

Supplemental Tables

PHYLOGEOGRAPHIC AND MORPHOGEOGRAPHIC OUTCOMES OF BROWN ANOLE COLONIZATION ACROSS THE CARIBBEAN PROVIDE INSIGHT INTO THE BEGINNING STAGES OF AN ADAPTIVE RADIATION

Supplemental Tables

*Large tables can be downloaded separately in the folder “Data and Trees”

Table S1. Individuals and sampling locations used to generate genetic data in this study.

[Download here.](#)

Table S2. Morphometric dataset. Individuals, sampling locations, accession numbers, and morphometric data. [Download here.](#)

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Table S3. Genetic distances among major mtDNA clades in *Anolis sagrei*. Tamura-Nei corrected distances below diagonal and uncorrected p-distances above diagonal.

	1	2	3	4	5	6	7	8	9	10	11	12
<i>1. A homolechis</i>	–	0.20	0.20	0.20	0.21	0.20	0.20	0.12	0.21	0.12	0.19	0.20
2. Clade A	0.24	–	0.08	0.09	0.11	0.11	0.11	0.10	0.10	0.10	0.11	0.13
3. Clade B	0.24	0.10	–	0.09	0.11	0.11	0.11	0.10	0.11	0.10	0.11	0.12
4. Clade C	0.24	0.10	0.10	–	0.12	0.10	0.10	0.10	0.10	0.10	0.11	0.12
5. Clade D	0.25	0.13	0.12	0.12	–	0.11	0.11	0.11	0.12	0.11	0.12	0.13
6. Clade E	0.20	0.13	0.12	0.12	0.12	–	0.11	0.12	0.12	0.12	0.13	0.12
7. Clade F	0.24	0.12	0.12	0.11	0.13	0.13	–	0.10	0.11	0.11	0.11	0.13
8. Clade G	0.24	0.11	0.11	0.11	0.13	0.14	0.11	–	0.06	0.08	0.08	0.12
9. Clade H	0.25	0.11	0.12	0.11	0.13	0.13	0.11	0.06	–	0.08	0.09	0.12
10. Clade I	0.24	0.11	0.11	0.11	0.12	0.13	0.12	0.08	0.08	–	0.09	0.12
11. Clade J	0.23	0.12	0.12	0.12	0.13	0.15	0.12	0.09	0.09	0.10	–	0.13
12. Clade K	0.23	0.14	0.13	0.14	0.15	0.14	0.14	0.14	0.13	0.14	0.14	–

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Table S4. Genetic distances among major genetic groups identified in SNP clustering analyses. Data are calculated from 31,678 SNP loci in *Anolis sagrei* and relatives. Above diagonal- Nei's distance, below diagonal, Cavalli-Sforza chord distances.

	1.	2.	3.	4.	5.	6.	7.	8.	9.	10	11.	12.	13.
1.West Bahamas	–	0.08	0.19	0.2	0.3	0.27	0.32	0.25	0.35	0.32	0.24	0.22	0.26
2.East Bahamas	0.09	–	0.17	0.17	0.26	0.23	0.28	0.21	0.31	0.28	0.21	0.19	0.23
3.West Cuba	0.21	0.18	–	0.06	0.24	0.21	0.26	0.19	0.29	0.26	0.17	0.11	0.19
4.West/Central Cuba	0.22	0.19	0.06	–	0.24	0.21	0.26	0.19	0.29	0.26	0.15	0.08	0.19
5.Swan Islands	0.31	0.27	0.24	0.25	–	0.05	0.08	0.07	0.21	0.18	0.27	0.26	0.26
6.South Cuba	0.28	0.24	0.21	0.22	0.06	–	0.07	0.05	0.18	0.16	0.24	0.23	0.24
7.Mesoamerica	0.33	0.29	0.26	0.27	0.09	0.08	–	0.09	0.23	0.2	0.29	0.28	0.28
8.East Cuba	0.27	0.23	0.19	0.2	0.08	0.05	0.1	–	0.19	0.16	0.22	0.21	0.22
9. Cayman Brac	0.36	0.33	0.31	0.31	0.24	0.21	0.25	0.21	–	0.11	0.32	0.31	0.32
10.Little Cayman	0.34	0.3	0.28	0.28	0.21	0.18	0.22	0.18	0.13	–	0.29	0.28	0.29
11. <i>A. bremeri</i>	0.27	0.23	0.19	0.16	0.28	0.25	0.29	0.23	0.33	0.31	–	0.09	0.18
12. <i>A. quadriocellifer</i>	0.24	0.21	0.13	0.09	0.27	0.24	0.28	0.22	0.32	0.3	0.11	–	0.18
13. <i>A. homolechis</i>	0.28	0.25	0.21	0.21	0.28	0.25	0.29	0.24	0.33	0.31	0.20	0.21	–

