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Meta-networks for the study of biogeographical traits in ecological networks: the

- **Mexican hummingbird-plant assemblage** 4
- **Ana M. Martín González¹ *, Juan Francisco Ornelas² , Bo Dalsgaard¹ , Ubaldo Márquez-Luna³ , Carlos Lara⁴** 6

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1 Center for Macroecology, Evolution and Climate, Natural History Museum of Denmark,

- University of Copenhagen, Universitetsparken 15, 2100 Copenhagen Ø, Denmark **2** Departamento de Biología Evolutiva, Instituto de Ecología, A.C. (INECOL), Carretera 10
- Antigua a Coatepec No. 351, El Haya, Xalapa, Veracruz 91070, Mexico **3** Doctorado en Ciencias Biológicas y de la Salud, Universidad Autónoma Metropolitana-12
- Iztapalapa, Av. San Rafael Atlixco 186, Col. Vicentina, Iztapalapa, C.P. 09340, Mexico, D.F **4** Centro de Investigación en Ciencias Biológicas, Universidad Autónoma de Tlaxcala, Km 14
- 10.5 Autopista Tlaxcala-San Martín Texmelucan, San Felipe Ixtacuixtla, Tlaxcala 90120, Mexico 16

*Corresponding author: *ana.maria.martingonzalez@gmail.com; amartingonzalez@snm.ku.dk*

ORCID 0000-0001-9429-7180 20

Juan Francisco Ornelas: *francisco.ornelas@inecol.mx* ORCID 0000-0002-1124-1163

- Bo Dalsgaard: *bo.dalsgaard@snm.ku.dk* Ubaldo Márquez-Luna: *marquezubaldo@gmail.com* 22
- Carlos Lara: *carlos.lara.rodriguez@gmail.com* 24

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Abstract

- Recent studies on ecological networks have quantified the contribution of ecological, historical and evolutionary factors on the structure of local communities of interacting 26
- species. However, the influence of species' biogeographical traits, such as migratory habits or phylogeographical history, on ecological networks is poorly understood. Meta-networks, i.e. 28
- networks that cover large spatial extensions and include species not co-occurring locally, enable us to investigate mechanisms that operate at larger spatial scales such as migratory 30
- patterns or phylogeographical distributions, as well as indirect relationships among species through shared partners. Using a meta-network of hummingbird-plant interaction across 32
- Mexico we illustrate the usefulness of this approach by investigating (1) how biogeographical and morphological factors associate with observed interactions, and (2) how species-specific 34
- biogeographical characteristics associate with species' network roles. Our results show that all studied hummingbird and plant species in the meta-network were interrelated, either 36
- directly or through shared partners. The meta-network was structured into modules, resulting from hummingbirds and plants interacting preferentially with subsets of species, which 38
- differed in biogeographical, and, to a lesser extent, morphological traits. Furthermore, migrants and hummingbirds from Nearctic, Transition and widespread regions had a higher 40
- topological importance in the meta-network. Taken together, this study illustrates how metanetworks may contribute to our current knowledge on species biogeographical traits and 42
- biotic interactions, providing a perspective complementary to local-scale networks. 44

Keywords biotic interactions, migration, modularity, morphology, phylogeny, pollination 46

INTRODUCTION

- Species interactions, such as pollination and other mutualistic associations, are widespread and crucial for the functioning of most ecological communities (Rech et al. 2016). An urgent 48
- challenge in ecology amidst global change is to quantify the contribution of ecological, historical, evolutionary and biogeographic mechanisms in the structuring of communities of 50
- interacting species (Ricklefs 1987; Cavender-Bares et al. 2009; Martín González et al. 2015; Heilmann-Clausen et al. 2017; Dalsgaard et al. 2018). This is a complex subject, as species 52
- typically show a context-dependent behavior reflecting their adaptation to a mosaic of factors presented in their local communities, which in turn interplay at different scales. Hence, the 54
- need of using a wide set of complementary analyses to study the effect of different factors and at different scales (Thuillier et al. 2013; Poisot et al. 2015). For instance, the study of 56
- interactions between plants and their pollinators over different seasons and years, including species whose phenophases may not fully overlap, has enabled us to explore the effect of 58
- climate, resource seasonality and species phenophases on community structure and species' roles. Besides a more accurate understanding of community structure and build up, these 60
- networks allow us to characterize more accurate the role of species and potential fluctuations over time (Martín González et al. 2012; Chacoff et al. 2017, Kantsa et al. 2018). Similarly, the 62
- study of "meta-networks", i.e. networks of biotic interactions covering large spatial scales, across biomes or in fragmented habitats, may give new insights into how species 64
- biogeographical traits such as phylogeographical distribution, range dynamics or migratory habits influence ecological networks, of which there is scarce knowledge (Heilmann-Clausen 66
- et al. 2016; Araujo et al., 2018; Emer et al. 2018). 68
- Meta-networks enable us to study indirect interactions among species, that is, relationships between species that do not co-occur spatially or temporally, but which may have an effect on 70
- each other through third species. For instance, two consumer species whose ranges may not overlap currently but which visit a similar array of resources, and hence may prevent the 72
- expansion into each other ranges. Hence, the study of meta-networks may be particularly useful to understand landscape dynamics, such as the effect of biotic interactions on range 74
- dynamics (e.g. Araújo and Luoto 2007), and the role and importance of species which, 76

