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## Supporting Online Material for

### **Founder Effects Persist Despite Adaptive Differentiation: A Field Experiment with Lizards**

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## Supporting Online Materials

### Summary of Methods and Supplementary Results

#### Field

In September 2004, the storm surge from Hurricane Frances submerged a number of small, low-lying islands near Great Abaco, Bahamas. Prior to the hurricane, these islands supported populations of the brown anole, *Anolis sagrei*. After the hurricane and before the start of the experiment, seven of these islands were thoroughly searched multiple times at varying times of day by up to four people in both November 2004 and May 2005. These searches did not find any lizards.

We collected adult *A. sagrei* from a single area (~350 m<sup>2</sup>) on Iron Cay in May 2005, then randomly chose one male and one female and placed them on each of seven experimental founder islands. A male was included to ensure that the introductions did not fail due to lack of fertilized females, although females were likely storing sperm (31). During our yearly censuses of Bahamian islands, we have observed natural instances of simultaneous colonization by two lizards (32). In further support that brown anole populations were extirpated by the hurricane, genetic analyses of non-founders captured in November 2005 ( $n = 3$ ) and May 2006 ( $n = 81$ ) were consistent with being either progeny of the founding pair ( $n = 79$ ) or offspring from stored sperm use by the founding female ( $n = 5$ ). Thus, our sampling over the first year did not detect any individuals with multilocus genotypes that would suggest they were either survivors of the hurricane that went undetected or immigrants within the first year. Not until 2007 do we detect unambiguous immigrants based on their multilocus genotype (see below). Population size on experimental founder islands was estimated in May of each year from 2006 to 2009 (and November 2006) using a multiple-recapture method adapted for multi-way contingency tables (see *ref.* 25 and references therein for details). Perch use by lizards was measured by recording perch height and diameter of undisturbed lizards during each visit to an island ( $n = 1,164$  observations on eight islands over four years). To determine if perch use changed over time on experimental founder islands, we used an analysis of variance (ANOVA) with island, year, and the island by year interaction as fixed effects.

In May 2009, we measured vegetation structure on the experimental islands as follows. Each island was approximated as an ellipse. A measuring tape was placed along the major axis of the island, from the beginning to the end of the vegetation, and perpendicular transects were placed at 3-m intervals along the major axis. At 2-m intervals along each transect, we measured the maximum height of the vegetation within a 0.5-m radius of a given point and the maximum diameter of the vegetation at 30.5-cm vertical intervals from above ground to the top of the vegetation at that point. On Iron Cay (the source population locality), a measuring tape was placed from the shore to 15 m inland at three different sites. At 3-m intervals along the line at each site, we measured the maximum height of the vegetation within a 0.5-m radius of a given point and the maximum diameter of the vegetation at 30.5-cm vertical intervals from the ground to 183 cm above ground.

#### Genetic

We extracted genomic DNA from tail tissue, amplified six microsatellite loci (15, 61, 70, 77, 91, 94) using PCR, and genotyped fragments with fluorescent-labeled primers

as in Kolbe et al. (33). We genotyped a total of 591 individuals sampled from Iron Cay, the seven experimental founder islands, and six reference islands from 2005 to 2009. Heterozygosity and allelic diversity were estimated for the source population (Iron Cay in 2005, that is, the founding pair from each island pooled,  $n = 14$ ) and compared to samples from the seven experimental founder islands in 2006 ( $n = 6-17$  lizards per island, mean = 11.6) using GenAEx version 6 (34). Sample sizes in subsequent years on Iron Cay and the seven experimental founder islands averaged 13.8 (range 3-23) in 2007 and 15.6 (range 6-24) in 2009. Islands were not sampled in 2008.

We tested for allelic differentiation between all pairs of populations using exact  $G$  (log likelihood ratio) tests in GENEPOP 4.1 (35). Results showed significant ( $P < 0.05$ ) allelic differentiation for at least one locus between each pair of populations, but more often 4-6 loci were significant (see Table S1). Additionally, we used Stouffer's  $z$  method to combine  $P$ -values for all six microsatellite loci as suggested by Whitlock (36), yielding significant pairwise allelic differences in 144 of 147 cases (Table S1, data sets A-C combined).

