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The macroecology of phylogenetically structured hummingbird-plant networks

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ABSTRACT

Aim To investigate the association between species richness, species' phylogenetic signal, insularity and historical and current climate with hummingbird-plant network structure.

Location 54 communities along a *c.* 10,000 kilometer latitudinal gradient across the Americas (39ºN - 32ºS), ranging from sea level to *c.* 3700 m asl, located on the mainland and on islands, and covering a wide range of climate regimes.

Methods We measured null-modeled corrected complementary specialization and bipartite modularity (compartmentalization) in networks of quantitative interactions between hummingbird and plant species. Using an ordinary least squares multi-model approach, we examined the influence of species richness, phylogenetic signal, insularity, and current and historical climate conditions on network structure.

Results Phylogenetically-related species, especially plants, showed a tendency to interact with a similar array of partners. The spatial variation in network structure exhibited a constant association with species' phylogeny (R^2=0.18-0.19). Species richness and environmental factors showed the strongest associations with network structure (R^2=0.20-0.44; R^2=0.32-0.45, respectively). Specifically, higher levels of complementary specialization and modularity were associated to species-rich communities and communities in which closely-related hummingbirds visited distinct sets of flowering species. On the mainland, warmer temperatures and higher historical temperature stability associated to higher levels of complementary specialization.

Main conclusions Previous macroecological studies of interaction networks have highlighted the importance of environment and species richness in determining network structure. Here, for the first time, we report an association between species phylogenetic signal and network structure at macroecological scale. Specifically, null model corrected complementary specialization and modularity exhibited a positive association with species

richness and a negative association with hummingbird phylogenetic signal, indicating that both high richness and high inter-specific competition among closely-related hummingbirds exhibit important relationships with specialization in hummingbird-plant networks. Our results document how species richness, phylogenetic signal and climate associate with network structure in complex ways at macroecological scale.

INTRODUCTION

An urgent challenge facing contemporary ecologists is to understand how ecological, evolutionary and environmental mechanisms affect the structure and function of ecological communities. Better understanding of how these processes form and maintain communities should help us to construct more robust theories and models of community dynamics that better predict how species and communities may respond to disturbance (Vázquez *et al.,* 2009a; Woodward *et al.,* 2010). For this purpose, the use of network approaches to study complex communities of interacting species, i.e. networks representing species as nodes and interactions as links between species, has significantly advanced our understanding of ecological systems (Woodward *et al*., 2010).

For instance, research on mutualistic networks such as plant-pollinator or plant-frugivore interactions, has revealed that these communities typically exhibit a number of architectural attributes, such as complementary specialization and modularity, which differ significantly from random interactions among species (Olesen *et al.*, 2007; Blüthgen 2010; Dalsgaard *et al.,* 2011, 2013; Schleuning *et al.,* 2012, 2014; Trøjelsgaard & Olesen, 2013; Dormann & Strauss, 2014; Sebastián González *et al.*, 2015). Complementary specialization measures the exclusiveness in species' interactions. Specifically, it is a measure of the deviation from a neutral scenario in which species interact solely according to their availability, measuring species' availability either as its abundance or its interaction frequency (Blüthgen *et al.*, 2006). Modularity quantifies whether species interact more frequently with subsets of available species within a community, forming modules of densely interacting plants and hummingbirds, with loose connections between them (Olesen *et al.*, 2007). Such modules have been suggested to reflect co-evolutionary units (Olesen *et al.*, 2007), within-network functional specialization (Maruyama *et al.*, 2014), and phenological units of species in environments with strong climatic seasonalities (Martín González *et al.*, 2012; Schleuning *et al.*, 2014).

These architectural attributes have a profound impact on the dynamics of ecological communities. For example, higher levels of complementary specialization have been linked to higher dependencies between species and hence, to a higher risk of secondary extinctions (Blüthgen, 2010), whereas high levels of modularity may at first provide higher network resilience to perturbations, as these are not typically spread across modules, but ultimately may result into unconnected modules, community fragmentation and rapid species loss (Thébault & Fontaine, 2010; Stouffer & Bascompte, 2011). Complementary specialization and modularity are typically related, as some degree of modularity necessarily implies a certain level of complementary specialization on a subset of species from the available species pool (Dormann & Strauss, 2014). Nevertheless, these metrics measure different aspects of interaction specialization and, hence, may show disparate associations with different ecological, evolutionary and environmental factors.

Thus, studies at macroecological scales, where differences among network structure can be associated to varying ecological, evolutionary and environmental factors, may provide valuable insights into the structure and dynamics of ecological networks (Dalsgaard *et al.,* 2011, 2013; Schleuning *et al.,* 2012, 2014; Trøjelsgaard & Olesen, 2013, Sebastián González *et al.*, 2015). For instance, species richness may promote higher degrees of complementary specialization and modularity by increasing interspecific competition and providing more species to interact with, i.e. allowing a finer niche partitioning (e.g. Dalsgaard *et al.,* 2011; Junker *et al.,* 2013). Additionaly, evolution may structure biotic interactions via niche conservatism, as closely-related species may display more similar phenotypes, spatial distributions, and ecological interactions than distantly-related species (Webb *et al.,* 2002; Ives & Godfray, 2006; Rezende *et al.,* 2007; Vázquez *et al*., 2009a). Alternatively, closely-related species experiencing strong interspecific competition may undergo niche partitioning, competitive exclusion, or resource-use complementarity (Webb *et al.,* 2002; Rezende *et al.,* 2009; Krasnov *et al.,* 2012). Environmental setting may also affect biotic interactions. Historical climatic stability may promote specialization and modularity by providing species more opportunity to co-evolve over longer periods of time compared to species from climatically more unstable areas. For example, large late Quaternary glacial-interglacial climate change is coupled with a decreased modularity in pollination networks (Dalsgaard *et al*., 2013), and decreased specialization in hummingbird-plant networks (Dalsgaard *et al.,* 2011). Likewise, current environmental conditions may influence the identity and strength of species interactions by altering species' spatial distribution, phenophases and foraging capability (Cruden, 1972; Martín González *et al.,* 2009; Dalsgaard *et al.,* 2011, 2013; Schleuning *et al*., 2012, 2014). For example, bird pollination has been reported to become increasingly important and specialized in areas of high precipitation and low temperatures, possibly because insect pollinator diversity and activity is lower in cold and wet environments due to thermoregulatory constraints (Cruden, 1972; Dalsgaard *et al*., 2009, 2011; Martín González *et al*., 2009). Finally, insularity may influence pollination network structure, with significantly lower levels of specialization and modularity on islands compared to the mainland (Olesen *et al.,* 2002; Dalsgaard *et al.,* 2013).

Despite the recently increasing interest in determining the influence of species richness, phylogenetic signal and past and current environmental conditions on network structure (Dalsgaard *et al*., 2011, 2013; Schleuning *et al*., 2012, 2014; Sebastián González *et al*., 2015), very little is known about the relative importance of these factors. Only Schleuning *et al.* (2014) studied their combined influence on the modular patterns of mutualistic networks. Specifically, they used a dataset of 18 frugivore bird-plant networks, and showed that modularity was high in areas having low temperatures and high temperature seasonality, whereas species' phylogenetic history and historical climate exhibited no detectable association to modularity. Here, we likewise examine how species richness, phylogenetic signal and environmental conditions associate to the structure of hummingbird-plant networks, another type of mutualistic assemblage. To do so, we compiled a data-set consisting of 54 high-resolution quantitative hummingbird-plant interaction networks, and combined them with state-of-the-art species phylogenies and simulations of paleo and current climate. In accordance with previous studies on pollination networks, we show that species richness and climatic conditions influence complementary specialization and modularity. Additionally, for the first time, we report an association between species phylogenetic signal and network structure at macroecological scale. Specifically, communities where closely-related hummingbirds interact with distinct sets of plant species exhibit higher levels of complementary specialization and modularity.

MATERIAL & METHODS

Hummingbird-plant interaction networks

We compiled a large data-set of 54 high-resolution and geographically widely distributed hummingbird-plant interaction networks from published and unpublished sources (Fig. 1; see Table S1 for full references, and Dalsgaard *et al.*, 2011 for a previous version of this dataset). This dataset does not include networks which have not sampled the entire floral community, i.e. we discarded studies which had focused only on ornithophilous species or on specific floral or hummingbird groups. We also discarded illegitimate interactions, i.e. our database focuses on interactions with potential for pollination. These networks describe the interaction frequency between plants and hummingbirds, recorded as number of observed visits. In total, our dataset is composed of 141 species of hummingbirds belonging to all major hummingbird lineages (about 42% of all described species; McGuire *et al.*, 2014) and 824 plant species belonging to 79 different plant families (Appendix S1).

Mutualistic hummingbird-plant interaction networks constitute a particularly suitable model system to explore large-scale patterns in network structure as there is ample knowledge of the historical biogeography of hummingbirds, these assemblages are widely distributed in a variety of ecosystems across the Americas, and they offer examples covering the entire interaction specialization-generalization spectrum (Bleiweiss, 1998; Dalsgaard *et al.,* 2011). Furthermore, our data consists of a single and monophyletic pollinator group (Brown & Bowers, 1985; McGuire *et al.,* 2014), allowing us to explore the association between phylogeny on overall network structure more precisely.

Finally, the spatial distribution of these networks extend from sea level to *c.* 3700 m a.s.l. and spans a *c.* 10,000 kilometer gradient from 39ºN to 32ºS, from tropical and subtropical ecosystems in South America to temperate communities in North America. The spatial distribution includes both mainland and insular communities (Fig. 1), and consists of communities from various environmental settings.

Network composition and network metrics

Network interactions were quantified in terms of the number of interaction events between hummingbird and plant species at particular locations. For each network we calculated two complementary metrics that describe the degree of specialization or specificity of hummingbird-plant interactions: complementary specialization (Blüthgen *et al.,* 2006) and quantitative bipartite modularity (Dormann & Strauss, 2014). These metrics were correlated in our dataset $R^2=0.78$ (Table S2) but were chosen to more fully characterize how evolutionary and environmental factors associate to specialized network structures. For the calculations we used the R package *bipartite 1.20* (Dormann *et al.*, 2009).

(1) *Complementary specialization (H_2')* describes how species restrict their interactions relative to random expectations based on species' abundances/interaction frequency.

Complementary specialization is calculated as $H_2 = -\sum_{i=1}^{r}\sum_{j=1}^{c}(p_{ij}\ln p_{ij})$, where p_{ij} reflects the proportional number of interactions of each species relative to their availability, i.e., for their respective marginal total (in our case total interaction frequency) for *r* plant and *c* animal species. We illustrate this in Figure 1; for instance, from the example community A from Fig. 1, p_{1A}=0.99 (which results from an interaction frequency of 155 between plant 1 and hummingbird A, over a marginal total of 155+1=156 for plant 1) and p_{A1}=1 (155 over 155). Hence the interaction A-1 exhibits a high complementary specialization, as hummingbird A visits exclusively plant 1 and at a high frequency, while plant 1 is only visited, and at a very low frequency, by another hummingbird species. If a community is composed majoritarily by interactions with such high complementarity, the community will exhibit high values of complementary specialization (Blüthgen *et al.*, 2006). On the other hand, species C and 4 also interact 155 times, but in this case hummingbird C interacts with many other plant species and has a higher marginal total, lowering the complementary specialization of this pair (p_{C4}=0.36, p_{4C}=1).

We standardized complementary specialization as $H_2' = \frac{H_{2\max} - H_2}{H_{2\max} - H_{2\min}}$, so that H_2' ranges from minimum (H_2'=0) to maximum (H_2'=1) link selectiveness where species establish distinct and highly specific interactions far different than expected interactions (Blüthgen *et al.,* 2006). Thus, H_2' quantifies the deviation of the observed interactions from those expected under a neutral assumption that species' interactions are entirely determined by partner availability. This assumption minimizes the influence of rare interactions by causing frequent interactions to dominate H_2'.

(2) *Quantitative bipartite modularity* (QuanBiMo) is an algorithm which places species among an *a priori* unespecified number of modules, such that species interact at high frequencies within their module, and show few links and/or low frequency links with species

outside their module (Dormann & Strauss, 2014; Schleuning *et al.,* 2014; Fig. 1). Such partition is based on a hierarchical representation of interaction frequencies and optimal allocation of species into modules. Specifically, the algorithm maximizes the bipartite version of Newman's modularity (*Q*), so that $Q=\frac{1}{2N}\Sigma(A_{ij}-K_{ij})\delta(m_i,m_j)$, where *N* reflects the total number of interactions, A_{ij} the normalized number of interactions between species *i* and *j*, K_{ij} the expected interaction probability between species *i* and *j* drawn from a neutral model of interactions, and the indicator function $\delta(m_i,m_j)$ equals 1 when species *i* and *j* are placed in the same module and 0 otherwise. Modularity ranges from no (*Q*=0) to maximum (*Q*=1) modularity. We ran the QuanBiMo algorithm following the methodology established by Schleuning *et al.* (2014) and the default specifications of the *computeModules* function in bipartite, that is, for each network we chose the partition showing highest modularity from five independent runs of the algorithm (Dormann & Strauss, 2014; Schleuning *et al.,* 2014). Variations in the likelihood values of modularity were negligible (all SD<0.05).

As raw values for network metrics may be affected by species frequencies and network connectance, network estimates for complementary specialization and modularity were corrected using null models (Schleuning *et al.*, 2012, 2014; Dormann & Strauss, 2014). Null models simulated matrices with the same number of species and interactions as the empirical network, and with a species' interaction probability distribution drawn from observed species' connectivity (vaznull model in bipartite; Vázquez *et al.,* 2007). Corrected metrics were then calculated as the difference between the value of the empirical network and the mean value obtained from 1000 and 100 null models for H_2' and QuanBiMo, respectively (as in e.g. Schleuning *et al.,* 2012, 2014). As for the calculation of empirical QuanBiMo values, for each of the 100 null matrices we used the maximum value of five independent runs of the QuanBiMo algorithm (Schleuning *et al.,* 2014). By extracting the network structure achieved under null conditions, corrected metrics quantify how much an empirical community departs from an average random one with an equivalent set of species, interactions and interaction probability distribution. Notice that for instance, as Figure 1 illustrates, a corrected value of 0.3 gives no information on the uncorrected values, only that there is a 0.3 difference between observed and null values, e.g. this value can result both from a raw observed value of 0.4 and a mean null value of 0.1 (Fig. 1 community A), and from a raw observed value of 0.5 and a mean null value of 0.2 (Fig. 1 community B), etc.

Analysis of phylogenetic signal in bipartite interaction networks

We measured the phylogenetic signal exhibited by hummingbird-plant networks by quantifying the degree to which closely-related species share more interaction partners than distantly-related species (Ives & Godfray, 2006). Species' interactions are considered to exhibit a higher phylogenetic signal, when closely-related species share relatively more interaction partners than distantly-related species (Ives & Godfray, 2006; Vázquez *et al*., 2009b).

We used state-of-the-art phylogenies of plants and hummingbirds to create variance-covariance matrices, which quantify the phylogenetic relatedness of plants or hummingbirds in each community, using the *"vcv"* function from the R package *ape* (Paradis *et al.,* 2004). We fitted these vcv matrices to each observed bipartite interaction matrix through a linear model using the *"pblm"* function from the R package *picante* (Kembel *et al*., 2010). This analysis results in two independent measures of the strength of the phylogenetic signal, one for plants (d_{plants}) and another for hummingbirds ($d_{hummingbirds}$), together with an overall measure of strength of the model fits for the entire community (measured as mean squared error of the model, MSE). We evaluated three different models, one assuming no phylogenetic signal (d_{plants}=$d_{hummingbirds}$=0; Star model), one assuming a maximum phylogenetic signal (d_{plants}=$d_{hummingbirds}$=1; Brownian model), and a final one which incorporated the observed phylogenetic signals combined (estimated d_{plants} and $d_{hummingbirds}$; Data model). We used the bootstrapping option to calculate confidence intervals for d_{plants} and $d_{hummingbirds}$. Networks where the these confidence intervals did not overlap zero or when the $MSE_{Data} < MSE_{Star}$ were considered to exhibit a significant phylogenetic signal (Ives & Godfray, 2006; Vázquez *et al.*, 2009b). For a list of all species included in this study and a detailed explanation of the phylogenetic analysis, refer to Appendices S1 and S2, respectively.

Environmental variables

We analyzed six variables describing contemporary and historical temperature and precipitation known or hypothesized to affect the structure of pollination networks. Four of the six variables describe contemporary climatic conditions: *mean annual temperature* (MAT, ºC), *temperature seasonality* (TS, standard deviation × 100), *mean annual precipitation* (MAP, mm) and *precipitation seasonality* (PS, coefficient of variation). We obtained these measurements from the WorldClim data set with spatial resolutions of 1 x 1 km (http://www.worldclim.org; see also Hijmans *et al.*, 2005). The historical climate variables, the *velocity of temperature change* and the *velocity of precipitation change,* reflect the speed of temperature and precipitation change between the Last Glacial Maximum (LGM) and pre-industrial times (VT, m/yr; VP, m/yr), following the definition of Loarie *et al.* (2009). Projections of the global climate during the LGM and pre-industry were generated by Hadley Centre Coupled Model Version 3 (HadCM3) with a resolution of 3.75 × 2.5 arc degrees (Singarayer & Valdes, 2010), and were downscaled to 0.1 × 0.1 arc degrees. For each study site, climate estimates were calculated as the average values of all 1 x 1 km grid cells (0.1 × 0.1 arc degrees for paleoclimate data) within a concentric distance of 10 km from the sampling location. Additionally, we scored whether a network was from the mainland (0) or an island

(1).

Macroecological models

We used a multi-model approach based on information theory as outlined in Diniz-Filho *et al*. (2008) to simultaneously evaluate the relationships between species richness, phylogenetic signal and environment and hummingbird-plant network structure. First, for each network metric, we calculated full ordinary least squares (OLS) regression models which included the following ten predictor variables: 1) species richness (network size), 2) the phylogenetic signal in the interaction pattern of plants' (d_{plants}) and 3) hummingbirds' ($d_{hummingbirds}$), 4) annual average temperature, 5) temperature seasonality, 6) annual average precipitation, 7) precipitation seasonality, 8) temperature-change velocity, 9) precipitation-change velocity and 10) insularity. Visually, OLS regression models minimize the distance between observed data points and those predicted by a linear approximation of the data. Second, for each network metric, we used the Akaike Information Criterion (AIC_C) aiming at identifying minimum adequate models (MAMs) among all possible model combinations of our ten predictor variables. MAMs were defined as models exhibiting a differences in AIC_C of at least two points lower than other models (i.e. a $\Delta AIC_C < 2$; Burnham & Anderson, 2002; Diniz-Filho *et al.,* 2008). As no single MAM was identified, often around 10 models had $\Delta AIC_C < 2$, we instead used a multi-model approach. Specifically, instead of calculating regression coefficients in a single best model (MAM), we calculated the overall importance of each model (w_i) as the relative likelihood of any given model *i* over the sum of the likelihoods of the entire dataset of models, such that $w_i = \dfrac{\exp(\frac{-1}{2}\Delta_i)}{\sum_{r=1}^{R}\exp(\frac{-1}{2}\Delta_R)}$, being Δ_i the differences in AIC between the set of *R* models, so that the relative strength of each model depends on the entire set of models. We report the standardized regression coefficients and the overall importance (Σ w_i) of each variable for ordinary least squares OLS regression for an averaged model based on weighted w_i (Burnham & Anderson, 2002; Diniz-Filho *et al.,* 2008), for which we adopted an importance cut-off value of ≥0.750. The standardized regression coefficients were also reported for the OLS regression model including all ten predictor variables ("full" model). For each network metric, we used partial regressions to separate the total, unique and shared variation explained by species richness, phylogenetic signal and environmental factors in the "full" models.

Previous studies suggest that the structure of mainland and island hummingbird-plant and pollination networks may differ (Olesen *et al.*, 2002; Dalsgaard *et al.,* 2009, 2013), and the colonization of the Caribbean by hummingbirds has been considerably more recent than mainland America (*c.* 5 million years ago versus 12-22 million years ago for North and South America, respectively). Consequently insular hummingbirds have had less time for specialization and coevolution with their nectar plants than their mainland counterparts (Bleiweiss, 1998; McGuire *et al.,* 2014). Together with the higher levels of generalization and less modularity predicted for insular pollinator communities (Olesen *et al*., 2002; Dalsgaard *et al.,* 2013), and a high level of periodic disturbances characteristic of Caribbean communities which may hinder high levels of specialization on islands (Graves & Olsen, 1987; Rivera-Marchand & Ackerman, 2006), the relationship between species richness, phylogenetic signal and environmental factors and network structure may differ between mainland and insular communities. For instance, the influence of historical climate change may be weaker on islands than on the mainland (Dalsgaard *et al.*, 2013, 2014). Our dataset contains too few island networks (n=9) to allow for a separate analysis for insular networks, hence, we explored putative differences in mainland and island networks by analyzing a subset of the dataset composed exclusively by networks from the mainland (Mainland, n=45 networks) and comparing these results to those of the entire dataset (Global dataset, which includes both mainland and insular communities, n=54 networks).

For all macroecological models, we $\log_{10}$-transformed species richness, temperature seasonality, temperature velocity, and precipitation velocity; we squared temperature, and square-root transformed precipitation. All other variables were left untransformed. In all spatial models we tested whether significant positive spatial autocorrelation remained in model residuals of the “full” models (i.e., whether $p<0.05$ in all distance classes, tested using 10 equally-spaced distance classes and applying a permutation test with 10,000 iterations). As no positive spatial autocorrelation was observed we did not build more sophisticated spatial models. All regression analyses were conducted using the software Spatial Analysis in Macroecology, SAM 4.0 (Rangel *et al.,* 2010).

To better support our findings, we performed a number of complementary macroecological models which included sampling effort as a predictor variable (Appendix S3), observed (uncorrected) metrics of network structure instead of null model corrected metrics (Appendix S4), and climate anomaly as a measure of historical climate stability instead of climate change velocity (Appendix S5).

RESULTS

Phylogenetic signal on species interaction patterns

Values for the independent phylogenetic signals of plants (d_{plants}) and hummingbirds ($d_{\text{hummingbirds}}$) were low but above zero in 85 and 65% of the networks, respectively, suggesting a significant relationship between phylogenetic signal and species interaction patterns. The confidence intervals (CI) of $d_{\text{hummingbirds}}$ overlapped with zero in a higher number of networks than did CIs of d_{plants} (82 and 57%; Table in Appendix S2), indicating that the significant association between phylogeny and interaction patterns was exhibited mostly by plant species.

We examined the overall association between phylogeny and the structure of bipartite interaction networks by comparing the mean squared error (MSE) of the model fit among models adjusted after observed phylogenetic signal (MSE_{data}), models which assumed no phylogenetic signal (MSE_{star}), and models which assume a maximum signal ($MSE_{Brownian}$). Results showed that most networks exhibited a significant phylogenetic signal (in 52 networks MSE_{data}<MSE_{star}, in 1 networks MSE_{data}=MSE_{star}, and in 1 MSE_{data}>MSE_{star}; in all cases $MSE_{Brownian}$ had clearly the highest values; Table in Appendix S2), e.g. in most communities the model which fitted best to the data (the one having the lowest error) was achieved when adjusting the model with observed phylogenetic signals of plants and hummingbirds (MSE_{data}). Nevertheless, most differences between MSE_{data} and MSE_{star} were small, and much smaller than between MSE_{data} and $MSE_{Brownian}$, indicating that in general, the association between phylogenetic signal and species interaction pattern was weak.