because of large spatial distributions (e.g. migrant species), may appear as peripheral in local

networks due a lower detection probability (Vázquez et al. 2009). 78

- Biogeographical factors may be especially important in areas with a complex geography and topography, in contact zones between biogeographical realms and in areas with communities 80
- containing species with large differences in range distributions or migratory habits. An outstanding combination of such factors is the Mexican hummingbird-plant assemblage. 82
- Mexico is located at the transition between the Nearctic and Neotropical realms (Halffter 1987; Rzedowski 1965), and exhibits a complex topography and geological history (Morrone 84
- 2010; Morrone et al. 2017; Fig. 1). Its wide array of ecological conditions has favoured population isolation and the action of *in situ* evolutionary processes (Navarro et al. 2002), 86
- enabling to find fauna, largely endemic, with different biogeographical and evolutionary origins. For instance, the Mexican hummingbird fauna appears to have arisen from multiple 88
- independent invasions of different phylogenetic lineages and at different times (Stiles 1981; Brown and Bowers 1985; Bleiweiss 1998; Licona-Vera and Ornelas 2017; see more details in 90
- methods). Several of the Mexican hummingbirds have very particular biogeographical and ecological restrictions, which entails both processes of diversification and endemism 92
- (Rodríguez-Gómez et al. 2013; Malpica and Ornelas 2014; Licona-Vera and Ornelas 2014; Ornelas et al. 2015). For instance, most of the 24 endemic Mexican hummingbirds are 94
- restricted to regions of narrow extensions, little landscape connectivity, and complex topography and floral composition. Furthermore, the Mexican hummingbird fauna includes a 96
- mixture of sedentary, altitudinal and short-distance migrants who track nectar availability of local resources, and obligate seasonal long-distance migrants who have latitudinally different 98
- winter and breeding grounds (e.g. Lara 2006; Licona-Vera and Ornelas 2017). 100
- Hence, given the large differences phylogeographical history, range distributions and migratory habits among Mexican species, we expect these biogeographical traits to exert a 102
- strong effect on hummingbird-plant interactions and, therefore, on network structure. However, most studies on hummingbird-plant assemblages have focused exclusively on the 104
- effect of morphological traits, which have been shown to regulate interactions in some but not 106

all communities (e.g. Maglianesi et al. 2014, 2015; Vizentin-Bugoni et al. 2014; Weinstein

- and Graham 2017; Dalsgaard et al. 2018). For instance, in the Brazilian Cerrado hummingbird traits have been shown to produce modules within local networks with their nectar-food plants 108
- (Maruyama et al. 2014). On the other hand, the role of biogeographical traits remains less well known (Sonne et al. 2016; Araujo et al. 2018). In this study we investigate the role of 110
- hummingbird's biogeographical and morphological traits in structuring a meta-network comprising all available information on hummingbird-plant interaction across Mexico. We 112
- expect that the Mexican meta-network will show a strong modular pattern in which modules can be interpreted in terms of species' biogeographical traits, an analogous outcome to the 114
- modular pattern of highly seasonal mutualistic assemblages where modules reflect species' staggered phenophases (Martín González et al. 2012). Specifically, we investigate (1) how 116
- hummingbird's biogeographical and morphological traits associate with the modular partition, and (2) how hummingbird's biogeographical and morphological traits may associate with the 118
- network role of hummingbirds in the meta-network. 120

Methods 122

Study area and study species

- Mexico is an outstanding example of complex biogeographical patterns (Morrone 2010; Morrone et al. 2017). The country currently stands out as a mega-diverse country, likely a 124
- consequence of its location at the transition between the Nearctic and Neotropical realms (Halffter 1964, 1987; Rzedowski 1965, 1992) and the close relationship between 126
- geological/climatic and speciation events (Croizat 1958, 1964; Rosen 1978; Halffter 1987; Liebherr 1991; Luna-Vega et al. 1999). In Mexico, the Nearctic realm comprises the arid 128
- subtropical areas that extend from northern to the high plateaus along the Volcanic Belt and the Sierras Madre, where it intermixes broadly with the Neotropical realm which includes 130
- humid and subhumid tropical areas in the central-south part of the country (Halffter 1964; Morrone and Márquez 2001; Morrone et al. 2017; Fig. 1). 132

Hummingbirds (Trochilidae) are the most highly specialized nectarivorous birds in the New