We used principal coordinates analysis (PCoA) of multilocus genotypes to reduce the dimensionality of the genetic data and facilitate visualization of genetic differences among islands and changes for each island through time. To test for a lasting influence of the founder effect, we calculated the correlation between genotype frequencies of the founding pair for each island and the average value in 2006, 2007, and 2009 on PCo axes 1-3, which explained a total of 66% of the variation in genotype frequencies. We also evaluated differences using separate ANOVAs for each PCo axis with island, year, and the island by year interaction as fixed effects. We calculated pairwise- $F_{ST}$  values among the source population (Iron Cay) and the seven experimental founder islands in 2006 (using 2005 samples for Iron Cay, which was not sampled in 2006), 2007, and 2009 using 999 random permutations to assess significant differences from zero. Recently established populations such as these are unlikely to be in equilibrium, an assumption of  $F$ -statistics, thus these results should be interpreted cautiously and only in conjunction with other tests of genetic divergence (i.e., allelic differentiation). To test for stability in among-population genetic differentiation, we conducted Mantel correlations of pairwise- $F_{ST}$  matrices from each year, assessing significance with 9,999 random permutations. For comparison to population-genetic differentiation found among reference islands, we calculated pairwise- $F_{ST}$  values for six reference islands in 2005 ( $n = 11-103$  lizards per island, mean = 43.5), the source population (Iron Cay, 2005) and the seven experimental founder islands in 2006. Genetic analyses were conducted using GenAEx version 6 (34).

We used assignment methods to estimate the likelihood that individuals sampled on experimental founder islands in 2007 and 2009 were first-generation immigrants based on their multilocus genotypes. We used the frequency-based method of Paetkau et al. (37) implemented in GENECLASS2 (38), and following the suggestion of the authors for situations where some potential source populations are clearly missing, we computed the likelihood of the individual genotype within the population where the individual was sampled ( $L_{home}$ ). We assessed significance ( $P < 0.05$ ) using a Monte Carlo resampling method of 10,000 simulated individuals. Nine individuals in 2007 and 12 individuals in 2009 (21 of 188 individuals sampled, or 11%) were excluded from originating on the island they were sampled, suggesting they are immigrants. This included individuals

from all seven experimental founder islands with at least 1 immigrant per sampling period on average for each island. The relatively small number of loci used for these assignment tests could lead to an overestimate of the number of migrants (39). We therefore constructed pedigrees for each island to identify individuals with previously undetected alleles, which could indicate offspring from stored sperm use, a first-generation immigrant, or a recent progeny of an immigrant. Pedigree analyses based on multilocus genotypes revealed 10 individuals with at least one previously undetected allele in 2007 and an additional 11 individuals in 2009. Ten of these 21 individuals had two or more new alleles. Although the pedigree analyses did not identify the same set of individuals as immigrants compared to the assignment tests; overall, the two methods detected the same number of individuals as immigrants. Thus, both the assignment tests and pedigree analyses estimate that 11% of the total number of individuals sampled in 2007 and 2009 were possible immigrants or the recent progeny of immigrants.

### **Morphology**

The same person measured snout-vent length (SVL) and hindlimb length (HL) measurements on each lizard by hand; HL for female founders ( $n = 7$ ) in 2005 was not measured. Only adult lizards were measured, corresponding to lower size limits of 38.5 mm SVL for males and 35 mm SVL for females. Both SVL and HL were log-transformed prior to all statistical analyses. We evaluated HL differences on experimental founder islands with analysis of covariance (ANCOVA) with SVL as a covariate. Independent variables consisted of island (seven experimental founder islands), year (2006, 2007, 2009), and sex (male and female) as fixed effects. Interaction effects between SVL and each independent variable and the island by year interaction were also tested. Non-significant interactions were removed in the final model. Our interpretation of HL differences focused on the year effect for adaptive differentiation, island effect for the founder effect (also tested for 2006 data only), and the year by island interaction for lack of persistence of the founder effect. To calculate the overall percent decrease in hindlimb length from 2006 to 2009 on experimental founder islands, we calculated regression equations for each year separately by sex and then compared predicted hindlimb values in 2006 and 2009 along the range of SVL values for each sex.