Macroecological models

Full OLS models on corrected network metrics were able to account for 54%-62% of the observed variation in network metrics across the sampled communities (Table 1, Table S3, Fig. 3). Species richness and environmental factors showed the strongest association with network structure, although with varying strengths across the "Global" and "Only Mainland" datasets and network metrics (Table 1, Table S3, Figure S1). On the contrary, the associations between phylogenetic signal and network structure remained constant, exhibiting low regression coefficients in both metrics and datasets (Table 1, Table S3). Collectively, complementary specialization exhibited a stronger association with current temperature and historical temperature stability, and to a lesser extent with species richness; whereas species richness had the strongest association with modularity (Fig. 3; Table S3).

When the ten predictor variables included in the full OLS models were examined in detail, species richness and hummingbird phylogenetic signal were the only variables showing an important, spatially consistent and widespread association to network structure, emerging as highly important for both network metrics and datasets. Species richness showed a strong positive relationship with complementary specialization and modularity (Table 1). On the contrary, a higher phylogenetic signal among hummingbirds was related with a lower complementary specialization and level of modularity. In other words, despite the association between phylogenetic signal and species' interaction pattern was weak and the weighted regression coefficients of $d_{\text{hummingbirds}}$ were low, complementary specialization and modularity consistently increased when closely-related hummingbirds visited distinct arrays of plant species (Table 1, Table S3, Fig. 3).

Complementary specialization was also highly associated with the environmental conditions, as the total variation explained by environmental factors was consistently higher than the variation attributed to species richness and phylogenetic signal in both the "Global" and "Only Mainland" datasets, and approximated to the variation explained by the full models (Table S3, Fig. 3). The amount of unique variation (i.e. variation explained exclusively by the predictor-type) explained by environmental factors was similar to the unique variation explained by species richness on the Global dataset (Table S3, Fig. 3). However, when examining only mainland networks, the unique variation explained by environmental factors was two times greater than the unique variation explained by the other two predictor-types (Table S3, Fig. 3). Among the seven environmental variables examined, only current temperature and historical temperature stability showed a strong relationship with complementary specialization, with increasing complementary specialization in communities with current warmer temperatures and with a higher historical temperature stability (Table 1).

Quantitative bipartite modularity showed the strongest association with species richness, particularly in the global dataset, with environmental conditions having a similar strength association among mainland communities (Table S3, Fig. 3).

Shared variability among species richness and phylogenetic signal (i.e. variability explained by these two predictor types) was non-existent, i.e. richness and phylogenetic signal were distinctly associated to specialization and modularity. Shared variability between environmental factors and species richness or phylogenetic signal was low (Table S3).

The remaining five environmental variables (insularity, temperature seasonality, mean annual precipitation, precipitation seasonality, and precipitation change velocity) as well as phylogenetic signal in the interaction pattern of plants, showed no important associations with null model corrected network structure (Table 1).

DISCUSSION

As previous macroecological studies of interaction networks, we found complementary specialization and modularity to vary along with environmental conditions and species richness. Additionally, for the first time, we report an association between phylogenetic signal and network structure at macroecological scale. Specifically, species richness and phylogenetic signal in hummingbird interaction patterns were the two predictor variables that associated most consistently to network structure, with an association between complementary specialization and current and historical temperature conditions limited to mainland networks.

Hummingbird phylogenetic signal had a constant association with both complementary specialization and modularity, and on both the Global and Only Mainland datasets, although the variability associated with phylogenetic signal was the lowest of all predictor types. A weak but significant relationship between phylogenetic signal and species' interaction pattern within ecological networks has also been reported by previous studies on food webs, host-parasite networks or plant-pollinator networks (Ives & Godfray, 2006; Vázquez *et al.,* 2009b;

Krasnov *et al.,* 2012; Rafferty & Ives, 2013). These studies also identified asymmetries in the phylogenetic signal between trophic levels, with the association between phylogenetic relatedness and species interaction pattern being stronger at lower trophic levels, i.e. plants in our system (but see Rezende *et al.,* 2007). According to these studies, such asymmetries may stem from a differential relationship between phylogeny and the interaction pattern of each trophic group, as species from the higher trophic group (“consumer” species) are more likely to adjust their feeding behavior according to local conditions. Our results corroborate this hypothesis: hummingbird phylogenetic signal showed a weaker relationship with their interaction pattern than plant species ($d_{hummingbirds}$ tends to be lower than d_{plants}, and CI $d_{hummingbirds}$ overlap with zero in more networks). Nevertheless, and unlike for plants which showed no association to the spatial variation in network structure, hummingbird phylogenetic signal was associated to network structure, with higher levels of complementary specialization and modularity consistently achieved when closely-related hummingbird species visited distinct sets of flowering plant species. This suggests that resource partitioning and inter-specific competition among closely-related hummingbirds might play an important role in structuring interactions in hummingbird-plant networks. Indeed, inter-specific competition is known to be strong among hummingbirds, and has been noted as a potential driver of patterns of hummingbird biodiversity (Brown & Bowers, 1985; Bleiweiss, 1998; Cotton, 1998).

Species richness had the strongest association with both metrics and in both the Global and Only Mainland datasets except for complementary specialization in the mainland. Higher species richness may result in a higher niche availability, thus providing ample opportunities for biotic specialization. At the same time, higher species richness may increase inter-specific competition, which may explain why high species richness lead to higher levels of complementary specialization and modularity (Rezende *et al.*, 2009; Dalsgaard *et al.*, 2011; Krasnov *et al.,* 2012; Junker *et al.*, 2013). Moreover, a higher plant richness may also translate into a temporally-stable availability of floral resources (or the establishment of a constant minimum local flower supply), enabling a locally constant hummingbird population and, hence, potential for biotic specialization (Montgomerie & Gass, 1981; Stiles, 1985; Araujo & Sazima, 2003; Cotton, 2007; Abrahamczyk *et al.*, 2011).

In the mainland, higher levels of complementary specialization were also found in warmer areas and in areas with higher historical temperature stability. The former may again be linked to higher inter-specific competition in warmer areas, and particularly in mainland settings, where hummingbird species and phylogenetic richness is highest (Bleiweiss, 1998; McGuire *et al.*, 2014). This relationship might be stronger on the mainland as insular pollinator faunas are typically depauperate (Olesen *et al.,* 2002). Moreover, in historically stable climates, hummingbirds have been able to establish long-term associations with plants, which may lead to higher levels of local adaptation, interaction specificity and specialization (see Dalsgaard *et al.*, 2011 for a study on a subset of the networks from the dataset used here). Such long associations may lead to higher complementary specialization in areas with low temperature-change velocity, such as montane habitats and tropical environments, leaving more generalized interaction patterns to areas with low topography and especially at higher latitudes where changes in temperature velocity have been greatest (Sandel *et al.*, 2011). Moreover, a higher complementary specialization in areas of high historical temperature stability is consistent with general hummingbird historical biogeography and speciation patterns, as the core area of hummingbird speciation and diversity occurs in Andean highland and in tropical lowland South-America (Brown & Bowers, 1985; Bleiweiss, 1998; McGuire *et al.,* 2014). We note that complementary macroecological analysis presented in Appendices S3-S5 generally confirmed the importance of species richness and hummingbird phylogenetic signal, and, additionally, showed an association between observed (uncorrected) complementary specialization/modularity and insularity and precipitation, with areas of high precipitation and mainland communities showing higher observed complementary specialization and modularity. Precipitation has previously been shown to influence both phenotypcal and network specialization of hummingbird-plant interactions and of entire pollination communities (Cruden, 1972; Dalsgaard *et al.*, 2009; Martín González *et al.*, 2009). The fact that precipitation and insularity only associated with observed complementary specialization and observed modularity and not with null model corrected values of these network metrics, may indicate that insularity and precipitation do not directly influence the interaction pattern of species, but rather associate indirectly with network structure through species richness and/or interaction probability distributions.

CONCLUSIONS

Characterizing potential ecological, evolutionary and environmental mechanisms associated with the structure of ecological communities is a critical first step towards understanding the determinants of community assembly and how climate-change may affect biodiversity (Woodward *et al.*, 2010; Schleuning *et al.*, 2014). By examining null model corrected network metrics, we are actively investigating how much observed communities depart from random ones with an equivalent set of species and interactions. Hence, we were able to investigate not only whether a community presents a structure which differs significantly from random, but also to associate the difference in complementary specialization and modularity to species richness, evolutionary history, and environmental conditions.

We have shown that complementary specialization and modularity in hummingbird-plant networks associate to species richness, hummingbird phylogenetic signal and environmental factors acting at varying spatio-temporal scales and in different aspects of network structure. Notably, species richness and hummingbird phylogenetic signal showed a consistent association with network structure, with a more restricted but still important role of contemporary temperature and historical temperature stability, which were only important among mainland communities. These results are markedly different to the ones for avian seed-dispersal networks for which species' phylogeny and historical climatic stability were unrelated to modularity and complementary specialization (Schleuning *et al.*, 2012, 2014; Sebastián González *et al.*, 2015). Such difference suggests that hummingbirds and flowers engage in tighter co-evolutionary associations than frugivore birds and their plants, and hence, historical and evolutionary factors may have a stronger role in hummingbird-plant assemblages than for frugivore birds-plant assemblages.

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REFERENCES

Abrahamczyk, S., Kluge, J., Gareca, Y., Reichle, S & Kessler, M. (2011) The influence of climatic seasonality on the diversity of different tropical pollinator groups. *PloS ONE*, **6**, e27115.

Araujo, A.C. & Sazima, M. (2003) The assemblage of flowers visited by hummingbirds in the "capões" of Southern Pantanal, Mato Grosso do Sul, Brazil. *Flora*, **198**, 427–435.

Bleiweiss, R. (1998) Origin of hummingbird faunas. *Biological Journal of the Linnean Society*, **6**, 77–97.

Blüthgen, N., Menzel, F. & Blüthgen, N. (2006) Measuring specialization in species interaction networks. *BMC Ecology,* 6:9.

Blüthgen, N. (2010). Why network analysis is often disconnected from community ecology: a critique and an ecologist's guide. *Basic and Applied Ecology*, **11**(3), 185-195.

Brown, J.H. & Bowers, M.A. (1985) Community organization in hummingbirds: relationships between morphology and ecology. *The Auk,***102**, 251–269.

Burnham, K.P. & Anderson, D.R. (2002) *Model Selection and Multimodel Inference: A Practical Information-Theoretic Approach* (2nd ed.), Springer-Verlag, New York.

Cotton, P.A. (1998) Coevolution in an Amazonian hummingbird-plant community. *Ibis,* **140**, 639-646.

Cotton, P.A. (2007) Seasonal resource tracking by Amazonian hummingbirds. *Ibis*, **149**, 135–142.

Cruden, R.W. (1972) Pollinators in high-elevation ecosystems: relative effectiveness of birds and bees. *Science*, **176,** 1439–1440.

Dalsgaard, B., Martín González, A.M., Olesen, J.M., Ollerton, J., Timmermann, A., Andersen, L. H. & Tossas, A. (2009) Plant–hummingbird interactions in the West Indies: floral specialisation gradients associated with environment and hummingbird size. *Oecologia,* ***159,*** 757–766.

Dalsgaard, B., Magård, E., Fjeldså, J., Martín González, A.M., Rahbek, C., Olesen, J.M., et al. (2011) Specialization in plant-hummingbird networks is associated with species richness, contemporary precipitation and quaternary climate-change velocity. *PloS ONE,* **6**, e25891.

Dalsgaard, B., Trøjelsgaard, K., Martín González, A.M., Nogués-Bravo, D., Ollerton, J., Petanidou, T., et al. (2013) Historical climate-change influences modularity and nestedness of pollination networks. *Ecography*, **36,** 1331–1340.

Dalsgaard, B., Carstensen, D.W., Fjeldså, J. Maruyama, P.K., Rahbek, C., Sandel, B., Sonne, J., Svenning, J.C., Wang, Z. & Sutherland, W.J. (2014) Determinants of bird species richness, endemism, and island network roles in Wallacea and the West Indies: is geography sufficient or does current and historical climate matter? *Ecology and Evolution*, **4**, 4019–4031.

Diniz-Filho, J.A.F., Rangel, T.F. L. & Bini, L.M. (2008) Model selection and information theory in geographical ecology. *Global Ecology and Biogeography*, **17,** 479–488.

Dormann, C.F. & Strauss, R. (2014) A method for detecting modules in quantitative bipartite networks: the QuanBiMo algorithm. *Methods in Ecology and Evolution*, **5**, 90–98.

Dormann, C.F., Fründ, J., Blüthgen, N. & Gruber, B. (2009) Indices, graphs and null models: analyzing bipartite ecological networks. *Open Ecology Journal*, **2**, 7–24.

Graves, G.R. & Olsen, S.L. (1987) *Chlorostilbon bracei lawrence*, an extinct species of hummingbird from New Providence Island, Bahamas. *Auk*, **104,** 296–302.

Hijmans, R.J., Cameron, S.E., Parra, J.L., Jones, P.G. & Jarvis, A. (2005) Very high resolution interpolated climate surfaces for global land areas. *International Journal of Climatology*, **25,** 1965–1978.

Ives, A.R. & Godfray, H.C.J. (2006) Phylogenetic analysis of trophic associations. *American Naturalist*, **168,** E1–E14.

Junker, R.R., Blüthgen, N., Brehm, T., Binkenstein, J., Paulus, J., Martin Schaefer, H., et al. (2013) Specialization on traits as basis for the niche-breadth of flower visitors and as structuring mechanism of ecological networks. *Functional Ecology*, **27**, 329–341.

Kembel, S.W., Cowan, P.D., Helmus, M.R., Cornwell, W.K., Morlon, H., Ackerly, D.D., et al. (2010) Picante: R tools for integrating phylogenies and ecology. *Bioinformatics*, **26,** 14631464.

Krasnov, B. R., Fortuna, M. A., Mouillot, D., Khokhlova, I. S., Shenbrot, G. I. & Poulin, R. (2012) Phylogenetic signal in module composition and species connectivity in compartmentalized host-parasite networks. *American Naturalist*, **179**, 501–511.

Loarie, S.R., Duffy, P.B., Hamilton, H., Asner, G.P., Field, C.B. & Ackerly, D.D. (2009) The velocity of climate change. *Nature*, **462,** 1052–1055.

Martín González, A.M., Dalsgaard, B., Ollerton, J., Timmermann, A., Olesen, J.M., Andersen, L. & Tossas, A. (2009) Effects of climate on pollination networks in the West Indies. *Journal of Tropical Ecology*, **25,** 493–506.

Martín González, A.M., Allesina, S., Rodrigo, A., & Bosch, J. (2012). Drivers of compartmentalization in a Mediterranean pollination network. *Oikos*, **121**(12), 2001-2013.

Maruyama, P.K., Vizentin-Bugoni, J., Oliveira, G.M., Oliveira, P.E. & Dalsgaard, B. (2014) Morphological and spatio-temporal mismatches shape a Neotropical savanna plant-hummingbird network. *Biotropica*, **46,** 740–747.

McGuire, J.A., Witt, C.C., Remsen, J.V., Jr., Corl, A., Rabosky, D.L., Altshuler, D.L., et al. (2014) Molecular phylogenetics and the diversification of hummingbirds. *Current Biology*, **24**, 910–916.

Montgomerie, R.D. & Gass, C.L. (1981) Energy limitations of hummingbird populations in tropical and temperate communities. *Oecologia,* **50**, 162–165.

Olesen, J.M., Eskildsen, L.I. & Venkatasamy, S. (2002) Invasion of pollination networks on oceanic islands: importance of invader complexes and endemic super generalists. *Diversity and Distributions*, **8**, 181–192.

Paradis, E., Claude, J., & Strimmer, K. (2004) APE: analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20,** 289–290.

Rafferty, N.E. & Ives, A.R. (2013) Phylogenetic trait-based analyses of ecological networks. *Ecology*, **94,** 2321–2333.

Rangel, T.F., Diniz-Filho, J.A.F. & Bini, L.M. (2010) SAM: a comprehensive application for spatial analysis in macroecology. *Ecography*, **33,** 46–50.

Rezende, E.L., Albert, E.M., Fortuna, M.A. & Bascompte, J. (2009) Compartments in a marine food web associated with phylogeny, body mass, and habitat structure. *Ecology Letters*, **12,** 779–788.

Rezende, E.L., Jordano, P. & Bascompte, J. (2007) Effects of phenotypic complementarity and phylogeny on the nested structure of mutualistic networks. *Oikos*, **116,** 1919–1929.

Rivera-Marchand, B. & Ackerman, J.D. (2006) Bat pollination breakdown in the Caribbean columnar cactus *Pilosocereus royenii*. *Biotropica*, **38,** 635–642.

Sandel, B., Arge, L., Dalsgaard, B., Davies, R.G., Gaston, K.J., Sutherland, W.J. & Svenning, J.-C. (2011) The influence of late Quaternary climate-change velocity on species endemism. *Science*, **334**, 660–664.

Schleuning, M., Fründ, J., Klein, A. M., Abrahamczyk, S., Alarcón, R., Albrecht, M.,et al. (2012) Specialization of mutualistic interaction networks decreases toward tropical latitudes. *Current Biology*, **22,** 1925–1931.

Schleuning, M., Ingmann, L., Strauss, R., Fritz, S.A., Dalsgaard, B., Matthias Dehling, D., et al. (2014) Ecological, historical and evolutionary determinants of modularity in weighted seed-dispersal networks. *Ecology Letters,* **17**, 454–463.

Sebastián González , E., Dalsgaard, B., Sandel, B. & Guimarães, P. (2015). Macroecological trends in nestedness and modularity of seed-dispersal networks: human impact matters. *Global Ecology and Biogeography*, **24,** 293–303.

Singarayer, J.S., & Valdes, P. J. (2010) High-latitude climate sensitivity to ice-sheet forcing over the last 120 kyr. *Quaternary Science Reviews*, **29,** 43–55.

Stiles, G.F. (1985) Seasonal patterns and coevolution in the hummingbird-flower community of a Costa Rican subtropical forest. *Ornithological Monographs*, **36**, 757–785.

Stouffer, D.B. & Bascompte, J. (2011) Compartmentalization increases food-web persistence. *Proceedings of the National Academy of Science USA*, **108**, 3648-3652.

Thébault, E., & Fontaine, C. (2010). Stability of ecological communities and the architecture of mutualistic and trophic networks. *Science*, **329**(5993), 853-856.

Trøjelsgaard, K. & Olesen, J.M. (2013) Macroecology of pollination networks. *Global Ecology Biogeography*, **22,** 149–162.

Vázquez, D.P., Melian, C.J., Williams, N.M., Blüthgen, N., Krasnov, B.R. & Poulin, R. (2007) Species abundance and asymmetric interaction strength in ecological networks. *Oikos,* **116**, 1120–1127.

Vázquez, D.P., Blüthgen, N., Cagnolo, L. & Chacoff, N.P. (2009a) Uniting pattern and process in plant–animal mutualistic networks: a review. *Annals of Botany*, **103,** 1445–1457.

Vázquez, D.P., Chacoff, N.P. & Cagnolo, L. (2009b) Evaluating multiple determinants of the structure of plant-animal mutualistic networks. *Ecology,* **90**, 2039–2046.

Webb, C.O., Ackerly, D.D., McPeek, M.A. & Donoghue, M.J. (2002) Phylogenetics and community ecology. *Annual Review of Ecology and Systematics*, **33,** 475–505.

Williams, R.J. (2010) *Network3D Software*. Microsoft Research, Cambridge, UK.

Woodward, G., Benstead, J.P., Beveridge, O.S., Blanchard, J., Brey, T., Brown, L., et al. (2010) Ecological networks in a changing climate. *Advanced Ecological Research,* **42,** 71–138.

Yoon, I., Williams, R.J., Levine, E., Yoon, S., Dunne, J.A. & Martinez, N.D. (2004) *Webs on the Web (WoW): 3D visualization of ecological networks on the WWW for collaborative research and education.* Proceedings of the IS&T/SPIE Symposium on Electronic Imaging, Visualization and Data Analysis, 5295, 124-132.

Biosketch: This work results from an ongoing collaboration among numerous researchers from different scientific backgrounds and institutions, who have gathered an extensive dataset of hummingbird plant interaction networks and complementary data on species traits, phylogeny, climate, etc. Such multidisciplinary information is allowing us to study in depth different aspects of hummingbird-plant interaction patterns at macroecological scales, and to identify potential mechanisms responsible for them. Our ultimate goal is to describe general macroecological patterns in biotic interactions using hummingbird-plant interactions as a model system.

Table 1. Relationship between species richness, phylogenetic signal and environment, and complementary specialization (*H_2'*) and modularity (QuanBiMo) across the Americas (Global dataset) and the mainland, i.e. when excluding insular communities (Only Mainland). Complementary specialization measures the exclusiveness of the interactions in the community, whereas modularity quantifies whether species interact more frequently with subsets of available species within a community. For each network metric, the standardized regression coefficients are reported for ordinary least squares regression for a model including all variables ("Full") and for a model averaged across all possible models using Akaike Weights (AICc w_i - "Averaged"). For the averaged models, the relative importance of each predictor variable ("Σw_i") is given by the Akaike Weights (AICc w_i). Predictors with high importance are marked in bold. Phylogenetic signal among plants and hummingbirds, d_p and d_h, respectively; Mean annual temperature, MAT; Temperature seasonality, TS; Mean annual precipitation, MAP; Precipitation seasonality, PS; Velocity of temperature change since the last Glacial Maximum, MAT velocity; Velocity of precipitation change since the last Glacial Maximum, MAP velocity. The significance of Moran's *I* was tested with 10 distance classes and a permutation test with 10,000 iterations. In all models multicollinearity was not an issue, i.e. VIF ≤ 3.4, CN ≤ 4.0, and there was no positive spatial autocorrelation, i.e. Moran's *I* was non-significant.