- World, relying almost exclusively on nectar as a food source (Stiles 1981). They distribute from Alaska through Patagonia, and their interactions with plants show strong 136
- biogeographical and evolutionary patterns, ranging from generalized to highly specialized (Stiles 1978; Dalsgaard et al. 2009, 2011; Abrahamczyk and Kessler 2014; Martín González 138
- et al. 2015; Sonne et al. 2016). Their adaptive radiation manifests them as a highly diverse clade, with more than 338 described species (McGuire et al. 2014). With approximately 58 140
- recognized species, Mexico hosts 17% of the described hummingbird species. The Mexican hummingbird fauna is relatively recent and results from various colonization waves from 142
- South America (McGuire et al. 2014; Ornelas et al. 2014). The high habitat diversity and abrupt environmental and climatic changes that characterize Mexico have played a key role 144
- on processes of divergence and speciation, resulting in a great level of endemism and varied migratory habits of Mexican hummingbirds (Malpica and Ornelas 2014; Licona-Vera and 146
- Ornelas 2017; Appendix 1). 148

Interaction data and species traits 150

We compiled 37 hummingbird-plant interaction networks describing feeding relationships

- between hummingbirds and plants throughout Mexico, spanning over nine different habitats and ten biogeographic provinces (as defined by Morrone et al. 2017), including both 152
- Neotropical and Nearctic realms and the Transition zone (Fig. 1, coordinates and references for details on Appendix 2). Overall, we compiled information on hummingbird visitation for 154
- 41 hummingbird species and 354 plant species, covering all but three of the nine taxonomically recognized phylogenetic lineages (McGuire et al. 2014) and comprising a wide 156
- range of body masses (2.5–11.9 g) and bill lengths (11.3–43.2 mm). Hummingbirds were classified following Escalante et al. (1993) as endemic, when their entire distribution is 158
- restricted to Mexico (8 species); semi-endemic, when the entire population is seasonally present in Mexico or in narrowly overlapping adjacent countries (<35000Km²; 9 species); and 160
- non-endemic (24 species). Some hummingbirds have long-distance migratory habits (7 species), others migrate locally (9 species) and others are year residents (25 species; 162
- Arizmendi and Berlanga 2014). The biogeographical distribution of hummingbirds was categorized as Nearctical, when the hummingbird was reported only in Nearctical or in 164
- Nearctical and Transition localities (6 species), as Neotropical when the hummingbird was reported only in Neotropical or in Neotropical and Transition localities (16 species), as 166
- Transition, when the hummingbird was reported only in Transition localities (8 species), or widespread if the hummingbird was present in Nearctical, Neotropical and Transition regions 168
- (11 species; Table 1). Plants belong to 66 different families, are mostly native species (271 species, 92% of total) and include both typical ornithophilous and non-ornithophilous floral 170

morphologies (see Appendix 2 for a list of plants present in the meta-network). 172

Meta-network analyses 174

To investigate the structure of the Mexican meta-network, we merged all information on the

- presence/absence of species interactions into a single meta-network describing whether each hummingbird and plant species interacted anywhere in Mexico (Appendix 2). We thereafter 176
- examined the potential modularity of this meta-network. Modularity was calculated in MODULAR (Marquitti et al. 2014) using Barber's metric for bipartite networks (Barber 178
- 2007), with simulated annealing as the searching algorithm and following the recommended program settings (Marquitti et al. 2014; Appendix 3). Barber's modularity divides the matrix 180
- into an a priori undefined number of modules using matrix's eigenvalues, minimizing the number of links between modules while maximizing within-module connectance (Barber 182
- 2007). Hence, in the resulting partition, species located in the same module interact more among themselves than with species from other modules. As MODULAR uses an iterative 184
- searching algorithm, we investigated the robustness of the resulting modular partition by running the analysis 30 times using different seed set numbers. In addition, we estimated the 186
- significance of each run against 100 null matrices obtained with MODULAR's Null Model 2, which creates matrices with the same number of species and interactions as the empirical one, 188
- and in which species interaction probability is based on their observed connectivity (Bascompte et al. 2003; Marquitti et al. 2014). 190

We examined the resulting modular partition in order to understand the underlying

- mechanisms associated with such pattern of interactions. We performed a non-metric multidimensional scaling (NMDS) of hummingbird morphological and biogeographical traits 194
- known or hypothesized to associate with hummingbird-plant interactions, namely bill length, body mass, degree of endemicity, migratory habits and biogeographical distribution. The 196
- NMDS was run following the approach recommended in the R package *vegan* (Oksanen et al. 2017), e.g. the ordination was run 5 times, with a minimum number of 200 iterations and 198
- using the previous best solution as starting point. To the resulting ordination, we fit a secondary matrix, which included group membership (e.g. which groups of hummingbirds 200
- were found in the same modules in the different runs of the modularity algorithm) and phylogenetic lineage as factors. Hence, we tested whether species from different groups or 202
- from different hummingbird phylogenetic lineages show different morphological or biogeographical traits. 204

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Finally, from the resulting modular partition we obtained information on the network role of

