

Velasco, Julián A. and Martínez-Meyer, Enrique and Flores-Villela, Oscar and García, Andrés and Algar, Adam C. and Köhler, Gunther and Daza, Juan M. (2016) Climatic niche attributes and diversification in Anolis lizards. Journal of Biogeography, 43 (1). pp. 134-144. ISSN 1365-2699

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1	Orig	inal	Arti	cle
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- 2 Title: Climatic niche attributes and diversification in Anolis lizards
- 3 Running header: Niche and speciation in lizards
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### 29 ABSTRACT

Aim The aim of this study was to test the link between climatic niche dynamics and species diversification in *Anolis* on islands and on the mainland. We tested the hypotheses that lineages in warmer climates and with narrow climate niches diversified more than lineages in cold climates and with broad climate niches. We also tested the hypothesis that species-rich clades exhibit greater niche diversity than species-poor clades.

36 **Location** Neotropics

Methods We collated occurrence records for 328 *Anolis* species to estimate niche
breadth, niche position and occupied niche space (as a proxy for niche diversity).
We compared niche breadth between insular and mainland *Anolis* species and
among *Anolis* clades, controlling for the potential confounding effect of range size.
Using two approaches (clade-based and QuaSSE) we explore the association
between niche metrics and diversification rates in *Anolis* lizards.

43 **Results** We found that Caribbean Anolis had a narrower niche breadth and niche 44 space occupation compared to mainland anoles after controlling for range size 45 differences. There was a significant association between niche traits (mean niche 46 position and niche breadth) and diversification in anoles. Anole lineages with 47 narrow niche breadths and that occupy warmer areas exhibited higher speciation 48 rates than those with broader niche breadths that occupy cold areas. In the same 49 way, clades with higher total diversification exhibit more niche diversity than clades with lower total diversification. 50

Main conclusions Climatic niche attributes play a role in anole diversification with
some differences between mainland and insular anole lineages. Climatic niche
differences between regions and clades likely are related to differences in niche
evolutionary rates. This also suggest that climate plays a strong role in shaping
species richness between and within mainland and islands.
Keywords Anolis, climate constraints, climatic space, evolution, Neotropics, niche
breadth, niche diversification, niche specialization, lizards, species richness

## 60 INTRODUCTION

61 Species richness in a clade or region results from the interplay of ecological and 62 evolutionary factors operating at different spatial and temporal scales (Wiens, 63 2011; Cornell, 2013). Species richness in a region can ultimately be explained by 64 differences in diversification rates (i.e., speciation minus extinction) and dispersal events (Wiens & Donoghue, 2004; Wiens, 2011). Although species diversification 65 66 is known to be influenced by ecological factors within a particular region (Wiens, 67 2011; Cornell, 2013; Machac et al., 2013), there is still little understanding of how 68 variation in ecological factors affects species diversification, and thus species 69 richness, across phylogenetic and geographic scales.

70 Ecology, diversification, and species richness are linked through the niche 71 concept (Hutchinson, 1957; Soberón & Nakamura, 2009; Ricklefs, 2012). For 72 instance, some recent studies have shown that speciation rates are coupled with 73 rates of niche evolution (Rabosky, 2012a; Rabosky & Adams, 2012; Rabosky et 74 al., 2013). Accordingly, clades displaying a high degree of species richness are 75 expected to have greater niche diversity than clades with low species richness 76 (Rabosky, 2012a; Ricklefs, 2012; Rabosky et al., 2013). This prediction is an 77 expected outcome during adaptive radiation where slowdowns in diversification 78 occur as ecological space is filled and species' niches become narrow due to 79 competition (Schluter, 2000; Rabosky, 2009). In this way, niche divergence can 80 drive cladogenesis. Alternatively, diversification may not be ecologically 81 constrained but rather, time or area dependent (Wiens, 2011). In cases where 82 cladogenesis is decoupled from niche evolution, we would expect lineages to

have greater niche similarity and large niche breadths (Cornell, 2013). The above
scenarios have been explored mostly using phenotypic traits related to habitat use
(Schluter, 2000; Harmon *et al.*, 2003). Only recently have some studies explored
the role of coarse-grain climatic niche attributes in clade diversification (Kozak &
Wiens, 2010; Pyron & Burbrink, 2012; Schnitzler *et al.*, 2012; Machac *et al.*, 2013;
Wiens *et al.*, 2013; Kostikova *et al.*, 2014).