					Species richness	**Phylogenetic signal**		**Environmental factors**						
		Model	**AICc**	**R^2**	**Network size**	**d_p**	**d_h**	**Insularity**	**MAT**	**TS**	**MAP**	**PS**	**MAT velocity**	**MAP velocity**
Global dataset (54 networks)	***H_2'***	Full	-54.368	0.543	**0.461**	-0.087	**-0.303**	-0.222	0.284	0.176	0.045	-0.209	-0.475	0.190
		Averaged			**0.520**	-0.143	**-0.361**	-0.121	0.137	0.121	0.085	-0.217	-0.270	0.106
		Σw_i			**0.999**	0.380	**0.962**	0.283	0.308	0.311	0.259	0.603	0.671	0.290
	QuanBiMo	Full	-99.867	0.638	**0.638**	-0.145	**-0.232**	-0.187	0.188	0.081	-0.003	-0.204	-0.132	-0.098
		Averaged			**0.652**	-0.183	**-0.283**	-0.137	0.080	0.058	0.097	-0.184	-0.098	-0.134
		Σw_i			**1.000**	0.619	**0.915**	0.341	0.257	0.237	0.286	0.567	0.288	0.392
Only Mainland (45 networks)	***H_2'***	Full	-55.244	0.581	**0.326**	-0.042	**-0.332**	na	**0.477**	0.125	-0.085	-0.261	**-0.714**	0.307
		Averaged			**0.324**	-0.048	**-0.358**	na	**0.451**	0.110	-0.044	-0.241	**-0.653**	0.359
		Σw_i			**0.807**	0.198	**0.919**	na	**0.854**	0.258	0.227	0.606	**0.931**	0.776
	QuanBiMo	Full	-76.885	0.567	**0.539**	-0.174	**-0.283**	na	0.289	0.046	-0.079	-0.248	-0.289	-0.093
		Averaged			**0.544**	-0.184	**-0.300**	na	0.231	0.021	0.096	-0.232	-0.237	-0.127
		Σw_i			**0.999**	0.476	**0.805**	na	0.414	0.201	0.257	0.592	0.427	0.304

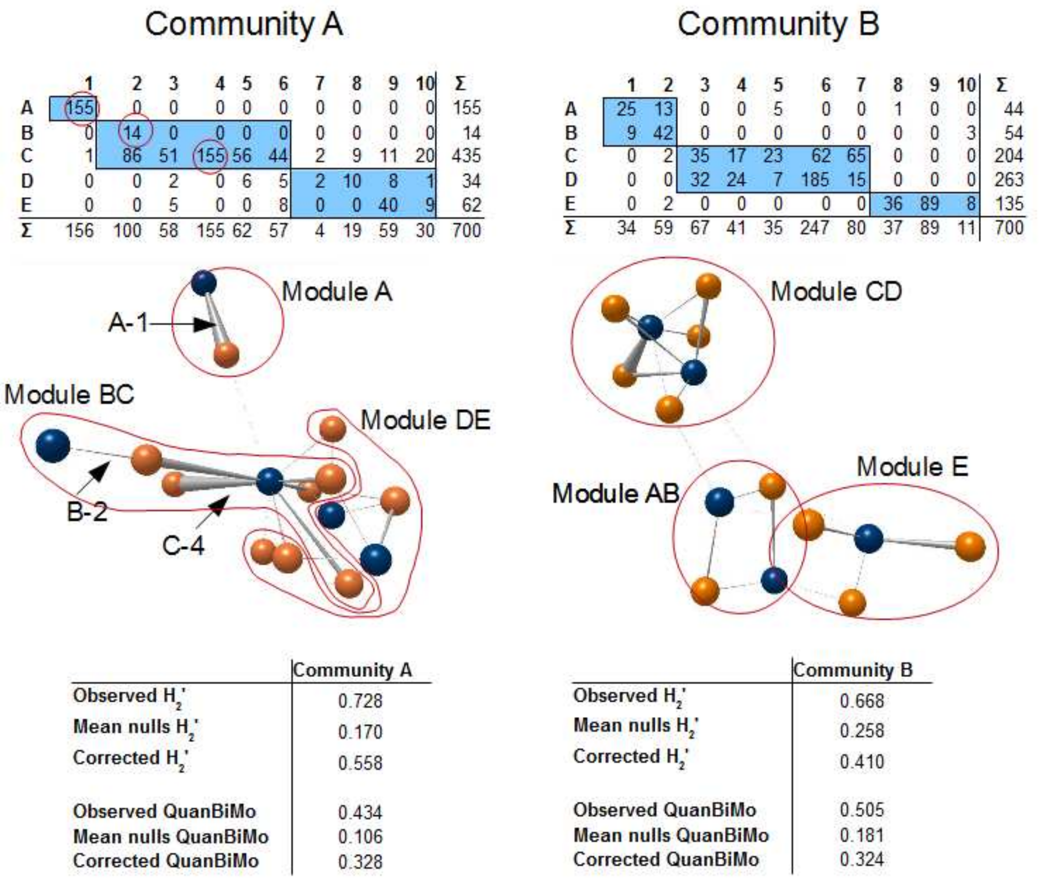
Figure 1. Cartoon illustrations depicting two different communities and the characteristics and relationship between complementary specialization (H_2') and quantitative bipartite modularity (QuanBiMo). Both communities depict 700 interaction events between 10 plants and 5 pollinators. Plants are labeled as numbers 1-10 in the matrix and as yellow nodes in the network representation, and pollinators by letters A-E in the matrix and as blue nodes in the network. Differences in interaction frequencies between plants and pollinators are illustrated as numbers of interaction events in the matrix format and as varying line widths in the network illustration. Complementary specialization measures the exclusiveness in species' interactions, whereas modularity quantifies whether species interact more frequently with subsets of available species within a community. Community A exhibits a moderate complementary specialization, with different species-pairs exhibiting various degrees of complementary specialization. For instance, species-pair A-1 shows a high complementary specialization, as hummingbird A visits exclusively and with high frequency (155 times) plant 1, which in turn is only visited once by another hummingbird. On the other hand, the complementary specialization or pair E-4 is lower than for the previous pair despite these species interact with the same frequency because hummingbird E also interacts with other plant species, i.e. the interaction E-4 is less exclusive. Interactions in community B are also somewhat specialized (species favored interactions with few of the available partners), but the exclusiveness of these interactions is lower than for community A. Both communities show very similar values for corrected modularity and can be divided into three distinct modules, although the modules are composed of a different array of species. By having different degree of complementary specialization but similar values of modularity, these communities show that although these metrics are positively related, measure complementary but different aspects of specialization. Network drawings were created using Network3D and energized with the 3D Force-directed algorithm to enhance visualization of modularity patterns (Yoon et al. 2004, Williams 2010).

Figure 2. Map of the American continent showing the location of the 54 study sites and a number of example networks located along a species richness gradient. Localities with darker shades of green denote networks with a higher richness. Some networks have been slightly moved horizontally to maximize visualization (exact coordinates of the localities on Table S1). For each illustrated network, the reference number and a concise description of the vegetation type is given, along with a network drawing. For the network drawings, blue and yellow nodes depict hummingbird and plant species, respectively, while line width depicts log+1 frequency of interaction among species. Notice that species-rich networks in general present more complex structures, with networks 11, 21 and 50 exhibiting the lowest corrected complementary specialization; networks 50, 11 and 21 the lowest corrected modularity; networks 53, 12 and 4 the highest corrected complementary specialization; and networks 10, 53 and 4 the highest corrected modularity, respectively. Complementary specialization measures the exclusiveness in species' interactions, whereas modularity quantifies whether species interact more frequently with subsets of available species within a community. Network drawings were created using Network3D and energized with the 3D Force-directed algorithm to enhance visualization of modularity patterns (Yoon et al. 2004, Williams 2010). The grey shading of the background illustrates altitude, with darker shades depicting higher altitudes.

Figure 3. Coefficients of determination (R^2) for complementary specialization and modularity obtained from partial regression of full models, i.e. in models including all ten predictor variables (see Table 1 for standardized coefficients of each variable and more details of model fit, and Table S3 for the R^2 values used in this figure). Complementary specialization measures the exclusiveness in species' interactions, whereas modularity quantifies whether species interact more frequently with subsets of available species within a community. We represent values for all networks in the study (Global dataset; n=54) and excluding insular communities (Only Mainland; n=45). Bars illustrate the association between the different

"predictor-types" and network structure. Predictor-types refers to (a) species richness (one variable), (b) phylogenetic signal (two variables: phylogenetic signal in the interaction pattern of plants and hummingbirds), and (c) environmental factors (eight variables: insularity, average annual temperature, temperature seasonality, total annual precipitation, precipitation seasonality, temperature and precipitation-change velocity between the Last Glacial Maximum and the present). The amount of variation explained by each pooled predictor-type is color-coded with different shades of blue: bars colored in darkest blue depict the overall variation explained by all factors together, whereas medium-blue illustrate the total variation explained by that predictor-type, and light-blue the unique variation explained by each predictor-type and not shared by other variable-types. H_2', complementary specialization; QuanBiMo, quantitative bipartite modularity.

Figure 1.



Community A

	1	2	3	4	5	6	7	8	9	10	Σ
A	155	0	0	0	0	0	0	0	0	0	155
B	0	14	0	0	0	0	0	0	0	0	14
C	1	86	51	155	56	44	2	9	11	20	435
D	0	0	2	0	6	5	2	10	8	1	34
E	0	0	5	0	0	8	0	0	40	9	62
Σ	156	100	58	155	62	57	4	19	59	30	700

Community B

	1	2	3	4	5	6	7	8	9	10	Σ
A	25	13	0	0	5	0	0	1	0	0	44
B	9	42	0	0	0	0	0	0	0	3	54
C	0	2	35	17	23	62	65	0	0	0	204
D	0	0	32	24	7	185	15	0	0	0	263
E	0	2	0	0	0	0	0	36	89	8	135
Σ	34	59	67	41	35	247	80	37	89	11	700

	Community A
Observed H_2'	0.728
Mean nulls H_2'	0.170
Corrected H_2'	0.558
Observed QuanBiMo	0.434
Mean nulls QuanBiMo	0.106
Corrected QuanBiMo	0.328

	Community B
Observed H_2'	0.668
Mean nulls H_2'	0.258
Corrected H_2'	0.410
Observed QuanBiMo	0.505
Mean nulls QuanBiMo	0.181
Corrected QuanBiMo	0.324

Figure 2.

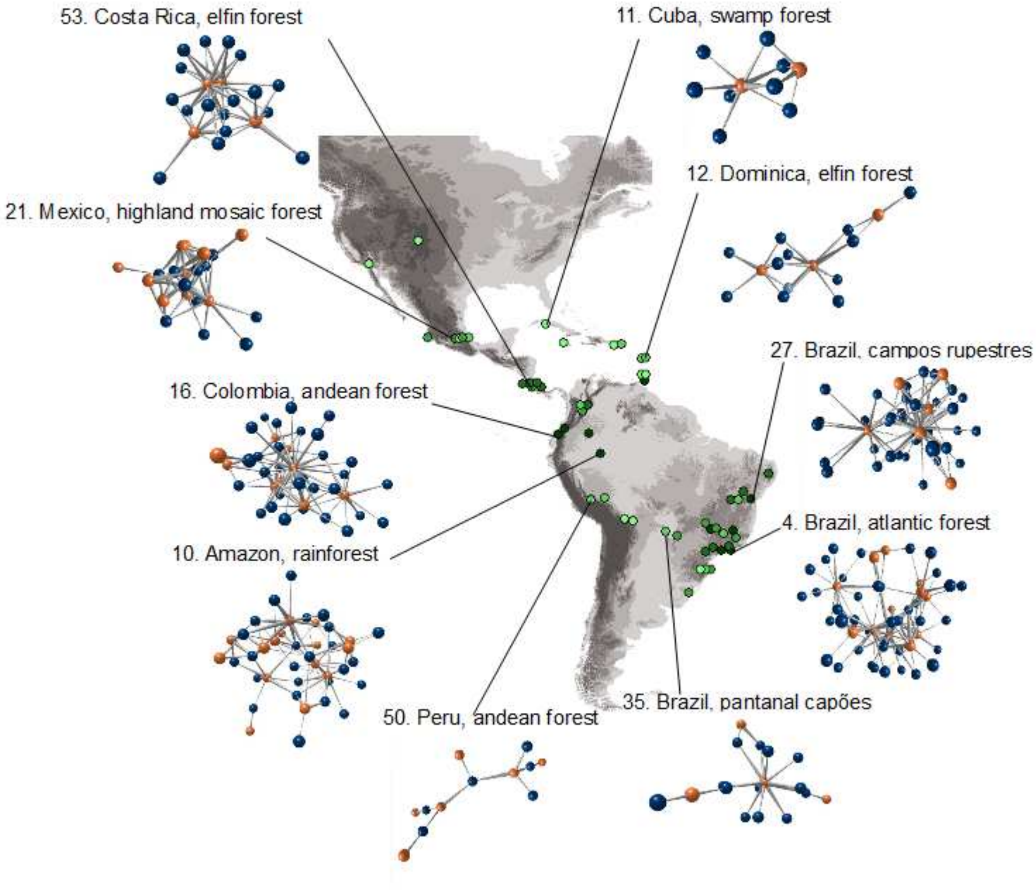
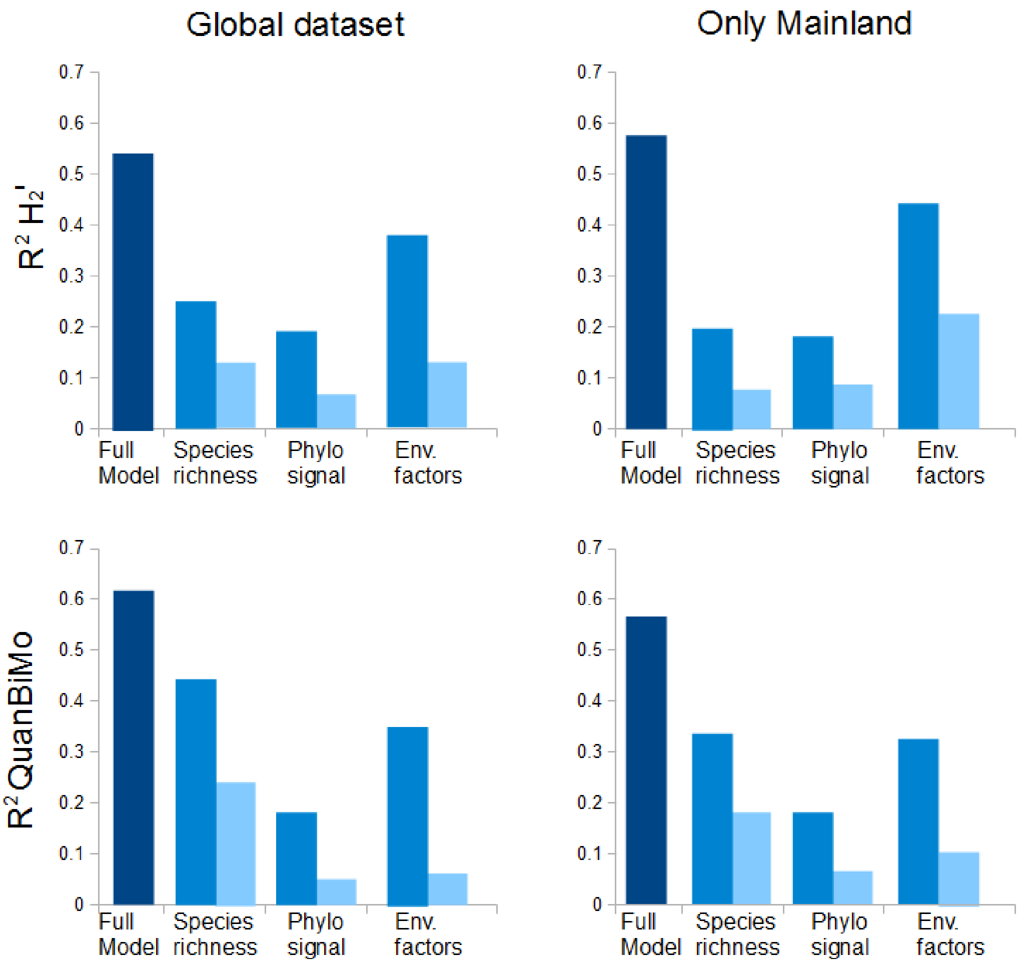

53. Costa Rica, elfin forest
11. Cuba, swamp forest
12. Dominica, elfin forest
21. Mexico, highland mosaic forest
27. Brazil, campos rupestres
16. Colombia, andean forest
4. Brazil, atlantic forest
10. Amazon, rainforest
35. Brazil, pantanal capões
50. Peru, andean forest

Figure 3.


Global dataset
Only Mainland
R^2 H_2'
R^2 QuanBiMo
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Full Model
Species richness
Phylo signal
Env. factors

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Appendix S1. List of all plant and hummingbird species present in the studied networks.

Plant species

Family	Plant Species
Acanthaceae	*Anisacanthus brasiliensis* Lindau
Acanthaceae	*Aphelandra aurantiaca* (Scheidw.) Lindl.
Acanthaceae	*Aphelandra colorata* (Vell.) Wassh.
Acanthaceae	*Aphelandra macrostachya* Nees
Acanthaceae	*Aphelandra sp. 1*
Acanthaceae	*Aphelandra sp. 2*
Acanthaceae	*Aphelandra storkii* Leonard
Acanthaceae	*Dicliptera pohliana* Nees
Acanthaceae	*Dicliptera squarrosa* Nees
Acanthaceae	*Geissomeria longiflora* Lindl.
Acanthaceae	*Geissomeria schottiana* Nees
Acanthaceae	*Geissomeria sp.*
Acanthaceae	*Justicia brasiliana* Roth
Acanthaceae	*Justicia candicans* (Nees) L.D.Benson
Acanthaceae	*Justicia carnea* Lindl.
Acanthaceae	*Justicia cuatrecasasii* Wassh.
Acanthaceae	*Justicia scheidweileri* V.A.W. Graham
Acanthaceae	*Justicia sebastianopolitanae* Profice
Acanthaceae	*Justicia secunda* Vahl
Acanthaceae	*Justicia sp. 1*
Acanthaceae	*Justicia sp. 2*
Acanthaceae	*Justicia tenuistachys* (Rusby) Wassh. & J.R.I. Wood
Acanthaceae	*Mendoncia sp.*
Acanthaceae	*Mendoncia coccinea* Ruiz & Pav.
Acanthaceae	*Odontonema barleriodes* Kuntze
Acanthaceae	*Pachystachys coccinea* (Aubl.) Nees
Acanthaceae	*Ruellia asperula* (Mart. & Nees) Lindau
Acanthaceae	*Ruellia brevifolia* (Pohl) C.Ezcurra
Acanthaceae	*Ruellia inflata* Rich.
Acanthaceae	*Ruellia sp.*
Acanthaceae	*Ruellia subsessilis* Lindau
Acanthaceae	*Sanchezia munita* (Nees) Planch.
Acanthaceae	*Sanchezia oblonga* Ruiz & Pav.
Acanthaceae	*Sanchezia putumayensis* Leonard
Acanthaceae	*Sanchezia scandens* (Lindau) Leonard & L.B. Sm.
Acanthaceae	*Staurogyne itatiaiae* (Wawra) Leonard
Acanthaceae	*Suessenguthia multisetosa* (Rusby) Wassh. & J.R.I. Wood
Adoxaceae	*Sambucus sp.*
Alstroemeriaceae	*Alstroemeria inodora* Herb.
Alstroemeriaceae	*Alstroemeria isabellana* Herb.
Alstroemeriaceae	*Alstroemeria rupestris* M.C.Assis
Alstroemeriaceae	*Alstroemeria sp.*

Family	**Plant Species**
Alstroemeriaceae	*Bomarea cf. carderi* Mast.
Alstroemeriaceae	*Bomarea costaricensis* Kraenzl.
Alstroemeriaceae	*Bomarea edulis* (Tussac) Herb.
Alstroemeriaceae	*Bomarea hirsuta* (Kunth) Herb.
Alstroemeriaceae	*Bomarea linifolia* (Kunth) Baker
Alstroemeriaceae	*Bomarea pardina* Herb.
Alstroemeriaceae	*Bomarea sp. 1*
Alstroemeriaceae	*Bomarea sp. 2*
Amaryllidaceae	*Hippeastrum aulicum* (Ker Gawl.) Herb.
Amaryllidaceae	*Hippeastrum aviflorum* (Ravenna) Dutilh
Amaryllidaceae	*Hippeastrum puniceum* (Lam.) Voss
Amaryllidaceae	*Hippeastrum cipoanum* (Ravenna) Meerow
Apocynaceae	*Allamanda blanchetii* A.DC.
Apocynaceae	*Blepharodon pictum* (Vahl) W.D.Stevens
Apocynaceae	*Ditassa retusa* Mart.
Apocynaceae	*Mandevilla aff. mollissima* (Kunth) K.Schum.
Apocynaceae	*Mandevilla funiformis* (Vell.) K.Schum.
Apocynaceae	*Mandevilla hirsuta* (Rich.) K.Schum.
Apocynaceae	*Mandevilla scabra* (Hoffmanns. ex Roem. & Schult.) K.Schum.
Apocynaceae	*Nephradenia asparagoides* (Decne.) E.Fourn.
Apocynaceae	*Pentalinon luteum* (L.) B.F.Hansen & Wunderlin
Apocynaceae	*Prestonia coalita* (Vell.) Woodson
Apocynaceae	*Stipecoma peltigera* (Stadelm.) Müll.Arg.
Apocynaceae	*Tabernaemontana alba* Mill.
Apocynaceae	*Tabernaemontana cymosa* Jacq.
Apocynaceae	*Tabernaemontana macrocalyx* Müll.Arg.
Araceae	*Philodendron fragrantissimum* (Hook.) G.Don
Asparagaceae	*Furcraea sp.*
Asteraceae	*Acritopappus longifolius* (Gardner) R.M.King & H.Rob.
Asteraceae	*Asteraceae sp.*
Asteraceae	*Baccharis salicina* Torr. & A.Gray
Asteraceae	*Barnadesia horrida* Muschl.
Asteraceae	*Barnadesia spinosa* L.f.
Asteraceae	*Chronopappus bifrons* (DC. ex Pers.) DC.
Asteraceae	*Cirsium subcoriaceum* (Less.) Sch.Bip. ex Sch.Bip.
Asteraceae	*Conocliniopsis prasiifolia* (DC.) R.M.King & H.Rob.
Asteraceae	*Dasyphyllum candolleanum* (Gardner) Cabrera
Asteraceae	*Diplostephium sp.*
Asteraceae	*Eremanthus crotonoides* (DC.) Sch.Bip.
Asteraceae	*Eremanthus erythropappus* (DC.) MacLeish
Asteraceae	*Espeletia sp.*
Asteraceae	*Gynoxys longifolia* Sch.Bip. ex Wedd.
Asteraceae	*Hololepis pedunculata* (DC. ex Pers.) DC.
Asteraceae	*Lepidaploa cotoneaster* (Willd. ex Spreng.) H.Rob.
Asteraceae	*Lepidaploa sp.*
Asteraceae	*Lessingianthus linearis* (Spreng.) H.Rob.
Asteraceae	*Moquinia kingii* (H.Rob.) Gamerro

Family	**Plant Species**
Asteraceae	*Mutisia speciosa* Aiton ex Hook.
Asteraceae	*Neomirandea eximia* (B.L.Rob.) R.M.King & H.Rob.
Asteraceae	*Peltophorum dubium* (Spreng.) Taub.
Asteraceae	*Piptocarpha notata* (Less.) Baker
Asteraceae	*Piptolepis leptospermoides* (Mart. ex DC.) Sch.Bip.
Asteraceae	*Pithecoseris pacourinoides* Mart. ex DC.
Asteraceae	*Trixis vauthieri* DC.
Asteraceae	*Vernonanthura phosphorica* (Vell.) H.Rob.
Balsaminaceae	*Impatiens sp.*
Balsaminaceae	*Impatiens walleriana* Hook.f.
Bignoniaceae	*Adenocalymma campicola* (Pilg.) L.G.Lohmann
Bignoniaceae	*Bignonia binata* Thunb.
Bignoniaceae	*Bignoniaceae sp.*
Bignoniaceae	*Campsis cf. Grandiflora* (Thunb.) K.Schum.
Bignoniaceae	*Cuspidaria inaequalis* (DC. ex Splitg.) L.G.Lohmann
Bignoniaceae	*Cuspidaria lateriflora* (Mart.) DC.
Bignoniaceae	*Cuspidaria simplicifolia* DC.
Bignoniaceae	*Dolichandra unguis-cati* (L.) L.G.Lohmann
Bignoniaceae	*Fridericia erubescens* (DC.) L.G.Lohmann
Bignoniaceae	*Fridericia florida* (DC.) L.G.Lohmann
Bignoniaceae	*Fridericia speciosa* Mart.
Bignoniaceae	*Fridericia triplinervia* (Mart. ex DC.) L.G.Lohmann
Bignoniaceae	*Handroanthus chrysotrichus* (Mart. ex DC.) Mattos
Bignoniaceae	*Handroanthus heptaphyllus* (Vell.) Mattos
Bignoniaceae	*Handroanthus impetiginosus* (Mart. ex DC.) Mattos
Bignoniaceae	*Handroanthus selachidentatus* (A.H.Gentry) S.O.Grose
Bignoniaceae	*Jacaranda irwinii* A.H.Gentry
Bignoniaceae	*Jacaranda mimosifolia* D.Don
Bignoniaceae	*Jacaranda puberula* Cham.
Bignoniaceae	*Jacaratia spinosa* (Aubl.) A.DC.
Bignoniaceae	*Lundia cordata* (Vell.) DC.
Bignoniaceae	*Pyrostegia venusta* (Ker Gawl.) Miers
Bignoniaceae	*Tabebuia aurea* (Silva Manso) Benth. & Hook.f. ex S.Moore
Bignoniaceae	*Tabebuia heterophylla* (DC.) Britton
Bignoniaceae	*Tabebuia orinocensis* (Sandwith) A.H.Gentry
Bignoniaceae	*Tabebuia sp.*
Bignoniaceae	*Tabebuia stenocalyx* Sprague & Stapf
Bignoniaceae	*Tecoma stans* (L.) Juss. ex Kunth
Bignoniaceae	*Zeyheria montana* Mart.
Boraginacea	*Cordia bullata var. globosa* (Jacq.) Govaerts
Boraginacea	*Cordia multispicata* Cham.
Boraginacea	*Cordia seleriana* Fernald
Boraginacea	*Cordia superba* Cham.
Boraginaceae	*Cordia bicolor* A.DC.
Boraginaceae	*Cordia curassavica* (Jacq.) Roem. & Schult.
Boraginaceae	*Cordia glabrata* (Mart.) A.DC.
Bromeliaceae	*Aechmea aquilega* (Salisb.) Griseb.

