

SUPPORTING INFORMATION

**A holistic view of the factors shaping the diversity of the lichen-forming fungal genus *Sticta*
(lichenized Ascomycota: Peltigerales) in the Caribbean**

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Appendix S1.1

DNA extraction, amplification and sequencing

DNA was extracted using the ZR Fungal/Bacterial DNA MiniPrep™ (Zymo Research, Irvine, CA, USA). Small portions of thalli were removed and manually grinded with mortar and pestle. Liquid nitrogen was used to facilitate tissue breakdown. Apart from these steps, extractions followed manufacturer's instructions.

Primers and PCR conditions used in this study are described in detail in Mercado-Díaz et al., 2020 and Widhelm et al., 2018. Briefly, PCR amplification was carried out using MyTaq™ Red DNA Polymerase (Bioline, Taunton, MA, USA) using previously reported aliquots of primers, water and template DNA. Amplification products were visualized on 1% agarose gels and subsequently purified with Exo SAP-IT (USB, Cleveland, OH, USA). Cycle sequencing was performed using Big Dye Terminator v.3.1 (Applied Biosystems, Foster City, CA, USA) and the same primers used for amplification. An ABI 3730 (Applied Biosystems) automatic sequencer was used to obtain sequences. Molecular work was carried out at the Pritzker Laboratory for Molecular Systematics at the Field Museum, Chicago, IL, USA.

Appendix S1.2

Environmental and geographic parameters for phylobetadiversity analysis

Environmental distances

Environmental parameters used for phylobetadiversity were obtained using GIS analysis and cloud computing for visualization of remotely sensed data. To do this, we first loaded specimen locality data in ArcGIS (ESRI, 2016) and defined 10 km² quadrats that captured most of the locality points within each of the sampling areas identified in Table 1. We characterized climate patterns for these areas by uploading and analyzing quadrats in the ClimateEngine web browser (<http://climateengine.org/app>), a cloud computing tool that uses Google's Earth Engine (Gorelick et al., 2017) for on-demand processing of satellite and climate data. The TerraClimate dataset, which is based on WorldClim and CRU Ts4.0 and JRA55 data, was used for obtaining data on precipitation (which was characterized using the Standardized Precipitation Index (SPI) (McKee, 1993)) and maximum and minimum temperatures. Data from the USGS MODIS Eta was used to estimate reference evapotranspiration (Eto). Estimates for the NDVI and the EVI indices were obtained using data from the USGS Modis Terra/Aqua sensor. Both NDVI and EVI are vegetation vigor, or “greenness” metrics but EVI minimizes adverse effects that derive from the soil background and atmospheric nuances (Alfredo Huete, Chris Justice, Wim van Leeuwen, 1999). Single-point estimates for all parameters were obtained by averaging monthly or bi-monthly values recorded for each island in 2019. On the other hand, values for the TRI index were obtained by implementing Riley et al., (1999) original algorithm. This analysis was carried out in Google Earth Engine and used the Shuttle Radar Topography Mission (SRTM, ver. 4) digital elevation dataset. Due to computing limitations, it was necessary to add a 1.2 scale factor to obtain TRI estimates. Calculations were therefore based on a 36 m resolution value (30 m

[native SRTM resolution] x 1.2 [scaling parameter]). This resulted in ruggedness ranging from 0.39 (less rugged) to 0.99 (more rugged). TRI estimates were first obtained for our sampling area quadrats and then averaged by island.

Geographic distances

To generate a matrix of inter-island geographic distances, we first used ArcGIS to draw for each island a polygon with vertices representing a single georeferenced sampling locality within each of our sampling areas. We then used the “Calculate Geometry” function in ArcGIS to obtain coordinates for polygon centroids and subsequently used R to calculate Euclidean distances between island centroids.

Table S1.1 Details about collecting areas for *Sticta* in the Caribbean. Vegetation types follow the “Terrestrial Ecoregions, Major Habitat Types, Biogeographic Realms” map from The Nature Conservancy (Olson et al., 2001). Due to similarities observed, two localities were attributed to ID "CUB03". The geographic distribution of localities is shown in Fig. 1.

ID	Geographic area	Island	Province	Vegetation type	Elevational range (m)	Collection dates
CUB01	Paisaje Natural Protegido Gran Piedra	Cuba	Santiago de Cuba	Tropical and Subtropical Moist Broadleaf Forests	920-1131	June 19 – July 17, 2016
CUB02	Parque Nacional Turquino	Cuba	Granma / Santiago de Cuba	Tropical and Subtropical Moist Broadleaf Forests	878-1955	July 7– July 9, 2016
CUB03	Parque Natural Protegido Topes de Collantes, Trinidad	Cuba	Sancti Spiritus	Tropical and Subtropical Moist Broadleaf Forests	650-860	March 19, 2018
CUB03	Las Vegas de Matagua, Cumanayagua	Cuba	Cienfuegos	Tropical and Subtropical Moist Broadleaf Forests	665	March 21, 2018
CUB04	El Yunque	Cuba	Guantánamo	Tropical and Subtropical Moist Broadleaf Forests	40-560	February 27, 2019
JAM01	Blue Mountains National Park	Jamaica	St. Thomas / Portland	Tropical and Subtropical Moist Broadleaf Forests	1684-2165	April 8 – April 23, 2018
JAM02	Cinchona Botanical Garden	Jamaica	St. Andrew	Tropical and Subtropical Moist Broadleaf Forests	1670-1680	
DOR01	Parque Nacional	Dominican Republic	Pedernales	Tropical and Subtropical Coniferous Forests	1410-1739	July 12 – July 14, 2017

	Sierra de Batoruco					
DOR02	Parque Nacional Sierra de Neiba	Dominican Republic	Independencia	Tropical and Subtropical Coniferous Forests	1684-1911	July 25 – July 26, 2017
DOR03	Parque Nacional Jose del Carmen Ramirez	Dominican Republic	San Juan / Manabao	Tropical and Subtropical Coniferous Forests	1115-2136	July 18 – July 21, 2017
PUR01	Puerto Rico	Puerto Rico	Several municipalities	Tropical and Subtropical Moist Broadleaf Forests	200-1,200	Continuously since 2015
GUAD01	Pitons de Bouillante – Parc National de la Guadeloupe	Guadeloupe	Vieux-Habitants	Tropical and Subtropical Moist Broadleaf Forests	621-957	May 2, 2019
GUAD02	Sentier d'interpretation du Matouba – Parc National de la Guadeloupe	Guadeloupe	Saint-Claude	Tropical and Subtropical Moist Broadleaf Forests	678-914	April 30 – May 4, 2019
DOM01	Syndicate Visitor Center – Morne Diablotin National Park	Dominica	St. Peter	Tropical and Subtropical Moist Broadleaf Forests	587-873	July 31 – Aug 11, 2017 and April 14 – 21, 2019
DOM02	Mourne Trois Pitons National Park	Dominica	St. Paul / St. George	Tropical and Subtropical Moist Broadleaf Forests	360-828	

DOM03	Soufriere Sulfur Springs National Park	Dominica	St. Mark	Tropical and Subtropical Moist Broadleaf Forests	90-100	
MAR01	Sentier PR Montagne Pelée par l'Aileron	Martinique	St. Pierre	Tropical and Subtropical Moist Broadleaf Forests	625-906	April 21 -28, 2019
MAR02	Piton Boucher / Piton Alma / Morne Bellevue / Mourne de Lorrain	Martinique	Fort-de-France / Gros Morne / La Trinite / St. Joseph	Tropical and Subtropical Moist Broadleaf Forests	408-745	
MAR03	Montagne du Vauclin	Martinique	Saint Esprit	Tropical and Subtropical Moist Broadleaf Forests	430-450	

Table S1.2. Voucher information and GenBank accession numbers for taxa used in phylogenetic analyses in this study. Newly generated sequences tentatively identified with an “x”.

ID	Taxon Corrected	Country	Collector	Voucher #	ITS	MCM7	mtSSU	nuLSU	RPB1	RPB2
DNA9930	<i>Lobaria pulmonaria</i>	U.S.A.	Widhelm	<i>s.n.</i>	MG367435	MF984336	MG754091	MG063078	MG754080	–
LG0688	<i>Pseudocyphellaria crocata</i>	France	Magain & Sérusiaux	<i>LG0688</i>	JQ735976	–	JQ736009	JQ735993	KT281770	–
RX50	<i>Ricasolia amplissima</i>	U.S.A.	Dillman	<i>2008-602</i>	KX385118	–	KC494188	–	–	KX385158
DNA4932	<i>Sticta aff. andina</i>	Colombia	Barragán	<i>12</i>	KC732476	MF984295	–	–	–	–
DNA7246	<i>Sticta aff. andreana</i>	Costa Rica	Moncada	<i>5620</i>	MG367402	MF984284	–	MG063062	–	–
DNA16979	<i>Sticta aff. andreana-2</i>	Jamaica	Mercado-Díaz	<i>3401</i>	x	–	x	x	–	x
DNA5443	<i>Sticta aff. arachnofuliginosa</i>	Colombia	Moncada	<i>4733</i>	KC732580	MF984309	MG754154	MG062948	–	–
DNA7291	<i>Sticta aff. arachnofuliginosa-2</i>	Colombia	Fonseca	<i>65</i>	MG367407	MF984213	–	–	–	–
DNA18170	<i>Sticta aff. borinquensis-2</i>	Martinique	Mercado-Díaz	<i>3981</i>	x	x	–	x	–	x
DNA15628	<i>Sticta aff. ciliata-2</i>	Dominican Republic	Mercado-Díaz	<i>3062e</i>	x	x	–	x	x	x
LG3539	<i>Sticta aff. ciliata-3</i>	France	Gérault	<i>LG3539</i>	KT281718	–	KT281674	KT281630	KT281774	–
DNA5474	<i>Sticta aff. ciliata-4</i>	Colombia	Moncada	<i>4678</i>	KC732607	MF984324	MG754144	MG063039	–	–
DNA15621	<i>Sticta aff. ciliata-5</i>	Dominican Republic	Mercado-Díaz	<i>3122b</i>	x	–	–	x	–	x
DNA7297	<i>Sticta aff. ciliosylvatica</i>	Colombia	Fonseca	<i>255</i>	MG367408	MF984209	MG754174	MG063061	–	–
DNA15654	<i>Sticta aff. cometiella</i>	Dominican Republic	Mercado-Díaz	<i>3034a</i>	x	x	x	x	–	x
DNA5022	<i>Sticta aff. cordillerana-2</i>	Colombia	Simijaca	<i>1731</i>	KC732553	MF984252	MG754120	MG062963	–	–
DNA7382	<i>Sticta aff. granatensis</i>	Ecuador	Dal Forno	<i>1787a</i>	MG367416	–	MG754117	MG062990	–	–
DNA15644	<i>Sticta aff. guilartensis-1</i>	Dominican Republic	Mercado-Díaz	<i>3072b</i>	x	x	x	x	x	
DNA17168	<i>Sticta aff. guilartensis-2</i>	Puerto Rico	Mercado-Díaz	<i>3660</i>	MN065865	x	MN065941	MN066012	MN066034	MN066103
MON6427	<i>Sticta aff. guilartensis-3</i>	Cuba	Mercado-Díaz	<i>44749</i>	x	x	–	x	–	x
DNA17162	<i>Sticta aff. harrisii</i>	Puerto Rico	Mercado-Díaz	<i>3646</i>	MN065842	MN065898	MN065949	MN066001	MN066038	MN066108
DNA16985	<i>Sticta aff. harrisii-1</i>	Jamaica	Mercado-Díaz	<i>3372</i>	x	–	–	x	–	x
DNA18160	<i>Sticta aff. harrisii-2</i>	Martinique	Mercado-Díaz	<i>3973a</i>	x	x	x	x	–	x
DNA15623	<i>Sticta aff. harrisii-3</i>	Dominican Republic	Mercado-Díaz	<i>3131e</i>	x	–	x	x	–	x
MON6798	<i>Sticta aff. hypoglabra</i>	Cuba	Mercado-Díaz	<i>46012</i>	x	–	–	x	–	x
DNA7226	<i>Sticta aff. laciniosa</i>	Costa Rica	Moncada	<i>5789</i>	MG367401	MF984240	–	MG062988	–	–
DNA18211	<i>Sticta aff. laciniosa-2</i>	Guadeloupe	Mercado-Díaz	<i>4043</i>	x	–	–	–	–	–
DNA16757	<i>Sticta aff. laciniosa-3</i>	Jamaica	Mercado-Díaz	<i>3542a</i>	x	x	x	x	–	x