- each hummingbird species by computing species' within-module degree (*z-values*) and among-module connectivity (*c-values*) in the *cz*-values function from the R package *bipartite* 208
- (Dormann 2012). Within and among module connectivities are calculated as $z = (k_{is} ks_{bar})/$ SD_{ks} and $c = 1 - \sum (k_{it}/k_i)^2$, respectively, where k_i is the degree of focal species *i*; k_{is} is the 210
- degree of focal species *i* to the rest of the species within i 's module; k_{Bar} is the average degree of all species in module s ; SD_{ks} is the standard deviation of the degrees of species in module s ; 212
- and k_{it} is the number of links of focal species *i* to species located in module *t* (Olesen et al. 2007; Dormann 2012). Hummingbirds can therefore be classified according to how their 214
- interactions distributed within and across modules as *hubs* when their z-values are high; as *connectors,* when their c-values are high; and as *peripherals,* when they are poorly connected 216
- and only within their module, and hence both their *c* and *z-values* are small. As hummingbird traits were a mixture of continuous (bill length and body mass), categorical ordered (degree 218
- of endemicity and migratory habits) and categorical unordered variables (biogeographical distribution), we used a non-parametric multiple regression with kernel estimation to examine 220
- whether their *z* and *c-values* associate with any of these traits, using the R package *np* (Hayfield and Racine 2017). All statistical analyses were performed in R 3.3.1 (R 222
- Development Core Team 2014). 224

Results 226

The meta-network consisted of 395 species and 1128 interactions, and had a connectance of

- 8%. All species conformed the giant component, that is, there were no separate subnetworks of species. The two most distant species in the meta-network were seven edges apart, while 228
- the average number of shortest paths between any two species in the meta-network was 3.389. Different runs of the MODULAR algorithm yielded different though relatively constant 230
- modularity values ($M = 0.466 \pm 0.004$), all of which were highly significant when compared to null models (all p-values <0.001; Appendix 3). Despite resulting partitions varied between 232
- five and eight different modules, species composition of modules was relatively constant, with all but five of the hummingbird species being placed over 87% of the runs together in the 234
- same module (that is, in 26 out of the 30 runs of the modularity algorithm; Fig. 2; group species compositions are given in Appendix 2; results from the modularity analysis are given 236

in Appendix 3). 238

- The NMDS analysis on the morphological and biogeographical traits of the 41 hummingbird species of the meta-network resulted in a two-dimensional solution with a stress value of 240
- 0.132 (Fig. 3). In axis 1 morphological traits and biogeographical distribution had positive scores whereas degree of endemism and migratory behavior had negative scores. The 242
- strongest associations were, in this order, with hummingbird migratory behavior and biogeographical distribution. All variables were negatively associated with axis 2 except for 244
- endemism, which was also the trait with the highest score, followed by bill length and body mass. Moreover, the resulting ordination was significantly correlated with hummingbird 246
- module composition ($R^2 = 0.426$, $p = 0.001$), that is, modules differed in the traits analyzed in the NMDS. 248

The two non-parametric multiple regressions performed between the *z-* and *c-values* and

- hummingbird traits resulted in strong and statistically significant associations (Table 2, Appendix 4). The *z-* and *c-values* were averaged across runs as different runs of the 252
- modularity algorithm yielded different partitions as species *z-* and *c-values* differed: range SD = 0.038–0.94 and 0.00–2.36 for *z* and *c-values*, respectively. Migratory behavior and 254
- biogeographical distribution showed a highly significant association with both *z* and *c-values* (Table 2, Fig. 4), with migratory and Nearctic/Widespread species showing higher within and 256
- among module connectivity values than non-migrants and Neotropical hummingbirds. Hummingbird *z-values* also correlated negatively with bill length and body mass, that is, large 258
- and long-bill hummingbirds tend to have a peripheral position in the meta-network (Table 2, Fig. 4). 260
- 262

Discussion

- In this study we explore the usefulness of meta-networks to investigate the effect of biogeographical traits on species interactions. In order to do so, we chose a study system of 264
- high geological complexity such as Mexico and a bird group model, which is broadly distributed and shows a wide array of biogeographical and morphological traits that may 266
- influence their interaction pattern with plants. By studying the Mexican hummingbird-plant assemblage at a macroecological scale, we included direct and indirect interactions among 268
- species. The resulting meta-network was fully connected; this indicates that all studied species had the capacity of influencing each other, even when not co-occurring at the same 270
- localities. Moreover, the average shortest path length of 3.389 indicates that even indirect interactions may exert relatively strong influences across the network. The meta-network was 272
- also highly modular, with modules reflecting differences in the migratory habits and degree of endemicity of hummingbirds. 274

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Our results highlight the large importance of migratory hummingbird species in the structure

of the meta-network. Migration in Mexican hummingbirds appears to be a highly labile and relatively recent trait, occurring repeatedly and independently on several species from basal 278