Family	**Plant Species**
Bromeliaceae	*Aechmea blumenavii* Reitz
Bromeliaceae	*Aechmea bromeliifolia* (Rudge) Baker
Bromeliaceae	*Aechmea chantinii* (Carrière) Baker
Bromeliaceae	*Aechmea contracta* (Mart. ex Schult. & Schult.f.) Baker
Bromeliaceae	*Aechmea corymbosa* (Mart. ex Schult. & Schult.f.) Mez
Bromeliaceae	*Aechmea cylindrata* Lindm.
Bromeliaceae	*Aechmea dichlamydea* Baker
Bromeliaceae	*Aechmea distichantha* Lem.
Bromeliaceae	*Aechmea fendleri* André ex Mez
Bromeliaceae	*Aechmea gamosepala* Wittm.
Bromeliaceae	*Aechmea longifolia* (Rudge) L.B.Sm. & M.A.Spencer
Bromeliaceae	*Aechmea mariae-reginae* H.Wendl.
Bromeliaceae	*Aechmea nudicaulis* (L.) Griseb.
Bromeliaceae	*Aechmea organensis* Wawra
Bromeliaceae	*Aechmea pectinata* Baker
Bromeliaceae	*Aechmea poitaei* (Baker) L.B.Sm. & M.A.Spencer
Bromeliaceae	*Aechmea recurvata* (Klotzsch) L.B.Sm.
Bromeliaceae	*Aechmea rubiginosa* Mez
Bromeliaceae	*Aechmea sp.*
Bromeliaceae	*Aechmea van-houtteana* (Van Houtte) Mez
Bromeliaceae	*Aechmea williamsii* (L.B.Sm.) L.B.Sm. & M.A.Spencer
Bromeliaceae	*Ananas ananassoides* (Baker) L.B.Sm.
Bromeliaceae	*Ananas comosus* (L.) Merr.
Bromeliaceae	*Billbergia amoena* (Lodd.) Lindl.
Bromeliaceae	*Billbergia decora* Poepp. & Endl.
Bromeliaceae	*Billbergia distachya* (Vell.) Mez
Bromeliaceae	*Billbergia pyramidalis* (Sims) Lindl.
Bromeliaceae	*Billbergia vittata* Brongn. ex C.Morel
Bromeliaceae	*Bromelia antiacantha* Bertol.
Bromeliaceae	*Bromelia balansae* Mez
Bromeliaceae	*Bromelia sp.*
Bromeliaceae	*Bromeliaceae sp. 1*
Bromeliaceae	*Bromeliaceae sp. 2*
Bromeliaceae	*Canistrum cyathiforme* (Vell.) Mez
Bromeliaceae	*Canistrum fragrans* (Linden) Mabb.
Bromeliaceae	*Canistrum giganteum* (Baker) L.B.Sm.
Bromeliaceae	*Canistrum perplexum* L.B.Sm.
Bromeliaceae	*Dyckia leptostachya* Baker
Bromeliaceae	*Dyckia sp.*
Bromeliaceae	*Encholirium brachypodum* L.B.Sm. & Read
Bromeliaceae	*Encholirium spectabile* Mart. ex Schult. & Schult.f.
Bromeliaceae	*Encholirium subsecundum* (Baker) Mez
Bromeliaceae	*Guzmania bakeri* (Wittm.) Mez
Bromeliaceae	*Guzmania berteroniana* (Schult. & Schult. f.) Mez
Bromeliaceae	*Guzmania candelabrum* (André) André ex Mez
Bromeliaceae	*Guzmania squarrosa* (Mez & Sodiro) L.B.Sm. & Pittendr.
Bromeliaceae	*Guzmania danielii* L.B.Sm.

Family	**Plant Species**
Bromeliaceae	*Guzmania jaramilloi* H.E.Luther
Bromeliaceae	*Guzmania monostachia* (L.) Rusby ex Mez
Bromeliaceae	*Guzmania nicaraguensis* Mez & C.F.Baker
Bromeliaceae	*Guzmania sp. 1*
Bromeliaceae	*Guzmania sp. 2*
Bromeliaceae	*Guzmania sp. 3*
Bromeliaceae	*Guzmania teuscheri* L.B.Sm.
Bromeliaceae	*Hohenbergia cf. catingae* Ule
Bromeliaceae	*Hohenbergia ridleyi* (Baker) Mez
Bromeliaceae	*Neoglaziovia variegata* (Arruda) Mez
Bromeliaceae	*Neoregelia bahiana* (Ule) L.B.Sm.
Bromeliaceae	*Nidularium rutilans* E. Morren
Bromeliaceae	*Nidularium innocentii* Lem.
Bromeliaceae	*Nidularium itatiaiae* L.B.Sm.
Bromeliaceae	*Nidularium marigoi* Leme
Bromeliaceae	*Nidularium procerum* Lindm.
Bromeliaceae	*Nidularium seidelii* L.B.Sm. & Reitz
Bromeliaceae	*Nidularium sp.*
Bromeliaceae	*Orthophytum albopictum* Philcox
Bromeliaceae	*Orthophytum lemei* E.Pereira & I.A.Penna
Bromeliaceae	*Pitcairnia brittoniana* (Mez) Mez
Bromeliaceae	*Pitcairnia flammea* Lindl.
Bromeliaceae	*Pitcairnia nigra* (Carrière) André
Bromeliaceae	*Pitcairnia sp.*
Bromeliaceae	*Pitcairnia sprucei* Baker
Bromeliaceae	*Puya clava-herculis* Mez & Sodiro
Bromeliaceae	*Puya ferruginea* (Ruiz & Pav.) L.B.Sm.
Bromeliaceae	*Quesnelia augusto-coburgii* Wawra
Bromeliaceae	*Quesnelia sp.*
Bromeliaceae	*Tillandsia aeranthos* (Loisel.) L.B.Sm.
Bromeliaceae	*Tillandsia aff. turneri* Baker
Bromeliaceae	*Tillandsia bartramii* Elliott
Bromeliaceae	*Tillandsia complanata* Benth.
Bromeliaceae	*Tillandsia dasyliriifolia* Baker
Bromeliaceae	*Tillandsia fasciculata* Sw.
Bromeliaceae	*Tillandsia gardneri* Lindl.
Bromeliaceae	*Tillandsia orbicularis* L.B.Sm.
Bromeliaceae	*Tillandsia paucifolia* Baker
Bromeliaceae	*Tillandsia sp. 1*
Bromeliaceae	*Tillandsia sp. 2*
Bromeliaceae	*Tillandsia stricta* Sol. ex Ker Gawl.
Bromeliaceae	*Tillandsia tetrantha* Ruiz & Pav.
Bromeliaceae	*Tillandsia utriculata* L.
Bromeliaceae	*Vriesea altodaserrae* L.B.Sm.
Bromeliaceae	*Vriesea carinata* Wawra
Bromeliaceae	*Vriesea chrysostachys* E.Morren
Bromeliaceae	*Vriesea ensiformis* (Vell.) Beer

Family	Plant Species
Bromeliaceae	*Vriesea erythrodactylon* (E.Morren) E.Morren ex Mez
Bromeliaceae	*Vriesea incurvata* Gaudich.
Bromeliaceae	*Vriesea jonghei* (K.Koch) E.Morren
Bromeliaceae	*Vriesea longicaulis* (Baker) Mez
Bromeliaceae	*Vriesea medusa* Versieux
Bromeliaceae	*Vriesea ororiensis* (Mez) L.B.Sm. & Pittendr.
Bromeliaceae	*Vriesea philippocoburgii* Wawra
Bromeliaceae	*Vriesea procera* (Mart. ex Schult. & Schult.f.) Wittm.
Bromeliaceae	*Vriesea procera var. tenuis* L.B.Sm.
Bromeliaceae	*Vriesea rodigasiana* E.Morren
Bromeliaceae	*Vriesea sceptrum* Mez
Bromeliaceae	*Vriesea simplex* (Vell.) Beer
Bromeliaceae	*Vriesea sp. 1*
Bromeliaceae	*Vriesea sp. 2*
Bromeliaceae	*Vriesea sp. 3*
Bromeliaceae	*Vriesea vagans* (L.B.Sm.) L.B.Sm.
Burseraceae	*Protium sp.*
Cactaceae	*Cipocereus minensis* (Werderm.) F.Ritter
Cactaceae	*Consolea rubescens* (Salm-Dyck ex DC.) Lem.
Cactaceae	*Melocactus concinnus* Buining & Brederoo
Cactaceae	*Melocactus ernestii* Vaupel
Cactaceae	*Melocactus intortus* (Mill.) Urb.
Cactaceae	*Melocactus zehntneri* (Britton & Rose) Luetzelb.
Cactaceae	*Micranthocereus flaviflorus* Buining & Brederoo
Cactaceae	*Micranthocereus purpureus* (Gürke) F. Ritter
Cactaceae	*Opuntia excelsa* Sánchez-Mej.
Cactaceae	*Opuntia karwinskiana* Salm-Dyck
Cactaceae	*Opuntia werneri* Eggli
Cactaceae	*Pilosocereus aurisetus* (Werderm.) Byles & G.D. Rowley
Cactaceae	*Pilosocereus gounellei* (F.A.C.Weber ex K.Schum.) Byles & G.D.Rowley
Cactaceae	*Pilosocereus pachycladus* F. Ritter
Cactaceae	*Pilosocereus royenii* (L.) Byles & G.D.Rowley
Cactaceae	*Pilosocereus sp.*
Cactaceae	*Tacinga inamoena* (K.Schum.) N.P.Taylor & Stuppy
Cactaceae	*Tacinga palmadora* (Britton & Rose) N.P.Taylor & Stuppy
Campanulaceae	*Burmeistera cyclostigmata* Donn.Sm.
Campanulaceae	*Burmeistera globosa* E.Wimm.
Campanulaceae	*Burmeistera parviflora* E.Wimm. ex Standl.
Campanulaceae	*Burmeistera sp.*
Campanulaceae	*Centropogon cornutus* (L.) Druce
Campanulaceae	*Centropogon costaricae* (Vatke) McVaugh
Campanulaceae	*Centropogon granulosus* C.Presl
Campanulaceae	*Centropogon solanifolius* Benth.
Campanulaceae	*Centropogon sp. 1*
Campanulaceae	*Centropogon sp. 2*
Campanulaceae	*Centropogon talamancensis* Wilbur
Campanulaceae	*Centropogon valerii* Standl.

Family	**Plant Species**
Campanulaceae	*Lobelia cirsiifolia* Lam.
Campanulaceae	*Lobelia fistulosa* Vell.
Campanulaceae	*Lobelia stricta* Sw.
Campanulaceae	*Siphocampylus bogotensis* E.Wimm.
Campanulaceae	*Siphocampylus cf. convolvulaceous* (Cham.) G.Don
Campanulaceae	*Siphocampylus fimbriatus* Regel
Campanulaceae	*Siphocampylus giganteus* (Cav.) G.Don
Campanulaceae	*Siphocampylus imbricatus* (Cham.) G.Don
Campanulaceae	*Siphocampylus longipedunculatus* Pohl
Campanulaceae	*Siphocampylus paramicola* McVaugh
Campanulaceae	*Siphocampylus sp.*
Campanulaceae	*Siphocampylus sulfureus* E.Wimm.
Campanulaceae	*Siphocampylus westinianus* (Thunb.) Pohl
Cannaceae	*Canna indica* L.
Cannaceae	*Canna paniculata* Ruiz & Pav.
Cannaceae	*Canna sp.*
Capparaceae	*Crateva tapia* L.
Caprifoliaceae	*Lonicera japonica* Thunb.
Caryocaraceae	*Caryocar brasiliense* A.St.-Hil.
Chrysobalanaceae	*Couepia schottii* Fritsch
Clusiaceae	*Clusia mangle* Rich. ex Planch. & Triana
Clusiaceae	*Clusia melchiorii* Gleason
Clusiaceae	*Clusia sp. 1*
Clusiaceae	*Clusia sp. 2*
Clusiaceae	*Symphonia globulifera* L.f.
Columelliaceae	*Desfontainia spinosa* Ruiz & Pav.
Combretaceae	*Combretum farinosum* Kunth
Combretaceae	*Combretum llewelynii* J.F.Macbr.
Convolvulaceae	*Aniseia martinicensis* (Jacq.) Choisy
Convolvulaceae	*Ipomoea aquatica* Forssk.
Convolvulaceae	*Ipomoea bracteata* Cav.
Convolvulaceae	*Ipomoea quamoclit* L.
Convolvulaceae	*Ipomoea sp. 1*
Convolvulaceae	*Ipomoea sp. 2*
Convolvulaceae	*Ipomoea sp. 3*
Convolvulaceae	*Ipomoea subincana* Meisn.
Convolvulaceae	*Jacquemontia sp. 1*
Convolvulaceae	*Jacquemontia sp. 2*
Convolvulaceae	*Merremia macrocalyx* (Ruiz & Pav.) O'Donell
Costaceae	*Costus curvibracteatus* Maas
Costaceae	*Costus lasius* Loes.
Costaceae	*Costus pulverulentus* C.Presl
Costaceae	*Costus scaber* Ruiz & Pav.
Costaceae	*Costus spiralis* (Jacq.) Roscoe
Costaceae	*Dimerocostus strobilaceus* Kuntze
Crassulaceae	*Kalanchoe sp.*
Cucurbitaceae	*Apodanthera villosa* C.Jeffrey

Family	Plant Species
Cucurbitaceae	*Gurania acuminata* Cogn.
Cucurbitaceae	*Gurania coccinea* Cogn.
Cucurbitaceae	*Gurania lobata* (L.) Pruski
Cucurbitaceae	*Gurania rhizantha* (Poepp. & Endl.) C.Jeffrey
Cucurbitaceae	*Gurania rufipila* Cogn.
Cucurbitaceae	*Psiguria ternata* (M.Roem.) C.Jeffrey
Ericaceae	*Agarista coriifolia* (Thunb.) Hook. ex Nied.
Ericaceae	*Agarista sp.*
Ericaceae	*Bejaria aestuans* Mutis ex L.
Ericaceae	*Cavendishia bracteata* (Ruiz & Pav. ex J.St.Hil.) Hoerold
Ericaceae	*Cavendishia callista* Donn.Sm.
Ericaceae	*Cavendishia complectens* Hemsl.
Ericaceae	*Cavendishia grandifolia* Herold
Ericaceae	*Cavendishia guatapeensis* Mansf.
Ericaceae	*Cavendishia pubescens* (Kunth) Hemsl.
Ericaceae	*Cavendishia quereme* (Kunth) Benth. & Hook.f.
Ericaceae	*Cavendishia sp.*
Ericaceae	*Cavendishia tarapotana* Benth. & Hook.f.
Ericaceae	*Disterigma codonanthum* S.F.Blake
Ericaceae	*Disterigma humboldtii* (Klotzsch) Nied.
Ericaceae	*Disterigma sp. 1*
Ericaceae	*Disterigma sp. 2*
Ericaceae	*Ericaceae sp. 1*
Ericaceae	*Ericaceae sp. 2*
Ericaceae	*Gaultheria erecta* Vent.
Ericaceae	*Gaultheria gracilis* Small
Ericaceae	*Gaultheria insipida* Benth.
Ericaceae	*Gaultheria myrsinoides* Kunth
Ericaceae	*Gaultheria sp.*
Ericaceae	*Gaylussacia brasiliensis* (Spreng.) Meisn.
Ericaceae	*Gaylussacia montana* (Pohl) Sleumer
Ericaceae	*Gaylussacia oleifolia* Dunal
Ericaceae	*Gaylussacia virgata* Mart. ex Meisn.
Ericaceae	*Gonocalyx pterocarpus* (Donn.Sm.) Luteyn
Ericaceae	*Macleania pentaptera* Hoerold
Ericaceae	*Macleania recumbens* A.C. Sm.
Ericaceae	*Macleania rupestris* (Kunth) A.C.Sm.
Ericaceae	*Psammisia aberrans* A.C. Sm.
Ericaceae	*Psammisia ecuadorensis* Hoerold
Ericaceae	*Psammisia falcata* Klotzsch
Ericaceae	*Psammisia oreogenes* Sleumer
Ericaceae	*Psammisia pauciflora* Griseb. ex A.C. Sm.
Ericaceae	*Psammisia penduliflora* (Dunal) Klotzsch
Ericaceae	*Psammisia ramiflora* Klotzsch
Ericaceae	*Psammisia sodiroi* Hoerold
Ericaceae	*Psammisia ulbrichiana* Hoerold
Ericaceae	*Satyria meiantha* Donn.Sm.

Family	Plant Species
Ericaceae	*Satyria panurensis* (Benth. ex Meisn.) Benth. & Hook.f. ex Nied.
Ericaceae	*Thibaudia costaricensis* Hoerold
Ericaceae	*Thibaudia rigidiflora* A.C.Sm.
Ericaceae	*Vaccinium consanguineum* Klotzsch
Ericaceae	*Vaccinium floribundum* Kunth
Ericaceae	*Vaccinium racemosum* (Vahl) Wilbur & Luteyn
Ericaceae	*Vaccinium poasanum* Donn.Sm.
Erythroxylaceae	*Erythroxylum vaccinifolium* Mart.
Euphorbiaceae	*Cnidoscolus halteris* Fern.Casas
Euphorbiaceae	*Cnidoscolus pubescens* Pohl
Euphorbiaceae	*Croton blanchetianus* Baill.
Euphorbiaceae	*Jatropha mollissima* (Pohl) Baill.
Euphorbiaceae	*Jatropha mutabilis* (Pohl) Baill.
Euphorbiaceae	*Manihot jacobinensis* Müll.Arg.
Euphorbiaceae	*Manihot reniformis* Pohl
Fabaceae	*Abarema brachystachya* (DC.) Barneby & J.W.Grimes
Fabaceae	*Albizia saman* (Jacq.) Merr.
Fabaceae	*Anadenanthera colubrina* (Vell.) Brenan
Fabaceae	*Bauhinia brevipes* Vogel
Fabaceae	*Bauhinia cheilantha* (Bong.) Steud.
Fabaceae	*Bauhinia forficata* Link
Fabaceae	*Bauhinia longifolia* (Bong.) Steud.
Fabaceae	*Bauhinia rufa* (Bong.) Steud.
Fabaceae	*Bauhinia ungulata* L.
Fabaceae	*Bauhinia variegata* L.
Fabaceae	*Bowdichia virgilioides* Kunth
Fabaceae	*Brownea coccinea subsp. capitella* (Jacq.) D.Velasquez & Agostini
Fabaceae	*Caesalpinia pyramidalis* Tul.
Fabaceae	*Calliandra brevipes* Benth.
Fabaceae	*Calliandra carbonaria* Benth.
Fabaceae	*Calliandra guildingii* Benth.
Fabaceae	*Calliandra hygrophila* Mackinder & G.P.Lewis
Fabaceae	*Calliandra mucugeana* Renvoize
Fabaceae	*Calliandra purdiaei* Benth.
Fabaceae	*Calliandra tweedii* Benth.
Fabaceae	*Calliandra viscidula* Benth.
Fabaceae	*Camptosema coriaceum* Benth.
Fabaceae	*Camptosema ellipticum* (Desv.) Burkart
Fabaceae	*Camptosema scarlatinum* (Benth.) Burkart
Fabaceae	*Centrosema brasilianum* (L.) Benth.
Fabaceae	*Centrosema coriaceum* Benth.
Fabaceae	*Chaetocalyx subulatus* Mackinder
Fabaceae	*Clathrotropis brachypetala* (Tul.) Kleinhoonte
Fabaceae	*Collaea speciosa* (Loisel.) DC.
Fabaceae	*Dahlstedtia pinnata* (Benth.) Malme
Fabaceae	*Dioclea grandiflora* Benth.
Fabaceae	*Dioclea sp.*