DNA5405	<i>Sticta aff. limbata</i>	Brazil	Lücking	30122	KC732568	MF984319	—	MG062954	—	—
DNA18220	<i>Sticta aff. maculofuliginosa</i>	Guadeloupe	Mercado-Díaz	4057	x	x	x	x	—	x
DNA8047	<i>Sticta aff. marginalis</i>	U.S.A.	Moncada	6916	MG754196	—	MG754095	MG062921	—	x
DNA17156	<i>Sticta aff. parvilobata</i>	Puerto Rico	Mercado-Díaz	3635	MN065887	MN065900	x	MN065979	MN066022	MN066124
DNA6299	<i>Sticta aff. pseudohumboldtii</i>	Colombia	Moncada	4928	KC732736	MF984307	—	MG062947	—	—
DNA16761	<i>Sticta aff. pseudolobaria</i>	Jamaica	Mercado-Díaz	3350	x	x	—	x	—	x
DNA15675	<i>Sticta aff. puracensis</i>	Dominican Republic	Mercado-Díaz	3155	x	—	x	—	x	x
DNA15659	<i>Sticta aff. roseocyphellata</i>	Dominican Republic	Mercado-Díaz	3062b	x	x	—	—	x	x
DNA7259	<i>Sticta aff. scabrosa</i>	Costa Rica	Moncada	5715b	—	MF984264	MG754121	MG063077	—	—
MON6447	<i>Sticta aff. sinuosa-2</i>	Cuba	Mercado-Díaz	45173	x	x	—	x	—	x
DNA18219	<i>Sticta aff. sinuosa-3</i>	Guadeloupe	Mercado-Díaz	4056	x	—	—	x	—	x
DNA18228	<i>Sticta aff. sinuosa-4</i>	Guadeloupe	Mercado-Díaz	4078	x	x	—	x	—	x
DNA6292	<i>Sticta aff. sublimbatoides-2</i>	Colombia	Moncada	4987	KC732732	MF984333	—	MG062964	—	—
DNA5541	<i>Sticta aff. subscrobiculata</i>	Colombia	Coca	1135	KC732639	—	MG754096	MG062985	—	—
DNA6288	<i>Sticta aff. subtomentella</i>	Colombia	Coca	1363	KC732730	MF984259	—	MG063059	—	—
DNA16989	<i>Sticta aff. tainorum</i>	Jamaica	Mercado-Díaz	3369a	x	x	—	x	—	x
DNA7260	<i>Sticta aff. tomentosa</i>	Costa Rica	Moncada	5694	MG367406	MF984315	MG754157	MG063051	—	—
DNA16981	<i>Sticta aff. tomentosa-2</i>	Jamaica	Mercado-Díaz	3384a	x	x	x	x	—	x
DNA18205	<i>Sticta aff. tomentosa-3</i>	Guadeloupe	Mercado-Díaz	4036	x	x	—	x	—	—
DNA5467	<i>Sticta aff. weigelii-1</i>	Colombia	Moncada & Lücking	4667	MG367390	MF984299	MG754103	MG062983	—	—
MON6448	<i>Sticta aff. weigelii-2</i>	Cuba	Mercado-Díaz	45218	x	x	x	x	—	x
DNA18115	<i>Sticta aff. weigelii-3</i>	Dominica	Mercado-Díaz	3884	x	x	x	x	x	x
DNA15673	<i>Sticta aff. weigelii-4</i>	Dominican Republic	Mercado-Díaz	3066	x	—	x	x	x	x
DNA7224	<i>Sticta aff. zahlbruckneri</i>	Costa Rica	Moncada	5785	MG367400	MF984318	—	MG062991	—	—
DNA5030	<i>Sticta albocyphellata</i>	Colombia	Moncada	4588	KC732557	—	MG754114	MG062937	—	—
DNA8197	<i>Sticta albohypoarbuscula</i>	U.S.A.	Moncada	7056	MG367434	MF984210	MG754094	MG062923	—	x
LG0992	<i>Sticta ambavillaria</i>	France	Magain & Sérusiaux	LG0992	JQ735978	—	JQ736011	JQ735995	—	—
DNA7373	<i>Sticta andensis</i>	Colombia	Lücking & Moncada	35422	KC732548	MF984317	MG754134	MG062956	—	—
DNA5003	<i>Sticta andina</i>	Colombia	Alfonso	4	KC732537	MF984248	MG754099	MG062967	MG754084	x
DNA6237	<i>Sticta andreana</i>	Colombia	Vargas & Herrera	634	MG367393	MF984331	—	MG063009	—	—
DNA4985	<i>Sticta arachnofuliginosa</i>	Colombia	Moncada	4007	KC732524	MF984306	—	MG062946	—	—
DNA5599	<i>Sticta arbuscula</i>	Colombia	Lücking & Moncada	33324	KC732682	—	—	MG063046	—	—

DNA5424	<i>Sticta arbusculotomentosa</i>	Colombia	Betancourt	326	KC732572	MF984220	–	MG063041	–	–
LG3858	<i>Sticta atlantica</i>	Azores		3858	KT281737	–	KT281693	KT281648	KT281784	–
DNA4999	<i>Sticta atroandensis</i>	Colombia	Fonseca	23	KC732533	MF984310	–	MG062952	MG754082	–
DNA14282	<i>Sticta babingtonii</i>	New Zealand	de Lange	12640	MF373808	MF984256	MG754167	MG063012	–	–
LG3303	<i>Sticta beauvoisii</i>	U.S.A.	Goffinet	11137	KT281725	–	KT281681	KT281636	KT281787	–
DNA17159	<i>Sticta borinquensis</i>	Puerto Rico	Mercado-Díaz	3639	MN065860	x	x	MN065966	MN066017	MN066122
DNA4914	<i>Sticta brevior</i>	Colombia	Moncada	4590b	MG367386	–	MG754108	MG062929	–	–
DNA13507	<i>Sticta caliginosa</i>	New Zealand	Lücking et. al.	39060a	MF373760	MF984229	MG754135	MG063035	–	–
LG3741	<i>Sticta canariensis</i>	Ireland	Sérusiaux	LG3741	KT281733	–	KT281689	KT281644	KT281779	–
LG0962	<i>Sticta caperata</i>	France	Magain & Sérusiaux	LG0962	JQ735979	–	JQ736012	JQ735996	KT281745	–
DNA16959	<i>Sticta carolinensis</i>	Jamaica	Mercado-Díaz	3356b	x	x	–	x	–	x
DNA15650	<i>Sticta cf. laciniata</i>	Dominican Republic	Mercado-Díaz	3149	x	–	–	x	–	–
DNA15648	<i>Sticta cf. laciniata-3</i>	Dominican Republic	Mercado-Díaz	3119a	x	–	–	x	–	–
DNA17048	<i>Sticta cf. laciniata-1</i>	Dominican Republic	Mercado-Díaz	2962	x	x	x	x	–	x
DNA5027	<i>Sticta cf. sinuosa</i>	Colombia	Simijaca	1725	KC732554	MF984296	–	MG062977	–	–
LG1605	<i>Sticta ciliata</i>	Rwanda	Sérusiaux	LG1605	KT281717	–	KT281673	KT281629	KT281763	–
DNA6336	<i>Sticta ciliosylvatica</i>	Colombia	Moncada	4870	MG367395	MF984205	–	MG063060	–	–
DNA13863	<i>Sticta cinereoglauca</i>	New Zealand	Lücking et. al.	38646	MF373798	MF984241	MG754140	MG063029	–	–
DNA5526	<i>Sticta cometia</i>	Colombia	Coca	1067	KC732626	MF984222	MG754178	MG062927	–	–
DNA4977	<i>Sticta cometiella</i>	Colombia	Moncada	4209	KC732517	MF984221	MG754177	MG062926	–	x
DNA14659	<i>Sticta corymbosa</i>	Puerto Rico	Mercado-Díaz	2380	MN065844	–	–	MN066003	MN066054	MN066098
DNA6179	<i>Sticta delicatula</i>	Colombia	Vargas & Herrera	556	MG367391	MF984237	MG754119	MG062998	–	–
DNA13875	<i>Sticta dendroides</i>	New Zealand	Lücking et. al.	38734	MF373799	MF984272	MG754188	MG063025	–	–
DNA18120	<i>Sticta densiphyllidiata</i>	Dominica	Mercado-Díaz	3892	x	x	x	x	–	x
LG0945	<i>Sticta dichotoma</i>	France	Magain & Sérusiaux	LG0945	JQ735981	–	JQ736014	JQ735998	KT281743	–
DNA5550	<i>Sticta dilatata</i>	Colombia	Coca	1077a	KC732647	–	MG754125	MG063057	–	–
LG1040	<i>Sticta duplolibata</i>	France	Magain & Sérusiaux	LG1040	JQ735984	–	JQ736001	JQ736017	KT281751	–
DNA12973	<i>Sticta filix</i>	New Zealand	de Lange	12284	MG367379	MF984228	–	MG063010	–	–
DNA7345	<i>Sticta fuliginoides</i>	Colombia	Buitrago	24	MG367410	MF984216	MG754158	MG063049	–	–
DNA7395	<i>Sticta fuliginosa</i>	Brazil	Gumboski	3536	MG367419	MF984303	MG754184	MG062939	–	x
DNA5568	<i>Sticta fuscotomentosa</i>	Colombia	Coca	1207	KC732661	MF984280	MG754126	MG063070	–	–
DNA4959	<i>Sticta gallowayana</i>	Colombia	Moncada	4637	KC732496	MF984285	–	MG062934	MG754087	x

