

Supplementary Material

Genetic drift or natural selection? Hybridization and asymmetric mitochondrial introgression in two Caribbean lizards (*Anolis pulchellus* and *Anolis krugi*)

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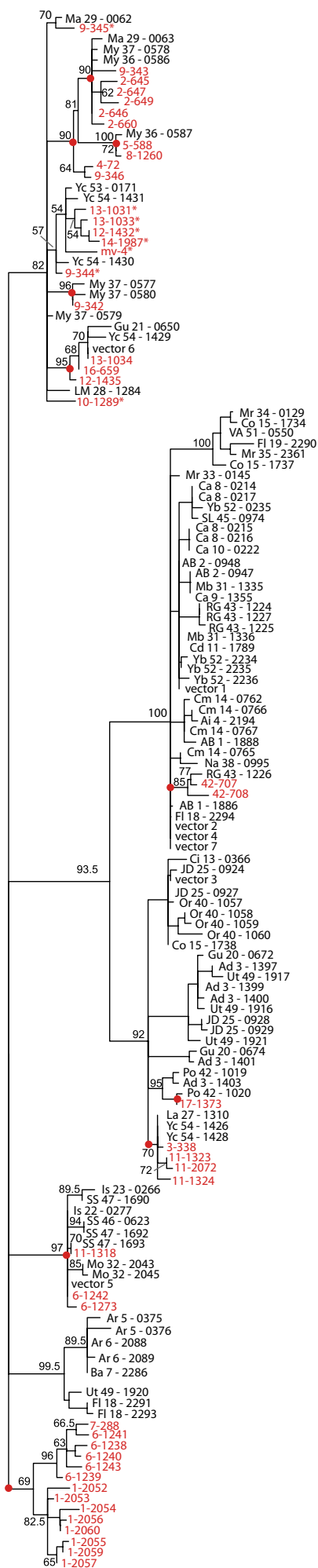
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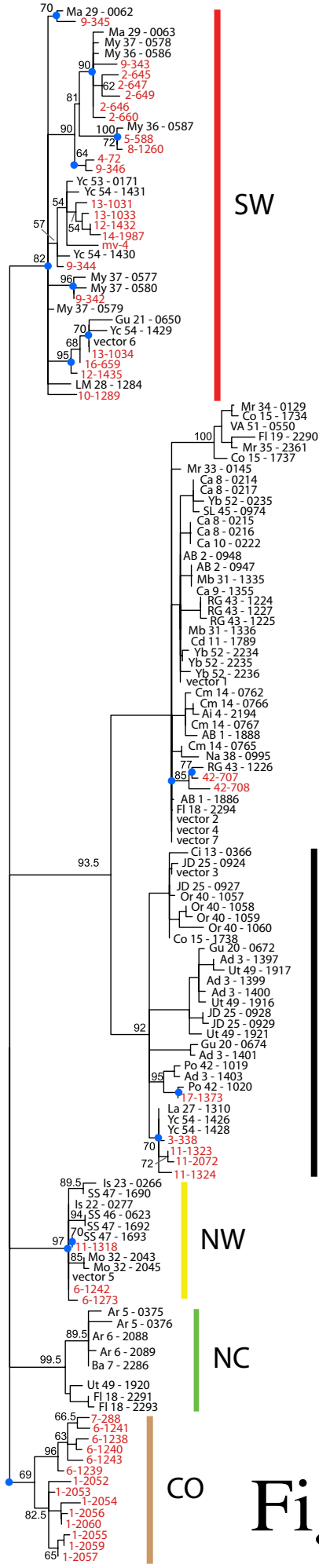
Supplementary Material, Figure S1. Minimum number of introgression events of *Anolis krugi*'s mtDNA into the genome of *A. pulchellus*, estimated from the ML tree for the combined datasets of all *A. krugi* sequences and the *A. krugi*'s mtDNA sequences in *A. pulchellus*. The number of introgression events was estimated as the minimum number of character state changes (i.e. shifts from mtDNA of *A. pulchellus* to mtDNA of *A. krugi*) necessary to explain the observed pattern of distribution of *A. krugi* mtDNA in the tree, under the assumption that the introgression occurred only in one direction, from *A. krugi* into *A. pulchellus*. For example, when two or more introgressed individuals of *A. pulchellus* shared the same most recent common ancestor (i.e. formed a monophyletic clade), we assumed that the clade originated from a single introgression event. Branches with (A) bootstrap values <90 and (B) bootstrap values <70 were collapsed to calculate more and less conservative estimates, respectively, of the number of introgression events. Asterisks on (A) indicate the eight star-contracted mtDNA haplotypes from the Southwestern Clade that we conservatively interpreted as representing a single introgression event (see *Geographic patterns of mtDNA introgression into Anolis pulchellus*, in the Discussion).