Family	**Plant Species**
Fabaceae	*Erythrina corallodendron* L.
Fabaceae	*Erythrina crista-galli* L.
Fabaceae	*Erythrina fusca* Lour.
Fabaceae	*Erythrina lanata* Rose
Fabaceae	*Erythrina poeppigiana* (Walp.) O.F.Cook
Fabaceae	*Erythrina sp.*
Fabaceae	*Erythrina speciosa* Andrews
Fabaceae	*Fabaceae sp.*
Fabaceae	*Inga edulis* Mart.
Fabaceae	*Inga ingoides* (Rich.) Willd.
Fabaceae	*Inga leiocalycina* Benth.
Fabaceae	*Inga luschnathiana* Benth.
Fabaceae	*Inga sessilis* (Vell.) Mart.
Fabaceae	*Inga sp. 1*
Fabaceae	*Inga sp. 2*
Fabaceae	*Inga sp. 3*
Fabaceae	*Inga venosa* Griseb.
Fabaceae	*Inga vera* Willd.
Fabaceae	*Lonchocarpus benthamianus* Pittier
Fabaceae	*Lysiloma latisiliquum* (L.) Benth.
Fabaceae	*Mucuna rostrata* Benth.
Fabaceae	*Mysanthus uleanus* (Harms) G.P.Lewis & A.Delgado
Fabaceae	*Neorudolphia volubilis* (Willd.) Britton
Fabaceae	*Periandra coccinea* (Schrad.) Benth.
Fabaceae	*Periandra mediterranea* (Vell.) Taub.
Fabaceae	*Phaseolus coccineus* L.
Fabaceae	*Abarema jupunba* (Willd.) Britton & Killip
Fabaceae	*Senna reticulata* (Willd.) H.S.Irwin & Barneby
Fabaceae	*Tachigali paniculata* Aubl.
Fabaceae	*Tephrosia noctiflora* Baker
Fabaceae	*Tipuana tipu* (Benth.) Kuntze
Fabaceae	*Viguieranthus alternans* (Benth.) Villiers
Fabaceae	*Zygia lathetica* Barneby & J.W. Grimes
Gentianaceae	*Chelonanthus alatus* (Aubl.) Pulle
Gentianaceae	Calolisianthus pendulus (Mart.) Gilg
Gentianaceae	*Lisianthius roseus* Sessé & Moc.
Gentianaceae	*Macrocarpaea cf. rubra* Malme
Gentianaceae	*Macrocarpaea sp.*
Gentianaceae	*Macrocarpaea valerioi* Standl.
Gentianaceae	*Symbolanthus tricolor* Gilg
Gentianaceae	*Tachia occidentalis* Maguire & Weaver
Gesneriaceae	*Alloplectus sp. 1*
Gesneriaceae	*Alloplectus sp. 2*
Gesneriaceae	*Besleria cf. solanoides* Kunth
Gesneriaceae	*Besleria columneoides* Hanst.
Gesneriaceae	*Besleria longimucronata* Hoehne
Gesneriaceae	*Besleria notabilis* C.V.Morton

Family	Plant Species
Gesneriaceae	*Besleria rotundifolia* Rusby
Gesneriaceae	*Besleria solanoides* Kunth
Gesneriaceae	*Besleria petiolaris* Griseb.
Gesneriaceae	*Columnea ciliata* (Wiehler) L.P.Kvist & L.E.Skog
Gesneriaceae	*Columnea ericae* Mansf.
Gesneriaceae	*Columnea magnifica* Klotzsch ex Oerst.
Gesneriaceae	*Columnea medicinalis* (Wiehler) L.E.Skog & L.P.Kvist
Gesneriaceae	*Columnea microcalyx* Hanst.
Gesneriaceae	*Columnea purpurata* Hanst.
Gesneriaceae	*Columnea querceti* Oerst.
Gesneriaceae	*Columnea sp.*
Gesneriaceae	*Columnea strigosa* Benth.
Gesneriaceae	*Drymonia coccinea* (Aubl.) Wiehler
Gesneriaceae	*Drymonia conchocalyx* Hanst.
Gesneriaceae	*Drymonia semicordata* (Poepp.) Wiehler
Gesneriaceae	*Gasteranthus sp.*
Gesneriaceae	*Gesneriaceae sp. 1*
Gesneriaceae	*Gesneriaceae sp. 2*
Gesneriaceae	*Gesneriaceae sp. 3*
Gesneriaceae	*Gesneriaceae sp. 4*
Gesneriaceae	*Glossoloma bolivianum* (Britton ex Rusby) J.L.Clark
Gesneriaceae	*Hypocyrta fritschii* (Hoehne) Handro
Gesneriaceae	*Kohleria spicata* (Kunth) Oerst.
Gesneriaceae	*Kohleria tigridia* (Ohlend.) Roalson & Boggan
Gesneriaceae	*Nematanthus aff. fritschii* Hoehne
Gesneriaceae	*Nematanthus australis* Chautems
Gesneriaceae	*Nematanthus crassifolius* (Schott) Wiehler
Gesneriaceae	*Nematanthus fluminensis* (Vell.) Fritsch
Gesneriaceae	*Nematanthus fornix* (Vell.) Chautems
Gesneriaceae	*Nematanthus gregarius* D.L. Denham
Gesneriaceae	*Nematanthus lanceolatus (*Poir.) Chautems
Gesneriaceae	*Nematanthus savannarum* (C.V.Morton) J.L.Clark
Gesneriaceae	*Nematanthus strigillosus* (Mart.) H.E. Moore
Gesneriaceae	*Paliavana sericiflora* Benth.
Gesneriaceae	*Sinningia cooperi* (J. Paxton) Wiehler
Gesneriaceae	*Sinningia douglasii* (Lindl.) Chautems
Gesneriaceae	*Sinningia elatior* (Kunth) Chautems
Gesneriaceae	*Sinningia gigantifolia* Chautems
Gesneriaceae	*Sinningia glazioviana* (Fritsch) Chautems
Gesneriaceae	*Sinningia rupicola* (Mart.) Wiehler
Heliconiaceae	*Heliconia acuminata* A.Rich.
Heliconiaceae	*Heliconia angusta* Vell.
Heliconiaceae	*Heliconia atropurpurea* G.S.Daniels & F.G.Stiles
Heliconiaceae	*Heliconia bihai* (L.) L.
Heliconiaceae	*Heliconia burleana* Abalo & G.Morales
Heliconiaceae	*Heliconia subulata* Ruiz & Pav. *subsp. subulata*
Heliconiaceae	*Heliconia episcopalis* Vell.

Family	Plant Species
Heliconiaceae	*Heliconia farinosa* Raddi
Heliconiaceae	*Heliconia hirsuta* L.f.
Heliconiaceae	*Heliconia imbricata* (Kuntze) Baker
Heliconiaceae	*Heliconia juruana* Loes.
Heliconiaceae	*Heliconia lankesteri* Standl.
Heliconiaceae	*Heliconia latispatha* Benth.
Heliconiaceae	*Heliconia marginata* (Griggs) Pittier
Heliconiaceae	*Heliconia mariae* Hook.f.
Heliconiaceae	*Heliconia mathiasiae* G.S.Daniels & F.G.Stiles
Heliconiaceae	*Heliconia metallica* Planch. & Linden ex Hook.
Heliconiaceae	*Heliconia pogonantha* Cufod.
Heliconiaceae	*Heliconia psittacorum* L.f.
Heliconiaceae	*Heliconia rostrata* Ruiz & Pav.
Heliconiaceae	*Heliconia schumanniana* Loes.
Heliconiaceae	*Heliconia sp. 1*
Heliconiaceae	*Heliconia sp. 2*
Heliconiaceae	*Heliconia sp. 3*
Heliconiaceae	*Heliconia sp. 4*
Heliconiaceae	*Heliconia spathocircinada* Aristeg.
Heliconiaceae	*Heliconia stricta* Huber
Heliconiaceae	*Heliconia subulata* Ruiz & Pav.
Heliconiaceae	*Heliconia vaginalis* Benth.
Heliconiaceae	*Heliconia wagneriana* Petersen
Humiriaceae	*Humiria balsamifera* Aubl.
Iridacea	*Iridaceae sp.*
Lamiaceae	*Aegiphila obducta* Vell.
Lamiaceae	*Aegiphila perplexa* Moldenke
Lamiaceae	*Amasonia campestris* (Aubl.) Moldenke
Lamiaceae	*Volkameria aculeata* L.
Lamiaceae	*Eriope latifolia* (Mart. ex Benth.) Harley
Lamiaceae	*Hyptidendron asperrimum* (Spreng.) Harley
Lamiaceae	*Hyptis atrorubens* Poit.
Lamiaceae	*Hyptis cuniloides* Epling
Lamiaceae	*Hyptis leptostachys* Epling
Lamiaceae	*Hyptis pectinata* (L.) Poit.
Lamiaceae	*Hyptis sp.*
Lamiaceae	*Lamiaceae sp.*
Lamiaceae	*Leonotis nepetifolia* (L.) R.Br.
Lamiaceae	Prunella vulgaris L.
Lamiaceae	*Salvia arenaria* A.St.-Hil. ex Benth.
Lamiaceae	*Salvia articulata* Epling
Lamiaceae	*Salvia carnea* Kunth
Lamiaceae	*Salvia elegans* Vahl
Lamiaceae	*Salvia mocinoi* Benth.
Lamiaceae	*Salvia sellowiana* Benth.
Lamiaceae	*Salvia sp.*
Lamiaceae	*Vitex cymosa* Bertero ex Spreng.

Family	Plant Species
Lamiaceae	*Vitex divaricata* Sw.
Lecythidaceae	*Lecythidoideae sp.*
Loganiaceae	*Spigelia pulchella* Mart.
Loranthaceae	*Gaiadendron punctatum* (Ruiz & Pav.) G.Don
Loranthaceae	*Ligaria teretiflora* (Rizzini) Kuijt
Loranthaceae	*Loranthaceae sp.*
Loranthaceae	*Loranthus bicalyculatus* Mart. ex Schult. & Schult.f.
Loranthaceae	*Psittacanthus cordatus* (Hoffmanns. ex Schult. f.) Blume
Loranthaceae	*Psittacanthus cucullaris* (Lam.) G.Don
Loranthaceae	*Psittacanthus dichrous* Mart.
Loranthaceae	*Psittacanthus flavo-viridis* Eichler
Loranthaceae	*Loranthus furcatus* Mart. ex Schult. & Schult.f.
Loranthaceae	*Psittacanthus lasianthus* Sandwith
Loranthaceae	*Tripodanthus acutifolius* (Ruiz & Pav.) Tiegh.
Loranthaceae	*Tristerix longebracteatus* (Desr.) Barlow & Wiens
Lythraceae	*Cuphea dipetala* (L.f.) Koehne
Lythraceae	*Cuphea ericoides* Cham. & Schltdl.
Lythraceae	*Cuphea melvilla* Lindl.
Lythraceae	*Lafoensia glyptocarpa* Koehne
Lythraceae	*Lafoensia sp.*
Malvaceae	*Abutilon aff. regnellii* Miq.
Malvaceae	*Abutilon bedfordianum* (Hook.) A.St.-Hil.
Malvaceae	*Abutilon darwinii* Hook.f.
Malvaceae	*Abutilon sp.*
Malvaceae	*Ceiba aesculifolia* (Kunth) Britten & Baker f.
Malvaceae	*Ceiba glaziovii* (Kuntze) K.Schum.
Malvaceae	*Ceiba pentandra* (L.) Gaertn.
Malvaceae	*Ceiba speciosa* (A.St.-Hil.) Ravenna
Malvaceae	*Dombeya wallichii* (Lindl.) K.Schum
Malvaceae	*Eriotheca gracilipes* (K.Schum.) A.Robyns
Malvaceae	*Eriotheca pentaphylla* (Vell.) A.Robyns
Malvaceae	*Guazuma ulmifolia* Lam.
Malvaceae	*Helicteres brevispira* A.Juss.
Malvaceae	*Helicteres eichleri* K. Schum.
Malvaceae	*Helicteres guazumifolia* Kunth
Malvaceae	*Helicteres sacarolha* A.Juss.
Malvaceae	*Helicteres velutina* K.Schum.
Malvaceae	*Hibiscus rosa-sinensis* L.
Malvaceae	*Luehea divaricata* Mart.
Malvaceae	*Malvaceae sp.*
Malvaceae	*Malvaviscus arboreus* Cav.
Malvaceae	*Malvaviscus palmanus* Pittier & Donn.Sm.
Malvaceae	*Melochia tomentosa* L.
Malvaceae	*Pavonia luetzelburgii* Ulbr.
Malvaceae	*Pavonia sp.*
Malvaceae	*Pavonia viscosa* A. St.-Hil.
Malvaceae	*Quararibea lasiocalyx* (K.Schum.) Vischer

Family	**Plant Species**
Malvaceae	*Spirotheca rivieri* (Decne.) Ulbr.
Malvaceae	*Urena lobata* L.
Malvaceae	*Waltheria cinerescens* A. St.-Hil.
Malvaceae	*Waltheria rotundifolia* Schrank
Marantaceae	*Calathea capitata* (Ruiz & Pav.) Lindl.
Marantaceae	*Calathea gymnocarpa* H.A.Kenn.
Marantaceae	*Calathea inocephala* (Kuntze) T.Durand & B.D.Jacks.
Marantaceae	*Calathea lasiostachya* Donn.Sm.
Marantaceae	*Calathea lutea* (Aubl.) E.Mey. ex Schult.
Marantaceae	*Calathea zingiberina* Körn.
Marantaceae	*Ischnosiphon arouma* (Aubl.) Körn.
Marantaceae	*Ischnosiphon hirsutus* Petersen
Marantaceae	*Ischnosiphon lasiocoleus* K.Schum. ex Loes.
Marantaceae	*Maranta furcata* Nees & Mart.
Marantaceae	*Monotagma secundum* (Petersen) K.Schum.
Marantaceae	*Stromanthe thalia* (Vell.) J.M.A.Braga
Marcgraviaceae	*Marcgravia myriostigma* Triana & Planch.
Marcgraviaceae	*Marcgravia polyantha* Delpino
Marcgraviaceae	*Norantea guianensis* Aubl.
Marcgraviaceae	*Sarcopera sp.*
Marcgraviaceae	*Schwartzia brasiliensis* (Choisy) Bedell ex Gir.-Cañas
Melastomataceae	*Acinodendron sintenisii* (Cogn.) Kuntze
Melastomataceae	*Brachyotum ledifolium* (Desr.) Triana
Melastomataceae	*Brachyotum lindenii* Cogn.
Melastomataceae	*Brachyotum nutans* Gleason
Melastomataceae	*Brachyotum sp.*
Melastomataceae	*Charianthus grenadensis* Penneys & Judd
Melastomataceae	*Huilaea minor* (L. Uribe) Lozano & N. Ruiz
Melastomataceae	*Melastomataceae sp.*
Melastomataceae	*Miconia purpurea* (D. Don) Judd & Skean
Melastomataceae	*Miconia sp. 1*
Melastomataceae	*Miconia sp. 2*
Musaceae	*Musa × paradisiaca* L.
Musaceae	*Musa sp. 1*
Musaceae	*Musa sp. 2*
Myrtaceae	*Callistemon speciosus* (Sims) Sweet
Myrtaceae	*Eucalyptus sp.*
Myrtaceae	*Melaleuca leucadendra* (L.) L.
Myrtaceae	*Myrcia lasiantha* DC.
Myrtaceae	*Myrcianthes oreophila* (Diels) McVaugh
Myrtaceae	*Psidium sp.*
Myrtaceae	*Syzygium jambos* (L.) Alston
Myrtaceae	*Syzygium malaccense* (L.) Merr. & L.M.Perry
Nyctaginaceae	*Bougainvillea sp.*
Onagraceae	*Fuchsia corollata* Benth.
Onagraceae	*Fuchsia macrostigma* Benth.
Onagraceae	*Fuchsia microphylla* Kunth

Family	Plant Species
Onagraceae	*Fuchsia regia* (Vand. ex Vell.) Munz
Onagraceae	*Fuchsia splendens* Zucc.
Orchidaceae	*Cattleya elongata* Barb.Rodr.
Orchidaceae	*Corymborkis flava* (Sw.) Kuntze
Orchidaceae	*Elleanthus aurantiacus* (Lindl.) Rchb.f.
Orchidaceae	*Elleanthus smithii* Schltr.
Orchidaceae	*Elleanthus sp.*
Orchidaceae	*Orchidaceae sp.*
Orobanchaceae	*Agalinis angustifolia* (Mart.) D'Arcy
Orobanchaceae	*Castilleja angustifolia* (Nutt.) G.Don
Orobanchaceae	*Castilleja fissifolia* L.f.
Orobanchaceae	*Castilleja irasuensis* Oerst.
Orobanchaceae	*Castilleja miniata* Douglas ex Hook.
Orobanchaceae	*Castilleja scorzonerifolia* Kunth
Orobanchaceae	*Castilleja tenuiflora* Benth.
Orobanchaceae	*Esterhazya splendida* J.C.Mikan
Orobanchaceae	*Vellosiella dracocephaloides* (Vell.) Baill.
Oxalidaceae	*Oxalis psoraleoides* Kunth
Passifloraceae	*Passiflora cf. skiantha* Huber
Passifloraceae	*Passiflora coccinea* Aubl.
Passifloraceae	*Passiflora edmundoi* Sacco
Passifloraceae	*Passiflora kermesina* Link & Otto
Passifloraceae	*Passiflora luetzelburgii* Harms
Passifloraceae	*Passiflora mixta* L.f.
Passifloraceae	*Passiflora quadriglandulosa* Rodschied
Passifloraceae	*Passiflora sp.*
Passifloraceae	*Passiflora speciosa* Gardner
Passifloraceae	*Passiflora spinosa* (Poepp. & Endl.) Mast.
Passifloraceae	*Passiflora vitifolia* Kunth
Passifloraceae	*Passifloraceae sp.*
Passifloraceae	*Turnera ulmifolia* L.
Phytolaccaceae	*Phytolacca rivinoides* Kunth & C.D.Bouché
Plantaginaceae	*Penstemon gentianoides* (Kunth) Poir.
Plantaginaceae	*Penstemon labrosus* (A. Gray) Mast. ex Hook. f.
Plantaginaceae	*Penstemon roseus* (Cerv. ex Sweet) G. Don
Plumbaginaceae	*Plumbago zeylanica* L.
Polygalaceae	*Monnina sp.*
Polygonaceae	*Antigonon leptopus* Hook. & Arn.
Proteaceae	*Grevillea banksii* R.Br.
Ranunculaceae	*Aquilegia formosa* Fisch. ex DC.
Ranunculaceae	*Delphinium barbeyi* (Huth) Huth
Rosaceae	*Rubus rosifolius* Sm.
Rosaceae	*Rubus sp. 1*
Rosaceae	*Rubus sp. 2*
Rubiaceae	*Augusta longifolia* (Spreng.) Rehder
Rubiaceae	*Bouvardia ternifolia* (Cav.) Schltdl.
Rubiaceae	*Cinchona cf. pitayensis* (Wedd.) Wedd.

Family	Plant Species
Rubiaceae	*Coussarea hydrangeifolia* (Benth.) Benth. & Hook.f. ex Müll.Arg.
Rubiaceae	*Erithalis fruticosa* L.
Rubiaceae	*Faramea eurycarpa* Donn.Sm.
Rubiaceae	*Ferdinandusa sprucei* K.Schum.
Rubiaceae	*Genipa americana* L.
Rubiaceae	*Gonzalagunia hirsuta* (Jacq.) K.Schum.
Rubiaceae	*Hamelia patens* Jacq.
Rubiaceae	*Hamelia rostrata* Bartl. ex DC.
Rubiaceae	*Hillia triflora* (Oerst.) C.M.Taylor
Rubiaceae	*Hoffmannia arborescens* Donn.Sm.
Rubiaceae	*Isertia hypoleuca* Benth.
Rubiaceae	*Isertia parviflora* Vahl
Rubiaceae	*Isertia rosea* Spruce ex K.Schum.
Rubiaceae	*Manettia aff. sabiceoides* Wernham
Rubiaceae	*Manettia coccocypseloides* Wernham
Rubiaceae	*Manettia cordifolia* Mart.
Rubiaceae	*Manettia dominicensis* Wernham
Rubiaceae	*Manettia mitis* (Vell.) K.Schum.
Rubiaceae	*Manettia pubescens* Cham. & Schltdl.
Rubiaceae	*Morinda citrifolia* L.
Rubiaceae	*Palicourea anderssoniana* C.M.Taylor
Rubiaceae	*Palicourea angustifolia* Kunth
Rubiaceae	*Palicourea aschersonianoides* (Wernham) Steyerm.
Rubiaceae	*Palicourea cf. anacardiifolia* (Humb. & Bonpl. ex Schult.) Standl.
Rubiaceae	*Palicourea cf. nigricans* K.Krause
Rubiaceae	*Palicourea cf. vagans* Wernham
Rubiaceae	*Palicourea coriacea* (Cham.) K.Schum.
Rubiaceae	*Palicourea crocea* (Sw.) Schult.
Rubiaceae	*Palicourea demissa* Standl.
Rubiaceae	*Palicourea fastigiata* Kunth
Rubiaceae	*Palicourea gomezii* C.M.Taylor
Rubiaceae	*Palicourea guianensis* Aubl.
Rubiaceae	*Palicourea lassiorrhachis* Oerst.
Rubiaceae	*Palicourea marcgravii* A.St.-Hil.
Rubiaceae	*Palicourea quadrifolia (*Rudge*)* DC.
Rubiaceae	*Palicourea rigida* Kunth
Rubiaceae	*Palicourea rudgeoides* (Müll.Arg.) Standl.
Rubiaceae	*Palicourea sodiroi* Standl.
Rubiaceae	*Palicourea sp. 1*
Rubiaceae	*Palicourea sp. 2*
Rubiaceae	*Palicourea subspicata* Huber
Rubiaceae	*Pentagonia monocaulis* C.M.Taylor
Rubiaceae	*Posoqueria sp.*
Rubiaceae	*Psychotria cf. nemorosa* Gardner
Rubiaceae	*Psychotria bahiensis* DC.
Rubiaceae	*Psychotria berteroana* DC.
Rubiaceae	*Psychotria capitata* Ruiz & Pav.