DNA5475	<i>Sticta globulifuliginosa</i>	Colombia	Moncada	4757	KC732608	–	–	MG062924	–	–
DNA17174	<i>Sticta guilartensis</i>	Puerto Rico	Mercado-Díaz	3671	MN065864	MN065906	MN065954	MN065959	MN066031	MN066120
DNA5457	<i>Sticta gyalocarpa</i>	Colombia	Moncada	4728	KC732594	MF984327	MG754111	MG063043	MG754089	–
DNA7250	<i>Sticta gyalocarpoides</i>	Costa Rica	Moncada	5649	MG367403	MF984326	–	MG063044	–	–
DNA17161	<i>Sticta harrisii</i>	Puerto Rico	Mercado-Díaz	3645	MN065838	MN065914	MN065947	MN066000	MN066039	MN066111
DNA5477	<i>Sticta hirsutofuliginosa</i>	Colombia	Moncada	4731	KC732610	MF984311	MG754152	MG062950	–	–
DNA6199	<i>Sticta humboldtii</i>	Colombia	Díaz-Escandón	L2	KC732702	MF984312	MG754118	MG062951	–	–
DNA5586a	<i>Sticta hypoglabra</i>	Colombia	Lücking & Moncada	33541	KC732667	MF984322	MG754104	MG063001	–	–
DNA5549	<i>Sticta impressula</i>	Colombia	Coca	1014	KC732646	MF984287	MG754110	MG062931	–	–
DNA6339a	<i>Sticta isidioimpressula</i>	Colombia	Moncada	4992	KC732761	MF984219	–	MG062936	–	–
DNA4982	<i>Sticta isidiokunthii</i>	Colombia	Moncada	4630	KC732522	MF984288	MG754189	MG062930	MG754088	–
DNA8081	<i>Sticta isidiopedunculata</i>	U.S.A.	Moncada	6949	MG367425	MF984211	MG754137	MG063037	–	x
DNA5607	<i>Sticta jaguirreana</i>	Colombia	Moncada	4804	MG754195	–	MG754162	MG062999	–	–
DNA7223	<i>Sticta laciniata</i>	Costa Rica	Moncada	5778	MG367399	–	MG754179	MG062984	–	–
DNA7301	<i>Sticta laevis</i>	Colombia	Fonseca	259	MG367409	MF984206	–	MG063052	–	–
DNA5589	<i>Sticta laselvae</i>	Colombia	Lücking & Moncada	33511	KC732673	MF984269	MG754145	MG063008	–	–
DNA13538	<i>Sticta latifrons</i>	New Zealand	de Lange	CH2517	MF373763	MF984230	MG754173	MG063015	–	–
DNA5460	<i>Sticta leucoblepharis</i>	Colombia	Moncada	4689	KC732597	MF984276	–	MG063063	–	–
DNA8131	<i>Sticta limbata</i>	U.S.A.	Moncada	6995	MG367428	MF984298	MG754181	MG062940	–	x
DNA5028	<i>Sticta lobarioides</i>	Colombia	Alfonso	5	KC732555	MF984238	MG754113	MG062992	–	x
DNA4939	<i>Sticta lobulata</i>	Colombia	Álvaro	41218a	KC732482	MF984271	MG754098	MG062960	–	x
DNA5436	<i>Sticta lumbschiana</i>	Colombia	Lücking & Moncada	33370	KC732575	MF984212	MG754124	MG063055	–	x
DNA5569	<i>Sticta macrocyphellata</i>	Colombia	Coca	1267	KC732662	MF984313	–	MG063056	–	–
DNA5511	<i>Sticta macrogyalocarpa</i>	Colombia	Fonseca	49	KC732619	–	MG754092	MG063045	MG754090	–
LG0946	<i>Sticta macrophylla</i>	France	Magain & Sérusiaux	LG0946	JQ735985	–	JQ736018	JQ736002	KT281744	–
DNA5539	<i>Sticta macrothallina</i>	Colombia	Coca	1115	KC732629	MF984208	MG754122	MG063034	–	–
DNA4975a	<i>Sticta maculofuliginosa</i>	Colombia	Moncada	4156	KC732514	MF984235	–	–	–	x
DNA8052	<i>Sticta maculohyposcrobiculata</i>	U.S.A.	Moncada	6920	MG367423	MF984302	MG754093	MG062922	–	x
LG1023	<i>Sticta marginalis</i>	France	Magain & Sérusiaux	LG1023	JQ735980	–	JQ736013	JQ735997	KT281748	–
DNA13522	<i>Sticta menziesii</i>	New Zealand	Lücking et. al.	39050	MF373761	MF984225	MG754191	MG063013	–	–
DNA5446	<i>Sticta minutula</i>	Colombia	Moncada	4753	KC732583	MF984297	–	MG063042	–	–
DNA5524	<i>Sticta neopulmonarioides</i>	Colombia	Coca	949	KC732625	MF984204	MG754115	–	–	–

DNA5021	<i>Sticta papillata</i>	Colombia	Alfonso	3	KC732552	MF984232	MG754123	MG063053	–	x
DNA5019	<i>Sticta parahumboldtii</i>	Colombia	Moncada	4016	KC732550	MF984308	MG754151	MG062949	–	–
DNA4921	<i>Sticta paralimbata</i>	Colombia	Valbuena	126	KC732466	–	–	MG062959	–	–
DNA17172	<i>Sticta parvilobata</i>	Puerto Rico	Mercado-Díaz	3667	MN065879	MN065922	–	MN065975	MN066019	MN066117
DNA4958	<i>Sticta phyllidiofuliginosa</i>	Colombia	Moncada	4051	KC732495	MF984329	–	–	–	–
DNA5456	<i>Sticta phyllidiokunthii</i>	Colombia	Moncada	4758	KC732593	MF984291	MG754112	MG062932	–	–
DNA6346	<i>Sticta plumbeociliata</i>	Colombia	Moncada	4820	KC732767	MF984290	–	MG062935	–	–
DNA4934	<i>Sticta pseudobeauvoisii</i>	Colombia	Ardila	1	KC732478	MF984265	MG754143	MG063007	–	–
DNA7254	<i>Sticta pseudodilatata</i>	Costa Rica	Moncada	5675	MG367405	MF984214	MG754127	MG063058	–	–
DNA4922	<i>Sticta pseudolimbata</i>	Colombia	Moncada	4009	KC732467	MF984316	MG754142	MG062955	–	–
DNA5556	<i>Sticta pseudolobaria</i>	Colombia	Coca	964	KC732650	–	–	MG062996	–	–
DNA16962	<i>Sticta pulmonarioides</i>	Jamaica	Mercado-Díaz	3436a	x	x	–	x	–	x
DNA6198	<i>Sticta puracensis</i>	Colombia	Díaz-Escandón	L1	KC732701	MF984243	MG754175	–	–	–
DNA4953	<i>Sticta rhizinata</i>	Colombia	Moncada	4638	KC732491	–	MG754097	MG062962	–	x
DNA17178	<i>Sticta riparia</i>	Puerto Rico	Mercado-Díaz	3684	MN065893	MN065928	MN065942	MN066008	MN066035	MN066105
DNA16987	<i>Sticta roseocyphellata</i>	Jamaica	Mercado-Díaz	3374b	x	x	x	x	–	x
DNA17157	<i>Sticta scabrosa</i>	Puerto Rico	Mercado-Díaz	3636a	MN065875	MN065929	x	MN065986	–	x
MON6812	<i>Sticta sp-1</i>	Cuba	Mercado-Díaz	46701	x	x	–	x	–	x
DNA16146	<i>Sticta sp-11</i>	Dominican Republic	Mercado-Díaz	3129b	x	x	x	x	–	x
DNA16971	<i>Sticta sp-13</i>	Jamaica	Mercado-Díaz	3510a	x	x	x	x	–	x
DNA16969	<i>Sticta sp-2</i>	Jamaica	Mercado-Díaz	3571	x	–	x	x	–	x
DNA16966	<i>Sticta sp-3</i>	Jamaica	Mercado-Díaz	3463a	x	x	–	x	–	x
DNA16960	<i>Sticta sp-4</i>	Jamaica	Mercado-Díaz	3462a	x	–	x	x	–	x
DNA6276	<i>Sticta sp-5</i>	Colombia	Suárez	306	KC732724	MF984335	–	MG062953	–	–
MON6423	<i>Sticta sp-7</i>	Cuba	Mercado-Díaz	44655	x	–	x	x	–	x
DNA16991	<i>Sticta sp-9</i>	Jamaica	Mercado-Díaz	3425b	x	–	–	x	–	–
DNA13526	<i>Sticta squamata</i>	New Zealand	Lücking et. al.	38562	MG367381	MF984260	MG754138	MG063030	–	–
DNA4925	<i>Sticta squamifera</i>	Colombia	Moncada	4026	KC732470	MF984217	–	MG062965	–	–
DNA14462	<i>Sticta stipitata</i>	Australia	Lumbsch et al.	2210	MG754197	MF984274	MG754141	MG063024	–	–
DNA13781	<i>Sticta subcaperata</i>	New Zealand	Lücking et. al.	38436	MG367383	MF984270	MG754172	MG063018	–	–
LG0885	<i>Sticta sublimbata</i>	D.R. Congo	Sérusiaux	LG0885	JQ735986	–	JQ736019	JQ736003	KT281771	–
LG3536	<i>Sticta sylvatica</i>	France	Gérault	LG3536	KT281726	–	KT281682	KT281637	KT281788	–

DNA17169	<i>Sticta tainorum</i>	Puerto Rico	Mercado-Díaz	3661	MN065868	MN065937	MN065940	MN065962	MN066055	MN066121
DNA8078	<i>Sticta tomentosa</i>	U.S.A.	Moncada	6946	MG367424	MF984278	MG754131	MG063069	–	x
LG0925	<i>Sticta umbilicariiformis</i>	Rwanda	Sérusiaux	LG0925	KT281697	–	KT281655	KT281652	KT281742	–
LG1037	<i>Sticta variabilis</i>	France	Magain & Sérusiaux	LG1037	JQ735987	–	JQ736020	JQ736004	KT281749	–
DNA5593	<i>Sticta viviana</i>	Colombia	Lücking & Moncada	33311	KC732680	–	MG754155	MG062925	–	–
DNA17160	<i>Sticta weigelii</i>	Puerto Rico	Mercado-Díaz	3643	MN065895	MN065938	x	MN066011	MN066057	MN066116

Table S1.3. Best partitioning schemes and best fit substitution models for multilocus datasets used in analyses presented in this work. Information on number of samples included in each analysis, number of loci and percent missing data is summarized first. Other columns show the following data: number of sequences in partition (*Seq*), total number of sites in partition (*Site*), number of unique site patterns (*Unique*), number of parsimony-informative sites (*Infor*), best substitution model for partition (*Model*), Bayesian information criterion scores (*BIC*). RAxML analysis used the same partitioning scheme as MrBayes but was based on the GTRGAMMA model.