We calculated mean relative HL for every island-year combination as the residuals of the regression of log-HL on log-SVL, treating each sex separately, pooling the residuals from each sex, and using only data from the experimental founder islands. To test for adaptive differentiation in 2006, we used a linear regression of mean relative HL and mean log-perch diameter among experimental founder islands. To control for measurement drift over time and possible unaccounted for global factors affecting all islands, we compared the experimental founder islands to a set of nearby reference islands (including the source Iron Cay) monitored over a similar period of time. We tested for a difference in HL using a mixed model ANCOVA, focusing on the island type by year interaction to test for a significantly greater decrease in HL for experimental founder islands compared to reference islands. Year, island type and sex were fixed effects and SVL nested within island was a random effect. Reference islands were measured in 2005 and 2008 (except Iron Cay which was measured in 2005 and 2009) and experimental founder islands were measured in 2006 and 2009. Non-significant interactions were removed from the final model.

To contrast adaptive differentiation and founder effects for producing HL differences among experimental founder islands in 2009, we conducted a multiple regression with relative HL in 2009 as the dependent variable and relative HL in 2006, vegetation-diameter availability, and perch-diameter use as independent variables, both diameter measures were log-transformed.

Table S1. Results of pairwise exact  $G$  (log likelihood ratio) tests for allelic differentiation evaluating the null hypothesis that alleles are drawn from the same distribution in both populations conducted in GENEPOP 4.1.0 (35). We report counts of significant ( $P < 0.05$ ) tests of allele frequency differences between populations for six microsatellite loci (below diagonal) and the combined  $P$ -value for the six loci using Stouffer's  $z$  method as recommended by Whitlock (36) (above diagonal). Pairwise comparisons between Iron Cay and the experimental founder islands are in bold.

A) Iron Cay founders (2005), experimental founder (2006), and reference islands (2005).

	Buddy	1	5	6	W2	X3	Iron Cay	N1	N2	N3	N4	N15	X3*	X10
Buddy		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
1	6		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
5	6	6		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
6	6	6	5		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
W2	6	6	6	6		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
X3	6	6	5	5	6		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
Iron Cay	6	6	6	6	5	6	<b>0.0006</b>	<b>0.0002</b>	<b>0.0469</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>
N1	6	5	6	6	6	6	<b>3</b>		<b>0.0424</b>	<b>&lt;0.0001</b>	<b>0.0159</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>
N2	6	5	6	6	5	6	<b>3</b>	<b>4</b>		<b>&lt;0.0001</b>	<b>0.0365</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>
N3	6	5	6	6	5	6	<b>1</b>	<b>4</b>	<b>3</b>		<b>&lt;0.0001</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>
N4	6	4	6	6	5	6	<b>3</b>	<b>4</b>	<b>3</b>	<b>4</b>		<b>&lt;0.0001</b>	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>
N15	6	5	6	6	6	6	<b>5</b>	<b>5</b>	<b>5</b>	<b>3</b>	<b>5</b>		<b>&lt;0.0001</b>	<b>&lt;0.0001</b>
X3*	5	5	6	5	5	6	<b>6</b>	<b>6</b>	<b>6</b>	<b>4</b>	<b>6</b>	<b>6</b>		<b>&lt;0.0001</b>
X10	6	5	5	5	5	5	<b>6</b>	<b>6</b>	<b>6</b>	<b>5</b>	<b>6</b>	<b>6</b>	<b>6</b>	

B) Iron Cay and experimental founder islands (2007)