Family	**Plant Species**
Rubiaceae	*Psychotria elata* (Sw.) Hammel
Rubiaceae	*Psychotria mapourioides* DC.
Rubiaceae	*Psychotria muscosa* (Jacq.) Steyerm.
Rubiaceae	*Psychotria nuda* (Cham. & Schltdl.) Wawra
Rubiaceae	*Psychotria platypoda* DC.
Rubiaceae	*Psychotria poeppigiana* Müll.Arg.
Rubiaceae	*Psychotria suterella* Müll.Arg.
Rubiaceae	*Psychotria urbaniana* Steyerm.
Rubiaceae	*Psychotria vellosiana* Benth.
Rubiaceae	*Retiniphyllum speciosum* (Spruce ex Benth.) Müll.Arg.
Rubiaceae	*Rubiaceae sp.*
Rubiaceae	*Rudgea loretensis* Standl.
Rubiaceae	*Sabicea aspera* Aubl.
Rubiaceae	*Sabicea villosa* Willd. ex Schult.
Rubiaceae	*Schradera exotica* (J.F.Gmel.) Standl.
Rubiaceae	*Staelia galioides* DC.
Rubiaceae	*Warszewiczia coccinea* (Vahl) Klotzsch
Rutaceae	*Decagonocarpus cornutus* R.S.Cowan
Rutaceae	*Erythrochiton fallax* Kallunki
Rutaceae	*Rutaceae sp.*
Salicaceae	*Ryania pyrifera (*Rich.) Uittien & Sleumer
Sapindaceae	*Serjania aff. caracasana* (Jacq.) Willd.
Sapindaceae	*Serjania coradinii* Ferrucci & Somner
Sapindaceae	*Serjania glutinosa* Radlk.
Schlegeliaceae	*Schlegelia brachyantha* Griseb.
Schlegeliaceae	*Schlegelia fastigiata* Schery
Scrophulariaceae	*Buddleja cf. brasiliensis* J.Jacq.
Solanaceae	*Brugmansia arborea* (L.) Steud.
Solanaceae	*Cestrum corymbosum* Schltdl.
Solanaceae	*Cestrum macrophyllum* Vent.
Solanaceae	*Cestrum schlechtendahlii* G.Don
Solanaceae	*Cestrum sp. 1*
Solanaceae	*Cestrum sp. 2*
Solanaceae	*Markea coccinea* Rich.
Styracaceae	*Styrax ferrugineus* Nees & Mart.
Theaceae	*Gordonia fruticosa* (Schrad.) H.Keng
Tropaeolaceae	*Tropaeolum moritzianum* Klotzsch
Tropaeolaceae	*Tropaeolum pentaphyllum* Lam.
Velloziaceae	*Barbacenia blanchetii* Goethart & Henrard
Velloziaceae	*Barbacenia flava* Mart. ex Schult. & Schult.f.
Velloziaceae	*Barbacenia gentianoides* Goethart & Henrard
Velloziaceae	*Barbacenia luzulifolia* Mart. ex Schult. & Schult.f.
Velloziaceae	*Barbacenia williamsii* L.B.Sm.
Velloziaceae	*Vellozia epidendroides* Mart.
Verbenaceae	*Citharexylum spinosum* L.
Verbenaceae	*Lantana camara* L.
Verbenaceae	*Lantana nivea* Vent.

Family	Plant Species
Verbenaceae	*Stachytarpheta crassifolia* Schrad.
Verbenaceae	*Stachytarpheta gesnerioides* Cham.
Verbenaceae	*Stachytarpheta glabra* Cham.
Verbenaceae	*Stachytarpheta jamaicensis* (L.) Vahl
Verbenaceae	*Stachytarpheta mexiae* Moldenke
Verbenaceae	*Stachytarpheta quadrangula* Nees & Mart.
Verbenaceae	*Stachytarpheta urticifolia* (Salisb.) Sims
Violaceae	*Paypayrola hulkiana* Pulle
Vitaceae	*Cissus simsiana* Roem. & Schult.
Vitaceae	*Cissus verticillata* (L.) Nicolson & C.E.Jarvis
Vochysiaceae	*Qualea grandiflora* Mart.
Vochysiaceae	*Qualea multiflora* Mart.
Vochysiaceae	*Qualea parviflora* Mart.
Vochysiaceae	*Salvertia convallariaeodora* A.St.-Hil.
Vochysiaceae	*Vochysia cinnamomea* Pohl
Vochysiaceae	*Vochysia emarginata* Vahl
Vochysiaceae	*Vochysia pyramidalis* Mart.
Vochysiaceae	*Vochysia rufa* Mart.
Vochysiaceae	*Vochysia sp.*
Vochysiaceae	*Vochysia tucanorum* Mart.
Xanthorrhoeaceae	*Phormium tenax* J.R.Forst. & G.Forst.
Zingiberaceae	*Hedychium coronarium* J.Koenig
Zingiberaceae	*Renealmia alpinia* (Rottb.) Maas
Zingiberaceae	*Renealmia breviscapa* Poepp. & Endl.
Zingiberaceae	*Renealmia cernua* (Sw. ex Roem. & Schult.) J.F.Macbr.
Zingiberaceae	*Renealmia krukovii* Maas
Zingiberaceae	*Renealmia pyramidalis* (Lam.) Maas
Zingiberaceae	*Renealmia sessilifolia* Gagnep.
Zingiberaceae	*Renealmia sp.*
Zingiberaceae	*Zingiberaceae sp.*

Hummingbird species

Phylogenetic lineage	Hummingbird Species
Bee	*Archilochus colubris*
Bee	*Atthis heloisa*
Bee	*Calothorax lucifer*
Bee	*Chaetocercus mulsant*
Bee	*Mellisuga helenae*
Bee	*Mellisuga minima*
Bee	*Selasphorus calliope*
Bee	*Selasphorus flammula*
Bee	*Selasphorus platycercus*
Bee	*Selasphorus rufus*

Phylogenetic lineage	Hummingbird Species
Bee	*Selasphorus sasin*
Bee	*Selasphorus scintilla*
Brilliant	*Aglaeactis castelnaudii*
Brilliant	*Aglaeactis cupripennis*
Brilliant	*Boissonneaua flavescens*
Brilliant	*Boissonneaua jardini*
Brilliant	*Clytolaema rubricauda*
Brilliant	*Coeligena helianthea*
Brilliant	*Coeligena lutetiae*
Brilliant	*Coeligena prunellei*
Brilliant	*Coeligena torquata*
Brilliant	*Coeligena wilsoni*
Brilliant	*Ensifera ensifera*
Brilliant	*Eriocnemis cupreoventris*
Brilliant	*Eriocnemis derbyi*
Brilliant	*Eriocnemis mosquera*
Brilliant	*Eriocnemis vestita*
Brilliant	*Heliodoxa aurescens*
Brilliant	*Heliodoxa imperatrix*
Brilliant	*Heliodoxa jacula*
Brilliant	*Heliodoxa rubinoides*
Brilliant	*Lafresnaya lafresnayi*
Brilliant	*Ocreatus underwoodii*
Brilliant	*Pterophanes cyanopterus*
Brilliant	*Urosticte benjamini*
Coquette	*Adelomyia melanogenys*
Coquette	*Aglaiocercus coelestis*
Coquette	*Aglaiocercus kingii*
Coquette	*Chalcostigma herrani*
Coquette	*Heliangelus amethysticollis*
Coquette	*Lesbia nuna*
Coquette	*Lophornis chalybeus*
Coquette	*Lophornis magnificus*
Coquette	*Metallura tyrianthina*
Coquette	*Oreonympha nobilis*
Coquette	*Oreotrochilus estella*
Emerald	*Amazilia beryllina*
Emerald	*Amazilia brevirostris*
Emerald	*Amazilia candida*
Emerald	*Amazilia cyanifrons*
Emerald	*Amazilia cyanocephala*
Emerald	*Amazilia fimbriata*
Emerald	*Amazilia franciae*
Emerald	*Amazilia lactea*
Emerald	*Amazilia rutila*
Emerald	*Amazilia tobaci*
Emerald	*Amazilia tzacatl*

Phylogenetic lineage	Hummingbird Species
Emerald	*Amazilia versicolor*
Emerald	*Amazilia yucatanensis*
Emerald	*Calliphlox amethystina*
Emerald	*Calliphlox mitchellii*
Emerald	*Campylopterus curvipennis*
Emerald	*Campylopterus hemileucurus*
Emerald	*Campylopterus largipennis*
Emerald	*Chlorestes notata*
Emerald	*Chlorostilbon canivetii*
Emerald	*Chlorostilbon gibsoni*
Emerald	*Chlorostilbon lucidus*
Emerald	*Chlorostilbon maugeaus*
Emerald	*Chlorostilbon mellisugus*
Emerald	*Chlorostilbon olivaresi*
Emerald	*Chlorostilbon poortmani*
Emerald	*Chlorostilbon ricordii*
Emerald	*Chrysuronia oenone*
Emerald	*Cyanophaia bicolor*
Emerald	*Cynanthus latirostris*
Emerald	*Eupetomena macroura*
Emerald	*Eupherusa nigriventris*
Emerald	*Hylocharis chrysura*
Emerald	*Hylocharis cyanus*
Emerald	*Hylocharis leucotis*
Emerald	*Klais guimeti*
Emerald	*Leucochloris albicollis*
Emerald	*Orthorhyncus cristatus*
Emerald	*Phaeochroa cuvieri*
Emerald	*Stephanoxis lalandi*
Emerald	*Thalurania colombica*
Emerald	*Thalurania fannyi*
Emerald	*Thalurania furcata*
Emerald	*Thalurania glaucopis*
Emerald	*Trochilus polytmus*
Gem	*Eugenes fulgens*
Gem	*Heliomaster constantii*
Gem	*Heliomaster squamosus*
Gem	*Lampornis amethystinus*
Gem	*Lampornis calolaema*
Gem	*Lampornis castaneoventris*
Gem	*Lampornis clemenciae*
Gem	*Lampornis hemileucus*
Gem	*Lamprolaima rhami*
Gem	*Panterpe insignis*
Hermit	*Anopetia gounellei*
Hermit	*Eutoxeres aquila*
Hermit	*Glaucis hirsutus*

Phylogenetic lineage	Hummingbird Species
Hermit	*Phaethornis bourcieri*
Hermit	*Phaethornis eurynome*
Hermit	*Phaethornis guy*
Hermit	*Phaethornis hispidus*
Hermit	*Phaethornis longirostris*
Hermit	*Phaethornis longuemareus*
Hermit	*Phaethornis malaris*
Hermit	*Phaethornis pretrei*
Hermit	*Phaethornis ruber*
Hermit	*Phaethornis squalidus*
Hermit	*Phaethornis striigularis*
Hermit	*Phaethornis stuarti*
Hermit	*Phaethornis subochraceus*
Hermit	*Phaethornis superciliosus*
Hermit	*Phaethornis syrmatophorus*
Hermit	*Ramphodon naevius*
Hermit	*Threnetes niger leucurus*
Hermit	*Threnetes ruckeri*
Mango	*Anthracothorax dominicus*
Mango	*Anthracothorax nigricollis*
Mango	*Anthracothorax prevostii*
Mango	*Anthracothorax viridis*
Mango	*Augastes lumachella*
Mango	*Augastes scutatus*
Mango	*Chrysolampis mosquitus*
Mango	*Colibri coruscans*
Mango	*Colibri delphinae*
Mango	*Colibri serrirostris*
Mango	*Colibri thalassinus*
Mango	*Doryfera ludoviciae*
Mango	*Eulampis holosericeus*
Mango	*Eulampis jugularis*
Mango	*Heliactin bilophus*
Mango	*Polytmus guainumbi*
Topaze	*Florisuga fusca*
Topaze	*Florisuga mellivora*
Topaze	*Topaza pyra*

Appendix S2 Phylogenetic methods

Plant phylogenies

For each community we extracted the phylogenetic relatedness of plants from Phylomatic's megatree (phylodiversity.net\phylomatic). Branch lengths were thereafter estimated with the *bladj* function from Phylocom (Webb *et al*., 2008), using calibration dates from Wikström *et al.* (2001).

Hummingbird phylogenies

For each community we extracted the phylogenetic relatedness of hummingbirds from the most complete to date hummingbird phylogeny, published in McGuire *et al.* (2014), which uses a time-calibrated, multi-locus Bayesian phylogenetic estimate constructed from DNA samples representing 284 hummingbird species.

The phylogenetic tree of McGuire *et al.* (2014) did not include eight hummingbird species represented in our networks, for which we had to approximate phylogenetic distances. Approximations were evaluated individually for each species, aiming to find the most accurate and conservative distance value in each case:

- Values for *Schistes geoffroy* were substituted for those of their most closely related species present in the phylogenetic tree: *Augastes lumachella* and *A. scutatus.*
- Values for *Amazilia saucerrottei* were substituted for those of their most closely related species present in the phylogenetic tree: *A. cyanifrons.*
- Values for *Campylopterus excellens* were substituted for those of their most closely related species present in the phylogenetic tree: *C. curvipennis.*
- Values for *Chlorostilbon mellisugus* were substituted for those of their most closely related species present in the phylogenetic tree: *C. gibsoni.*
- We loosely placed *Phaethornis gounellei* in the base of its clade using the minimum

value among *Phaethornis* species.

- We placed *P. stuarti* similarly using the minimum value of the “Pygmornis” clade within *Phaethornis*.
- Values for *Chlorostilbon olivaresi* and *Mellisuga helenae* were assigned as the average distance from the con-genera species present in the phylogenetic tree.

Analysis of phylogenetic signal on bipartite interaction networks

Following the methodology described in Ives & Godfray (2006), we examined whether closely related species interact with a similar array of partners. In other words, we quantified the effect of phylogeny on species interaction pattern. To do so, first, for each community and both for plant and hummingirds, we used the above described phylogenies to calculate variance-covariance matrices (vcv), which represent the phylogenetic distance among species. Variance-covariance matrices were constructed using the *“vcv”* function from the R package *ape* (Paradis *et al.,* 2004). This approach assumes that the interaction frequency between plants and hummingbirds is given by the product of the vcv matrices. Therefore, for a given plant species *i*, the phylogenetic correlation between visits from hummingbirds *a* and *b* is given by the hummingbird phylogeny, and *vice versa* for hummingbirds. If both plants and hummingbirds are closely-related, visits between plant *i* and hummingbird *a* and plant *j* and hummingbird *b* are correlated. The strength of the phylogenetic association between plants and hummingbirds was then modeled statistically by fitting vcv matrices to each observed bipartite interaction matrix through a linear model using the *“pblm”* function from the R package *picante* (Kembel *et al*., 2010). This analysis results in a parameter *d* which determines the strength of the phylogenetic signal on species' interaction pattern. Specifically, this analysis provides two independent measures of phylogenetic signal (*d*), one for each trophic group (d_{plants} and $d_{hummingbirds}$ in our case), calculated statistically through an estimated generalized least squares model (EGLS), which does not assume that phylogenetic distance nor the interaction frequencies are normally distributed. Values of d=0 represent a lack of phylogenetic correlation, whereas d=1 represents a maximum correlation of phylogenetic signals. Disruptive selection processes show values above 1 (Ives & Godfray, 2006). We truncated the d-value to a maximum of d=2, as d_{plants} values for network 11 (Cuba) had an initial value of 6.43, being clearly an outlier (Table Appendix S2). Confidence intervals for d were calculated by bootstrap replication data from standardized residuals through the same EGLS used to fit the original data over 2000 replication sets. Thereafter, we calculated the overall strength of the phylogenetic signal on the interaction matrix by evaluating three different models, one assuming no phylogenetic signal ($d_{\mathrm{plants}}=d_{\mathrm{hummingbirds}}=0$; Star model), one assuming a maximum phylogenetic signal ($d_{\mathrm{plants}}=d_{\mathrm{hummingbirds}}=1$; Brownian model), and a final one which incorporated the observed phylogenetic signals combined (estimated d_{plants} and $d_{\mathrm{hummingbirds}}$; Data model). Again, these models were fitted through an EGLS approximation. To choose the model which best describes the data we quantified the goodness of fit of each model as mean squared error (MSE), so that the lowest value of MSE indicate the best fit.

Notice however that this analysis should not be acknowledged as a test for particular phylogenetic hypothesis, but rather a measure of how much does the phylogenetic relatedness among species affect their interaction pattern.

REFERENCES

Ives, A.R. & Godfray, H.C.J. (2006) Phylogenetic analysis of trophic associations. *American Naturalist*, **168,** E1–E14.

Kembel, S.W., Cowan, P.D., Helmus, M.R., Cornwell, W.K., Morlon, H., Ackerly, D.D., et al. (2010) Picante: R tools for integrating phylogenies and ecology. *Bioinformatics*, **26,** 14631464.

McGuire, J.A., Witt, C.C., Remsen, J.V., Jr., Corl, A., Rabosky, D.L., Altshuler, D.L., et al. (2014) Molecular phylogenetics and the diversification of hummingbirds. *Current Biology*, **24**, 910–916.

Paradis, E., Claude, J., & Strimmer, K. (2004) APE: analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20,** 289–290.

Webb, C.O., Ackerly, D.D. & Kembel, S.W. (2008) Phylocom: software for the analysis of phylogenetic community structure and trait evolution. *Bioinformatics*, **24,** 2098–2100.

Wikström, N., Savolainen, V., & Chase, M.W. (2001). Evolution of the angiosperms: Calibrating the family tree. *Proceedings of the Royal Society of London B*, **268,** 2211–2220.

Appendix S2 Table A. Results of the phylogenetic analysis for each community

Dataset ID number	MSE$_{Data}$	MSE$_{Star}$	MSE$_{Brownian}$	CI MIN d$_{plants}$	d$_{plants}$	CI MAX d$_{plants}$	CI MIN d$_{hummingbirds}$	d$_{hummingbirds}$	CI MAX d$_{hummingbirds}$
1	15.468	19.632	36.420	0.000	0.094	0.452	0.002	0.243	0.467
2	9.887	13.973	16.665	0.000	0.293	0.639	0.000	0.310	2.395
3	25.700	25.277	183.797	0.955	0.883	1.056	0.000	0.000	0.114
4	14.194	15.611	34.123	0.000	0.161	0.403	0.000	0.043	0.257
5	54.965	59.220	101.878	0.000	0.263	0.642	0.000	0.092	0.330
6	2.270	4.220	5.354	0.354	0.700	1.018	0.000	0.000	0.156
7	109.205	116.143	207.956	0.000	0.252	0.521	0.000	0.053	0.284
8	69.545	78.534	122.920	0.000	0.093	0.364	0.000	0.295	0.574
9	16.398	21.877	40.001	0.181	0.587	1.009	0.000	0.000	0.119
10	139.116	139.116	336.877	0.000	0.000	0.000	0.000	0.000	0.000
11	137.292	247.429	242.988	0.931	2.000	17.038	0.000	0.098	0.765
12	6.258	7.458	13.106	0.034	0.654	1.280	0.000	0.000	0.293
13	36.780	37.552	55.636	0.000	0.041	0.637	0.000	0.119	0.787
14	37.913	38.519	60.741	0.000	0.041	1.873	0.000	0.120	1.400
15	16.017	16.433	25.504	0.000	0.151	2.000	0.000	0.000	0.838
16	1.454	1.642	2.379	0.068	0.290	0.499	0.000	0.155	0.319
17	1.017	1.577	1.124	0.089	1.056	2.452	0.000	0.261	1.888
18	4.161	4.471	5.857	0.118	0.706	1.387	0.000	0.065	0.377
19	12.602	21.129	18.718	0.042	1.119	3.076	0.000	0.060	0.514
20	28.627	28.718	43.951	0.000	0.000	0.734	0.000	0.000	0.458
21	1.552	2.167	2.627	0.032	0.383	0.804	0.057	0.310	0.520
22	1.761	2.415	3.948	0.268	1.703	5.247	0.000	0.000	0.291
23	1.490	1.785	1.933	0.000	0.000	0.877	0.000	0.396	0.706
24	63.498	67.344	119.495	0.071	0.420	0.841	0.000	0.006	0.268
25	9.717	9.889	21.005	0.000	0.046	0.232	0.000	0.052	0.213
26	7.456	7.581	15.548	0.000	0.045	0.396	0.000	0.000	0.237
27	2.885	3.426	3.618	0.168	0.397	0.599	0.000	0.292	0.779
28	41.405	42.071	63.699	0.000	0.112	0.423	0.000	0.053	0.306
29	15.717	18.415	29.404	0.025	0.611	1.223	0.000	0.000	0.246
30	52.055	56.779	132.613	0.000	0.009	0.331	0.000	0.084	0.413
31	3.738	4.052	9.265	0.057	0.306	0.546	0.000	0.000	0.095
32	2.873	3.296	4.361	0.056	0.271	0.455	0.056	0.267	0.436
33	0.603	0.723	0.865	0.000	0.066	0.379	0.026	0.405	0.674
34	2.385	2.397	5.426	0.000	0.000	0.186	0.000	0.000	0.130
35	12.454	19.826	23.805	0.257	1.150	2.362	0.000	0.013	0.330
36	6.404	7.762	7.988	0.000	0.240	0.827	0.000	0.499	1.383
37	10.555	10.837	13.897	0.000	0.284	2.633	0.000	0.000	1.158
38	6.022	6.340	11.381	0.007	0.214	0.430	0.000	0.028	0.197
39	23.433	23.874	44.968	0.000	0.000	0.272	0.000	0.136	0.390
40	1.956	2.205	3.601	0.132	0.350	0.551	0.000	0.000	0.142
41	1.616	2.121	2.510	0.108	0.235	0.359	0.266	0.409	0.514
42	1.716	2.047	2.875	0.000	0.009	0.296	0.047	0.388	0.607
43	1.075	1.083	2.293	0.000	0.045	0.178	0.000	0.000	0.085
44	1.783	2.562	2.289	0.157	0.668	1.275	0.001	0.340	0.609
45	1.165	1.168	1.778	0.000	0.000	0.150	0.001	0.143	0.316

Dataset ID number	MSE_{Data}	MSE_{Star}	$MSE_{Brownian}$	CI MIN d_{plants}	d_{plants}	CI MAX d_{plants}	CI MIN $d_{hummingbirds}$	$d_{hummingbirds}$	CI MAX $d_{hummingbirds}$
46	0.931	0.935	2.388	0.000	0.000	2.800	0.000	0.008	0.412
47	0.472	0.493	1.565	0.000	0.426	1.899	0.000	0.000	0.470
48	10.432	11.690	16.730	0.000	0.033	0.961	0.000	0.350	0.971
49	134.072	149.850	165.457	0.174	0.553	0.932	0.000	0.255	0.519
50	0.649	0.701	3.976	0.000	0.310	0.871	0.000	0.000	0.159
51	4.974	6.059	6.535	0.000	0.107	0.476	0.102	0.547	0.798
52	1.289	1.600	1.505	0.182	0.427	0.765	0.204	0.397	0.614
53	11.288	11.288	35.158	0.000	0.000	0.228	0.000	0.000	0.186
54	0.797	0.821	1.811	0.000	0.144	0.340	0.000	0.000	0.132

Appendix S3 Effect of the differences in sampling effort among data sets on network structure

Network data were collected from various studies employing different sampling efforts, which could potentially bias resulting differences in network structure among communities. We measured sampling effort as sampling intensity, i.e. the ratio between number of interactions and the geometric mean of the number of plants and hummingbirds in the community as in Schleuning et al. (2014). Simple correlations presented in Table S2 show a relationship between sampling intensity and corrected complementary specialization and with observed modularity, both in the global and mainland datasets. Therefore, in order to reveal whether these correlations had any repercussions in the conclusions obtained from the macroecological models, we repeated the macroecological models presented in the main manuscript including sampling intensity as a predictor variable (Table Appendix S3).

Overall trends remained constant. For corrected complementary specialization (H_2'), the inclusion of sampling intensity had no overall effects on the other predictor variables in the global model, while in the mainland analysis network size lost some of its importance, but the rank of importance remained the same. For observed modularity, the only difference was that $d_{\text{hummingbirds}}$ lost some of its importance in the global dataset, while insularity became an important predictor, with islands showing a lower modularity than mainland communities (Table Appendix S3), confirming findings from other performed complementary macroecological analysis (Appendix S4) which suggest differences between mainland and island communities.

REFERENCES

Schleuning, M., Ingmann, L., Strauss, R., Fritz, S.A., Dalsgaard, B., Matthias Dehling, D., et al. (2014) Ecological, historical and evolutionary determinants of modularity in weighted seed-dispersal networks. *Ecology Letters,* 17, 454–463.