Analysis	Number of species	# loci included	Missing data	Partitions	Seq	Site	Unique	Infor	Model	BIC
MrBayes	162	6	22.70%	18s_rRNA+28S_rRNA+MCM7_pos2+RPB1_pos2+RPB2_pos2	162	930	385	20	HKY+F+G4	4252.308
				ITS1+ITS2	161	412	376	236	GTR+F+G4	20171.5
				5-8_rRNA+MCM7_pos1	162	373	169	38	K2P+I+G4	3389.296
				MCM7_pos3	114	216	205	136	K2P+G4	8645.254
				mtSSU	107	1189	653	221	GTR+F+I+G4	15803.69
				nuLSU	152	594	295	103	SYM+I+G4	8401.774
				RPB1_pos1+RPB2_pos1	85	645	252	22	GTR+F+I	3269.073
				RPB1_pos3+RPB1_intron+RPB2_pos3	85	709	556	306	SYM+G4	11839.7
				Alignment length:	5068					
Divergence dating + biogeographic reconstruction + BAMM (BEAST)	162	4	16.57%	18s_rRNA+28S_rRNA+MCM7_pos2	161	285	163	8	K2P+G4	1614.749
				ITS1+ITS2	161	412	376	236	TIM2+F+G4	19921
				5-8_rRNA+MCM7_pos1	162	373	169	38	K2P+I+G4	3427.689
				MCM7_pos3	114	216	205	136	K2P+G4	8727.049
				mtSSU	107	1189	653	221	TVM+F+I+G4	15753.16
				nuLSU	152	594	295	103	TIM2e+I+G4	8412.017
				Alignment length:	3069					
GeoSSE (BEAST)	119	4	20.59%	18s_rRNA+5-8_rRNA+28S_rRNA+MCM7_pos1+nuLSU	119	1036	466	116	TNe+I+G4	9535.6
				ITS1+ITS2	118	412	324	184	TIM2+F+G4	14021.92
				MCM7_pos2	89	216	96	4	K2P	933.6638
				MCM7_pos3	89	216	198	122	K2P+G4	6887.524
				mtSSU	67	1189	497	144	TPM3u+F+I+G4	10294.67

				<i>Alignment length:</i>		3069				
Phylo- betadiversity (BEAST)	62	6	10.01%	18s_rRNA+MCM7_pos1+nuLSU+RPB1_pos1+RPB2_pos1	63	1483	531	98	TIM+F+I+G4	8285.173
				ITS1+ITS2	63	412	282	158	TIM+F+G4	8255.405
				5-8_rRNA+28S_rRNA+MCM7_pos2+RPB1_pos2+RPB2_pos2	63	1059	300	15	TIM2+F+I	3984.908
				MCM7_pos3+RPB1_pos3+RPB1_intron+RPB2_pos3	58	925	548	258	TIM3e+G4	10456.79
				mtSSU	40	1189	397	107	TPM3u+F+I+G4	7478.221
				<i>Alignment length:</i>		5068				

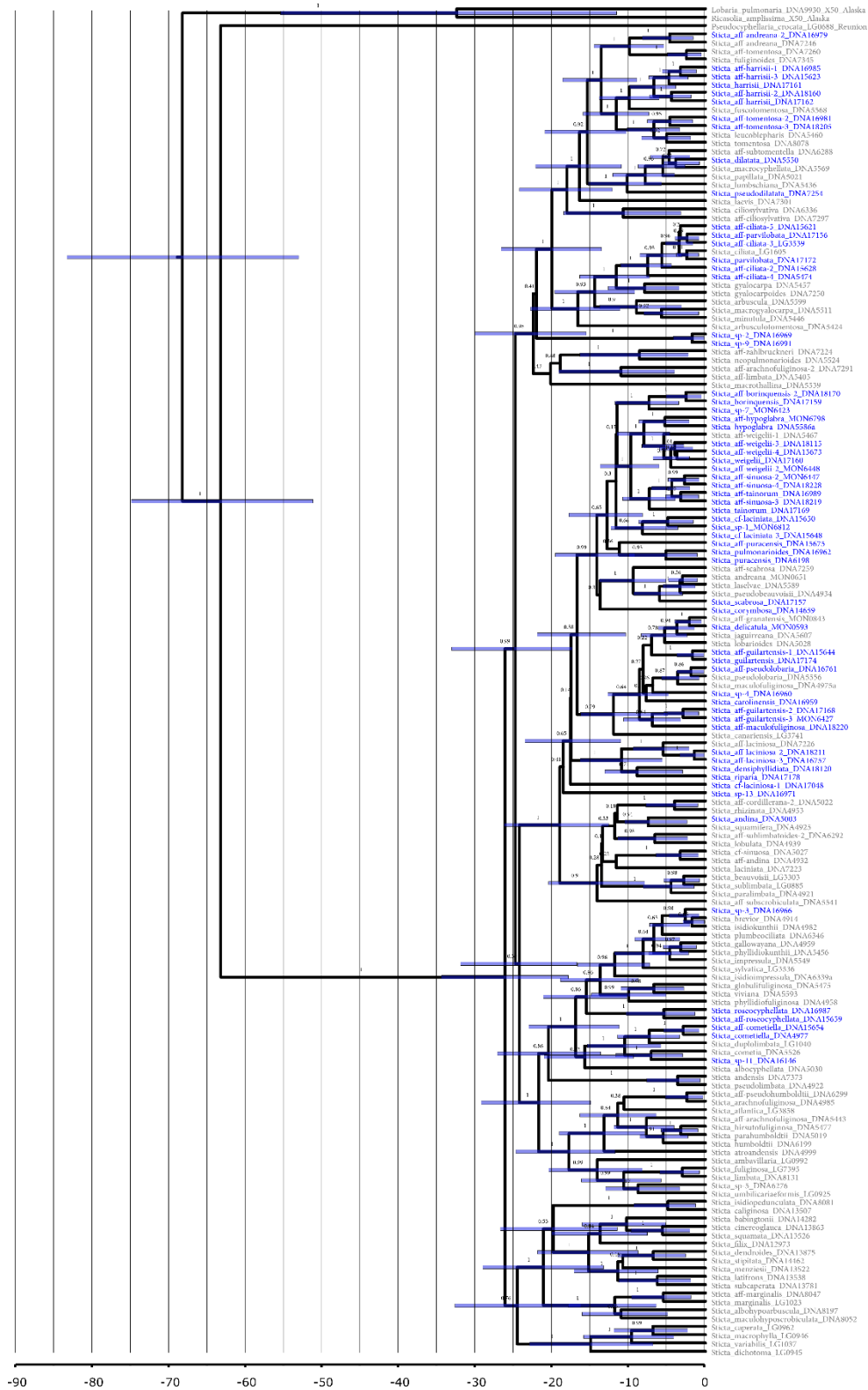
Table S1.4. Values for environmental variables obtained for island-level communities analyzed.

Island	Elev (mean)	Elev (median)	Elev (max)	Precip	MaxTemp	MinTemp	Eta	NDVI	EVI	TRI
Cuba	941.75	941.75	1648.00	127.58	27.44	18.65	113.83	0.86	0.61	0.67
Dominica	619.18	612.25	873.00	123.85	28.25	20.65	132.00	0.86	0.59	0.62
Dominican Republic	1635.66	1605.00	2136.00	115.63	22.03	10.07	88.43	0.78	0.45	0.52
Guadeloupe	808.67	824.25	957.00	97.20	27.10	19.70	120.50	0.85	0.53	0.72
Jamaica	1728.33	1696.25	2165.00	158.20	22.35	15.55	106.55	0.79	0.52	0.93
Martinique	676.57	710.00	906.00	130.60	28.00	20.90	129.35	0.80	0.56	0.73
Puerto Rico	901.32	919.00	1185.00	150.57	26.60	17.17	125.57	0.83	0.57	0.54

Table S1.5. PCA loadings for environmental variables used for taxonomic and phylobetadiversity analysis.

	Elev_max	Precip	MaxTemp	MinTemp	Eta	NDVI	EVI	TRI
PC1	0.896205	0.175755	-0.97938	-0.94513	-0.93532	-0.83248	-0.86843	0.0428
PC2	-0.2058	-0.82049	0.123948	-0.22217	-0.19563	0.170839	-0.26831	-0.78763
PC3	-0.14505	-0.5123	-0.01639	0.23162	-0.00599	-0.13405	-0.32312	0.586151
PC4	-0.35574	0.177334	0.036813	0.024802	0.278196	-0.48476	-0.24374	-0.1842
PC5	0.081449	-0.03977	0.150745	0.054781	-0.09383	-0.15689	0.097071	-0.01537
PC6	0.015511	-0.02051	-0.03331	0.010065	0.025996	-0.01489	0.024313	-0.00873
PC7	0.589854	-0.12828	-0.65193	-0.41624	-0.63308	-0.62892	-0.67955	0.566829

Figure S1.1. Maximum Clade Credibility tree from BEAST. Caribbean taxa are highlighted in blue. Node bars show 95% HPD values whereas values above branches indicate posterior probabilities. Horizontal scale in millions of years.



