**Title:** Varyingly Hungry Caterpillars: Predictive Models and Foliar Chemistry Suggest How to Eat a Rainforest

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**Supplementary Material Figure Legends**

**Figure S1**. A schematic diagram of our analytical steps. All predictive analyses included the standardised Madang data set (Input 1). Firstly, we fit a linear model to the association strengths of our bipartite data set, with a phylogenetic correlation between interacting species (Input 1). We then used the community covariance matrices and phylogenetically standardized interactions strengths derived from this model to perform sequential removal and host prediction for each interactant from the matrix. This allowed us to generate a predicted binary host use matrix filled with the most probable interactions (Output 1). These predictions were then validated by correlating matrix fill and using null models (Validation). Finally the quantitative data set (Input 1) was extended to include a phylogeny in which the position of hosts from the expanded data set was known, but all additional host associations were predicted based on the original covariance matrices and phylogenetically standardized interactions strengths and this new phylogeny.

**Figure S2**. The phylogeny of plant hosts sampled for either geometrids or pyraloids. The 34 hosts only sampled in the Wanang data set are marked with a star. Branch lengths are equal to substitutions per site.

**Figure S3**. The phylogeny of pyraloids sampled in this study and used for analysis. The species only sampled in the Wanang data set is marked with a star. Branch lengths are equal to substitutions per site.

**Figure S4**. The phylogeny of geometrids sampled in this study and used for analysis. The species only sampled in the Wanang data set is marked with a star. Branch lengths are equal to substitutions per site.

**Figure S5**. A histogram of mean oxidative activity (mg/g) (± one s.e.) for all 88 species analysed. Species are ordered by the maximum number of days between intra-specific collections.

**Figure S6**. A histogram of mean protein precipitation (mg/g) (± one s.e.) for all 88 species analysed. Species are ordered by the maximum number of days between intra-specific collections.

**Figure S7**. Plots of fitted quasibinomial regressions for both oxidative activity (mg/g) and protein precipitation (mg/g). Plots i) and ii) include only the significant phylogenetic axes common to both moth families, while plots ii) and v) include only the chemical traits, plots iii) and vi) include both phylogenetic axes and chemical traits.

**Figure S8**. A heatmap of geometrid abundance, oxidative activity (mg/g) and predicted occurrence derived from phylogenetic eigenvectors regression (PVR) including all significant phylogenetic axes. Geometrid abundance was not included as a model term in any PVR analysis.

**Figure S9**. Correlations between Euclidean distance matrices derived from observed and predicted association between plant hosts a i) geometrid caterpillars (r=0.72, p=0.001) and ii) pyraloid caterpillars (r=0.94, p=0.001).

**Appendix 1**. Detailed methods and results section.

**Appendix 2**. A list of individuals sequenced for each gene included in this study, including from published studies (Haines and Rubinoff, 2012; Sihvonen et al., 2011). Red text indicates individuals where close relatives were used as BOLD extracts were not available for the exact specimen.

**Appendix 3**. A description of taxonomic updates published since Novotny et al. (2010) or resulting from this study.

**Appendix 4**. Literature review and summary of Geometroidea, Pyraloidea and Thyrididae host use in the oriental region.