Appendix S3 Table A. Relationship between species richness, phylogenetic signal and environment, and corrected complementary specialization (*H_2'*) and observed modularity (QuanBiMo) across the Americas (Global dataset) and the mainland, i.e. when excluding insular communities (Only Mainland), when including Sampling effort as a predictor variable, as these network metrics appeared to be correlated with sampling intensity (Table S2). For each network metric, the standardized regression coefficients are reported for ordinary least squares regression for a model including all variables ("Full") and for a model averaged across all possible models using Akaike Weights (AICc w_i - "Averaged"). For the averaged models, the relative importance of each predictor variable ("Σ w_i") is given by the Akaike Weights (AICc w_i). Predictors with high importance are marked in bold. Phylogenetic signal among plants and hummingbirds, d_p and d_h, respectively; Mean annual temperature, MAT; Temperature seasonality, TS; Mean annual precipitation, MAP; Precipitation seasonality, PS; Velocity of temperature change since the last Glacial Maximum, MAT velocity; Velocity of precipitation change since the last Glacial Maximum, MAP velocity. The significance of Moran's *I* was tested with 10 distance classes and a permutation test with 10,000 iterations. In all models multicollinearity was not an issue, i.e. VIF≤ 3.3, CN ≤ 4.2, and there was no positive spatial autocorrelation, i.e. Moran's *I* was non-significant.

					Species richness	Phylogenetic signal		Environmental factors							Sampling effort
		Model	AICc	R^2	Network size	d_p	d_h	Insularity	MAT	TS	MAP	PS	MAT velocity	MAP velocity	Sampling intensity
Global dataset (54 networks)	***H_2'* corrected**	Full	-60.862	0.620	**0.346**	-0.027	**-0.228**	-0.311	0.285	0.138	0.237	-0.165	-0.485	0.140	**0.341**
		Averaged			**0.415**	-0.089	**-0.297**	-0.245	0.200	0.103	0.305	-0.206	-0.289	0.069	**0.342**
		Σ w_i			**0.956**	0.264	**0.868**	0.521	0.385	0.272	0.646	0.516	0.734	0.254	**0.944**
	QuanBiMo *observed*	Full	-69.765	0.658	**0.371**	-0.170	-0.181	**-0.373**	0.202	-0.044	0.138	-0.087	-0.052	-0.085	**-0.289**
		Averaged			**0.380**	-0.202	-0.225	**-0.345**	0.192	-0.071	0.305	-0.098	-0.063	-0.091	**-0.304**
		Σ w_i			**0.953**	0.653	0.659	**0.886**	0.447	0.235	0.710	0.279	0.252	0.266	**0.872**
Only Mainland (45 networks)	***H_2'* corrected**	Full	-59.753	0.652	0.212	-0.045	**-0.281**	na	**0.478**	0.091	0.114	-0.223	**-0.708**	0.240	**0.344**
		Averaged			0.249	-0.057	**-0.305**	na	**0.512**	0.044	0.208	-0.266	**-0.680**	0.277	**0.370**
		Σ w_i			0.641	0.195	**0.871**	na	**0.961**	0.191	0.340	0.736	**0.985**	0.614	**0.956**
	QuanBiMo *observed*	Full	-54.411	0.619	**0.262**	-0.217	**-0.280**	na	0.313	-0.118	0.052	-0.103	-0.184	-0.075	**-0.311**
		Averaged			**0.309**	-0.239	**-0.292**	na	0.287	-0.168	0.327	-0.105	-0.221	-0.086	**-0.347**
		Σ w_i			**0.756**	0.694	**0.754**	na	0.583	0.356	0.549	0.262	0.373	0.237	**0.809**

Appendix S4 Results of macroecological models on observed network metrics

As an additional analysis, we performed an equivalent macroecological analysis on observed network metrics instead of on null model corrected metrics as presented in the main manuscript. By analyzing observed network metrics, we are investigating the "raw" level of specialization, regardless of the community context (species and interaction richness, interaction frequency distribution). This complementary analysis allow us to understand more fully the effect of correcting for network metrics and the relationships between the studied variables (Tables S4A and S4B).

The amount of variability explained by the models is similar to that of corrected metrics, but important differences in the role of the different predictor variables arose. First of all, species richness lost its high importance except for modularity in the global dataset. In other words, in general, larger communities did not show higher levels of observed specialization (complementary specialization and modularity). Together with the results from the corrected-metrics analysis, where species richness exhibited a strong and widespread association with higher levels of specialization, we can conclude that *only when compared to communities with the same attributes as empirical matrices* do species richness impact network structure.

Similarly, hummingbird phylogenetic signal, the other variable exhibiting a constant association with corrected network structure, is only related with complementary specialization, and not modularity, when examining observed metrics. As our null model correction does not account for species' phylogenetic relatedness, we may conclude that higher levels of corrected modularity are indeed achieved when closely-related hummingbirds form distinct modules.

As with corrected metrics, mean annual temperature and temperature velocity were related only to higher levels of complementary specialization on mainland communities, both showing the highest regression coefficients of all predictors in the full models.

Additionaly, insularity and mean annual precipitation became important determinants of observed specialization, with mainland and humid communities showing higher levels of complementary specialization and modularity than insular communities or networks from drier environments. The effect of these predictor variables disappeared when modeling corrected metrics, suggesting that insularity and MAP may affect either species/interaction richness or interaction distribution, leading to higher observed levels of specialization (Dalsgaard *et al.*, 2011).

REFERENCES

Dalsgaard, B., Magård, E., Fjeldså, J., Martín González, A.M., Rahbek, C., Olesen, J.M., et al. (2011) Specialization in plant-hummingbird networks is associated with species richness, contemporary precipitation and quaternary climate-change velocity. *PloS ONE,* **6**, e25891.

Appendix S4 Table A. Relationship between species richness, phylogenetic signal and environment, and complementary specialization (H_2') and modularity (QuanBiMo) across the Americas (Global dataset) and the mainland, i.e. when excluding insular communities (Only Mainland). Complementary specialization measures the exclusiveness of the interactions in the community, whereas modularity describes a community pattern where species interact more frequently within subsets of species and loosely among subsets. For each network metric, the standardized regression coefficients are reported for ordinary least squares regression for a model including all variables ("Full") and for a model averaged across all possible models using Akaike Weights (AICc w_i - "Averaged"). For the averaged models, the relative importance of each predictor variable ("$\Sigma\ w_i$") is given by the Akaike Weights (AICc w_i). Phylogenetic relatedness among plants and hummingbirds, d_p and d_h, respectively; Mean annual temperature, MAT; Temperature seasonality, TS; Mean annual precipitation, MAP; Precipitation seasonality, PS; Velocity of temperature change since the last Glacial Maximum, MAT velocity; Velocity of precipitation change since the last Glacial Maximum, MAP velocity. The significance of Moran's *I* was tested with 10 distance classes and a permutation test with 10,000 iterations. In all models multicollinearity was not an issue, i.e. VIF ≤ 4.0, CN ≤ 3.3, and there was no positive spatial autocorrelation, i.e. Moran's *I* was non-significant.

					Species richness	Phylogenetic signal		Environmental factors						
		Model	**AICc**	**R^2**	**Network size**	**d_p**	**d_h**	**Insularity**	**MAT**	**TS**	**MAP**	**PS**	**MAT velocity**	**MAP velocity**
Global dataset (54 networks)	H_2'	Full	-35.112	0.578	0.210	-0.069	**-0.231**	**-0.453**	0.355	0.085	**0.344**	-0.085	-0.317	0.129
		Averaged			0.249	-0.119	**-0.254**	**-0.401**	0.290	0.040	**0.423**	-0.101	-0.225	0.115
		$\Sigma\ w_i$			0.659	0.323	**0.767**	**0.916**	0.573	0.218	**0.965**	0.268	0.417	0.295
	QuanBiMo	Full	-65.124	0.602	**0.273**	-0.119	-0.117	**-0.449**	0.203	-0.076	**0.301**	-0.049	-0.037	-0.128
		Averaged			**0.259**	-0.139	-0.112	**-0.446**	0.202	-0.098	**0.446**	-0.028	-0.063	-0.095
		$\Sigma\ w_i$			**0.794**	0.411	0.324	**0.993**	0.483	0.276	**0.989**	0.216	0.261	0.280
Only Mainland (45 networks)	H_2'	Full	-31.253	0.574	0.076	-0.067	**-0.300**	na	**0.518**	0.001	0.238	-0.105	**-0.491**	0.197
		Averaged			0.145	-0.094	**-0.382**	na	**0.525**	-0.065	0.327	-0.167	**-0.475**	0.223
		$\Sigma\ w_i$			0.325	0.250	**0.858**	na	**0.924**	0.223	0.731	0.351	**0.832**	0.477
	QuanBiMo	Full	-51.864	0.561	0.159	-0.221	-0.234	na	0.314	-0.149	**0.232**	-0.069	-0.179	-0.136
		Averaged			0.181	-0.232	-0.210	na	0.298	-0.181	**0.455**	-0.047	-0.230	-0.101
		$\Sigma\ w_i$			0.412	0.637	0.496	na	0.585	0.383	**0.938**	0.221	0.384	0.261

Appendix S4 Table B. Coefficients of determination (R^2) from partial regression local models separating the effect of species richness, species' evolutionary history and environmental factors as predictors of corrected network structure of American communities, when including climate change velocity as an estimate of historical climate stability. We estimated R^2 values in "full" models, i.e. in models including all ten predictor variables (see Appendix S4 Table A). "Total model" reflects the total amount of variation in network structure explained by the full model; "Total species richness", "Total phylogenetic signals" and "Total environmental factors" reflect the variation explained by species richness, phylogenetic signal and environmental factors, respectively; "Only species richness", "Only phylogenetic signal" and "Only environmental factors" reflect the amount of variation in network structure explained by the specified predictor-type and not by any other (i.e. the unique variation); Finally, "shared" reflects the variation attributable to the pair of specified predictor types or to all factors combined. See Table S4A for standardized coefficients of each variable and more details of model fit.

	Global dataset (54 networks)		**Only Mainland (45 networks)**	
	H_2' observed	**QuanBiMo observed**	**H_2' observed**	**QuanBiMo observed**
Total model	0.58	0.60	0.57	0.56
Total species richness	0.19	0.27	0.11	0.14
Total phylogenetic signal	0.23	0.18	0.25	0.23
Total environmental factors	0.52	0.54	0.51	0.48
Unique species richness	0.03	0.04	0.00	0.02
Unique phylogenetic signal	0.04	0.02	0.06	0.07
Unique environmental factors	0.19	0.21	0.23	0.23
Shared species richness – phylogeny	0.00	0.00	0.00	0.00
Shared species richness – environmental factors	0.14	0.17	0.09	0.08
Shared phylogeny – environmental factors	0.16	0.11	0.17	0.12
Shared all factors	0.04	0.06	0.02	0.05

Appendix S5 Complementary macroecological analyses

As different climate change metrics may capture different aspects important for biodiversity (Garcia *et al*., 2014), to evaluate more comprehensively the impact of historical climate-change we calculated another summarizations of historical climatic stability: *the anomaly of mean annual temperature and mean annual precipitation* between the LGM and the present, calculated as pre-industrial minus LGM precipitation/temperature (i.e. positive values indicate that conditions were drier or colder at LGM than at present). Whereas climate change velocities reflect the speed of climate change irrespective of the direction of the change, anomalies reflect the direction of climate change. As with climate change velocities, projections of the global climate during the LGM and pre-industry were generated by Hadley Centre Coupled Model Version 3 (HadCM3) with a resolution of 3.75 × 2.5 arc degrees (Singarayer & Joy 2010), and were downscaled to 0.1 × 0.1 arc degrees.

We performed a set of models equivalent to those presented in the main text (Diniz-Filho et al. 2008) but which included climate change anomaly instead of climate change velocity. Temperature anomaly was $\log_{10}$-transformed. Models including climatic anomaly gave a poorer fit to our data, explaining less variability and raising multicollinearity concerns. Nevertheless, strong patterns disclosed by the macroecological models with climatic velocity persisted (Tables S4A-B).

The significance and importance of species richness and hummingbird phylogenetic signal was again widespread and showed similar values than the models which included change velocity as measure of historical climate stability. We found a stronger role, although still non-significant, of the phylogenetic signal of plants, associated with lower levels of modularity on both datasets. Finally, and most importantly, neither temperature nor precipitation anomaly had any effect on any of the studied variables.

REFERENCES

Diniz-Filho, J.A.F., Rangel, T.F. L. & Bini, L.M. (2008) Model selection and information theory in geographical ecology. *Global Ecology and Biogeography*, **17,** 479–488.

Garcia, R.A., Cabeza, M., Rahbek, C., & Araújo, M.B. (2014) Multiple Dimensions of Climate Change and Their Implications for Biodiversity. *Science*, **344**, 6183.

Singarayer, J.S,. & Valdes, P. J. (2010) High-latitude climate sensitivity to ice-sheet forcing over the last 120 kyr. *Quaternary Science Reviews*, **29,** 43–55.

Appendix S5 Table A. Relationship between species richness, phylogenetic signal and environment, and complementary specialization (H_2') and modularity (QuanBiMo) across the Americas (Global dataset) and the mainland, i.e. when excluding insular communities (Only Mainland), when including historical climate anomaly as a predictor of historical climatic stability. Complementary specialization measures the exclusiveness of the interactions in the community, whereas modularity describes a community pattern where species interact more frequently within subsets of species and loosely among subsets. For each network metric, the standardized regression coefficients are reported for ordinary least squares regression for a model including all variables (“Full”) and for a model averaged across all possible models using Akaike Weights (AICc w_i - “Averaged”). For the averaged models, the relative importance of each predictor variable (“$\Sigma\ w_i$”) is given by the Akaike Weights (AICc w_i). Phylogenetic signal among plants and hummingbirds, d_p and d_h, respectively; Mean annual temperature, MAT; Temperature seasonality, TS; Mean annual precipitation, MAP; Precipitation seasonality, PS; Velocity of temperature change since the last Glacial Maximum, MAT velocity; Velocity of precipitation change since the last Glacial Maximum, MAP velocity. The significance of Moran’s *I* was tested with 10 distance classes and a permutation test with 10,000 iterations. In all models multicollinearity was not an issue, i.e. VIF ≤ 5.1, CN ≤ 4.9, and there was no positive spatial autocorrelation, i.e. Moran's *I* was non-significant.

					Species richness	**Phylogenetic signal**		**Environmental factors**						
		Model	**AICc**	**R^2_{adj}**	**Network size**	**d_p**	**d_h**	**Insularity**	**MAT**	**TSN**	**MAP**	**PSN**	**MAT anomaly**	**MAP anomaly**
Global dataset (54 networks)	***H_2'***	Full	-46.828	0.474	**0.512**	-0.168	**-0.306**	-0.046	-0.004	0.111	0.026	-0.251	0.009	-0.046
		Averaged			**0.516**	-0.165	**-0.328**	-0.067	-0.024	0.080	0.101	-0.249	0.004	-0.023
		$\Sigma\ w_i$			**0.999**	0.458	**0.936**	0.240	0.218	0.261	0.276	0.738	0.216	0.224
	QuanBiMo	Full	-99.080	0.619	**0.630**	-0.186	**-0.237**	-0.210	0.110	0.075	-0.087	-0.242	0.022	-0.217
		Averaged			**0.636**	-0.194	**-0.277**	-0.141	0.024	0.054	0.118	-0.214	-0.053	-0.124
		$\Sigma\ w_i$			**1.000**	0.667	**0.908**	0.362	0.227	0.239	0.317	0.696	0.242	0.343
Only Mainland (45 networks)	***H_2'***	Full	-45.189	0.477	**0.422**	-0.146	**-0.337**	na	0.135	0.019	-0.388	-0.350	0.216	-0.215
		Averaged			**0.424**	-0.116	**-0.330**	na	0.079	0.039	-0.067	-0.275	-0.218	-0.047
		$\Sigma\ w_i$			**0.968**	0.282	**0.839**	na	0.237	0.217	0.246	0.695	0.479	0.229
	QuanBiMo	Full	-76.043	0.558	**0.539**	-0.217	**-0.301**	na	0.169	0.028	-0.285	-0.291	-0.081	-0.332
		Averaged			**0.534**	-0.192	**-0.293**	na	0.101	0.019	0.079	-0.251	-0.135	-0.183
		$\Sigma\ w_i$			**0.999**	0.510	**0.794**	na	0.265	0.209	0.282	0.676	0.312	0.410

Appendix S5 Table B. Coefficients of determination (R^2) from partial regression local models separating the effect of species richness, environmental factors and species' evolutionary history as predictors of corrected network structure of American communities when using climatic anomaly as an estimate for historical climatic stability. We estimated R^2 values in "full" models, i.e. in models including all ten predictor variables (see Appendix S5 Table A for standardized coefficients of each variable and more details of model fit). "Total model" reflects the total amount of variation in network structure explained by the model; "Total species richness", "Total phylogenetic signals" and "Total environmental factors" reflect the total variation explained by species richness, phylogenetic signal and environmental factors, respectively, whereas "Only species richness", "Only phylogenetic signal" and "Only environmental factors" reflect the unique variation in network structure explained by species richness, phylogenetic signal and environmental factors, respectively. Finally, "shared" reflect the shared variation described by the specified predictor sets, and "shared all factors" reflect variation attributable to species richness, phylogenetic signal and environmental factors.

	Global dataset (54 networks)		**Only Mainland (45 networks)**	
	H_2'	**QuanBiMo**	H_2'	**QuanBiMo**
Total model	0.47	0.62	0.48	0.56
Total species richness	0.25	0.44	0.20	0.33
Total phylogenetic signal	0.19	0.19	0.18	0.19
Total environmental factors	0.25	0.32	0.28	0.28
Unique species richness	0.16	0.24	0.12	0.20
Unique phylogenetic signal	0.08	0.06	0.08	0.08
Unique environmental factors	0.06	0.06	0.11	0.09
Shared species richness – phylogeny	0.00	0.00	0.00	0.00
Shared species richness – environmental factors	0.07	0.14	0.06	0.09
Shared phylogeny – environmental factors	0.08	0.07	0.08	0.06
Shared all factors	0.04	0.06	0.03	0.05

Table S1. Coordinates, description, location and data references for each studied community.

ID number	Latitude	Longitude	Site description and general location	Data Source Reference
1	-20.75	-42.92	Atlantic forest, SE Brazil	Abreu, C.R.M. & Vieira, M.F. (2004) Os beija-flores e seus recursos florais em um fragmento florestal de Viçosa, sudeste brasileiro. *Lundiana,* **5**, 129–134.
2	34.22	-116.95	Montane meadow, SW USA	Alarcón, R., Waser, N.M & Ollerton, J. (2008) Year-to-year variation in the topology of a plant-pollinator interaction network. *Oikos,* **117**, 1796–1807.
3	38.98	-106.97	Sub-alpine meadow, Central USA	Ollerton, J., Alarcón, R., Waser, N.M, Price, M.V., Watts, S., Cranmer, L., Hingston, A., Peter, C. & Rotenberry, J. (2009) A global test of the pollination syndrome hypothesis. *Annals of Botany,* **103**, 1471–1480.
4	-23.35	-44.83	Atlantic forest, SE Brazil	Araujo, A.C. (1996) Beija-flores e seus recursos florais numa área de planicie costeira do litoral norte de São Paulo, sudeste do Brasil. *MSc. Thesis*. Universidade Estadual de Campinas, Brazil.
5	19.50	-105.05	Tropical dry deciduous forest, W Mexico	Arizmendi, M.C. & Ornelas, J.F. (1990) Hummingbirds and their floral resources in a tropical dry forest in Mexico. *Biotropica,* **22**, 172–180.
6	-31.80	-52.42	Pampa, S Brazil	Vizentin-Bugoni, J. & Rui, A.M. *Unpublished data*.
7	-22.50	-44.83	Highland Atlantic forest, SE Brazil	Canela, M.B.F. (2006) Interações entre plantas e beija-flores numa comunidade de floresta atlântica montana em Itatiaia, RJ. *Ph.D thesis.* Universidade Estadual de Campinas, Brazil.
8	-7.87	-36.40	Caatinga, NE Brazil	Las Casas, F.M.G., Azevedo Júnior, S.M. & Dias Filho, M.M. (2012) The community of hummingbirds (Aves: Trochilidae) and the assemblage of flowers in a Caatinga vegetation. *Brazilian Journal of Biology*, **72**, 51–58.
9	-11.48	-41.32	Altitudinal caatinga, NE Brazil	Moura, A.C. & Machado, C.G. Hummingbirds and their flowers at altitudinal dryland vegetation in Chapada Diamantina, northeast Brazil. *In preparation.*
10	-3.82	-70.27	Amazonian rainforest, SE Colombia	Cotton, P.A. (1998) The hummingbird community of a lowland Amazonian rainforest. *Ibis*, **140**, 512–521.
11	22.28	-81.20	Swamp forest, Hurricane disturbed, Cuba	Baquero, A.C. (2014) Evolutionary and ecological insight into hummingbird-plant communities in the Caribbean. *MSc Thesis.* University of Copenhagen, Denmark.
12	15.35	-61.30	Elfin forest, Dominica	Dalsgaard, B., Martín González, A.M., Olesen, J.M., Ollerton, J., Timmermann, A., Andersen, L.H. & Tossas, A.G. (2009) Plant–hummingbird interactions in the West Indies: floral specialisation gradients associated with environment and hummingbird size. *Oecologia,* **159**, 757–766.
13	15.25	-61.37	Coastal dry scrubland, Dominica	Dalsgaard, B., Martín González, A.M., Olesen, J.M., Ollerton, J., Timmermann, A., Andersen, L.H. & Tossas, A.G. (2009) Plant–hummingbird interactions in the West Indies: floral specialisation gradients associated with environment and hummingbird size. *Oecologia,* **159**, 757–766.