Appendix S2.1

DEC analysis with dispersal limitations

Dispersal limitations were set by analyzing area–dispersal matrices which allocated different dispersal probabilities to different periods of time (see table below). We applied a dispersal constraint scheme similar to (Cano *et al.*, 2018) which assigns a dispersal probability of $p = 1$ for dispersal between adjacent areas, $p = 0.5$ for dispersal over the Caribbean Sea or over non-adjacent areas and 0.01 for dispersal over oceans. Sensitivity tests were not carried out since no significant differences in terms of loglikelihoods for biogeographic reconstruction have been found under different dispersal probabilities (e.g. $p = 0.1$ vs. $p = 0.001$) (Cano *et al.*, 2018).

We evaluated the four time periods defined by Cano *et al.*, 2018 using adjustments that accounted for our biogeographic areas: (1) 90–33 Mya: increase probability of dispersal between NA and PA, (2) 33–15 Mya: land bridges connecting NA and PA were no longer available (Brikiatis, 2014); (3) 15–7 Mya: Panama Isthmus closure (Montes *et al.*, 2015); and (4) 7 Mya-present: final uplift of the Northern Andes acting as a barrier for dispersal between Amazonia and the Chocó region (Luebert & Weigend, 2014). Results are presented in Fig. 1.

Time: 0-7 MY

	SA	CA	CAM	NA	AF	PA	OR	HA	AU
SA	1	0.5	1	0.01	0.01	0.01	0.01	0.01	0.01
CA	0.5	1	0.5	0.5	0.01	0.01	0.01	0.01	0.01
CAM	1	0.5	1	1	0.01	0.01	0.01	0.01	0.01
NA	0.01	0.5	1	1	0.01	0.01	0.01	0.01	0.01
AF	0.01	0.01	0.01	0.01	1	0.5	0.5	0.01	0.01
PA	0.01	0.01	0.01	0.01	0.5	1	1	0.01	0.01
OR	0.01	0.01	0.01	0.01	0.5	1	1	0.01	0.01
HA	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1	0.01
AU	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1

Time: 7-15 MY

	SA	CA	CAM	NA	AF	PA	OR	HA	AU
SA	1	0.5	1	0.5	0.01	0.01	0.01	0.01	0.01
CA	0.5	1	0.5	0.5	0.01	0.01	0.01	0.01	0.01
CAM	1	0.5	1	1	0.01	0.01	0.01	0.01	0.01
NA	0.5	0.5	1	1	0.01	0.01	0.01	0.01	0.01
AF	0.01	0.01	0.01	0.01	1	0.5	0.5	0.01	0.01
PA	0.01	0.01	0.01	0.01	0.5	1	1	0.01	0.01
OR	0.01	0.01	0.01	0.01	0.5	1	1	0.01	0.01
HA	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1	0.01
AU	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1

Time: 15-33 MY

	SA	CA	CAM	NA	AF	PA	OR	HA	AU
SA	1	0.5	0.5	0.5	0.01	0.01	0.01	0.01	0.01
CA	0.5	1	0.5	0.5	0.01	0.01	0.01	0.01	0.01
CAM	0.5	0.5	1	1	0.01	0.01	0.01	0.01	0.01
NA	0.5	0.5	1	1	0.01	0.01	0.01	0.01	0.01

AF	0.01	0.01	0.01	0.01	1	0.5	0.5	0.01	0.01
PA	0.01	0.01	0.01	0.01	0.5	1	1	0.01	0.01
OR	0.01	0.01	0.01	0.01	0.5	1	1	0.01	0.01
HA	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1	0.01
AU	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1

Time: 33-90 MY

	SA	CA	CAM	NA	AF	PA	OR	HA	AU
SA	1	0.5	0.5	0.5	0.01	0.01	0.01	0.01	0.01
CA	0.5	1	0.5	0.5	0.01	0.01	0.01	0.01	0.01
CAM	0.5	0.5	1	1	0.01	0.01	0.01	0.01	0.01
NA	0.5	0.5	1	1	0.01	1	0.01	0.01	0.01
AF	0.01	0.01	0.01	0.01	1	0.5	0.5	0.01	0.01
PA	0.01	0.01	0.01	1	0.5	1	1	0.01	0.01
OR	0.01	0.01	0.01	0.01	0.5	1	1	0.01	0.01
HA	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1	0.01
AU	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1

Matrix of dispersal constraint multipliers indicating the probability of dispersal between each set of areas in different time periods. SA: South America, CA: Caribbean, CAM: Central America, NA: North America, AF: Afrotropical, PA: Palearctic, OR: Oriental, HA: Hawaiian, AU: Australasian.

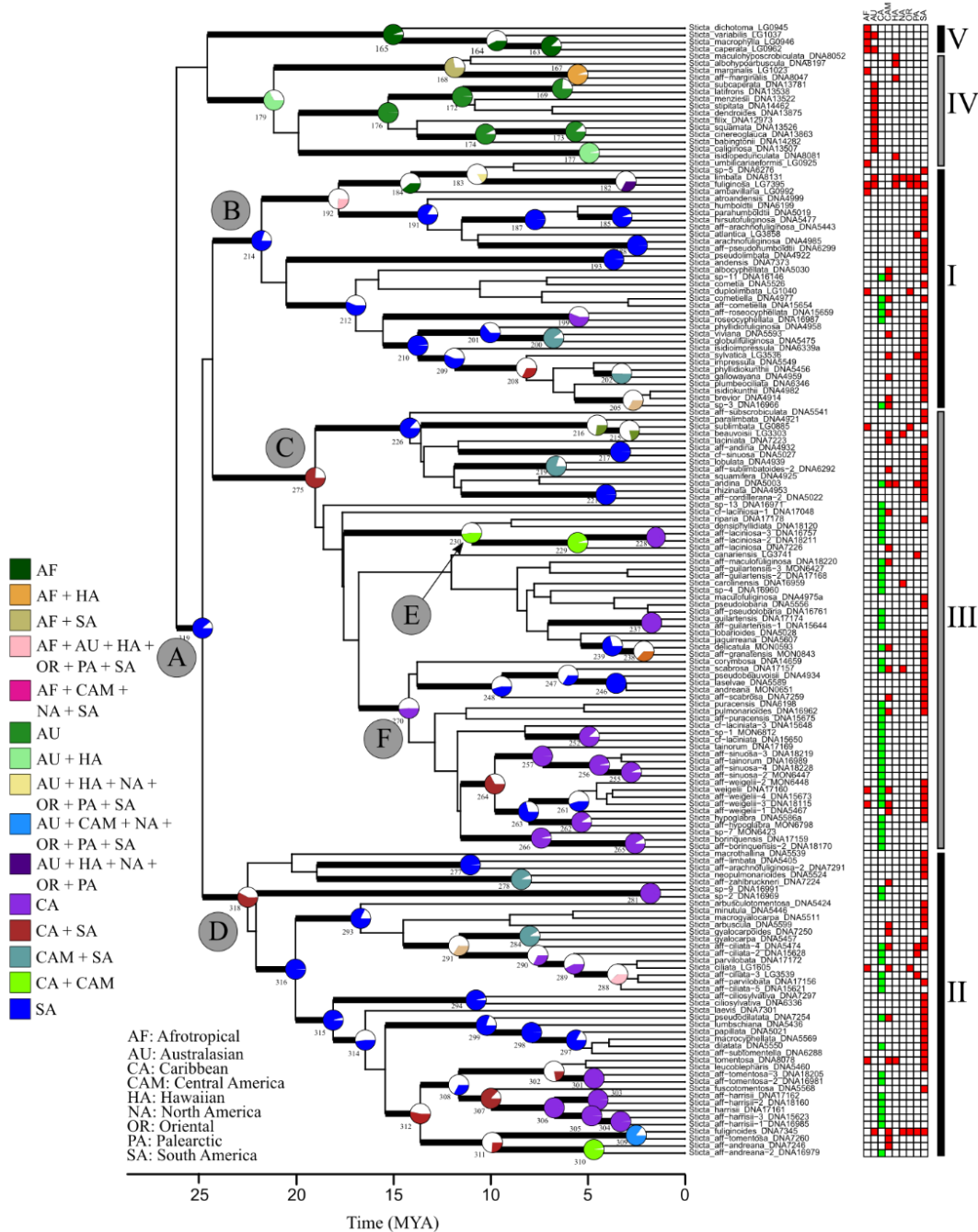


Table S2.1. Differences in ancestral ranges inferred with and without dispersal constraints for strongly supported nodes containing Caribbean taxa.

Clade	Node #	Taxa	+ dispersal constraints	- dispersal constraints
I	199	<i>S. roseocyphellata</i> , <i>S. aff. roseocyphellata</i>	CA	SA
I	205	<i>S. brevior</i> , <i>Sticta</i> sp. 3, <i>S. isidiokunthii</i>	CAM	SA, CAM
I	208	<i>S. sylvatica</i> , <i>S. impressula</i> , <i>S. phyllidiokunthii</i> , <i>S. gallowayana</i> , <i>S. plumbeociliata</i> , <i>S. isidiokunthii</i> , <i>S. brevior</i> , <i>Sticta</i> sp. 3	SA, PA	SA
II	288	<i>S. parvilobata</i> , <i>S. ciliata</i> , <i>S. aff. ciliata-3</i> , <i>S. aff. parvilobata</i> , <i>S. aff. ciliata-5</i>	CA, CAM, AF, OR	CA
II	290	<i>S. aff. ciliata-4</i> , <i>S. aff. ciliata-2</i> , <i>S. parvilobata</i> , <i>S. ciliata</i> , <i>S. aff. ciliata-3</i> , <i>S. aff. parvilobata</i> , <i>S. aff. ciliata-5</i>	CA	SA, CA
II	291	<i>S. gyalocarpoides</i> , <i>S. gyalocarpa</i> , <i>S. aff. ciliata-4</i> , <i>S. aff. ciliata-2</i> , <i>S. parvilobata</i> , <i>S. ciliata</i> , <i>S. aff. ciliata-3</i> , <i>S. aff. parvilobata</i> , <i>S. aff. ciliata-5</i>	CAM	SA
II	311	<i>S. aff. andreana</i> , <i>S. aff. tomentosa</i> , <i>S. fuliginoides</i>	CA, CAM, NA, PA, OR, AU	SA, CAM
II	312	<i>S. tomentosa</i> , <i>S. leucoblepharis</i> , <i>S. aff. tomentosa-3</i> , <i>S. aff. tomentosa-2</i> , <i>S. fuscotomentosa</i> , <i>S. aff. harrisii</i> , <i>S. aff. harrisii-2</i> , <i>S. harrisii</i> , <i>S. aff. harrisii-3</i> , <i>S. aff. harrisii-1</i> , <i>S. fuliginoides</i> , <i>S. aff. tomentosa</i> , <i>S. aff. andreana</i> , <i>S. aff. andreana-2</i>	CA, CAM, NA, PA, OR, AU	SA
II	318	All species within Clade II (Node "D" in Fig. 3)	SA, CA	SA
III	230	<i>S. riparia</i> , <i>S. densiphyllidiata</i> , <i>S. aff. laciniosa</i> , <i>S. aff. laciniosa2</i> , <i>S. aff. laciniosa-3</i> (Node "E" in Fig. 3)	CA, CAM	CA
III	238	<i>S. delicatula</i> , <i>S. granatensis</i>	SA, CAM, CA	SA, CA
III	239	<i>S. jaguirreana</i> , <i>S. delicatula</i> , <i>S. aff. granatensis</i>	SA	SA, CA
III	247	<i>S. andreana</i> , <i>S. laselvae</i> , <i>S. pseudobeauvoisii</i> , <i>S. scabrosa</i>	SA	SA, CA
III	248	<i>S. aff. scabrosa</i> , <i>S. andreana</i> , <i>S. laselvae</i> , <i>S. pseudobeauvoisii</i> , <i>S. scabrosa</i>	SA	SA, CA