- sedentary ancestors (Licona-Vera and Ornelas 2017). Migratory hummingbirds have significantly higher *c-values*, that is, a relatively high proportion of their interactions are with 280
- plant species from other modules, increasing overall network cohesiveness (Olesen et al. 2007; Tylianakis et al. 2010; Stouffer and Bascompte 2011) and the potential importance of 282
- indirect interactions. In highly seasonal pollination networks this role is achieved by pollinator species with long phenophases, who connected species with much more restricted 284
- activity periods (Martín González et al. 2012; Kantsa et al. 2018). Modular networks are expected to be highly resilient, as disturbances are less likely to spread beyond modules 286
- (Olesen et al. 2007; Tylianakis et al. 2010; Stouffer and Bascompte 2011). However, at the same time, this particular topological configuration renders connectors a foremost 288
- importance, as they are able to affect rapidly the rest of the species in the network. Migratory Mexican hummingbirds show an interaction behavior relatively robust to changes in habitat 290
- conditions and in plant distributions and phenologies. By experimentally simulating changes in the environment, Ornelas and Lara (2015) showed that some migratory Mexican 292
- hummingbird species included in this study (i.e. Emerald *Amazilia beryllina* and Bee *Selasphorus rufus*) are able to quickly change and adjust their colour preferences of the 294
- flowers they visit due to the short time spent in a given novel environment, whereas resident hummingbirds also included in this study (i.e. Emerald *Hylocharis leucotis* and Gem 296
- *Lampornis amethystinus*) usually prefer visiting their natural red flower type and they take longer to change their colour preferences. This apparent neophilia in the migratory 298
- hummingbirds could favor the easy incorporation of non-familiar resources, such as invasive plant species, into their interaction networks. 300
- 302

The biogeographical distribution of species was strongly associated with the role of species in

- the network. Nearctic, Transition and widespread hummingbirds showed a higher withinmodule and among-module connectivity. Most of these hummingbirds are also migrants 304
- (Table 1), and hence have wider range distributions and habitat preferences. Another possible explanation for the higher importance of Nearctic and widespread hummingbirds involves the 306
- divergence time of hummingbirds and their floral preferences. For example, hummingbird species from the Bees and Mountain Gems clades are distributed particularly in North 308
- America and Central America (mostly in the Nearctic realm), being the only lineages that expanded and diversified in these regions (∼12 million years ago, McGuire et al. 2014; 310
- Licona-Vera and Ornelas 2017) and show a significantly higher mean *c-value* (Appendix 5). Altogether, these species seem to be more evolutionary and ecologically dynamic. In contrast, 312
- Neotropical clades such as Hermits (e.g. *Phaethornis* spp.) and Emeralds (e.g. *Amazilia* spp.) had more recent invasions from South America and a subsequent diversification in the 314
- Mesoamerican zone (Ornelas et al. 2014), and have a more peripheral role in the metanetwork. 316
- 318

The most common ancestral condition for the hummingbird flowers of North America is a

- bee-pollinated system (Grant and Grant 1968), promoting hummingbirds to be particularly generalist in their interactions with plants in the Nearctic realm. North-American 320
- hummingbirds have a closer phenotype than other hummingbird assemblages (Stiles 1981; Brown and Bowers 1985), which also translates into a higher congruence in the floral 322
- phenotypes. By contrast, ornithophilous genera of plants are centred in subtropical or tropical America, where hummingbird-plant interactions show higher levels of specialization and 324
- morphological complementarity (Stiles 1978; Dalsgaard et al. 2011). Hence, in Mexican hummingbird-plant assemblages, morphological traits may be, *a priori*, not as important as 326
- other mechanisms in structuring interactions at the community level. Our results show that both the length of the bill and the body mass of the hummingbirds affect the number of 328
- interactions hummingbirds establish within their module, with short-bill and smaller species showing a tendency to interact with a higher number of plants within their modules than long-330
- bill and larger hummingbirds. Long bills restrict the number of plants from which a hummingbird can effectively extract nectar, while larger hummingbirds have higher energetic 332
- demands which constrain their available floral choices to flowers providing mid-high amounts of nectar, of which the North American flora is relatively scarce (Stiles 1981; Brown and 334
- Bowers 1985). Hence, in the Mexican hummingbird-plant assemblage there seems to be a preference for not establishing strong morphological or energetic barriers between 336
- hummingbirds and their nectar plants. 338
- Taken together, our study of the Mexican hummingbird-plant meta-network illustrates how meta-networks may provide a more complete view on the dynamics of ecological 340
- communities, particularly as the importance and behavior of migrant species may not be fully characterize when studying only local-scale networks. Notably, through a meta-network, we 342
- have been able to capture the direct and indirect interactions between hummingbirds and their nectar plants across Mexico, resulting in relevant insights on the importance of 344
- biogeographical traits for such assemblages. This emphasizes the usefulness of metanetworks for the characterization of the factors shaping species communities and how they 346
- interact across large spatial scales. This approach may be extended to other taxa and biogeographical regions, and may prove valuable in order to asses the effects of mechanisms 348
- that operate at large spatial scales such as habitat fragmentation, species invasions, the effect of biotic interactions on range dynamics and changes in species phenophases (Araújo and 350
- Luoto 2007; Araujo et al. 2018; Emer et al. 2018). 352

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TABLES

- Table 1. Hummingbird species and the traits examined in this study. Phylogenetic lineages were obtained from McGuire et al. (2014), biogeographical species distribution from their 514
- observed community location, body mass and bill length from Arizmendi and Berlanga (2014) and from Carlos Lara's own measurements (marked with and asterisk *), degree of 516
- endemism from Escalante (1993) and species migratory behavior from Arizmendi and 518

Berlanga (2014).

