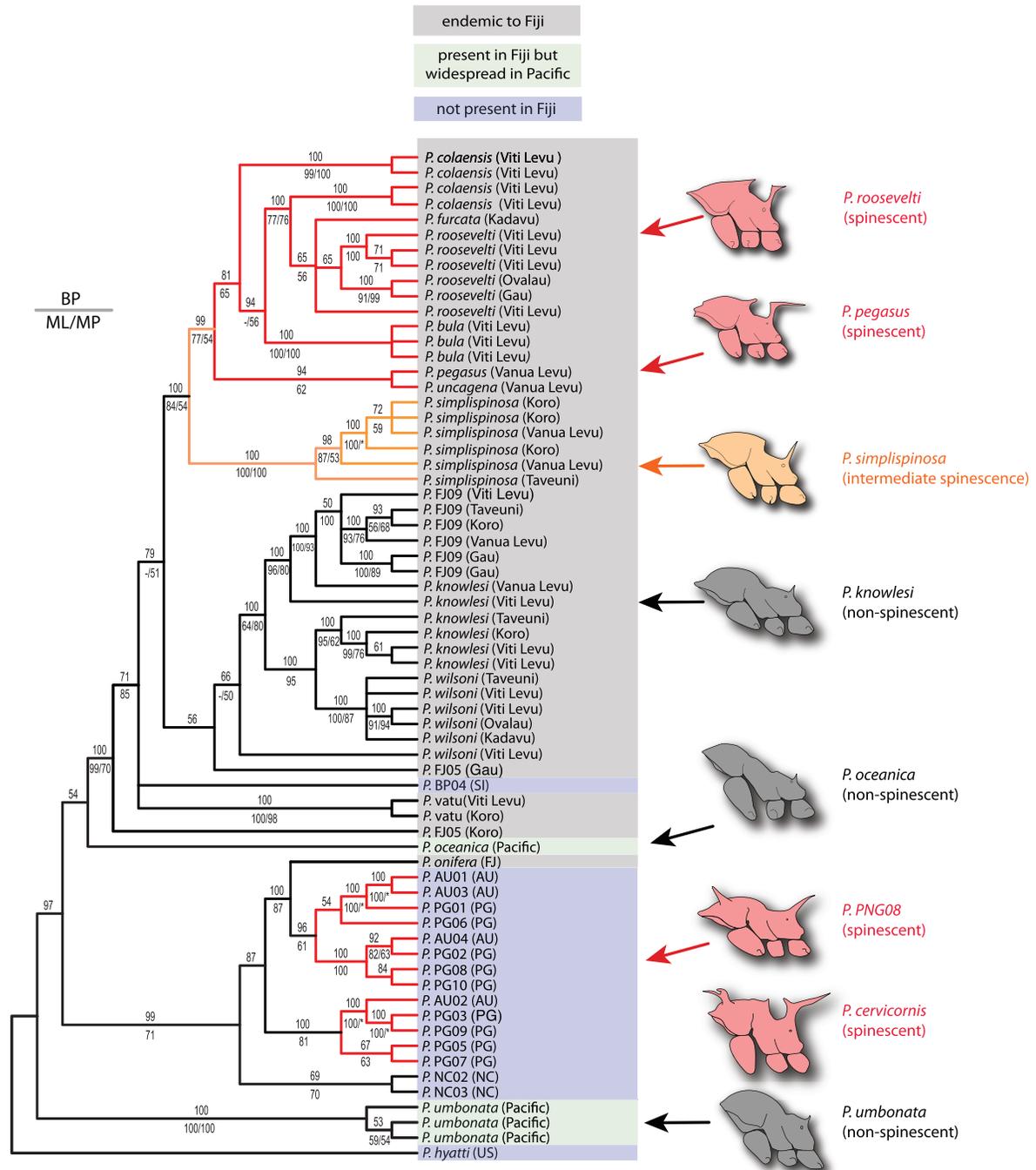


Figure A4: Regional *Pheidole* phylogeny (redrawn from Sarnat and Moreau 2011).