III	261	<i>S. aff. weigeli-2, S. weigeli, S. aff. weigeli-4, S. aff. weigeli-3, S. aff. weigeli-1</i>	SA	SA, CA
III	263	<i>S. aff. weigeli-2, S. weigeli, S. aff. weigeli-4, S. aff. weigeli-3, S. aff. weigeli-1, S. hypoglabra, S. aff. hypoglabra</i>	SA	CA
III	264	<i>S. tainorum, S. aff. sinuosa-3, S. aff. tainorum, S. aff. sinuosa-4, S. aff. sinuosa-2, S. aff. weigeli-2, S. weigeli, S. aff. weigeli-4, S. aff. weigeli-3, S. aff. weigeli-1, S. hypoglabra, S. aff. hypoglabra</i>	SA, CA	CA

Appendix S3.1

GeoSSE analysis

Analysis with GeoSSE requires lineages to be assigned one of three geographic character states: either present in one of two regions (i.e. endemic to region “A” or region “B”) or present in both regions (i.e. “AB” distribution). Accordingly, and following indications above, we used BEAST to generate a time-calibrated tree (119 tips) that included species restricted to either the continental Neotropics (65) or the Caribbean islands (36), and species that occur in both regions (18). Sampling fractions were based on the global ITS dataset used for candidate species delimitation and were set as follows: 70% (both regions), 35% (endemic to the continental Neotropics), and 90% (endemic to the Caribbean).

ML model construction and constraining were carried out with *diversitree* functions “make.geosse” and “constrain”, respectively. Parameter estimates for the different models were obtained with the function “find.mle”. Models were compared using likelihood ratio tests. A posterior probability distribution of parameter estimates for the full model was also generated with the “mcmc” function in *diversitree* (nsteps = 10,000). The chain started with parameter estimates obtained from Maximum Likelihood and used a broad exponential prior probability distribution of 1/2. A burnin of 1,000 was applied. Lastly, root states of two additional unconstrained models were fixed to either the continental Neotropics or the Caribbean. We compare model selection and parameter estimates from fixed and unfixed root models to better understand dispersal asymmetries.

Figure S3.1. Distribution of geographic character states in 119-tip MCC tree used for GeoSSE analysis.

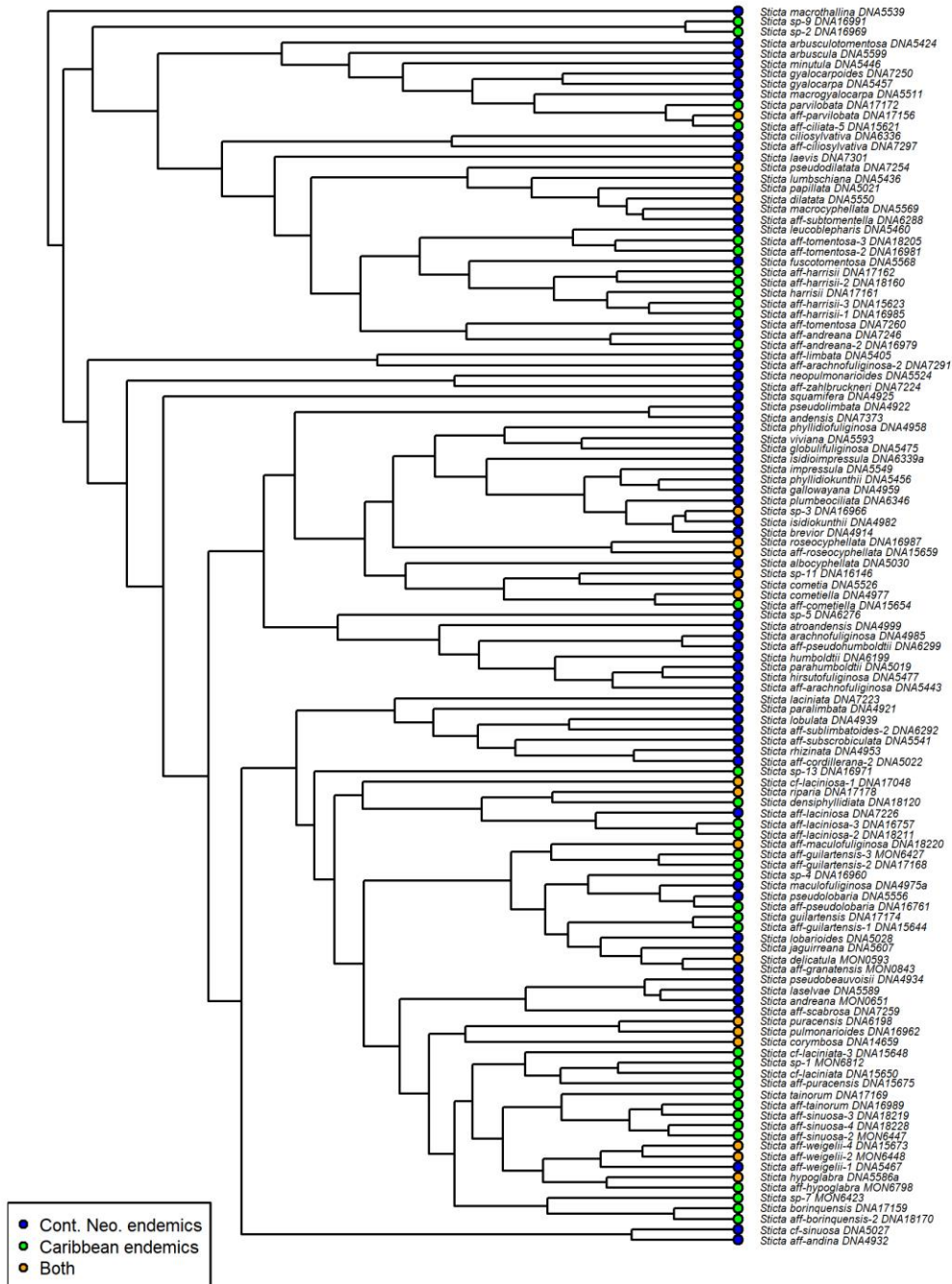


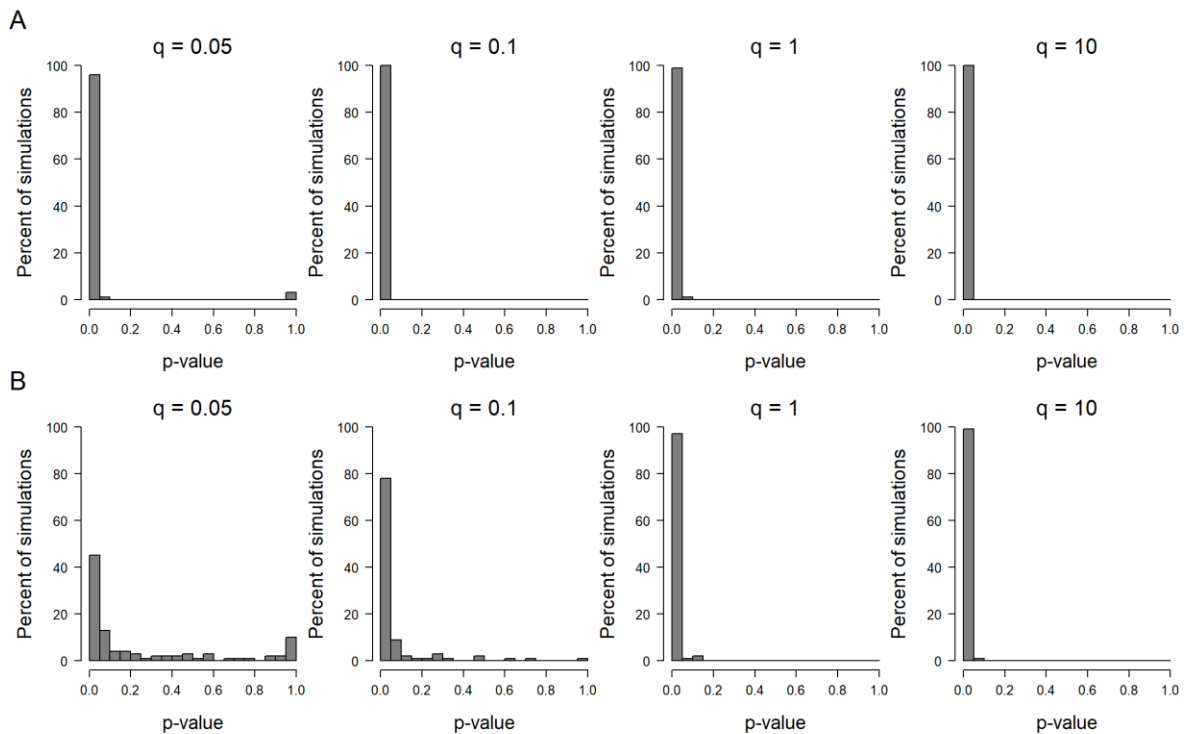
Table S3.1. Model selection results and parameter estimates for three full GeoSSE models (unfixed root, fixed root: Cont. Neo., fixed root: Caribbean) and nine models were constraints on speciation (sA, sB, sAB), extinction (xA, xB), and dispersal (dA, dB) were performed to evaluate different macroevolutionary scenarios.