A

90% bootstrap threshold

**B**

70% bootstrap threshold



SW

E

C

NW

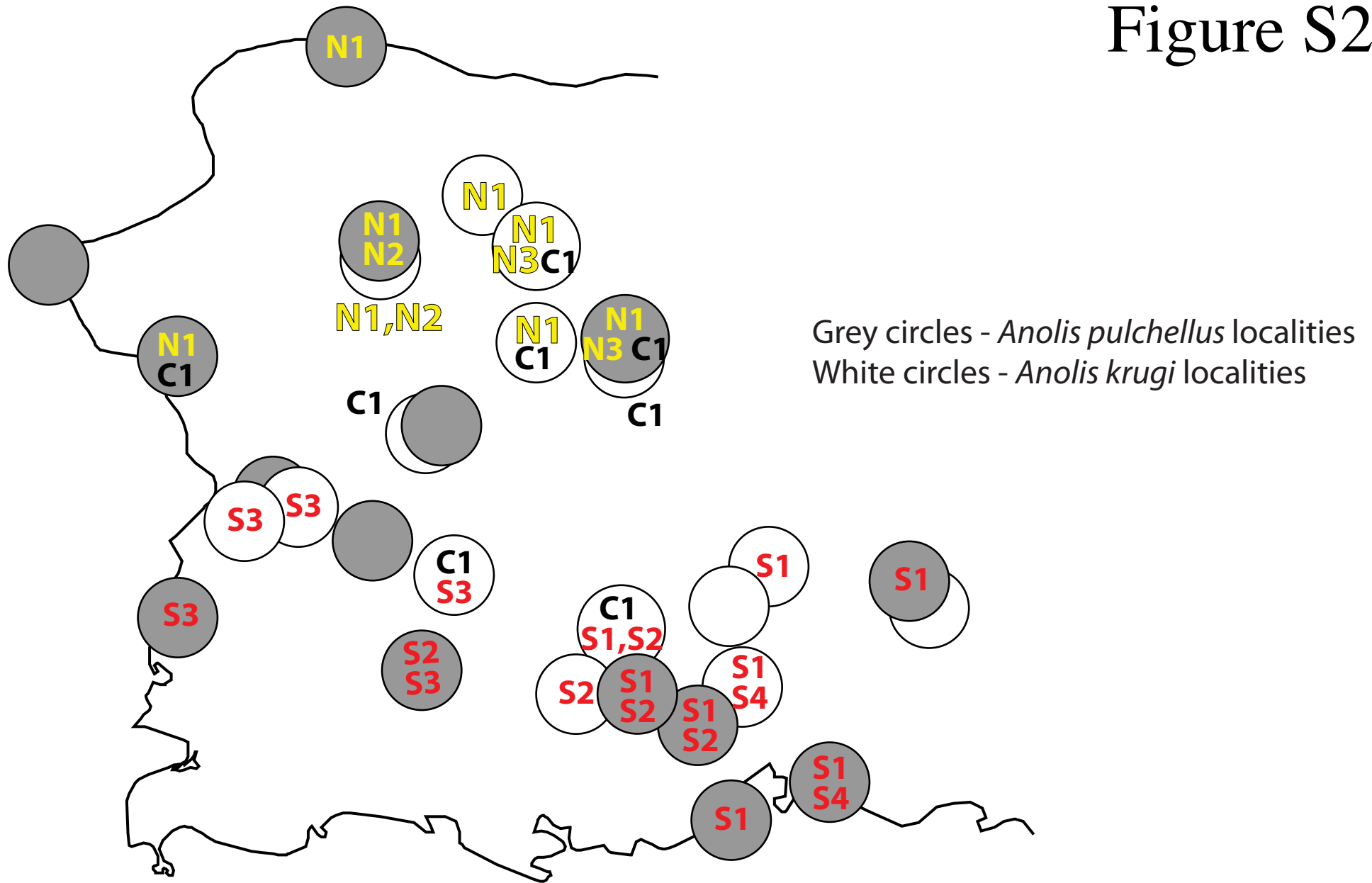
NC

CO

Figure S1

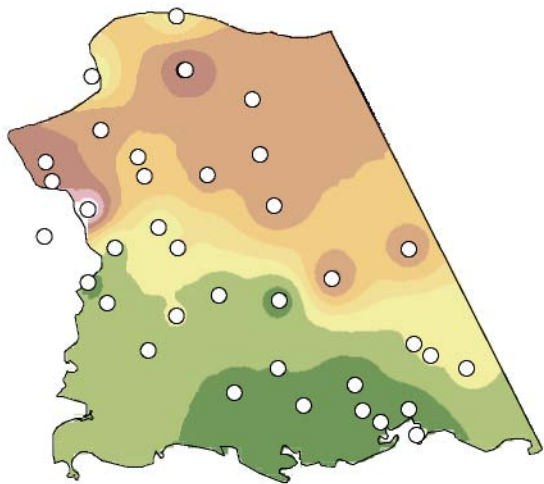
Supplementary Material, Figure S2. Star-contracted *Anolis krugi* mtDNA haplotypes shared between *A. pulchellus* and *A. krugi*. The star-contraction method identifies star-like clusters of haplotypes representing newly emerging mutations (also called satellite haplotypes) around a founder (ancestral) node. Each star-contraction haplotype therefore represents an ancestral haplotype and its satellite haplotypes (Forster *et al.*, 2001). Because we used a contraction value of five mutational steps, satellite haplotypes can be up to five mutations apart from the founder node. We identified eight star-contracted haplotypes. We plotted all shared star-contracted haplotypes between *A. pulchellus* and *A. krugi* on a map of western Puerto Rico, and the resulting distribution indicated that shared star-contracted haplotypes for *A. pulchellus* and *A. krugi* occur in nearby localities.

Figure S2



S1, S2, S3, S4 - shared star-contracted haplotypes belonging to the *Anolis krugi* Southwestern mtDNA clade
N1, N2, N3 - shared star-contracted haplotypes belonging to the *Anolis krugi* Northwestern mtDNA clade
C1 - shared star-contracted haplotype belonging to the *Anolis krugi* Central clade

Supplementary Material, Figure S3. Interpolated genetic distances among populations of *Anolis pulchellus* with *A. krugi* mtDNA. We calculated genetic distances among populations of *A. pulchellus* with *A. krugi* mtDNA, and interpolated them across the landscape. The genetic distances were represented by mismatch distances between sequences from neighboring sampling sites, calculated in the program Alleles in Space (Miller, 2005). These pairwise genetic distances were assigned to mid-points (shown as white circles in the map) between sampling sites using the Delaunay triangulation-based connectivity network (Miller *et al.