89 The climatic niche is defined as the set of climatic variables at a coarse-90 resolution with an influence on the intrinsic and instantaneous population growth 91 rates of a species at a geographic scale (Soberón, 2007; Peterson et al., 2011). It 92 is useful to establish whether climatic niche requirements can explain differences 93 in species richness and diversification among regions and clades. This definition 94 considers climatic niche as a population-level trait and not as an individual-level 95 trait, which is implicit in definitions incorporating critical physiological boundaries. 96 Accordingly, several studies have explored the link between climatic niche 97 attributes and diversification (Kozak & Wiens, 2010; Schnitzler et al., 2012). For 98 instance, Kozak & Wiens (2010) suggested that high rates of climatic-niche 99 evolution might promote increases in diversification rates. However, a causal link 100 between diversification rate and climatic niche evolution is difficult to establish 101 (Schnitzler et al., 2012). In order to clarify the link between niche dynamics, 102 diversification and species richness, clear predictions about how climatic niche 103 attributes (e.g., niche space and niche breadth) facilitate increases or slowdowns 104 in diversification rates are needed.

105 In this paper, first, we hypothesize a link between climatic niche metrics 106 (i.e., niche position and niche breadth) and diversification in Anolis lizards. For 107 niche position, we predict that lineages occupying warmer and drier areas (where 108 anole diversity is higher; Algar & Losos, 2011; Losos, 2009) tend to diversify more 109 than lineages adapted to cold and very humid conditions (where their diversity is 110 lower). For niche breadth, we predict that clades composed of climatic niche 111 specialist species (i.e., with narrow niche breadths) will have higher diversification 112 rates than lineages composed of climatic niche generalist species (i.e., wide niche 113 breadths) (Futuyma & Moreno, 1988; Cantalapiedra et al., 2011; Cadena et al., 114 2012; Wiens et al., 2013). This hypothesis predicts a negative relationship 115 between diversification rates and niche breadth, a relationship that likely is 116 mediated by climatic niche conservatism (Gómez-Rodríguez et al., 2015). Second, 117 we hypothesize that clades with high species richness (and likely high 118 diversification rates) will have a high degree of niche diversity (i.e., more occupied 119 niche space) than clades poor in species (Ricklefs, 2012). This is consistent with a 120 scenario where cladogenesis is driven by niche evolution rates (Harmon et al., 121 2003; Rabosky et al., 2013). 122 We test these hypotheses for *Anolis* lizards, which occur mainly in the 123 Caribbean islands and on the mainland from Mexico to southern Brazil. They are 124 species-rich on both the islands (~160 species) and the mainland (~230 species;

125 Table 1). The evolutionary history of Caribbean Anolis has been subjected to

126 intense research in the last several decades (Losos, 2009). There is evidence that

127 their diversification in the Greater Antilles is related to island size and colonizing

time, with speciation rates declining over time as a function of area (Rabosky &
Glor, 2010). This pattern suggests that regional species richness in the Greater
Antilles is controlled by area and potentially by competitive interactions (Losos &
Schluter, 2000; Rabosky & Glor, 2010). Specifically, we predict that *Anolis* lizards
with narrow climatic niches and specialization toward particular climate regimes
have diversified more than those that tolerate a wide range of climate conditions
(Kozak & Wiens, 2010).

In this paper, we compare climatic niche attributes in *Anolis* between
regions and clades, to assess whether niche position and specialization have
driven diversification in these lizards. We evaluate the available climatic space in
each region to explore patterns of niche occupation in *Anolis* clades inhabiting the
islands and the mainland. Although there are substantial niche differences
between insular and mainland anoles, niche traits were associated with

141 cladogenesis in both anole faunas.

## 142 MATERIALS AND METHODS

### 143 Anolis records

144 We mapped 13,580 georeferenced locality records for 328 Anolis species from the

- 145 Caribbean islands (145 species, 3,134 locality records) and the mainland (183
- 146 species, 10,445 locality records), drawn from the Global Biodiversity Information
- 147 Facility (GBIF, http://gbif.org), HerpNET (http://www.herpnet.org/), Algar and
- 148 Losos (2011), Ochoa-Ochoa & Flores-Villela (2006) and other databases not
- 149 publicly available (e.g., GK database). Some herpetological collections for which
- 150 *Anolis* locality data is not available via the Internet (e.g., GBIF or HerpNet), namely

151 ICN (Colección de Anfibios y Reptiles, Instituto de Ciencias Naturales, Bogotá 152 Colombia), MHUA (Museo de Herpetología de la Universidad de Antioquia, 153 Medellin, Colombia), and QCAZ (Colección de Anfibios y Reptiles, Pontificia 154 Universidad Católica de Ecuador, Quito, Ecuador) were georeferenced using 155 national gazetteers and the point-georeferencing method with a spatial precision 156 of ~1 km (Chapman & Wieczorek, 2006). We carefully revised each record in our 157 database and eliminated erroneous, doubtful and duplicate records (i.e., identical 158 records from two or more sources).