- Table 2. Results from the non-parametric multiple regression with kernel variable estimation between species within and between module connectivity (*z* and *c* value, respectively) and 520
- their morphological and biogeographical traits. Regression was performed with the 41 hummingbird species and using the 5 studied variables. We used a local-linear kernel 522
- regression estimator, using a second-order Gaussian kernel function for the two continuous explanatory variables (bill length and body mass), an Aitchison and Aitken kernel function 524
- for the unordered categorical variable (biogeographical distribution) and a Li and Racine kernel function for the two ordered categorical variable (degree of endemism and migratory 526
- behavior). Bandwidths were computed using an adaptive k-nearest neighbor algorithm and selected through a least squares cross-validation (Hayfield and Racine 2008, 2017). 528
- Significance tests were performed with 399 bootstraps. Significant variables are marked in bold. 530

FIGURES

- **Figure 1**. Map of Mexico showing the different biogeographical regions conforming the Nearctical realm (in blue), the Neotropical realm (in orange) and Transition provinces (in 534
- green) as defined by Morrone et al. (2017). Dots pinpoint the localities where the hummingbird-plant networks were collected. Note that some of the points may overlap. 536

538

Figure 2. Illustration of the Mexican bipartite meta-network. Hummingbirds in blue and

- plants in orange, and the interactions between them in grey. The width of the species' bars represents species' number of interactions. Hummingbirds are also divided according to their 540
- resulting modules. The picture shows a female *Selasphorus platycercus* visiting a flower of *Penstemon roseus*. Photo by Carlos Lara. 542

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Figure 3. Results of the non-metric muldimensional scaling ordination of five hummingbird

- species traits (bill length, body mass, biogeographical distribution, degree of endemism and migratory behavior). Ellipses in the NMDS indicate 95% confidence intervals around the 546
- centroids of each group. Note that modules 6-10 (colored in different shades of red) are conformed of only one hummingbird species, as these hummingbirds appeared in different 548
- modules in the different runs of the modularity algorithm. Notice also that these hummingbirds do not show biogeographical or morphological differences from 550
- hummingbirds with constant module partners. 552
- **Figure 4**. Plots illustrating the significant correlations between *z* and *c* values and migratory behavior (a,b), biogeographical distribution (c,d), bill length (e) and body mass (f) of 554
- hummingbirds. Pirateplots show raw data as points, the median as a horizontal line surrounded by a Bayesian 95% Inference Highest Density Interval as a horizontal bar, and a 556

smoothed density bean surrounding the raw data points. 558

560

 \overline{a}

SUPPORTING INFORMATION 568

Appendix 1. Details about the Mexican biogeography and hummingbird fauna and

- biogeographical characteristics. 570
- Mexico is an outstanding example of complex biogeographical patterns (Morrone 2010; Morrone et al. 2017). The Mexican Transition Zone (Halffter 1987), which marks the 572
- transition between the Neotropical and the Nearctic biota, is considered a critical area for understanding not just diversification in the region, but also the evolution of migratory 574
- systems of various animal species. This zone includes the Isthmus of Tehuantepec in southern Mexico, formed c. 3 Ma, and the Trans-Mexican Volcanic Belt (TMVB) across central 576
- Mexico, formed c. 10–7 Ma (Gómez-Tuena et al. 2007). The Isthmus of Tehuantepec divides mountain ranges along the Sierra Madre Oriental and Oaxaca from those in Chiapas and 578
- Guatemala. Its formation was followed by changes in sea levels caused by glaciation cycles, with rising sea levels and marine transgression during interglacials inundating much of the 580
- coastal plains and isolating montane habitats on either side (Barrier et al. 1998). At present, the lowlands in the area are occupied by dry scrubby habitats that are very different from the 582
- moist mountainous areas on either side. The TMVB was formed during four main episodes of volcanic activity from the middle-to-late Miocene to the Holocene (Gómez-Tuena et al. 584
- 2005), resulting in a continental magmatic arc of nearly 8000 volcanic chain of mountains (reaching over 4000 m above sea level), extending west to east and virtually cutting Mexico 586
- into northern and southern halves. The TMVB acts as an effective geographic barrier to the dispersal of most hummingbird species, producing abrupt environmental changes, which may 588
- explain the existence of such high number of endemic hummingbird species. Recent phylogeographic studies have shown that species level population divergence of terrestrial 590
- species post-dates Pliocene faulting and marine inundations across the Isthmus of Tehuantepec (Barber and Klicka 2010; Ornelas et al. 2013 and references therein). 592
- 594