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Table S5. Individual coefficients from the principal components analysis of nine quantitative traits from the *Anolis sagrei* morphological dataset. The first three PC axes are shown, with proportion of variance explained by each of the three axes.

QT Coefficient	PC1 (63.6%)	PC2 (16.8%)	PC3 (9.5%)
HL	0.07	0.17	-0.09
SW	0.12	0.66	-0.06
SL	0.13	0.67	-0.17
JL	0.06	0.13	-0.04
HW	0.11	0.03	0.09
TL	0.01	0.08	0.44
FL	0.03	0.09	0.61
MTL	0.06	0.12	0.62
LAM	0.97	-0.21	-0.03

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Table S6. Coefficients from linear discriminant function analysis for the *Anolis sagrei* morphological dataset. The data are residuals for each trait from a regression on body size (SVL). Six *a priori* groupings were used to test for discriminatory ability based on quantitative trait variation. PoV is the proportion of group variance explained by each of the first two discriminant axes. Note that PoV is always equal to 1 when only two groups are present (Venables and Ripley, 2002).

<i>mtDNA</i>	LD1	LD2	<i>DAPC</i>	LD1	LD2	<i>STRUCTURE</i>	LD1	LD2
HL	17.48	-18.48	HL	20.98	7.22	HL	9.95	20.06
SW	83.80	-21.33	SW	24.25	13.37	SW	27.57	23.19
SL	-77.02	62.62	SL	-57.77	-15.00	SL	-55.20	5.50
JL	-10.22	-42.58	JL	58.19	3.49	JL	44.73	-46.12
HW	-29.30	1.78	HW	-30.22	-28.53	HW	-26.99	-19.25
TL	-158.34	-6.83	TL	34.34	33.26	TL	-18.03	-64.40
FL	87.82	87.75	FL	-79.54	-63.85	FL	-43.37	93.80
MTL	25.67	-54.46	MTL	35.74	-0.77	MTL	41.60	-27.95
LAM	6.79	-11.58	LAM	16.02	-4.39	LAM	20.45	7.93
PoV	31.9	28.1	PoV	37.1	21.6	PoV	32.7	27.1
<i>Region</i>	LD1	LD2	<i>Subspecies</i>	LD1	LD2	<i>Cuba Diaspora</i>	LD1	
HL	-0.06	7.84	HL	10.25	-2.53	HL	-3.64	
SW	26.17	-41.00	SW	-25.26	41.71	SW	23.45	
SL	-40.53	35.04	SL	41.12	-33.45	SL	-42.93	
JL	50.99	9.13	JL	-52.29	-14.29	JL	52.47	
HW	-43.44	-5.42	HW	30.82	2.00	HW	-35.38	
TL	-28.99	127.67	TL	52.00	-119.63	TL	-25.41	
FL	0.90	-86.41	FL	0.23	92.15	FL	-33.74	
MTL	5.32	-36.76	MTL	-22.58	28.36	MTL	24.96	
LAM	25.06	5.18	LAM	-22.75	-5.94	LAM	19.26	
PoV	34.2	28.3	PoV	39.3	33.2	PoV	1.00	

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Table S7. Tests for phylogenetic signal in quantitative traits using Pagel's λ . P values are based on 1000 Brownian motion simulations. Here the null hypothesis is no phylogenetic signal.

Trait	λ	P
SVL	0.42	0.008
TL	<0.001	1
JL	<0.001	1
HW	<0.001	1
HL	<0.001	1
FL	0.46	0.24
MTL	0.06	0.82
SL	<0.001	1
SW	<0.001	1
Lamellae	0.08	0.9

LITERATURE CITED

Venables, W. N., & Ripley, B. D. (2002). Modern applied statistics with S. Fourth edition. New York, NY; Springer.