159

## 160 Climatic niche metrics in Anolis lizards

161 We estimated the climatic niche represented by temperature and precipitation 162 variables drawn from the WorldClim database (Hijmans et al., 2005) using the 163 occurrence records of 328 species. Our climatic niche estimates encompass the 164 realized niche as is common in GIS approaches (Peterson et al., 2011). To 165 estimate the niche breadth for each Anolis species, we used maximum 166 Mahalanobis distances (Rotenberry et al., 2006); a statistical technique for 167 ecological niche modelling based on presence-only records (Peterson et al., 168 2011). The Mahalanobis distance measures the space between two points in a *n*-169 dimensional coordinate system accounting for unequal variances and correlation 170 between variables (Xian et al., 2008). Distances are simply calculated as a 171 standardized difference between the value of any point (i.e., a species' record) 172 and the mean values from all points from the climate space (Rotenberry et al.,

173 2006). Also, we estimated niche breadth using Euclidean distances and ran a 174 correlation of niche breadth between both distance methods, which was highly 175 significant (p < 0.0001).

176 We characterized the available climatic space for each region in which each 177 clade occurs. For each island in the Greater Antilles we extracted values for bioclimatic variables for all pixels (1 km<sup>2</sup> pixel size). For the mainland, we 178 179 generated a minimum convex polygon for Middle American and South American 180 anole records with a buffer of 1,000 km in each area. Note that here Middle 181 America refers to the countries of Central America and Mexico. This polygon 182 potentially represents at least the dispersal or movement area for mainland anole 183 species (Peterson & Soberón, 2012; Saupe et al., 2012). We clipped all bioclimatic 184 rasters using this polygon and extracted values for all 19 variables from a random set of pixels (>100,000 pixels of 1 km<sup>2</sup> each for South America, and >25,000 pixels 185 186 of 1 km<sup>2</sup> each for Middle America). We conducted a Principal Components 187 Analysis (PCA) with all 19 bioclimatic variables from species records and points 188 from each region (see Appendix S1 in Supporting Information). For each anole 189 species we calculated the mean of the scores of the first PC as an estimate of 190 niche position. Finally, we calculated range size for each species as the area 191 within the minimum convex polygon (MCP) enclosing all records for individual 192 species and for anole clades. The MCP was only used to calculate range sizes, 193 which were used as covariates for comparisons of niche breadth between clades 194 and regions.

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## 196 Phylogenetic estimation

197 We generated a time-calibrated phylogeny using an Anolis dataset extracted from 198 a recent Squamata phylogeny (Pyron et al., 2013). Our anole tree comprises 207 199 anole species, representing 53% of the total number of recognized anole species 200 (Uetz, 2014). Although sampling was very complete for the Caribbean anole 201 species (87%, 19 species missing), and was very incomplete for the mainland 202 species (76 species, 32% of all known species). We also included 32 outgroups 203 based on the topological position of *Anolis* in the Iguania phylogeny (Townsend et 204 al., 2011). The assembled matrix included 233 taxa and 12,896 sites 205 corresponding to 9 genes included in Pyron et al. (2013). We used their alignment 206 to maintain consistency among studies. We used only two calibration points due 207 to the low availability of fossil samples. First, using a normal distribution prior we 208 calibrated the root with the crown-group pleurodont iguanian Saichangurvel 209 (Conrad & Norell, 2007) from the Late Campanian (70.6 ± 0.6 Ma; Townsend et al., 210 2011). Second, a lognormal prior with a minimum age of 23 Ma was used to 211 calibrate the Anolis chlorocyanus group based an unnamed fossil from the 212 Dominican Republic putatively assigned to this clade (de Queiroz et al., 1998). We 213 placed this anole fossil at the stem of the chlorocyanus group (A. aliniger, A. 214 chlorocyanus, A. coelestinus, A. singularis) following Nicholson et al. (2012). We 215 implemented a relaxed clock method with uncorrelated rates among branches 216 using the software BEAST 1.8.0 (Drummond et al., 2012). We did not implement a 217 highly parameterized partitioned analysis as the ingroup (Anolis) is represented 218 almost entirely by one single gene (ND2). As suggested by iModeltest v.2