Table A1. Fitted coefficients for the multinomial logistic regression models selected under Akaike Information Criterion (AIC) minimization

Data set (species detections, samples or localities)	AIC _{null}	AIC _{best}	Endemism		Elevation	Elevation ²	Distance	Distance ²	Elevation × distance
			class	Intercept					
All methods by sample (6,415, 2,132)	9,835	7,970	ex.	0	0	0	0	0	0
			w.n.	-4.72	1.3×10^{-3}	-3.4×10^{-6}	2.27	-.23	1.5×10^{-4}
			e.a.	-10.71	2.7×10^{-3}	-4.8×10^{-6}	4.14	-.44	1.0×10^{-3}
			d.e.	-8.07	1.3×10^{-3}	-3.6×10^{-6}	3.62	-.40	9.6×10^{-4}
All methods by locality (3,616, 434)	3,992	2,680	ex.	0	0	0	0	0	0
			w.n.	-3.8	2.2×10^{-3}	-2.6×10^{-6}	1.6	-.15	1.1×10^{-4}
			e.a.	-11.4	3.1×10^{-3}	-4.3×10^{-6}	4.6	-.50	8.0×10^{-4}
			d.e.	-8.1	2.3×10^{-3}	-2.7×10^{-6}	3.4	-.35	5.4×10^{-4}
Hand collections only by sample (1,366, 1,196)	3,310	2,397	ex.	0	0	...	0	0	...
			w.n.	-3.6	4.9×10^{-5}	...	1.5	-.10	...
			e.a.	-9.3	3.3×10^{-3}	...	2.6	-.17	...
			d.e.	-8.7	3.0×10^{-3}	...	3.3	-.29	...
Hand collections by locality (1,187, 300)	1,968	1,220	ex.	0	0	...	0
			w.n.	-2.7	3.1×10^{-4}8
			e.a.	-7.7	3.4×10^{-3}	...	1.4
			d.e.	-5.7	2.8×10^{-3}	...	1.3
Malaise samples, forest only (2,831, 617)	3,733	3,497	ex.	0	0	0
			w.n.	1.0	2.3×10^{-3}	-2.8×10^{-6}
			e.a.	-1.1	5.2×10^{-3}	-2.9×10^{-6}
			d.e.	.6	3.4×10^{-3}	-2.5×10^{-6}
Leaf litter samples, forest only (649, 56)	486	419	ex.	0	0
			w.n.	.6	1.8×10^{-3}
			e.a.	-4	4.4×10^{-3}
			d.e.	-.5	5.1×10^{-3}
Hand collections, forest only (505, 648)	1,343	1,218	ex.	0	0
			w.n.	1.1	3.8×10^{-3}
			e.a.	-1.2	4.3×10^{-3}
			d.e.	-.2	4.0×10^{-3}

Note: The AIC_{null} represents the AIC from an intercepts-only model. Exotics were used as the reference category, and thus, all coefficients were set to zero; the coefficients of the other three classes are sufficient to describe changes in relative probability. ex. = exotic, w.n. = widespread native, e.a. = endemic allopecies, d.e. = deep endemic.

Table A2. Fitted coefficients and Akaike Information Criterion (AIC) values for the binomial logistic regression models selected under AIC minimization

Data set (n), endemic class	AIC _{null}	AIC _{best}	Intercept	Elevation	Elevation ²
Leaf litter samples (56):					
ex.	156	111	-1.5	-4.2×10^{-3}	...
w.n.	294	195	-1.5	3.2×10^{-3}	-7.1×10^{-6}
e.a.	250	226	-2.1	3.3×10^{-3}	-4.3×10^{-6}
d.e.	269	247	-3.9	4.9×10^{-3}	-5.1×10^{-6}
Malaise trap samples (719):					
ex.	1,130	1,124	-2.4	-8.5×10^{-4}	...
w.n.	2,253	2,176	-2.6	5.8×10^{-4}	1.6×10^{-6}
e.a.	1,473	1,326	-4.7	3.8×10^{-3}	1.9×10^{-6}
d.e.	2,169	2,138	-4.5	1.7×10^{-3}	1.3×10^{-6}