<i>Models</i>	<i>Df</i>	<i>lnLik</i>	<i>AIC</i>	full		full (fixed root: Cont. Neo.)		full (fixed root: Caribbean)		Rates						
				<i>ChiSq</i>	<i>Pr(> Chi)</i>	<i>ChiSq</i>	<i>Pr(> Chi)</i>	<i>ChiSq</i>	<i>Pr(> Chi)</i>	<i>sA</i>	<i>sB</i>	<i>sAB</i>	<i>xA</i>	<i>xB</i>	<i>dA</i>	<i>dB</i>
full	7	-451.63	917.26	–	–	–	–	–	–	0.15	0.14	0.08	0.00	0.00	0.01	0.09
full (fixed root: Cont. Neo.)	7	-450.99	915.98	–	–	–	–	–	–	0.15	0.14	0.09	0.00	0.00	0.01	0.09
full (fixed root: Caribbean)	7	-454.82	923.64	–	–	–	–	–	–	0.15	0.16	0.07	0.00	0.06	0.01	0.10
no.sAB (sAB ~ 0)	6	-453.75	919.50	4.24	0.04	5.52	0.02	-2.14	1.00	0.18	0.14	0.00	0.03	0.00	0.01	0.08
eq.div (sA ~ sB, xA ~ xB)	5	-451.84	913.69	0.43	0.81	1.71	0.43	-5.95	1.00	0.15	0.15	0.08	0.00	0.00	0.01	0.09
eq.disp (dA ~ dB)	6	-455.75	923.50	8.24	0.00	9.52	0.00	1.85	0.17	0.16	0.12	0.06	0.00	0.00	0.02	0.02
eq.sp (sA ~ sB)	6	-451.84	915.69	0.43	0.51	1.71	0.19	-5.95	1.00	0.15	0.15	0.08	0.00	0.00	0.01	0.09
eq.sp_no.sAB (sA ~ sB, sAB ~ 0)	5	-453.83	917.66	4.40	0.11	5.68	0.06	-1.98	1.00	0.16	0.16	0.00	0.00	0.04	0.01	0.07
eq.sp_eq.ex_no.sAB (sA ~ sB, sAB ~ 0, xA ~ xB)	4	-454.09	916.19	4.93	0.18	6.21	0.10	-1.46	1.00	0.16	0.16	0.00	0.02	0.02	0.01	0.08
eq.ex_no.sAB (xA ~ xB, sAB ~ 0)	5	-453.82	917.63	4.38	0.11	5.65	0.06	-2.01	1.00	0.17	0.15	0.00	0.02	0.02	0.01	0.08
no.dB (dB ~ 0)	6	-458.20	928.40	13.14	0.00	14.42	0.00	6.76	0.01	0.17	0.11	0.06	0.00	0.01	0.03	0.00
no.dA (dA ~ 0)	6	-454.94	921.87	6.62	0.01	7.89	0.00	0.23	0.63	0.12	0.13	0.28	0.00	0.00	0.00	0.22

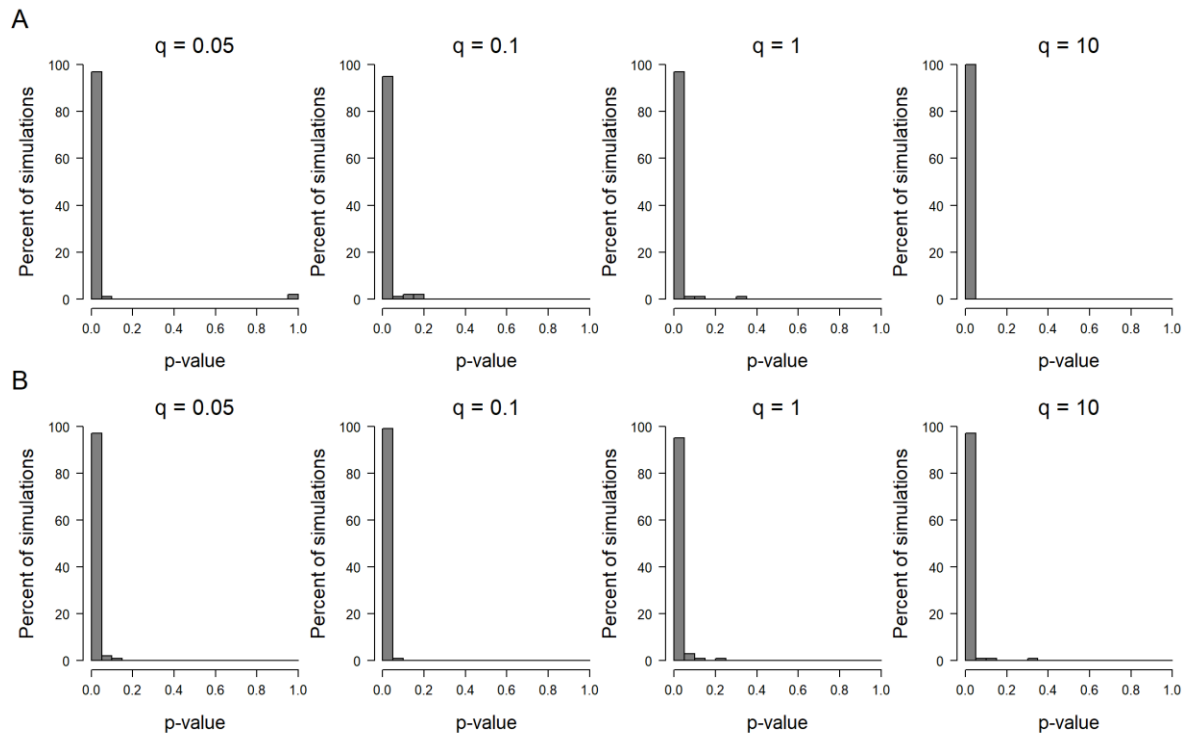
Appendix S4.1

GeoSSE simulation analysis

We used four different transition rates (q) (0.05, 0.1, 1, and 10) to simulate the evolution of neutral and random traits on our MCC tree. Only simulated trees (100) with three states and more than 10% of species in each state were allowed to avoid biases related to sampling (Davis *et al.*, 2013). Simulation was similar for both trait types, except that tip states were reshuffled for random traits trees. A full GeoSSE model was fit to simulated trees using the same sampling fraction of our empirical analysis. Two additional (null) models, one without between-region speciation ($sAB \sim 0$) (Fig. 1) and another without regional dependence of dispersal rates ($dA \sim dB$) (Fig. 2) were generated by constraining the full (alternative) model. Models were compared using likelihood ratio tests and p-values were extracted to estimate error rates (i.e. visualize how often the null models were rejected when they were true).



Results from simulation analysis to estimate error rates of between-region speciation in GeoSSE. The evolution of three-state random (A) and neutral (B) traits were simulated on our MCC tree using four transition rates: 0.05, 0.1, 1, 10. Bars indicate the distribution of p-values obtained for all simulations. In each graph, the first bar to the left (p-values < 0.05) indicate the proportion of simulations in which the null hypothesis ($sAB \sim 0$) was incorrectly rejected in favor of the alternative hypothesis of differences in between-region speciation.

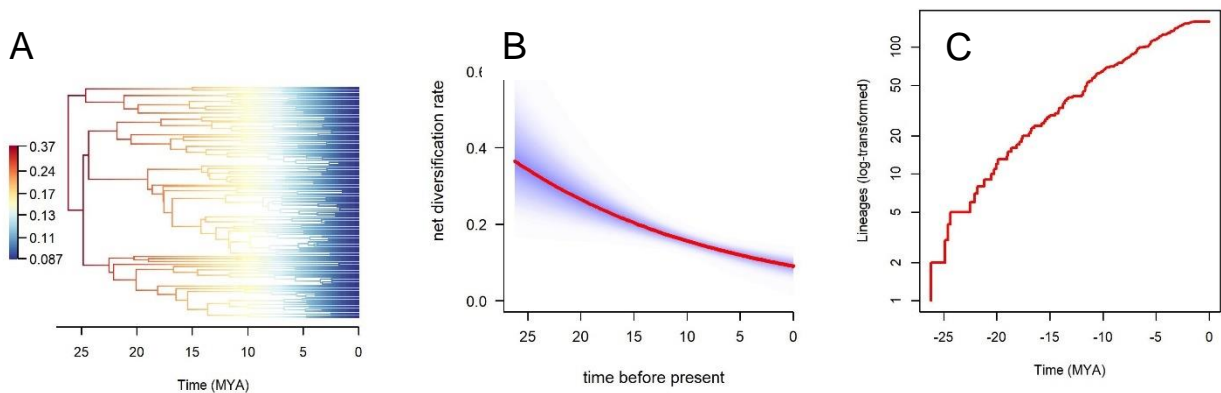


Results from simulation analysis to estimate error rates in dispersal asymmetries inferred in GeoSSE. The evolution of three-state random (A) and neutral (B) traits were simulated on our MCC tree using four transition rates: 0.05, 0.1, 1, 10. Bars indicate the distribution of p-values obtained for all simulations. In each graph, the first bar to the left (p-values < 0.05) indicate the proportion of simulations in which the null hypothesis ($dA \sim dB$) was incorrectly rejected in favor of the alternative hypothesis of dispersal asymmetries between regions.

Appendix S5.1

BAMM

BAMM is a statistical framework that uses a reversible jump Markov chain Monte Carlo (rjMCMC) sampler to ultimately identify the number and location of so called “rate shifts”, transitions in evolutionary parameters along branches of a phylogenetic tree. Except for Clades IV and V, sampling fractions used by Widhalm *et al.*, 2018 were updated according to the global ITS dataset used for candidate species delimitation and set using the “SamplesProbsFilename” argument in the control file (Clade I: 65%, Clade II: 60%, Clade III: 50%). Outgroups were removed from analysis as Widhalm *et al.*, 2018 showed they had no noticeable effect on BAMM inferences. The function “setBAMMpriors” from the R package *BAMMtools* (Rabosky *et al.*, 2014) was used to find appropriate prior parameters. We ran four parallel chains of 10,000,000 generations with sampling frequency set at 5000. Output files “mcmcout” and “eventdata” were analyzed with *BAMMtools* and used to assess convergence, calculate effective sample sizes (ESS) of parameters and visualize rates. The R package *coda* v. 0.19-4 (Plummer *et al.*, 2006) was used to estimate ESS values. Twenty percent of trees were discarded as burnin. Our phylorate plot was generated with the “plot.bammdata” function, the net diversification rate through time plot with the function “plotRateThroughTime” whereas the lineage through time plot was obtained with the “lft.plot” function (Fig. 1).