219 (Guindon & Gascuel 2003: Darriba et al., 2012) we used the GTRGI model of 220 evolution for the entire dataset. We initiated two runs starting from a random tree 221 and ran these for 40 million generations sampling every 1,000 following a burn-in 222 of 2 million generations. The number of generations required to reach stationarity 223 was determined by examining marginal probabilities in Tracer v1.6 (Rambaut et 224 al., 2014). For each run, the posterior sampling of trees yielded an effective 225 sample size (ESS) of >200 for all parameter models. Both runs were combined as 226 they gave similar results, and node and branch parameters were summarized on 227 the maximum clade credibility tree (see Fig. S1 in Appendix S2). The resulting tree 228 was very similar in topology to recent phylogenetic estimates of Anolis lizards 229 using the same datasets (Mahler et al., 2010; Nicholson et al., 2012; Gamble et al., 230 2014; Prates et al., 2015). In particular, Prates et al. (2015) generated a calibrated 231 tree for a subset of Anolis species (some species from Dactyloa clade, Anolis 232 carolinensis and some species from Norops clade) using three fossils as 233 calibration points and lying outside of the Anolis ingroup (one in the root, and two 234 inside the outgroup). Their estimated dates for the most recent common ancestor 235 (MRCA) of Anolis are very similar to our estimated dates (see Prates et al., 2015). 236

# 237 Climatic niche attributes and diversification in Anolis lizards

238 i) The clade-based approach

239 We implemented a clade-based approach to correlate occupied climatic niche

- space with species richness. Nicholson *et al.* (2012, their figure 4) recognized
- eight clades in the Anolis phylogeny and raised them to the rank of genus (but see

242 Poe. 2013). We used these same names as clades to compare niche attributes. 243 Although the criteria to delimit these clades is arbitrary, the same problem occurs 244 with the use of recognized taxa of a given rank (e.g., family or genus level); 245 additionally, some of these clade names for anoles have been used by some 246 herpetologists for almost three decades (Guyer & Savage, 1986; Savage, 2002). 247 We separated the Norops clade into three: Cuban Norops, Jamaican Norops and 248 mainland Norops, and also split the Dactyloa clade: Lesser Antillean Dactyloa and 249 mainland *Dactyloa* (Table 1). We obtained species richness data for each clade 250 from Nicholson et al. (2012). For each clade, we calculated occupied niche space 251 as the summed variances of the first four PC scores (see above). This measure of 252 occupied niche space can be considered a proxy for niche diversity, analogous to the measures of morphological variance used in studies of morphological disparity 253 254 (Foote, 1997; Wainwright, 2004; Ricklefs, 2012). We can use the species richness 255 (In species richness) of anole clades as a direct estimator of the total 256 diversification in each clade (the  $\Omega$  estimator in Rabosky, 2009) because anole 257 clade diversity was not correlated with age ( $R^2 = 0.30$ , p = 0.124) (Rabosky, 2009, 258 2012b; Rabosky & Adams, 2012). In addition, we calculated net diversification 259 rates for each anole clade using the method-of-moments estimator (Magallón & 260 Sanderson, 2001), based on the crown-group age (obtained from our calibrated 261 tree) and the total number of described species for each clade, and using two 262 values for relative extinction rate (0.9 and 0.1). We tested for a relationship 263 between occupied niche space, clade area (log10 geographical area) and species 264 richness (In species richness) and net diversification rates in Anolis clades using a

path analysis. We repeated the same analysis using only insular clades. This
approach allowed us to incorporate all of the anole species for which we had
compiled climate data.

268 *ii) The QuaSSE approach* 

269 We implemented a quantitative-state speciation and extinction model (QUASSE;

270 FitzJohn, 2012) to correlate niche attributes (mean niche position and niche

breadth) with diversification rates (FitzJohn, 2010). The QuaSSE approach uses a

272 maximum likelihood method to evaluate whether a distribution of continuous

273 character states is associated with higher or lower speciation rates (FitzJohn,

274 2010). This method has been used previously to find associations between climate

and diversification rates in other taxonomic groups (Pyron & Wiens, 2013;

276 Kostikova *et al.*, 2014). We explored whether mean niche position and niche

277 breath were associated with speciation rates in *Anolis* lizards. These niche metrics

278 describe the ecological niche of a species across a set of environmental axes

279 (Schoener, 1989; Thuiller *et al.*, 2005). The QuaSSE approach identifies whether

280 lineages exhibiting lower or higher niche positions/broader or narrower niche

281 breadths are correlated with higher speciation rates in *Anolis*.