ID number	Latitude	Longitude	Site description and general location	Data Source Reference
14	12.10	-61.70	Elfin forest, Grenada	Dalsgaard, B., Martín González, A.M., Olesen, J.M., Ollerton, J., Timmermann, A., Andersen, L.H. & Tossas, A.G. (2009) Plant–hummingbird interactions in the West Indies: floral specialisation gradients associated with environment and hummingbird size. *Oecologia,* **159**, 757–766.
15	12.10	-61.68	Rainforest, Grenada	Dalsgaard, B., Martín González, A.M., Olesen, J.M., Ollerton, J., Timmermann, A., Andersen, L.H. & Tossas, A.G. (2009) Plant–hummingbird interactions in the West Indies: floral specialisation gradients associated with environment and hummingbird size. *Oecologia,* **159**, 757–766.
16	1.25	-77.43	High andean forest, Colombia	Gutierrez Zamora, E.A. & Rojas Nossa, S.V. (2001) Dinámica anual de la interacción colibrí-flor en ecosistemas altoandinos del volcán Galeras, Sur de Colombia. *BSc. Thesis*. Universidad Nacional de Colombia, Colombia.
17	18.35	-77.65	Evergreen lowland rainforest, Jamaica.	Ingversen, T. (2006) Plant-Pollinator Interactions on Jamaica and Dominica – The Centrality, Asymetry, and Modularity of Networks. *MSc. Thesis*. University of Aarhus, Denmark.
18	-27.27	-49.01	Atlantic Forest, low elevation	Kohler, G. (2011) Redes de interação planta-beija-flor em um gradiente altitudinal de Floresta Atlântica no Sul do Brasil. *MSc. Thesis*. Universidade Federal do Paraná, Brazil.
19	-27.26	-49.02	Atlantic Forest, mid elevation	Kohler, G. (2011) Redes de interação planta-beija-flor em um gradiente altitudinal de Floresta Atlântica no Sul do Brasil. *MSc. Thesis*. Universidade Federal do Paraná, Brazil.
20	-27.26	-49.02	Atlantic Forest, high elevation	Kohler, G. (2011) Redes de interação planta-beija-flor em um gradiente altitudinal de Floresta Atlântica no Sul do Brasil. *MSc. Thesis*. Universidade Federal do Paraná, Brazil.
21	19.23	-98.97	Highland temperate mosaic forest, Central Mexico	Lara, C. (2006) Temporal dynamics of flower use by hummingbirds in a highland temperate forest in México. *Ecoscience,* **13**, 23–29.
22	19.28	-98.23	Suburban forest, Central Mexico	Lara, C. *Unpublished data.*
23	19.40	-96.80	Protected cloud forest, Central Mexico	Lara, C. *Unpublished data.*
24	0.07	-72.45	Rainforest, Colombia	Rosero, L. (2003) Interações planta/beija-flor em três comunidades vegetais da parte sul do Parque Nacional Natural Chiribiquete, Amazonas (Colombia). *Ph.D. Thesis.* Universidade Estadual de Campinas, Brazil. Rosero-Lasprilla, L. & Sazima, M. (2004) Interacciones planta-colibrí en tres comunidades vegetales de la parte suroriental del Parque Nacional Natural Chiribiquete, Colombia. *Ornitologia Neotropical*, **15** (Suppl.), 183–190.
25	-13.12	-41.58	Highland caatinga, NE Brazil	Machado, C.G. (2009) Hummingbirds (Aves: Trochilidae) and their floral resources in an area of caatinga vegetation in the Chapada Diamantina, Bahia State, Northeast Brazil. *Zoologia*, **26**, 55–65.
26	-13.12	-41.57	Open cerrado, NE	Machado, C.G. (2014) The hummingbird community and the plants which they visit at a savannah in the

ID number	Latitude	Longitude	Site description and general location	Data Source Reference
			Brazil	Chapada Diamantina, Bahia, Brazil. *Bioscience Journal*, **30**, 1578–1587.
27	-12.98	-41.33	Campos rupestres, NE Brazil	Machado, C.G., Coelho, A.G., Santana, C.S., Rodrigues, M. (2007) Hummingbirds and their flowers in the 'campos rupestres' of Chapada Diamantina, Bahia, northeastern Brazil. *Revista Brasileira de Ornitologia*, **15**, 215–227.
28	10.44	-84.01	Cloud forest, low elevation, Costa Rica	Maglianesi, M.A., Blüthgen, N., Böhning–Gaese, K. & Schleuning, M. (2014) Morphological traits determine specialization and resource use in plant–hummingbird networks in the Neotropics. *Ecology,* http://dx.doi.org/10.1890/13-2261.1
29	10.27	-84.08	Cloud forest, mid elevation, Costa Rica	Maglianesi, M.A., Blüthgen, N., Böhning–Gaese, K. & Schleuning, M. (2014) Morphological traits determine specialization and resource use in plant–hummingbird networks in the Neotropics. *Ecology,* http://dx.doi.org/10.1890/13-2261.1
30	10.18	-84.11	Cloud forest, high elevation, Costa Rica	Maglianesi, M.A., Blüthgen, N., Böhning–Gaese, K. & Schleuning, M. (2014) Morphological traits determine specialization and resource use in plant–hummingbird networks in the Neotropics. *Ecology,* http://dx.doi.org/10.1890/13-2261.1
31	-18.99	-48.30	Cerrado, Central Brazil	Araújo, F.P., Sazima, M. & Oliveira, P.E. (2013) The assembly of plants used as nectar sources by hummingbirds in a Cerrado area of Central Brazil. *Plant Systematics and Evolution,* **299**, 1119–1133. Machado, A.O. (2012) Diversidade de recursos florais para beija-flores nos cerrados do Triângulo mineiro e região. *Ph.D Thesis*. Universidade Federal de Uberlândia, Brazil. Maruyama, P.K., Oliveira, G.M., Ferreira, C., Dalsgaard, B. & Oliveira, P.E. (2013) Pollination syndromes ignored: importance of non-ornithophilous flowers to Neotropical savanna hummingbirds. *Naturwissenschaften*, **100**, 1061–1068.
32	-19.16	-48.39	Cerrado, Central Brazil	Araújo, F.P., Sazima, M. & Oliveira, P.E. (2013) The assembly of plants used as nectar sources by hummingbirds in a Cerrado area of Central Brazil. *Plant Systematics and Evolution,* **299**, 1119–1133. Machado, A.O. (2012) Diversidade de recursos florais para beija-flores nos cerrados do Triângulo mineiro e região. *Ph.D Thesis*. Universidade Federal de Uberlândia, Brazil. Maruyama, P.K., Oliveira, G.M., Ferreira, C., Dalsgaard, B. & Oliveira, P.E. (2013) Pollination syndromes ignored: importance of non-ornithophilous flowers to Neotropical savanna hummingbirds. *Naturwissenschaften*, **100**, 1061–1068.
33	-17.78	-48.68	Cerrado, Central Brazil	Machado, A.O. (2012) Diversidade de recursos florais para beija-flores nos cerrados do Triângulo mineiro e região. *Ph.D Thesis*. Universidade Federal de Uberlândia, Brazil.
34	19.50	-96.95	Protected cloud forest, Central Mexico	Ornelas, J.F. *Unpublished data.*
35	-19.52	-56.98	Pantanal wetland, SW Brazil	Araujo, AC & Sazima, M 2003. The assemblage of flowers visited by hummingbirds in the "capões" of Southern Pantanal, Mato Grosso do Sul, Brazil. *Flora,* **198**, 427–435

ID number	Latitude	Longitude	Site description and general location	Data Source Reference
36	18.13	-66.76	Elfin forest, Puerto Rico	Dalsgaard, B., Martín González, A.M., Olesen, J.M., Ollerton, J., Timmermann, A., Andersen, L.H. & Tossas, A.G. (2009) Plant–hummingbird interactions in the West Indies: floral specialisation gradients associated with environment and hummingbird size. *Oecologia,* **159**, 757-766.
37	17.95	-66.82	Highly preserved coastal dry scrubland, Puerto Rico	Dalsgaard, B., Martín González, A.M., Olesen, J.M., Ollerton, J., Timmermann, A., Andersen, L.H. & Tossas, A.G. (2009) Plant–hummingbird interactions in the West Indies: floral specialisation gradients associated with environment and hummingbird size. *Oecologia,* **159**, 757-766.
38	-19.25	-43.52	Campos rupestres, SE Brazil	Rodrigues, L.C. & Rodrigues, M. (2014) Flowers visited by hummingbirds in the open habitats of the southeastern Brazilian moutaintops: species composition and seasonality. *Brazilian Journal of Biology*, **74**, 659–676.
39	-20.44	-54.65	Cerrado, W Brazil	Rodrigues, L.C. & Araujo, A.C. (2011) The hummingbird community and their floral resources in an urban forest remnant in Brazil. *Brazilian Journal of Biology*, **71**, 611–622.
40	-22.73	-45.58	Montane Forest, SE Brazil	Sazima, I., Buzato, S. & Sazima, M. (1996) An assemblage of hummingbird-pollinated flowers in a montane forest in southeastern Brazil. *Botanica Acta,* **109**, 149–160.
41	10.67	-61.28	Mixed forest, Trinidad	Snow, B.K. & Snow, D.W. (1972) Feeding niches of humingbirds in a Trinidad Valley. *The Journal of Animal Ecology*, **41**, 471–485.
42	4.53	-73.85	Andean forest, Colombia	Snow, D.W. & Snow, B.K. (1980) Relationships between hummingbirds and flowers in the Andes of Colombia. *Bulletin of the British Museum of Natural History (Zoology),* **38**, 105–139.
43	5.90	-73.42	Andean forest, Colombia	Snow, D.W. & Snow, B.K. (1980) Relationships between hummingbirds and flowers in the Andes of Colombia. *Bulletin of the British Museum of Natural History (Zoology),* **38**, 105–139.
44	5.92	-73.53	Andean forest, Colombia	Snow, D.W. & Snow, B.K. (1980) Relationships between hummingbirds and flowers in the Andes of Colombia. *Bulletin of the British Museum of Natural History (Zoology),* **38**, 105–139.
45	-23.63	-45.85	Coastal cloud forest, SE Brazil	Snow D.W. & Snow, B.K. (1986) Feeding ecology of hummingbirds in the Serra do Mar, southeastern Brazil. *Hornero,* **012**, 286–296.
46	-17.51	-63.64	Primary forest, Bolivia	Abrahamczyk, S. & Kessler, M. (2010) Hummingbird diversity, food niche characters, and assemblage composition along a latitudinal precipitation gradient in the Bolivian lowlands. *Journal of Ornithology,* **151**, 615–625.
47	-16.96	-65.41	Primary forest, Bolivia	Abrahamczyk, S. & Kessler, M. (2010) Hummingbird diversity, food niche characters, and assemblage composition along a latitudinal precipitation gradient in the Bolivian lowlands. *Journal of Ornithology,* **151**, 615–625.
48	-19.95	-43.90	Campo rupestre, W Brazil	Vasconcelos, M.F. & Lombardi, J.A. (1999) Padrão sazonal na ocorrência de deis espécie de beija-flores (Apodiformes: Trochilidae) em uma localidade de campo rupestre na Serra do Curral, Minas Gerais. *Ararajuba,* **7**, 71–79.

ID number	Latitude	Longitude	Site description and general location	Data Source Reference
49	-23.28	-45.05	Atlantic forest, SE Brazil	Vizentin–Bugoni, J., Maruyama, P.K. & Sazima, M. (2014) Processes entangling interactions in communities: forbidden links are more important than abundance in a hummingbird–plant network. *Proceedings of the Royal Society of London B,* **281**,1–8.
50	-13.22	-72.12	Subtropical humid montane forest, Perú	Watts, S. (2008) Plant-flower visitor interaction in the Sacred Valley of Perú. *PhD. Thesis.* University of Northampton, UK.
51	-12.85	-69.37	Lowland primary forest, Perú	Watts, S. (2008) Plant-flower visitor interaction in the Sacred Valley of Perú. *PhD. Thesis.* University of Northampton, UK.
52	-0.02	-78.77	Andean rainforest, mid-elevation, Ecuador.	Walther, B.A. & Brieschke, H. (2001) Hummingbird-flower relationships in a mid-elevation rainforest near Mindo, northwestern Ecuador. *International Journal of Ornithology*, **4**, 115–135.
53	9.57	-83.73	Elfin forest, Costa Rica	Wolf, L.L., Stiles, F.G. & Hainsworth, F.R. (1976) Ecological organzation of a tropical, highland hummingbird community. *The Journal of Animal Ecology*, **45**, 349–379.
54	9.48	-83.48	Undisturbed highland páramo, Costa Rica	Wolf, L.L., Stiles, F.G. & Hainsworth, F.R. (1976) Ecological organzation of a tropical, highland hummingbird community. *The Journal of Animal Ecology*, **45**, 349–379.

Table S2. Correlations between corrected and observed indices of network structure (H_2', complementary specialization; and QuanBiMo, quantitative bipartite modularity) and the predictor variables included in the OLS models: species richness/network size, phylogenetic signal in the interaction pattern of plants (d_p) and of hummingbirds (d_h), and all included environmental variables (except insularity as it is a dummy variable) calculated within a 10km buffer zone around each locality. MAT, Mean annual temperature; TS, Temperature seasonality; MAP, mean annual precipitation; PS, precipitation seasonality; MAT vel, velocity of temperature change; MAP vel, velocity of precipitation change; MAT anom, temperature anomaly; MAP anom, precipitation anomaly, SE, Sampling effort/intensity. Correlations for the global dataset are below the diagonal (N = 54), and for mainland networks above the diagonal (N = 45). $^{**}P<0.01$; $^{*}P<0.05$ when significance level is based on degrees of freedom corrected for spatial auto-correlation using Dutilleul's (1993) method; †significant when using traditional non-spatial statistics, but non-significant when correcting for spatial auto-correlation; ^{ns} non-significant. Significant correlations are marked in bold.

	H_2' *observed*	H_2' *corrected*	QuanBiMo *observed*	QuanBiMo *corrected*	Species richness	d_p	d_h	MAT	TS	MAP	PS	MAT vel	MAP vel	MAT anom	MAP anom	SE
H_2' *observed*	-	$\mathbf{+0.77^{**}}$	$\mathbf{+0.77^{**}}$	$\mathbf{+0.65^{**}}$	$\mathbf{+0.33^{*}}$	-0.17^{NS}	$\mathbf{-0.43^{**}}$	$\mathbf{+0.42^{**}}$	-0.29^{ns}	$\mathbf{+0.56^{**}}$	$\mathbf{-0.34^{*}}$	-0.01^{ns}	$+0.09^{ns}$	$\mathbf{-0.47^{**}}$	$+0.31^{\dagger}$	-0.28^{NS}
H_2' *corrected*	$\mathbf{+0.82^{**}}$	-	$\mathbf{+0.51^{**}}$	$\mathbf{+0.78^{**}}$	$\mathbf{+0.45^{*}}$	-0.14^{ns}	$\mathbf{-0.37^{*}}$	$+0.23^{ns}$	-0.17^{ns}	$\mathbf{+0.34^{*}}$	$-0.36^{\dagger}$	-0.14^{ns}	$+0.19^{ns}$	$\mathbf{-0.40^{*}}$	-0.15^{ns}	$+0.27^{NS}$
QuanBiMo *observed*	$\mathbf{+0.78^{**}}$	$\mathbf{+0.55^{**}}$	-	$\mathbf{+0.76^{**}}$	$\mathbf{+0.38^{**}}$	$\mathbf{+0.32^{*}}$	$\mathbf{-0.30^{*}}$	$\mathbf{+0.34^{*}}$	$-0.43^{\dagger}$	$\mathbf{+0.61^{**}}$	-0.27^{ns}	-0.09^{ns}	-0.11^{ns}	$\mathbf{-0.43^{**}}$	$+0.40^{\dagger}$	$\mathbf{-0.41^{*}}$
QuanBiMo *corrected*	$\mathbf{+0.70^{**}}$	$\mathbf{+0.78^{**}}$	$\mathbf{+0.81^{**}}$	-	$\mathbf{+0.57^{**}}$	-0.26^{ns}	$\mathbf{-0.30^{*}}$	$+0.26^{ns}$	-0.27^{ns}	$\mathbf{+0.42^{**}}$	$-0.30^{\dagger}$	-0.10^{ns}	$+0.03^{ns}$	$\mathbf{-0.38^{\dagger}}$	$+0.25^{ns}$	$+0.14^{NS}$
Species richness	$\mathbf{+0.44^{**}}$	$\mathbf{+0.50^{**}}$	$\mathbf{+0.52^{**}}$	$\mathbf{+0.66^{**}}$	-	-0.23^{ns}	$+0.05^{ns}$	$+0.21^{ns}$	$\mathbf{-0.41^{*}}$	$\mathbf{+0.31^{*}}$	$+0.01^{ns}$	-0.06^{ns}	$+0.22^{ns}$	$-0.34^{\dagger}$	$+0.13^{ns}$	$+0.14^{NS}$
d_p	-0.26^{ns}	-0.25^{ns}	$\mathbf{-0.34^{*}}$	$\mathbf{-0.33^{*}}$	-0.26^{ns}	-	-0.19^{ns}	-0.11^{ns}	$+0.21^{ns}$	-0.14^{ns}	-0.07^{ns}	$+0.11^{ns}$	-0.05^{ns}	$+0.05^{ns}$	-0.07^{ns}	$+0.07^{NS}$
d_h	$\mathbf{-0.36^{**}}$	$\mathbf{-0.32^{*}}$	-0.21^{ns}	-0.24^{ns}	$+0.09^{ns}$	-0.14^{ns}	-	-0.28^{ns}	-0.05^{ns}	$\mathbf{-0.29^{*}}$	$\mathbf{+0.36^{*}}$	-0.26^{ns}	-0.12^{ns}	$+0.12^{ns}$	$+0.03^{ns}$	-0.03^{NS}
MAT	$+0.15^{ns}$	$+0.05^{ns}$	$+0.06^{ns}$	$+0.05^{ns}$	-0.01^{ns}	$+0.01^{ns}$	-0.21^{NS}	-	-0.09^{ns}	$+0.25^{ns}$	$+0.02^{ns}$	$\mathbf{+0.66^{**}}$	$\mathbf{+0.32^{\dagger}}$	-0.10^{ns}	-0.16^{ns}	$+0.00^{NS}$
TS	-0.20^{ns}	-0.13^{ns}	$-0.30^{\dagger}$	-0.20^{ns}	$\mathbf{-0.30^{*}}$	$+0.21^{ns}$	-0.06^{ns}	-0.17^{ns}	-	$-0.47^{\dagger}$	$+0.14^{ns}$	$+0.18^{ns}$	$+0.02^{ns}$	$+0.17^{ns}$	$-0.35^{\dagger}$	$+0.23^{NS}$
MAP	$\mathbf{+0.51^{**}}$	$\mathbf{+0.34^{**}}$	$\mathbf{+0.50^{**}}$	$\mathbf{+0.36^{**}}$	$+0.25^{ns}$	-0.15^{ns}	-0.20^{ns}	$+0.25^{ns}$	$-0.48^{\dagger}$	-	$\mathbf{-0.47^{*}}$	-0.14^{ns}	-0.20^{ns}	$\mathbf{-0.53^{**}}$	$\mathbf{+0.71^{**}}$	$\mathbf{-0.47^{*}}$
PS	-0.25^{ns}	$-0.28^{\dagger}$	-0.15^{ns}	-0.19^{ns}	$+0.08^{ns}$	-0.03^{ns}	$\mathbf{+0.29^{*}}$	-0.08^{ns}	$+0.20^{ns}$	$\mathbf{-0.50^{*}}$	-	$+0.06^{ns}$	-0.03^{ns}	$+0.21^{ns}$	-0.20^{ns}	$+0.12^{NS}$
MAT vel	-0.03^{ns}	-0.13^{ns}	-0.05^{ns}	-0.06^{ns}	$+0.01^{ns}$	$+0.19^{ns}$	-0.22^{ns}	$\mathbf{+0.53^{**}}$	$+0.22^{ns}$	-0.20^{ns}	$+0.13^{ns}$	-	$\mathbf{+0.58^{**}}$	$\mathbf{+0.42^{*}}$	$\mathbf{-0.37^{*}}$	$+0.21^{NS}$
MAP vel	$+0.01^{ns}$	$+0.07^{ns}$	-0.13^{ns}	-0.01^{ns}	$+0.17^{ns}$	$+0.08^{ns}$	-0.09^{ns}	$\mathbf{+0.29^{*}}$	$+0.05^{ns}$	-0.24^{ns}	$+0.03^{ns}$	$\mathbf{+0.61^{**}}$	-	$\mathbf{+0.40^{**}}$	$\mathbf{-0.41^{*}}$	$\mathbf{-0.39^{*}}$
MAT anom	-0.23^{ns}	-0.13^{ns}	-0.24^{ns}	-0.17^{ns}	-0.16^{ns}	-0.16^{ns}	$+0.07^{ns}$	-0.14^{ns}	$-0.46^{\dagger}$	$\mathbf{-0.43^{**}}$	$+0.18^{ns}$	$\mathbf{+0.33^{*}}$	$+0.30^{\dagger}$	-	$\mathbf{-0.49^{*}}$	$\mathbf{+0.32^{*}}$
MAP anom	$+0.14^{ns}$	$+0.04^{ns}$	-0.15^{ns}	$+0.08^{ns}$	-0.04^{ns}	-0.03^{ns}	$+0.05^{ns}$	$+0.04^{ns}$	$-0.37^{\dagger}$	$\mathbf{+0.67^{*}}$	$+0.27^{\dagger}$	$\mathbf{+0.38^{**}}$	$\mathbf{+0.38^{**}}$	$\mathbf{-0.44^{*}}$	-	$-0.37^{\dagger}$
SE	-0.18^{NS}	$\mathbf{+0.29^{*}}$	$\mathbf{-0.33^{*}}$	$+0.16^{NS}$	$+0.11^{ns}$	-0.07^{ns}	-0.07^{ns}	$+0.04^{ns}$	$-0.29^{\dagger}$	$\mathbf{-0.38^{*}}$	$+0.08^{ns}$	$+0.15^{ns}$	$\mathbf{+0.32^{*}}$	$\mathbf{+0.36^{**}}$	$-0.29^{\dagger}$	-

REFERENCES Dutilleul, P. (1993) Modifying the t test for assessing the correlation between two spatial processes. *Biometrics*, **49**, 305–314.

Table S3. Coefficients of determination (R^2) from partial regression local models separating the effect of species richness, phylogenetic signal and environmental factors as predictors of corrected network structure when including climate change velocity as an estimate of historical climate stability. We estimated R^2 values in "full" models, i.e. in models including all ten predictor variables (see Table 1). "Total model" reflects the total amount of variation in network structure explained by the full model; "Total species richness", "Total phylogenetic signals" and "Total environmental factors" reflect the variation explained by species richness, phylogenetic signal and environmental factors, respectively; "Only species richness", "Only phylogenetic signal", "Only environmental factors" reflect the amount of variation in network structure explained by the specified predictor-type and not by any other (i.e. the unique variation); Finally, "shared" reflects the variation attributable to the pair of specified predictor types or to all factors combined. See Table 1 for standardized coefficients of each variable and more details of model fit, and Figure 3 for a graphical representation of these results.

	Global dataset (54 networks)		**Only Mainland (45 networks)**	
	H_2'	**QuanBiMo**	H_2'	**QuanBiMo**
Total model	0.54	0.62	0.58	0.57
Total species richness	0.25	0.44	0.20	0.33
Total phylogenetic signal	0.19	0.19	0.18	0.19
Total environmental factors	0.38	0.35	0.45	0.32
Unique species richness	0.13	0.24	0.07	0.19
Unique phylogenetic signal	0.06	0.05	0.08	0.07
Unique environmental factors	0.13	0.06	0.22	0.10
Shared species richness – phylogeny	0.00	0.00	0.00	0.00
Shared species richness – environmental factors	0.10	0.14	0.11	0.09
Shared phylogeny – environmental factors	0.10	0.08	0.09	0.07
Shared all factors	0.05	0.08	0.03	0.06

Figure S1. Scatter plots showing the linear associations between corrected complementary specialization, H_2', and corrected quantitative bipartite modularity, *QuanBiMo,* and species richness and hummingbird phylogenetic signal, the predictor variables exhibiting the most consistent relationships. Complementary specialization measures the exclusiveness of the interactions in the community, whereas modularity quantifies whether species interact more frequently with subsets of available species within a community. Full and open circles denote mainland and island networks, respectively. Notice the differences in the regression lines fitted to the Global and Only Mainland datasets, in thick and dashed lines, respectively.