	Iron Cay	N1	N2	N3	N4	N15	X3*	X10
Iron Cay		<0.0001	<0.0001	0.0007	<0.0001	<0.0001	<0.0001	<0.0001
N1	3		<0.0001	0.0002	<0.0001	<0.0001	<0.0001	<0.0001
N2	4	4		0.0006	0.0004	<0.0001	<0.0001	<0.0001
N3	3	1	2		0.0018	<0.0001	0.1411	<0.0001
N4	2	4	5	2		<0.0001	<0.0001	<0.0001
N15	5	5	6	4	6		<0.0001	<0.0001
X3*	5	5	5	4	4	6		<0.0001
X10	5	6	6	4	6	5	6	

C) Iron Cay and experimental founder islands (2009)

	Iron Cay	N1	N2	N3	N4	N15	X3*	X10
Iron Cay		0.0004	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
N1	1		0.2667	<0.0001	0.4956	<0.0001	<0.0001	<0.0001
N2	4	3		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
N3	5	5	6		<0.0001	<0.0001	<0.0001	<0.0001
N4	3	3	4	5		<0.0001	<0.0001	<0.0001
N15	4	5	5	5	5		<0.0001	<0.0001
X3*	5	6	6	5	6	6		<0.0001
X10	2	5	4	5	6	3	6	

Table S2. Pairwise- $F_{ST}$  values (below diagonal) and significance values (above diagonal) for Iron Cay (source population), experimental founder islands (N1, N2, N3, N4, N15, X3\*, and X10), and reference islands (Buddy, 1, 5, 6, W2, and X3). The significance of pairwise- $F_{ST}$  values from zero was assessed with 999 random permutations (34).

Pairwise comparisons between Iron Cay and the experimental founder islands are in bold. These results should be interpreted cautiously because recently founded populations such as these are unlikely to be in migration-drift-mutation equilibrium, an assumption of  $F$ -statistics.

A) Iron Cay founders (2005), experimental founder (2006), and reference islands (2005).

	Buddy	1	5	6	W2	X3	Iron Cay	N1	N2	N3	N4	N15	X3*	X10
Buddy		0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
1	0.378		0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
5	0.352	0.220		0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
6	0.358	0.290	0.181		0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
W2	0.250	0.341	0.305	0.337		0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
X3	0.314	0.298	0.220	0.156	0.294		0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
Iron Cay	0.169	0.192	0.170	0.192	0.207	0.181	<b>0.009</b>	<b>0.001</b>	<b>0.063</b>	<b>0.018</b>	<b>0.100</b>	<b>0.001</b>	<b>0.001</b>	<b>0.002</b>
N1	0.189	0.295	0.279	0.214	0.311	0.217	<b>0.051</b>		<b>0.001</b>	<b>0.001</b>	<b>0.002</b>	<b>0.001</b>	<b>0.001</b>	<b>0.001</b>
N2	0.310	0.339	0.312	0.289	0.342	0.322	<b>0.084</b>	<b>0.165</b>		<b>0.001</b>	<b>0.001</b>	<b>0.001</b>	<b>0.001</b>	<b>0.001</b>
N3	0.243	0.302	0.239	0.288	0.338	0.311	<b>0.038</b>	<b>0.152</b>	<b>0.206</b>		<b>0.001</b>	<b>0.004</b>	<b>0.001</b>	<b>0.001</b>
N4	0.226	0.149	0.226	0.219	0.267	0.218	<b>0.043</b>	<b>0.104</b>	<b>0.191</b>	<b>0.174</b>		<b>0.001</b>	<b>0.001</b>	<b>0.001</b>
N15	0.264	0.255	0.200	0.258	0.262	0.219	<b>0.019</b>	<b>0.148</b>	<b>0.181</b>	<b>0.105</b>	<b>0.130</b>		<b>0.001</b>	<b>0.005</b>
X3*	0.228	0.337	0.322	0.327	0.272	0.320	<b>0.143</b>	<b>0.275</b>	<b>0.294</b>	<b>0.241</b>	<b>0.239</b>	<b>0.260</b>		<b>0.001</b>
X10	0.306	0.336	0.247	0.284	0.334	0.260	<b>0.080</b>	<b>0.181</b>	<b>0.192</b>	<b>0.250</b>	<b>0.190</b>	<b>0.078</b>	<b>0.330</b>	