We generated four models in which speciation rates were fitted according to a particular function: (i) constant function (trait variation has no influence on speciation rate); (ii) linear function (a linear increase in a trait is associated with a linear increase in speciation rate); (iii) a sigmoid function (there is an association between speciation rates and a continuous trait exhibiting a sigmoidal function), 287 and (iv) a modal function (where intermediate values for a trait are associated with 288 a higher speciation rate). In addition, we generated another set of models, but 289 assuming a directional trend in the evolution of the particular trait (FitzJohn, 2012). 290 We kept extinction rates constant among models because QuaSSE is known for 291 its difficulty detecting differences in extinction rates (FitzJohn, 2010). We 292 conducted the same analysis but only for the Caribbean species by pruning all 293 mainland species from the phylogeny. We did not conduct a specific analysis for 294 mainland species only due to the limited taxon sampling for these species (see 295 above). Models were compared using the Akaike Information Criterion (Burnham & 296 Anderson, 2002) and we selected as the best models those with the lowest AIC 297 scores (Burnham & Anderson, 2002). As QuaSSE calculations are guite complex 298 and computationally extensive (FitzJohn, 2012), we only performed a QuaSSE 299 analysis for each variable with the best topology selected from our BEAST 300 analysis. Therefore, we were not able to evaluate the potential effects of 301 phylogenetic uncertainty on correlations between speciation rates and niche traits. 302 Finally, we performed a rarefaction analysis for the Caribbean anole tree to 303 evaluate the impact of missing species on the QuaSSE analysis. We randomly 304 pruned species in a sequence of percentages (10%, 15%, 20%, 25%, 30%, 35%, 305 40%, 45% and 50%) and generated a QuaSSE analysis for each dataset with 306 these pruned trees. The aim was to evaluate whether QuaSSE is sensitive to 307 missing species and therefore to explore the potential impact of taxon 308 incompleteness on the association between traits and diversification (see 309 Appendix S3).

### 310 **RESULTS**

#### 311 Anole climatic niches

312 The first two axes of the PCA explained 46.6% and 22.4% of the total variance of 313 climatic variables in Anolis lizards (69% in total). Both axes were mainly related to 314 temperature variables (see Appendix S1). The first axis was mainly associated with 315 the minimum temperature of the coldest month (bio 6) and the second axis was 316 mainly associated with the maximum temperature of the warmest month (bio 5; 317 see Appendix S1). We used the mean PC scores of the first axis for each species 318 as a metric of average niche position. 319 320 Niche breadth between insular and mainland Anolis lizards and among Anolis 321 clades 322 Caribbean Anolis species did not have lower niche breadth values than their mainland counterparts (Fig. 1a;  $F_{1.330} = 3.32$ , p < 0.069). However, after 323 324 controlling for geographical range size effects, niche breadths do differ between 325 regions (ANCOVA;  $F_{1.308} = 4.24$ , p < 0.040). Furthermore, we did not find any 326 differences in niche breadth between clades (Fig. 1b;  $F_{10,321} = 1.57$ , p < 0.114), 327 but we did detect differences after controlling for range size differences (ANCOVA; 328  $F_{10,299} = 2.35, p = 0.011$ ). 329 330 Occupied niche space in Anolis clades and available climate space

331 Comparisons of occupied niche space with available climate conditions across

regions revealed that the occupation of niche space differed strikingly between

insular and mainland lineages (Fig. 2 and 3). Insular anole clades seem to occupy
almost all climate conditions available on each of the Greater Antilles islands,
except Jamaica (Fig. 2). In contrast, mainland anoles occupy only a portion of all
available climate conditions both in Middle America and South America. The *Norops* clade occupies a larger thermal and water niche space than *Dactyloa*does in Middle America, but in South America both clades occupy similar portions
of the niche space (Fig. 3).