Table A3. Fiji Islands species list

Taxon	Level of endemism	Species group/complex	Island distribution in Fiji ^a
Subfamily Amblyoponinae:			
<i>Amblyopone zwaluwenburgi</i> (Williams)	Quasi-endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Prionopelta kraepelini</i> Forel	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
Subfamily Cerapachyinae:			
<i>Cerapachys cryptus</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys fuscior</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys lindrothi</i> Wilson	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys majusculus</i> Mann	Deep endemic	Excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys sculpturatus</i> Mann	Deep endemic	Excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys vitiensis</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys zimmermani</i> Wilson	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys</i> sp. FJ01	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys</i> sp. FJ04	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys</i> sp. FJ05	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys</i> sp. FJ06	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys</i> sp. FJ07	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys</i> sp. FJ08	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cerapachys</i> sp. FJ10	Deep endemic	Excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
Subfamily Dolichoderinae:			
<i>Iridomyrmex anceps</i> (Roger)	Exotic	Native to Indo-Pacific but classified exotic due to documented human introduction to Fiji (Wilson and Taylor 1967)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Iridomyrmex ignobilis</i> Mann	Endemic allospecies	<i>anceps</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Ochetellus sororis</i> (Mann)	Endemic allospecies	<i>glaber</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Philidris nagasau</i> (Mann)	Endemic allospecies	<i>cordatus</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tapinoma melanocephalum</i> (Fabricius)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tapinoma minutum</i> Mayr	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tapinoma</i> sp. FJ01	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tapinoma</i> sp. FJ02	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Technomyrmex vitiensis</i> Mann	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
Subfamily Ectatomminae:			
<i>Gnamptogenys aterrima</i> (Mann)	Endemic allospecies	<i>albiclava</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
Subfamily Formicinae:			
<i>Acropyga lauta</i> Mann	Quasi-endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Acropyga</i> sp. FJ02	Endemic allospecies	<i>myops</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Anoplolepis gracilipes</i> (Smith, F.)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus fijianus</i> Ödzikmen	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus bryani</i> Santschi	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus chloroticus</i> Emery	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus cristatus</i> Mayr	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus dentatus</i> (Mayr)	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus kadi</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus laminatus</i> Mayr	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus lauensis</i> Mann	Deep endemic	Excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus levuanus</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus maafui</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus manni</i> Wheeler	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus oceanicus</i> (Mayr)	Deep endemic	Excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus polynesianus</i> Emery	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus sadinus</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus schmeltzi</i> Mayr	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus umbratilis</i> Wheeler	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus vitiensis</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus</i> sp. FJ02	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus</i> sp. FJ03	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Camponotus</i> sp. FJ04	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Nylanderia glabrior</i> (Forel)	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Nylanderia vaga</i> (Forel)	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Nylanderia vitiensis</i> (Mann)	Endemic allospecies	<i>glabrior</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK

Table A3 (Continued)

Taxon	Level of endemism	Species group/complex	Island distribution in Fiji ^a
<i>Nylanderia</i> sp. FJ03	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Paraparatrechina oceanica</i> Mann	Endemic allospecies	<i>minutula</i> complex	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Paratrechina longicornis</i> (Latreille)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Plagiolepis alluaudi</i> Emery	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
Subfamily Myrmicinae:			
<i>Adelomyrmex hirsutus</i> Mann	Endemic allospecies	Closely allied to undescribed species from New Caledonia	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Adelomyrmex samoanus</i> Wilson & Taylor	Quasi-endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cardiocondyla emeryi</i> Forel	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cardiocondyla kagutsuchi</i> Terayama	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cardiocondyla minutior</i> Forel	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cardiocondyla nuda</i> (Mayr)	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Cardiocondyla obscurior</i> Wheeler	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Carebara atoma</i> (Emery)	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Eurhopalothrix emeryi</i> (Forel)	Endemic allospecies		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Eurhopalothrix insidiatrix</i> Taylor	Endemic allospecies		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Eurhopalothrix</i> sp. FJ52	Endemic allospecies		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma curvata</i> Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma desupra</i> Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma levifrons</i> (Mann)	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma polita</i> (Mann)	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma rugosa</i> (Mann)	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma stoneri</i> (Mann)	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma striatella</i> (Mann)	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma sukuna</i> Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma tortuosa</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma vanua</i> Lucky & Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Lordomyrma vuda</i> Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Metapone</i> sp. FJ01	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Monomorium destructor</i> (Jerdon)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Monomorium floricola</i> (Jerdon)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Monomorium pharaonis</i> (Linnaeus)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Monomorium sechellense</i> Emery	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Monomorium vitiense</i> Mann	Endemic allospecies	<i>talpa</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Monomorium</i> sp. FJ02	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Myrmecina cacabau</i> (Mann)	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Myrmecina</i> sp. FJ01	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole bula</i> Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole caldwelli</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole colaensis</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole fervens</i> Smith, F.	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole furcata</i> Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole knowlesi</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole megacephala</i> (Fabricius)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole oceanica</i> Mayr	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole onifera</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole pegasus</i> Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole roosevelti</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole simplispinosa</i> Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole umbonata</i> Mayr	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole uncagena</i> Sarnat	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole vatu</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole wilsoni</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole</i> sp. FJ05	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pheidole</i> sp. FJ09	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Poecilomyrma myrmecodiae</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Poecilomyrma senirewae</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Poecilomyrma</i> sp. FJ03	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Poecilomyrma</i> sp. FJ05	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Poecilomyrma</i> sp. FJ06	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Poecilomyrma</i> sp. FJ07	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Poecilomyrma</i> sp. FJ08	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pristomyrmex mandibularis</i> Mann	Endemic allospecies	<i>laevigatus</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK

Table A3 (Continued)