B) Iron Cay and experimental founder islands (2007)

	Iron Cay	N1	N2	N3	N4	N15	X3*	X10
Iron Cay			0.009	0.001	0.002	0.001	0.001	0.001
N1	0.041			0.001	0.004	0.001	0.001	0.001
N2	0.141	0.171			0.002	0.001	0.001	0.001
N3	0.153	0.165	0.193			0.017	0.013	0.011
N4	0.115	0.142	0.202	0.137			0.001	0.001
N15	0.063	0.123	0.211	0.125	0.167			0.001
X3*	0.186	0.176	0.258	0.191	0.208	0.249		0.001
X10	0.145	0.148	0.258	0.296	0.283	0.124	0.296	

C) Iron Cay and experimental founder islands (2009)

	Iron Cay	N1	N2	N3	N4	N15	X3*	X10
Iron Cay			0.002	0.001	0.001	0.001	0.001	0.001
N1	0.064			0.001	0.001	0.004	0.001	0.001
N2	0.094	0.098			0.001	0.001	0.001	0.002
N3	0.153	0.191	0.204			0.001	0.001	0.001
N4	0.086	0.078	0.188	0.189			0.001	0.001
N15	0.062	0.128	0.170	0.169	0.150			0.001
X3*	0.187	0.193	0.269	0.213	0.189	0.196		0.001
X10	0.113	0.165	0.116	0.264	0.209	0.090	0.292	

Table S3. A) Founder effect in hindlimb length (HL) in 2006. Results of an analysis of covariance (ANCOVA) testing for differences in hindlimb length among islands (fixed effect) in 2006 with SVL as a covariate. The non-significant island by SVL interaction ( $P = 0.17$ ) was removed from the final model. Tukey's honestly significant difference (HSD) post hoc test showed a significant difference between the islands with the relatively longest (N1) and shortest (N2) hindlimbs at the  $\alpha = 0.05$  level.

Source	DF	Sum of squares	F	P-value
Island	6	0.00216626	4.0783	0.0015
Sex	1	0.00936198	105.7532	< 0.0001
SVL	1	0.01012160	114.3339	< 0.0001
Sex by SVL	1	0.00090735	10.2494	0.0021
Error	68	0.00601982		

Note: Whole model  $R^2 = 0.983$ .

B) Results of an analysis of variance (ANOVA) on the residuals from the log-HL on log-SVL regression, calculated separately by sex and using the 2006 data only. Tukey's HSD post hoc test showed a significant difference only between the islands with the relatively longest (N1) and shortest (N2) hindlimbs at the  $\alpha = 0.05$  level. Although some have criticized the use of residuals in favor of analysis of covariance (40), one or the other method can be more conservative (41). We present both ANCOVA and ANOVA of residuals for comparison. In each case, results are robust to the methods and qualitative conclusions are the same. For analyses using residuals, we subtracted one degree of freedom from the error degrees of freedom as in *ref.* 40.

Source	DF	Sum of squares	F	P-value
Island	6	0.00211400	4.062	0.0015
Error	70	0.00607207		

Note: Whole model  $R^2 = 0.258$ .

Table S4. A) Results of an ANCOVA for hindlimb length differences among island, year, and sex (fixed effects) with SVL as a covariate. This analysis tested for a founder effect (7 islands), adaptation (3 years), and lack of founder effect persistence, drift or idiosyncratic effects over time (island by year interaction) on hindlimb length using the experimental founder island data only. Non-significant island by year by SVL ( $P = 0.32$ ) and island by SVL ( $P = 0.31$ ) were removed from the final model. Although the year by SVL interaction is significant, slopes for hindlimb on SVL among the three years are almost identical for males (slopes = 0.86, 0.86, and 0.84) and very similar for females (slopes = 0.49, 0.58, and 0.59) in 2006, 2007, and 2009, respectively for each sex. In fact, the year by SVL interaction is non-significant when analyzing females only and the Johnson-Neyman procedure (42) does not identify any regions of non-significance when comparing females in 2006 and 2009. This suggests interpreting the highly significant main effect of year is appropriate (see Table S5 and Fig. S4 for an analysis of % hindlimb change for various SVL values). Tukey's HSD post hoc test showed a significant difference between the islands with the relatively longest (N1) and shortest (N2 & X10) hindlimbs and among all three years at the  $\alpha = 0.05$  level.