340

## 341 The clade-based approach

342 Path analysis revealed a significant correlation between species richness (total 343 diversification) and occupied niche space for all anole clades (R=0.71, p=0.015; 344 Fig. 4a). Furthermore, occupied niche space had an indirect influence on species 345 richness through clade area (partial r = 0.79). Average niche breadth was not 346 correlated with species richness (R=0.02, p=0.950; Fig. 4b), nor did it have any 347 indirect influence on species richness through clade area (partial r = 0.22). For 348 insular clades, niche attributes (occupied niche space and average niche breadth) 349 were not correlated with species richness (Fig. 4c,d). Similar results were obtained 350 using net diversification rates for Anolis clades (see Fig. S2 in Appendix S2). This 351 suggests that our results are robust to differences in the diversification metrics 352 used (i.e., total diversification and net diversification rates).

## 353 The QuaSSE approach

We found an association between niche attributes (niche position and niche
breadth) and speciation rates for all *Anolis* lizards (Table 2). For niche position and

356 niche breadth, we found that the best model was one with a humped directional 357 trend (Table 2, Fig. 5 upper; though according to AIC values for niche breadth this 358 model had no more support than the linear model with a directional trend). This 359 suggests that speciation rates are higher in lineages occupying warmer areas and 360 for lineages with very narrow niches and some with large niches. For Caribbean 361 anoles, we found that the best model for niche position was one with a directional 362 linear trend (Table 2, Fig. 5 bottom left; again, comparing AIC values for this model 363 had no more support than the hump model with a directional trend). The best 364 model for niche breadth for Caribbean anoles was one with a humped directional 365 trend (Table 2; Fig. 5 bottom right). This suggests that speciation rates are higher 366 in Caribbean anole lineages occupying warmer regions and with very small niches 367 than in lineages occupying cold climates and with large niches. Finally, the 368 association between niche traits and speciation rates for Caribbean Anolis lizards 369 found here was stable to the different percentage of random taxon pruning (see 370 Appendix S3). Therefore our QuaSSE analyses were robust to the taxonomic 371 incompleteness in our dataset.

## 372 **DISCUSSION**

In this study, we found evidence of an association between niche traits and cladogenesis in *Anolis* lizards. First, we found that anole species occurring in warmer and drier regions tend to diversify more than species in humid and cold regions. This result was consistent for mainland and Caribbean anole species. In particular, Caribbean anole clades tend to occupy all available climate space in

378 comparison with mainland anoles. This suggests that Caribbean clades are not 379 likely constrained by an inability to expand their climatic niche limits, but rather, by 380 the limited Caribbean climate space (Algar & Mahler, 2015). In fact, Caribbean 381 species might not be prevented from inhabiting cold conditions by evolutionary 382 constraints on cold tolerance, which can evolve guickly (Leal & Gunderson, 2012; 383 Muñoz et al., 2014), but rather by climatic availability in the region (Algar & Mahler, 384 2015). The limited climatic space, coupled with the high species richness of these 385 clades, suggests substantial niche overlap in insular species, though this may be 386 mediated in part by narrower niche breadths. Furthermore, the high degree of 387 similarity in niche traits for Caribbean anoles, suggests that climate niche 388 convergence might be a widespread phenomenon across the Greater Antilles, as 389 found for phenotypic traits (Losos et al., 1998; Mahler et al., 2013). This pattern 390 might be the result of a combination of reduced climatic space in the region and a 391 strong effect of stabilizing selection on climatic niches (Sedio et al. 2013; Wüest et al., 2015). 392

393 Mainland clades occupy only a portion of the climatic space within their 394 accessible area (Peterson et al., 2011), but these clades still exhibited greater 395 niche breadth and broader niche space values than insular clades. Mainland 396 clades may have been prevented from exploiting the complete available climate 397 space either because of insufficient time for niche diversification (though this is 398 unlikely for the *Dactyloa* clade given its age: 30 Ma; see Table 1), inability to adapt 399 to extreme climate conditions, strong biotic interactions, or dispersal constraints. 400 As mainland anole species tend be absent from regions with extreme

401 temperatures (e.g., mountaintops exceeding 3,000 m or desert areas) anoles may
402 have physiological constraints that prevent them from inhabiting regions with
403 these extreme climate conditions. However, whether mainland anoles are more
404 limited in range by current climate, dispersal limitations or biotic interactions than
405 Caribbean anoles are (Algar *et al.*, 2013), remains unknown.