The Mexican hummingbird fauna (including all North American species) began with a single invasion from South America by the common ancestor of the Bee and Mountain Gem clades ca. 12–14 million years ago (McGuire et al. 2014; Licona-Vera and Ornelas 2017). After this 596

- invasion, there have been multiple independent invasions of North America by Emeralds, Coquettes, Mangoes, and Hermits and single invasions by Brilliants and Topazes, presumably 598
- all of which occurred prior to or after the Panamanian land bridge formation (McGuire et al. 2014; Ornelas et al. 2014). Species accumulation in North America proceeded slowly at first 600
- and a rapid increase during the past 7 Ma, which reflects not only in situ diversification of Mountain Gems and Bees, but also a heterogeneous diversification dynamics during the 602
- history of hummingbirds and an extraordinary high rate of net diversification in the Bee clade (McGuire et al. 2014), potentially linked to the evolution of migratory behavior (Licona-Vera 604
- and Ornelas 2017). In the Nearctic-Neotropical migration systems, analyses of molecular data suggest that many bird species colonized northern areas when they became available after the 606
- Last Glacial Maximum (LGM) event (Hewitt 2000). For example, the ancestral sedentary ranges of the Bee clade (such as *Selasphorus* species) expanded into northern latitudes 608
- following the LGM, until they reached limits for residency imposed by the local seasonality of the floral resources and migration was selectively favoured (Malpica and Ornelas 2014). 610
- These migrations were followed by rapid radiations and local adaptations to both xeric and humid conditions in different regions of Mexico, and produced both sedentary and migratory 612
- populations (Licona-Vera and Ornelas 2017). In a phylogenetic framework, the repeated evolution of long-distance migratory behavior is observed at different times in the radiation of 614
- the Bee clade, highlighting the key role of the environment (local topographical features and climatic changes) on processes of divergence and speciation. These repeated gains of 616
- migration at the phylogenetic scale seem to have occurred linked to certain patterns of climatic change during the Late Pliocene and Pleistocene glaciations, whereas the evolution of 618
- long-distance seasonal migration within species seems to have occurred during the last glacial-interglacial cycles of the Pleistocene (Rodríguez-Gómez et al. 2013; Malpica and 620
- Ornelas 2014; Licona-Vera and Ornelas 2017). 622

Study #	Author		Mexican state Main Vegetation type	Latitude	Longitude	Biogeographical province	Biogeographical realm
$\mathbf{1}$	Rodríguez-Flores, C.I.	Jalisco	Cloud forest	$19°34'14"$ - 19°37'30"	$104^{\circ}14'49''$ - 104°18'16"	Sierra Madre del Sur	Transition
$\overline{2}$	Ortiz-Pulido, R.	Veracruz	Pine forest	19°29'59.86"	97° 8'12.08"	Trans-Mexican Volcanic Belt	Transition
$\overline{3}$	Arizmendi, M.C.	Jalisco	Tropical deciduous forest	$19^{\circ} 30'$	$105^{\circ} 03'$	Pacific Lowlands	Neotropical
$\overline{4}$	Arizmendi, M. C.	Jalisco	Cloud forest	$19^{\circ} 35'$	$104^{\circ} 16'$	Sierra Madre del Sur	Transition
5	Des Granges, J.-L.	Colima	Pine-oak forest	19°31'3.18"	103°37'5.55"	Trans-Mexican Volcanic Belt	Transition
6	Partida Lara, R.	Chiapas	Cloud forest	16°44'38"	92°40'15"	Chiapas Highlands	Transition
$\overline{7}$	Arizmendi, M. C.	Guerrero	Pine-oak forest	$17^{\circ}19'53.1"$ - 17°25'47.8"	100° 09' 56.1" - 100°11'48.5"	Sierra Madre del Sur	Transition
8	Lyon, D.L.	Oaxaca	Pine forest	17° 8'26.67"	96°41'21.55"	Sierra Madre del Sur	Transition
9	Arriaga, L.	Baja California Surk forest		24°-22°50'	109°60'-110°10'	Baja Californian	Nearctica
10	Reyna Bustos, O.	Jalisco	Tropical deciduous forest	$21°45'08"$ - 21°44'50"	103°15'	Pacific Lowlands	Neotropical
11	De la Cruz, F.	Oaxaca	Xeric shrubland	17°04'04"	96°43'12"	Sierra Madre del Sur	Transition
12	Jimenez Sierra, L.	Hidalgo	Xeric shrubland	20°45'26"	98°57'08"	Sierra Madre Oriental	Transition
13	Toledo, V.	Veracruz	Evergreen tropical forest	18°32'	$95^{\circ} 04'$	Veracruzan	Neotropical
14	Van Devender, T.	Sonora	Foothills thorn scrubs	28°34'40"	109°33'09"	Sonoran	Nearctica
15	Van Devender, T.	Sonora	Tropical deciduous forest	28254'48"	109°11'31"	Sonoran	Nearctica
16	Van Devender, T.	Sonora	Oak woodland	28°22'18"	109°03'53"	Sonoran	Nearctica
17	Van Devender, T.	Sonora	Pine-oak forest	28°19'31"	109°02'00"	Sonoran	Nearctica

Appendix 2. Table S2. Geographical and habitat details for each hummingbird-plant network.