Source	DF	Sum of squares	F	P-value
Island	6	0.00516070	7.6852	< 0.0001
Year	2	0.01591637	71.1069	< 0.0001
Sex	1	0.02341087	209.1777	< 0.0001
Island by Year	12	0.00100612	0.7491	0.7020
SVL	1	0.05504884	491.8652	< 0.0001
Year by SVL	2	0.00098810	4.4144	0.0133
Sex by SVL	1	0.00184610	16.4951	< 0.0001
Error	200	0.02238371		

Note: Whole model  $R^2 = 0.976$ .

B) Results on an ANOVA on residuals from the log-HL on log-SVL regression, calculated separately by sex.

Source	DF	Sum of squares	F	P-value
Island	6	0.00491181	6.9768	< 0.0001
Year	2	0.01683958	71.7573	< 0.0001
Island by Year	12	0.00155107	1.1016	0.3604
Error	204	0.02393675		

Note: Whole model  $R^2 = 0.514$ .

C) As an alternative to analyzing individual lizards as above, this analysis uses mean values for islands in each year. Analysis at the level of island, calculating year-island means ( $n = 21$ ) after residuals by sex. No replication of island or year exists with mean values, so we followed recommendations from Legendre et al. (43) and used their Model 5 to test the island by year interaction ( $P = 0.937$ ), then as suggested by Legendre et al. (43), we used a standard two-way ANOVA on year-island means to test the main effects.

Source	DF	Sum of squares	F	P-value
Island	6	0.00053108	5.8589	0.0047
Year	2	0.00168614	55.8048	< 0.0001
Error	12	0.00018129		

Note: Whole model  $R^2 = 0.909$ .

Table S5. Percent decrease in hindlimb length on experimental founder islands from 2006 to 2009. Using regression equations calculated separately for each sex in 2006 and 2009, we show the predicted difference in HL between years along the range of SVL values. Males show little variation along the range of SVL values due to similar HL-SVL slopes (0.86 and 0.84 in 2006 and 2009, respectively), whereas females show slightly more variation due to a slope difference of 0.49 versus 0.59 in 2006 and 2009, respectively.

SVL quartiles	Males (log SVL)	% HL decrease	Females	% HL decrease
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		from 2006 to 2009	(log SVL)	from 2006 to 2009
100	1.7653	6.76%	1.64345	3.02%
75	1.72016	6.58%	1.61278	3.68%
50	1.69897	6.49%	1.59797	3.99%
25	1.67036	6.38%	1.57978	4.38%
0	1.58546	6.03%	1.54407	5.14%

Table S6. A) Mixed model ANCOVA testing for hindlimb differences between reference and experimental founder islands over time implemented in R. Year, island type and sex were fixed effects and SVL nested within island was a random effect. Reference islands were measured in 2005 and 2008 (except Iron Cay which was measured in 2005 and 2009) and experimental founder islands were measured in 2006 and 2009. Non-significant year by island type by SVL ( $P = 0.12$ ) and island type by SVL ( $P = 0.90$ ) interactions were removed from the final model. Significant year by SVL ( $P < 0.0001$ ) and sex by SVL ( $P < 0.0001$ ) were retained. The key test of the year by island type interaction was highly significant ( $P < 0.0001$ ). Hindlimb length on founder islands decreased significantly more over time than the reference islands (see Fig. 4).