406 We found strong evidence of a negative relationship between niche breadth 407 and diversification rates. This suggests that niche specialization, particularly 408 toward warmer and drier climates, has driven anole diversification. This 409 association between niche specialization and cladogenesis suggest a strong role 410 of climate in anole diversification. Similar results have been found in lampropeltine 411 snakes, for which lineages occurring in warm conditions had higher speciation 412 rates (Pyron & Burbrink, 2012). Finally, we found that clades with higher species 413 richness tend to exhibit more niche diversity (occupied niche space) than species-414 poor clades. These results support the hypothesis that cladogenesis is coupled 415 with climate niche divergence in Anolis lizards (Rabosky 2012a, Rabosky et al., 416 2013). Recently, Gómez-Rodríguez et al. (2015) suggested that a negative 417 relationship between niche width and diversification rates would be expected 418 under a scenario of niche conservatism (Wiens, 2004). In contrast, they suggested 419 that a positive relationship would be expected under a scenario of climatic niche 420 divergence (Moritz et al., 2000). However, it is not clear how these niche 421 conservatism or niche divergence patterns can shape diversification dynamics at 422 regional scales. In our opinion, the evolutionary mechanisms underlying the

423 correlation between climatic niche traits and speciation dynamics are still424 unknown.

425 Our study is the first to examine how climatic niches vary among Anolis 426 lizards at large phylogenetic and geographical scales, and how climatic niche 427 traits are related to species diversification. We found that Caribbean and mainland 428 anoles exhibit striking differences in niche traits (after controlling for range size 429 effects) and these are correlated with speciation rates. Specifically, we found that 430 lineages with narrow niches and that are specialized to warmer areas have 431 diversified more than lineages with large niches and specialized to cold regions. 432 Niche differences in insular and mainland anoles suggest that different 433 evolutionary processes (niche divergence or niche conservatism) might be 434 operating between regions, as in the case of ecomorphological traits (Pinto et al., 435 2008). However, it is crucial that a more comprehensive phylogeny for mainland 436 anoles be incorporated to corroborate these findings using comparative 437 phylogenetic methods. Finally, our study found interesting macroecological and 438 macroevolutionary patterns, but more research is necessary to identify the 439 potential evolutionary mechanisms driving these patterns.

440

## 441 **ACKNOWLEDGEMENTS**

442 JAV is grateful to the Posgrado de Ciencias Biológicas (PCB) at the Universidad

443 Nacional Autónoma de México and to the Consejo Nacional de Ciencia y

444 Tecnología (Conacyt) for graduate scholarship No. 262590. This paper fulfils one

445 of the requirements for the PhD in Sciences of the PCB. JAV thanks M. J.

- 446 Londoño, D. Osorio, L. Valenzuela, S. Poe, and three anonymous reviewers for
- their useful comments. JAV also thanks G. Uguetto for sharing some distribution
- 448 data on Venezuelan species and S. Claramunt for helping with R code to generate
- 449 figures from QuaSSE analyses. OFV is grateful for funding from the NSF (grant
- 450 DEB-0613802) awarded to J. Campbell and OFV.
- 451

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## **Supporting Information**

- 650 Additional Supporting Information may be found in the online version of this article:
- 652 Appendix S1 Results of the Principal Components Analysis for 19 bioclimatic653 variables.

- 655 Appendix S2 Supplementary figures.
- **Appendix S3** Effects of missing species on the QuaSSE analysis.

- 660 Biosketch
- 661 Julián A. Velasco is carrying out his Ph.D studies at the Instituto de Biología,
- 662 Universidad Nacional Autónoma de México. His doctoral research focuses on
- 663 understanding the ecological and evolutionary processes responsible for species
- richness gradients and diversification in *Anolis* lizards. He addresses several
- 665 evolutionary and ecological topics using a combination of conceptual and
- 666 methodological approaches including niche modelling, geospatial analysis,
- 667 historical biogeography and macroecology.
- 668
- 669 Author contributions: JAV conceived the ideas and analysed the data; EMM,
- 670 OFV and AGA, and ACA provided feedback and contributed ideas; ACA, GK and
- 671 OFV collected the occurrence records for Anolis species; JMD performed the
- 672 phylogenetic analysis; JAV led the writing and had the approval of all the authors.
- 673

674 Editor: Kostas Triantis

## 675 Tables

Table 1. Clades recognized in *Anolis* radiation, species richness, range size (log10 km<sup>2</sup>), age, net diversification rates (Net div. rates; extinction fraction 0.9/0.1), occupied niche space (Occ. niche space), niche breadth (log10) and distribution.