*, 2006). We used residual genetic distances derived from the linear regression of genetic versus geographical distance to account for correlation between these two distances (Manni *et al.*, 2004; Miller *et al.*, 2006). The residual genetic distances were interpolated across uniformly spaced 30-second grids (*ca.* 1 km) using the inverse distance weighted interpolation procedure (Watson & Philip, 1985) in ArcGIS 9.2 (ESRI, Redlands, CA, USA) across western Puerto Rico. The shading gradation progresses from green (lowest genetic distance) to yellow, brown, and white (highest genetic distance).



LITERATURE CITED

- Forster, P., Torroni, A., Renfrew, C. & Röhl, A. 2001. Phylogenetic star contraction applied to Asian and Papuan mtDNA evolution. *Mol. Biol. Evol.* **18**: 1864-1881.
- Manni, F., Guérard, E. & Heyer, E. 2004. Geographic patterns of (genetic, morphologic, linguistic) variation: how barriers can be detected by using Monmonier's algorithm. *Hum. Biol.* **76**: 173-190.
- Miller, M.P. 2005. Alleles In Space (AIS): computer software for the joint analysis of interindividual spatial and genetic information. *J. Hered.* **96**: 722-724.
- Miller, M.P., Bellinger, M.R., Forsman, E.D. & Haig, S.M. 2006. Effects of historical climate change, habitat connectivity, and vicariance on genetic structure and diversity across the range of the red tree vole (*Phenacomys longicaudus*) in the Pacific Northwestern United States. *Mol. Ecol.* **15**: 145-159.
- Watson, D.F. & Philip, G.M. 1985. A refinement of inverse distance weighted interpolation. *Geo-Processing* **2**: 315-327.