Taxon	Level of endemism	Species group/complex	Island distribution in Fiji ^a
<i>Pristomyrmex</i> sp. FJ02	Endemic allospecies	<i>laevigatus</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pyramica membranifera</i> (Emery)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pyramica trauma</i> Bolton	Endemic allospecies	<i>capitata</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pyramica</i> sp. FJ02	Endemic allospecies	<i>capitata</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Rogeria stigmatica</i> Emery	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Romblonella liogaster</i> (Santschi)	Endemic	Excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Solenopsis geminata</i> (Fabricius)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Solenopsis papuana</i> Emery	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys basiliska</i> Bolton	Endemic allospecies	<i>biroi</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys chernovi</i> Dlussky	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys daithma</i> Bolton	Endemic allospecies	<i>caniophanes</i> group, excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys ekasura</i> Bolton	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys frivola</i> Bolton	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys godeffroyi</i> Mayr	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys jepsoni</i> Mann	Quasi-endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys mailei</i> Wilson & Taylor	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys nidifex</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys panaulax</i> Bolton	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys praefecta</i> Bolton	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys rogeri</i> Emery	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys scelestia</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys sulcata</i> Bolton	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys tumida</i> Bolton	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys</i> sp. FJ01	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys</i> sp. FJ13	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys</i> sp. FJ17	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys</i> sp. FJ18	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Strumigenys</i> sp. FJ19	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tetramorium bicarinatum</i> (Nylander)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tetramorium caldarium</i> (Roger)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tetramorium insolens</i> Smith, F.	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tetramorium lanuginosum</i> Mayr	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tetramorium manni</i> Bolton	Endemic allospecies	<i>szalayi</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tetramorium pacificum</i> Mayr	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tetramorium simillimum</i> (Smith, F.)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Tetramorium tonganum</i> Mayr	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Vollenhovia denticulata</i> Emery	Quasi-endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Vollenhovia</i> sp. FJ01	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Vollenhovia</i> sp. FJ03	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Vollenhovia</i> sp. FJ04	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Vollenhovia</i> sp. FJ05	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
Subfamily Ponerinae:			
<i>Anochetus graeffei</i> Mayr	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Hypoponera confinis</i> (Roger)	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Hypoponera eutrepta</i> (Wilson)	Endemic allospecies	<i>biroi</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Hypoponera monticola</i> (Mann)	Endemic allospecies	<i>pruinosa</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Hypoponera opaciceps</i> (Mayr)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Hypoponera pruinosa</i> (Forel)	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Hypoponera punctatissima</i> (Roger)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Hypoponera turaga</i> (Mann)	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Hypoponera vitiensis</i> (Mann)	Deep endemic	Excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Hypoponera</i> sp. FJ16	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Leptogenys foveopunctata</i> Mann	Deep endemic	Excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Leptogenys fugax</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Leptogenys humiliata</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Leptogenys letilae</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Leptogenys navua</i> Mann	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Leptogenys vitiensis</i> Mann	Deep endemic	Excluded (no ecological data)	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Leptogenys</i> sp. FJ01	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Odontomachus angulatus</i> Mayr	Endemic allospecies	<i>saevissimus</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Odontomachus simillimus</i> Smith, F.	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Pachycondyla stigma</i> (Fabricius)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Platythyrea parallela</i> (F. Smith)	Widespread native		VL-VN-TA-KV-GA-KR-LA-ML-LK

Table A3 (Continued)

Taxon	Level of endemism	Species group/complex	Island distribution in Fiji ^a
<i>Ponera colaensis</i> Mann	Endemic allospecies	<i>taipingensis</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Ponera manni</i> Taylor	Endemic allospecies	<i>japonica</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Ponera swazeyi</i> (Wheeler)	Exotic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Ponera</i> sp. FJ02	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
Subfamily Proceratiinae:			
<i>Discothyrea</i> sp. FJ01	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Discothyrea</i> sp. FJ02	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Discothyrea</i> sp. FJ04	Deep endemic		VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Proceratium oceanicum</i> De Andrade	Endemic allospecies	<i>silaceum</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Proceratium relictum</i> Mann	Endemic allospecies	<i>silaceum</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK
<i>Proceratium</i> sp. FJ01	Endemic allospecies	<i>silaceum</i> group	VL-VN-TA-KV-GA-KR-LA-ML-LK

Note: List is from Sarnat and Economo, forthcoming. The AIC_{null} represents the AIC from an intercepts-only model. ex. = exotic, w.n. = widespread native, e.a. = endemic allospecies, d.e. = deep endemic.

^aBold = observed; roman = not observed. See figure 1 for island abbreviations.