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Clade	Species richness	Range size	Age (Ma)	Net divers. rates	Occ. niche space	Niche breadth	Distribution
Anolis	44	5.095	30.090	0.054/0.102	3.076	1.542	Bahamas, Cayman islands, Cuba, Hispaniola, south of Florida.
Lesser Antilles Dactyloa	9	3.210	25.510	0.021/0.059	1.34	1.513	Southern Lesser Antilles.
Mainland Dactyloa	83	7.053	30.980	0.072/0.122	16.496	2.640	Lower Central America and South America.
Audantia	9	4.921	22.860	0.023/0.059	7.968	1.779	Hispaniola and satellite islands.
Chamaelinorops	16	4.863	30.850	0.028/0.067	7.432	1.704	Hispaniola and satellite islands.
Ctenonotus	36	4.945	30.870	0.047/0.093	5.2	1.779	Bahamas, Hispaniola, Puerto Rico, Virgin Islands, Northern Lesser Antilles.
Deiroptyx	21	5.270	32.100	0.033/0.073	4.861	1.704	Cuba, Hispaniola, Puerto Rico.
Xiphosurus	11	5.170	30.030	0.021/0.057	4.199	1.736	Cuba, Hispaniola, Puerto Rico and satellite islands.

	Cuban Norops	18	5.110	28.950	0.029/0.068	1.986	2.640	Cuba.
	Jamaican Norops	7	4.090	25.270	0.016/0.049	2.575	1.382	Jamaica.
	Mainland Norops	150	7.140	32.310	0.090/0.142	14.148	2.707	Middle and South America.
070								

681 Table 2. QuaSSE models of the relationship between climatic niche metrics (niche position and niche breadth) and

682 speciation rates in all Anolis and only Caribbean Anolis lizards. Best-fitting models according to delta AIC (Akaike

683 information criterion) values are in bold. Pars: Number of parameters; InL: In Likelihood; AIC: Akaike Information Criterion;

684  $\triangle$ AIC: Delta AIC; Weights: model weights.

	Niche position					Niche breadth				
	Model	Pars	InL	AIC	ΔAIC	Weights	InL	AIC	ΔAIC	Weig
	Minimal	3	-937.95	1881.9	48	0.00	-683.31	1372.6	45	0.0
	Linear	4	-937.89	1883.8	50	0.00	-683.22	1374.5	47	0.0
	Sigmoidal	6	-937.06	1886.1	52	0.00	-682.91	1377.8	51	0.0
All Anolis	Hump	6	936.28	1884.5	51	0.00	-682.81	1377.6	50	0.0
	Linear (drift)	5	-917.36	1844.7	11	0.00	-659.16	1328.3	1	0.2
	Sigmoidal (drift)	7	-917.92	1849.8	16	0.00	-662.35	1338.7	12	0.0
	Hump (drift)	7	-909.91	1833.8	0	0.38	-656.58	1327.2	0	0.3

	Sigmoidal	6	-651	1314	27	0.00	-391.7	795.3
Caribbean Anolis	Hump	6	-649.4	1310.8	24	0.00	-391.7	795.3
	Linear (drift)	5	-638.4	1286.8	0	0.38	-391.4	792.7

7

-641.2

-637.2

1296.3

1288.3

9

1

0.00

0.23

Sigmoidal (drift)

Hump (drift)

16

18

22

22

20

0

24

773.1

797.3

-379.5

-391.7

0.0

0.0

0.0

0.0

0.0

0.3

0.0

685

34

686

## 688 Figure Legends

689 Figure 1. Box plots of niche breadth values for Caribbean and mainland *Anolis* species

690 (a) and *Anolis* clades (b). Niche breadth was estimated using maximum Mahalanobis

691 distances to the niche centroid for 19 bioclimatic variables in a multidimensional

692 climatic niche space. *Dactyloa* LA: *Dactyloa* Lesser Antilles.

Figure 2. Occupied climate niche space for Caribbean anole clades in each one of the Greater Antilles islands. Light grey points represent the available climate conditions in each island extracted from each pixel (see text for details).

Figure 3. Occupied climate niche space for mainland anole clades in Middle America
and South America. Light grey points represent the available climate conditions in each
mainland region extracted from a random sample of pixels (see text for details)

Figure 4. Direct and indirect effects of climatic niche traits (occupied niche space and

niche breadth) on species richness for all anole clades (a,b), and only for insular clades

701 (c,d). Statistically significant correlation coefficients are in bold (p < 0.05).

Figure 5. Relationships between niche traits (mean niche position and niche breadth)
and speciation rates for all anoles lizards (upper) and Caribbean anoles only (bottom)
using the QuaSSE approach. Dotted lines represent alternative models according to
delta AIC values (see table 2).

706

707







715 Figure 2



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Figure 4



Figure 5