Source of variation	Sum of squares	DF	Mean square	F	P-value
Year	0.39784	1	0.39784	659.356	< 0.0001
Island type	0.01905	1	0.01905	31.571	< 0.0001
Sex	2.85517	1	2.85517	4731.975	< 0.0001
SVL	1.4961	1	1.4961	2479.537	< 0.0001
Year by Island type	0.03703	1	0.03703	61.377	< 0.0001
Year by SVL	0.04366	1	0.04366	72.362	< 0.0001
Sex by SVL	0.03613	1	0.03613	59.88	< 0.0001
Error	0.27514128	456	0.00060338		

B) Results of repeated-measures ANOVA testing an island type by year interaction, residuals by sex and mean values for each island-year combination. Iron Cay data are from 2005 and 2009 (4 years instead of the 3 years as for all other reference and founder islands). Results are the same if Iron Cay values (2005) are either 2005 compared to the midpoint between 2007/2009 or the midpoint between 2005/2007 compared to 2009.

Source of variation	DF	F	P-value
Between subjects:			
Island type	1,18	0.2377	0.6318
Within subject:			
Year	1,18	40.4363	< 0.0001
Island type by Year	1,18	19.1322	0.0004

## Supplementary Figure Legends

Fig. S1. Vegetation profile of the source population on Iron Cay and experimental founder islands. The source population on Iron Cay (A, B) mostly consists of taller and broader vegetation (mean vegetation height = 384 cm and mean vegetation diameter = 11.1 cm) compared to the experimental founder islands (C, D), which have much shorter and narrower vegetation (mean vegetation height ranged from 62-107 cm and mean vegetation diameter ranged from 1.6-5.4 cm). [Photos taken by JJK in 2009].

Fig. S2. Vegetation diameter availability on the seven experimental founder islands and source population on Iron Cay in 2009 (mean values are shown in Fig. 1). Within each bin (i.e., 0-1 cm, 1-2 cm, etc.), gray bars show the experimental founder islands in the following order: N4, N2, N3, N1, N15, X3\* and X10, and the black bar is the source population on Iron Cay.

Fig. S3. Mean relative hindlimb length calculated as the residual values from the log-hindlimb length on log-SVL regression, separately for each sex, and using the 2006 data for the experimental founder islands and founder males (2005) pooled for the Iron Cay estimate. As a result of the founder effect, populations on some experimental founder islands have relatively longer hindlimbs compared to the source population, whereas hindlimbs are shorter on other islands.

Fig. S4. Relationship between hindlimb length and SVL for males and females on experimental founder islands in each year. See Table S5 for percent decrease in hindlimb length from 2006 to 2009 for each sex. Regression equations are as follows for males in 2006 ( $\log \text{HL} = 0.1191541 + 0.8552145 * \log \text{SVL}$ ), 2007 ( $\log \text{HL} = 0.0909974 + 0.8601324 * \log \text{SVL}$ ), and 2009 ( $\log \text{HL} = 0.1217093 + 0.8365524 * \log \text{SVL}$ ), and females in 2006 ( $\log \text{HL} = 0.6623623 + 0.4888146 * \log \text{SVL}$ ), 2007 ( $\log \text{HL} = 0.5119675 + 0.5766003 * \log \text{SVL}$ ), and 2009 ( $\log \text{HL} = 0.4902570 + 0.5854430 * \log \text{SVL}$ ).

Fig. S5. Relative hindlimb lengths (mean  $\pm$  SE) for broad and narrow perch treatments from a previous plasticity experiment (30), the source population (Iron Cay in 2005, 2007 & 2009) and experimental founder islands (2006, 2007 & 2009) from this study, reference islands (2005 & 2008), natural islands ( $n = 13$  islands) across the Bahamas (44), and an experimental-island introduction ( $n = 16$  islands) over a 10-14 year period sampled from a single source, Staniel Cay (open circle), Exuma, Bahamas (45). Relative hindlimb lengths are the residual values from the log-HL on log-SVL regression, separately for each sex, combining data from all studies into a single analysis. The same person measured SVL and HL measurements on each lizard by hand. Mean island values are arranged from largest to smallest in each group and alternate between solid circles/lines and open circles/dashed lines for reference and experimental founder islands for clarity.