31, 32 Puch-Chávez R (2012) Flora visitada por colibríes en selvas maduras y sitios

Appendix 3. Adjacency matrix for the Mexican meta-network. Hummingbird species in columns, plants in rows, 1 depicts at least an observed interaction somewhere in the Mexican territory, 0 otherwise. Hummingbirds are ordered by module membership, as result of running 30 times a modular partition in MODULAR (Marquitti et al. 2014). Hummingbirds are placed in the same module when in 87% of the times (i.e. more than 26 out of the 30 runs of the modularity algorithm) result in the same module, and are labeled NA when they have no constant module partners.

Appendix 4. Results from the modularity analysis. Modularity was calculated in MODULAR

- (Marquitti et al. 2014) using Barber's metric for bipartite networks (Barber 2007), with simulated annealing as the searching algorithm and following the recommended program 634
- settings: an initial temperature of 2.0, a cooling factor of 1.01, and an iteration factor of 1 (Marquitti et al. 2014). Barber's modularity divides the matrix into an a priori undefined 636
- number of modules using matrix's eigenvalues, minimizing the number of links between modules while maximizing within-module connectance (Barber 2007). We estimated the 638
- significance of each run against 100 null matrices obtained with MODULAR's Null Model 2, which creates matrices with the same number of species and interactions as the empirical one, 640
- and in which species interaction probability is based on their observed connectivity (Bascompte et al. 2003; Marquitti et al. 2014). As MODULAR uses an iterative searching 642
- algorithm, we investigated the robustness of the resulting modular partition by running the analysis 30 times using different seed set numbers. The resulting 30 partitions showed similar 644
- levels of modularity but differed in the resulting number of modules (Table S3.1). Hence, we further explored the species composition of the modules in the different runs. Species 646
- composition of modules was relatively constant, with all but five of the hummingbird species being placed over 87% of the runs together in the same module (that is, in 26 out of the 30 648
- runs). This threshold value for establishing modules was chosen through a hierarchical agglomerative cluster analysis of dissimilarity data (Figure S3.1). Supporting this partition, 650
- hummingbirds with variable module partners were not randomly scattered but tended to be placed together with specific modules (Figure S3.1) and showed no differences in any of the 652
- studied traits with species forming constant groups (Table 1, Figure S3.2). 654

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Zhao S, Guo Y, Sheng Q, Shyr Y (2016) An improved heatmap package. Package "heatmap3" 660

- Table S4.1. Results from the 30 runs of the MODULAR (Marquitti et al. 2014) modularity analysis. Notice that the resulting number of modules varies between 5 and 8. Modularity
- values average M=0.466, with a standard deviation of SD=0.004. All runs were significantly modular when compared against matrices of same number of species and interactions as the
- empirical one, and where species have a probability of interaction derived from their observed connectivity (NM2).

Figure S4.1. Heatmap illustrating the frequency each pair of hummingbird species was placed

- in the same module in each modularity run. The modularity algorithm was run 30 times. Clustering analysis was performed with a fast hierarchical and agglomerative routine of 674
- dissimilarity data from the *fastcluster* package in R (Müllner 2017) resulting in five clusters. Arrows mark the five hummingbird species without constant partners. Heatmap compiled in 676
- the *heatmap3* package in R (Zhao et al. 2016). 678

- Figure S4.2. Results of the non-metric muldimensional scaling ordination of five hummingbird species traits (bill length, body mass, biogeographical distribution, degree of 682
- endemism and migratory behavior). The illustration shows (a) how hummingbirds without fixed module-partners do not differ in traits from hummingbirds with fixed module partners, 684
- and (b,c) the lack of significant differences when considering modules conformed of only constant partners (bottom left, the partition showed in the main text) and when considering 686
- modules derived from the cluster partition (bottom right). Ellipses in the NMDS indicate 95% confidence intervals around the centroids of each group. Note that analyzing only constant 688
- groups of partners or clusters result in virtually identical ellipses. 690

 $MDS1$ Goodness of fit = 0.426 , p-value = 0.001 Goodness of fit = 0.345 , p-value = 0.001

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Module₅

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\bullet \bullet \bullet 45\n \end{array}$

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Appendix 5. Partial regression plots for the asymptotic errors of the non-parametric multiple regression with kernel smoothing analysis. 692

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ordered(migratoryhabits)

 $\mathbf{1}$

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 $\overline{2}$

Appendix 6. Differences in average *c* values in the various hummingbird phylogenetic lineages (KW $X^2 = 13.751$, df = 5, p-value = 0.017). 700

