Detailed Phylogenetic Analyses

Local plant communities are often dominated by species rich genera, and this is especially true in the tropics. We therefore used rbcL sequences in combination with additional sequence data for the following groups: Euphorbiaceae (ndhF), *Ficus* (ITS) and Rubiaceae (RpS16). We used the resultant topologies as constraints in a larger rbcl only analysis for all 88 plant species from 31 families. We also used the ordinal and family level relationships as derived from the APGIII [1] tree for constraining the higher level angiosperm relationships [2].We used published sequence data and subfamily level constraints from Sihvonen *et al.* [3] for geometrids (159 additional taxa and a total of 209) and Haines & Rubinoff [4] for pyraloids (53 additional taxa and a total of 130). This approach meant that we could include a much wider taxonomic context into our analyses and estimate more robust phylogenies that were not as heavily influenced by missing data or the unbalanced taxonomic composition of our community samples. We estimated ultrametric phylogenies using BEAST v2.3.1 [5] using substitution models derived from jMODEL Test 2 [6] and a relaxed log-normal molecular clock (set to a rate of 1.0). We partitioned our five gene data set, grouping codons one and two (modelling codon three separately) and defined a separate substitution model for each partition. We ran three (geometrids) or six (pyraloids) separate MCMC chains for 40,000,000 generations and assessed the effective sample sizes (ESS) of the combined chains using Tracer v1.6 [7] to ensure adequate sampling and convergence of the analysis (ESS values over 200 for all parameters sampled). We used the CIPRES portal v3.3 for all phylogenetic analyses [8].

Detailed Insect Collection Protocol

In the Madang area, we hand collected caterpillars from host plants for at least one year per tree species between 1995 and 2008, sampling ca 1500 m^2 of foliage per species. We sampled accessible branches from the understory and the forest canopy. In the laboratory, each caterpillar was offered foliage from its host plant and only feeding caterpillars were included in subsequent analyses.

For the felled plots in Wanang care was taken while felling to ensure minimum disturbance to other trees within the plot, this involved directional felling in an orderly manner beginning with the shortest trees and those with the least lianas. Trees tangled with lianas had the potential for damaging other trees when felled, and in general were difficult to fell, thus lianas were cut with machetes where possible. We felled small trees in the understory first, following with larger trees and finally canopy trees. Felling was directed into gaps created by previous plot clearance, allowing for easier collection and minimising disturbance to the tree being sampled, reducing caterpillar loss and exchange between trees. Collection from the entire foliage of the felled trees was carried out immediately upon felling by a team of ~15 locally recruited collectors supervised by on-sight researchers. Collection involved searching for live caterpillars (Lepidoptera), both free feeding and semi concealed, and placing them in plastic collections pots before being brought back to the field laboratory. Our extensive use of both standarised collections and felling suggests that caterpillars are much more resistant to felling disturbance than beetles and flying insects. In the field laboratory, trophic links were confirmed using no-choice feeding trials, which involved supplying collected herbivores with leaves of the host they were found upon. This ensured that 'tourist' species, or those from other hosts, were not assigned as feeding individuals.

Detailed Laboratory Protocol

We collected and silica-gel dried duplicate samples to find out the dry weight percentage of leaves stored into acetone. Once in laboratory, collection acetone of each sample was carefully collected into a new Falcon tube and the remaining leaf material was transferred into a new Ultra Turrax Tube Dispenser capsule. The material was cut into small pieces and extracted with 30 mL acetone/water (80:20, v/v) at 4000 rpm for 3 x 5 mins, then left to maserate overnight at +5°C and the extraction was repeated for another 3 x 5 mins. After centrifugation, the supernatant was pooled with the collection acetone and acetone was evaporated under nitrogen. The aqueous phase was frozen and freeze-dried. 5 mL of ultra-pure water was added to the freeze-dried sample and the polyphenol extract was filtered via 0.20 µm PTFE filters before analysis.

Intra- vs. Inter-Specific Variation

Linear regressions of the coefficient of variation for oxidative activity and protein precipitation capacity per species against the maximum difference between collection dates within species revealed no significant relationships ($t=1.302_{60,1}$, $p=0.198$, $R^2=0.028$, $t=0.487_{46,1}$, $p=0.628$, $R^2=0.005$, respectively) (Figures S5 and S7). We also compared the contribution of intra- and inter-species variation using mixed models (LMMs) including individual samples. We included the response variables oxidative activity and protein precipitation (for individual samples) in two separate LMMs, both with the categorical explanatory variable 'replicate' (time ordered categorical variable). We grouped all samples using the random effect 'species' and fit models using maximum likelihood with the function 'lme' in the R package 'nlme' [9]. We used the function 'r.squaredGLMM' in the R package 'MuMIn' [10] to determine both the marginal R^2 (fixed effects) and conditional R^2 (whole model) for each model. Finally, we tested the significance of the random effects by using a likelihood ratio test (full mixed effect model vs. linear model without random effects). We limited the comparison to three replicates per species to keep group sizes even. Overall replicate means were not significantly different for oxidative activity ($F=2.04_{,146}$, $p=0.134$) or protein precipitation capacity ($t=2.57_{,146}$, $p=0.0799$) and the amount of variance explained by replicate was small for both oxidative activity ($R^2=0.005$) and protein precipitation capacity ($R^2=0.007$) compared to the full model with species identity included ($R^2=0.737$, $R^2=0.708$). However, replicate group three did have a significantly higher mean protein precipitation capacity than replicate group one after species identity had been taken into account ($t=2.255_{,146}$, $p=0.026$). For both oxidative activity (Likelihood Ratio=137.704, $p<0.001$) and protein precipitation capacity (Likelihood Ratio=115.994, $p<0.001$) the full model was significantly better, indicating a much larger contribution of species identity than time ordered replicate in explaining the variance in chemical activity between samples.

We further analysed replicate samples from three highly variable species (*Leea indica*, *Homalanthus novoguineensis* and *Macaranga densiflora*) using UPLC-QqQ-MS/MS [11], confirming that each species did have their specific metabolite profiles, i.e. the within-species variation came from differences in

compound concentrations, rather than their composition. Finally, we note that interspecific variation in secondary metabolite profile has been shown to be considerably higher than intraspecific variation in tropical plants, even when sampling across seasons [12].

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