Results from state-independent diversification analysis using Bayesian Analysis of Macroevolutionary Mixtures (BAMM) based on our 162 tips multilocus tree (outgroups removed). A. Mean phylorate plot on diversification rate (breaksmethod = 'jenks'), B. Net diversification through time plot, C. Lineage through time plot

Figure S5.1 Procrustes superimposition to assess the relationship between TBD, tPBD and bPBD metrics with environmental distances.

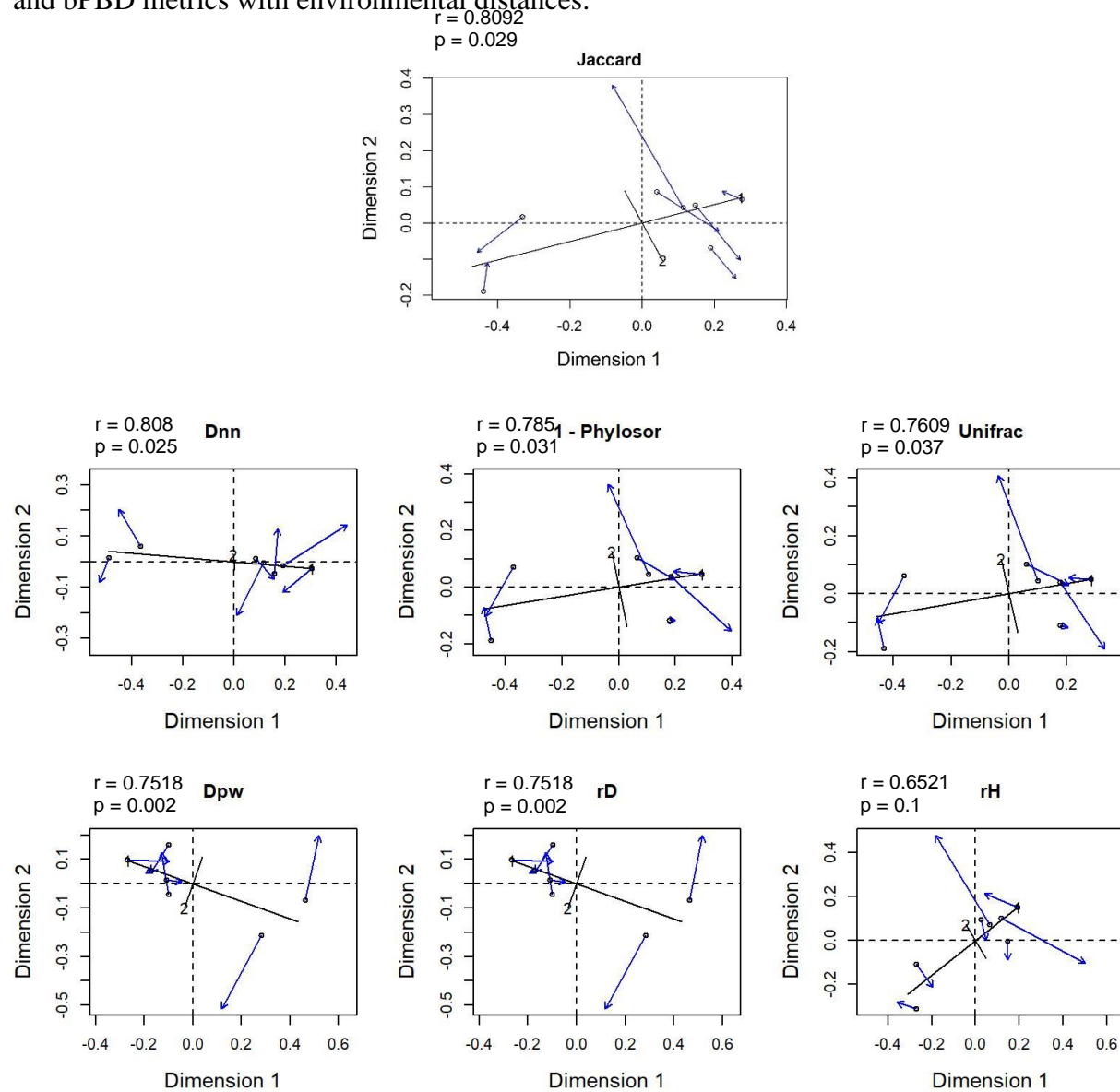


Figure S5.2. Relationship between TBD, tPBD and bPBD metrics with geographic distance. A) Jaccard, B) Dnn1, C) 1-Phylosor, D) UniFrac, E) Dpw, F) Rao's D, G) Rao's H. None of the associations were statistically significant according to Mantel tests.

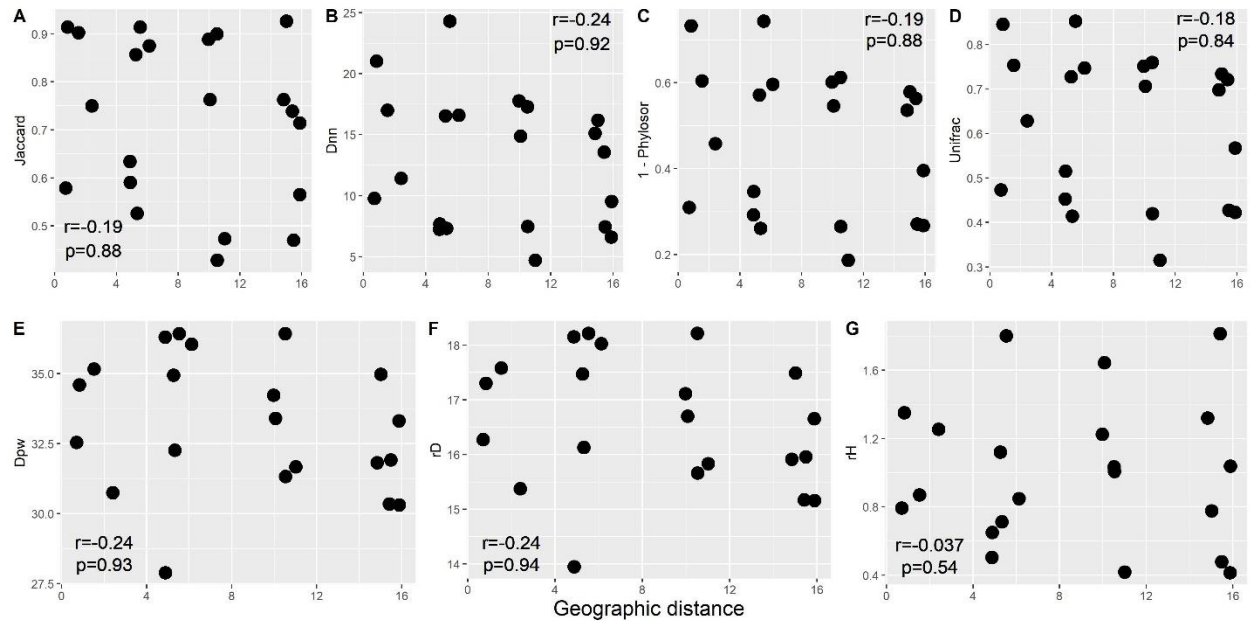


Figure S5.3. Relationships between A) species richness vs. phylogenetic diversity, B) species richness vs. elevation, C) phylogenetic diversity vs. elevation, in *Sticta* communities from islands in the Caribbean.

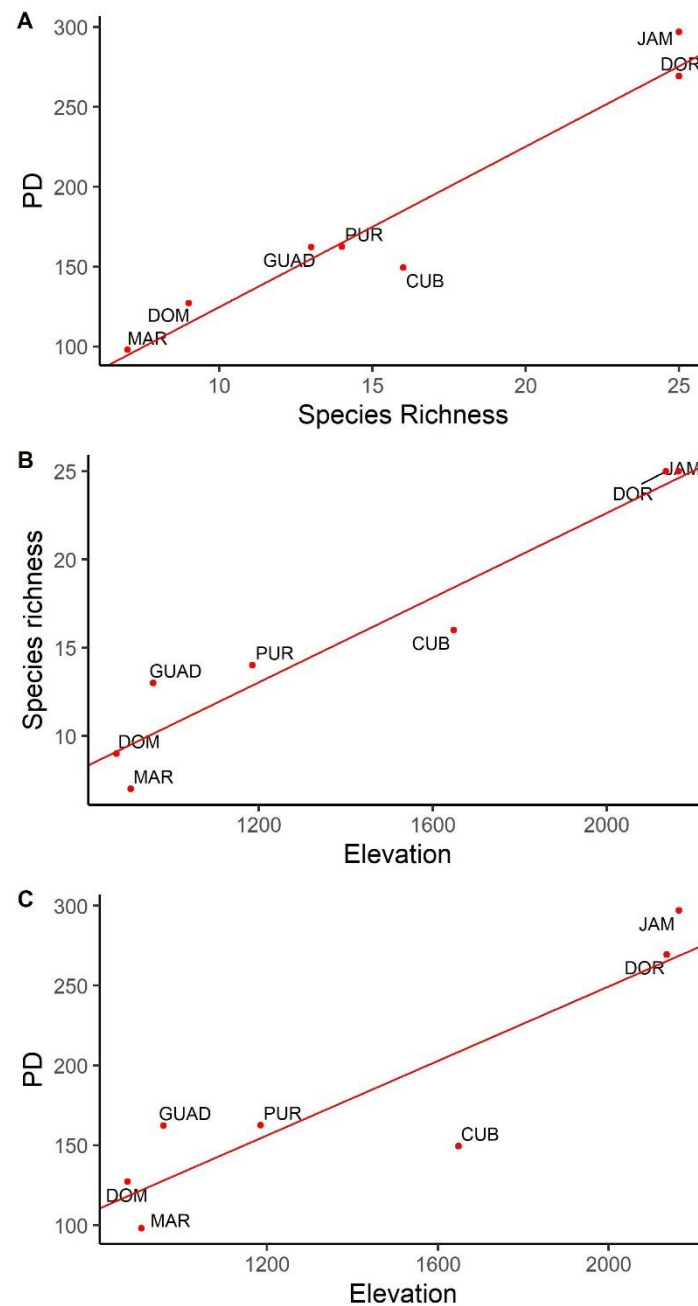


Figure S5.4 Distribution of values for “turnover” and “nestedness” components of A) taxonomic and B) phylogenetic beta diversity.