Fig. S1



Fig. S2

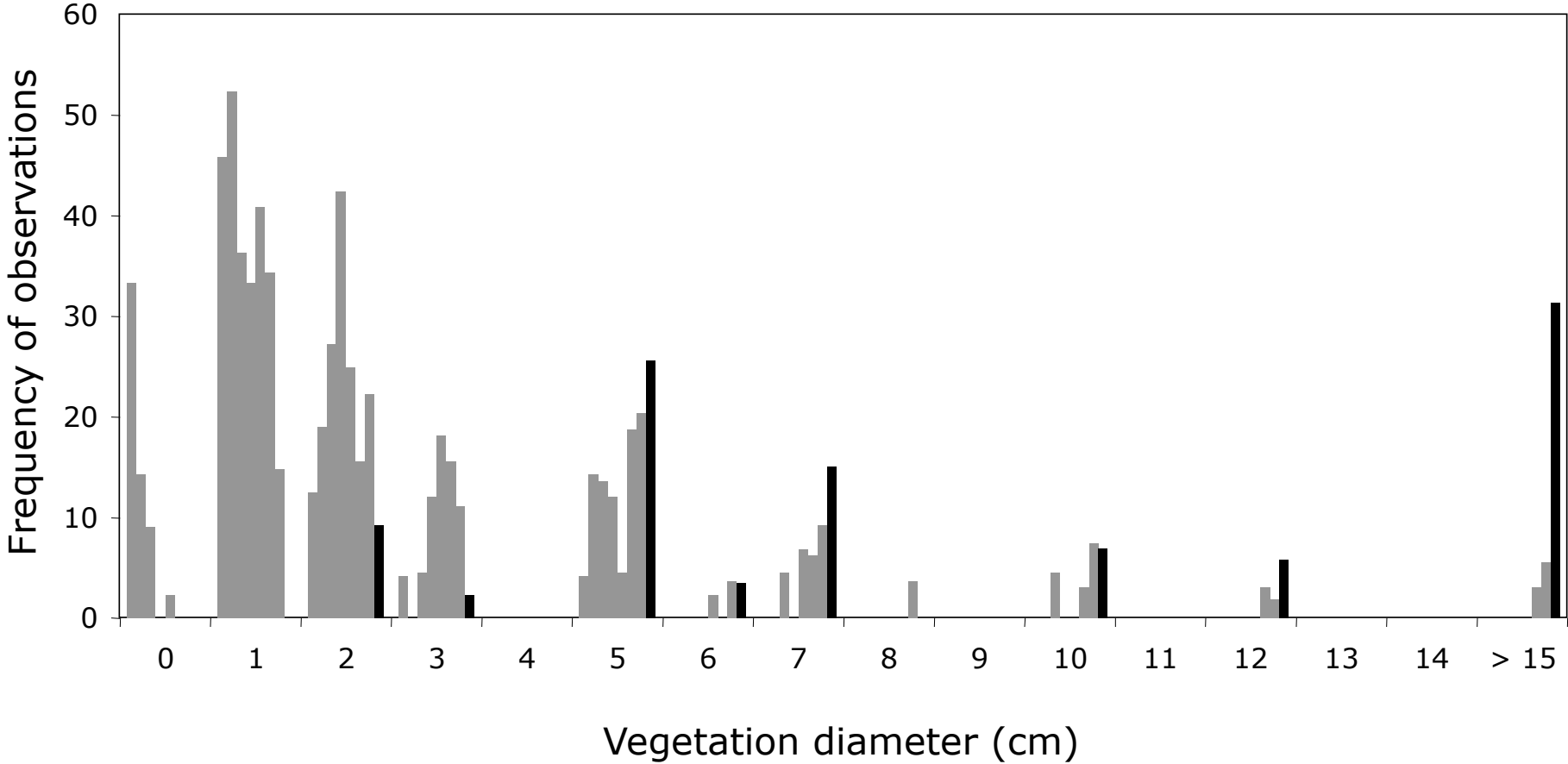


Fig. S3

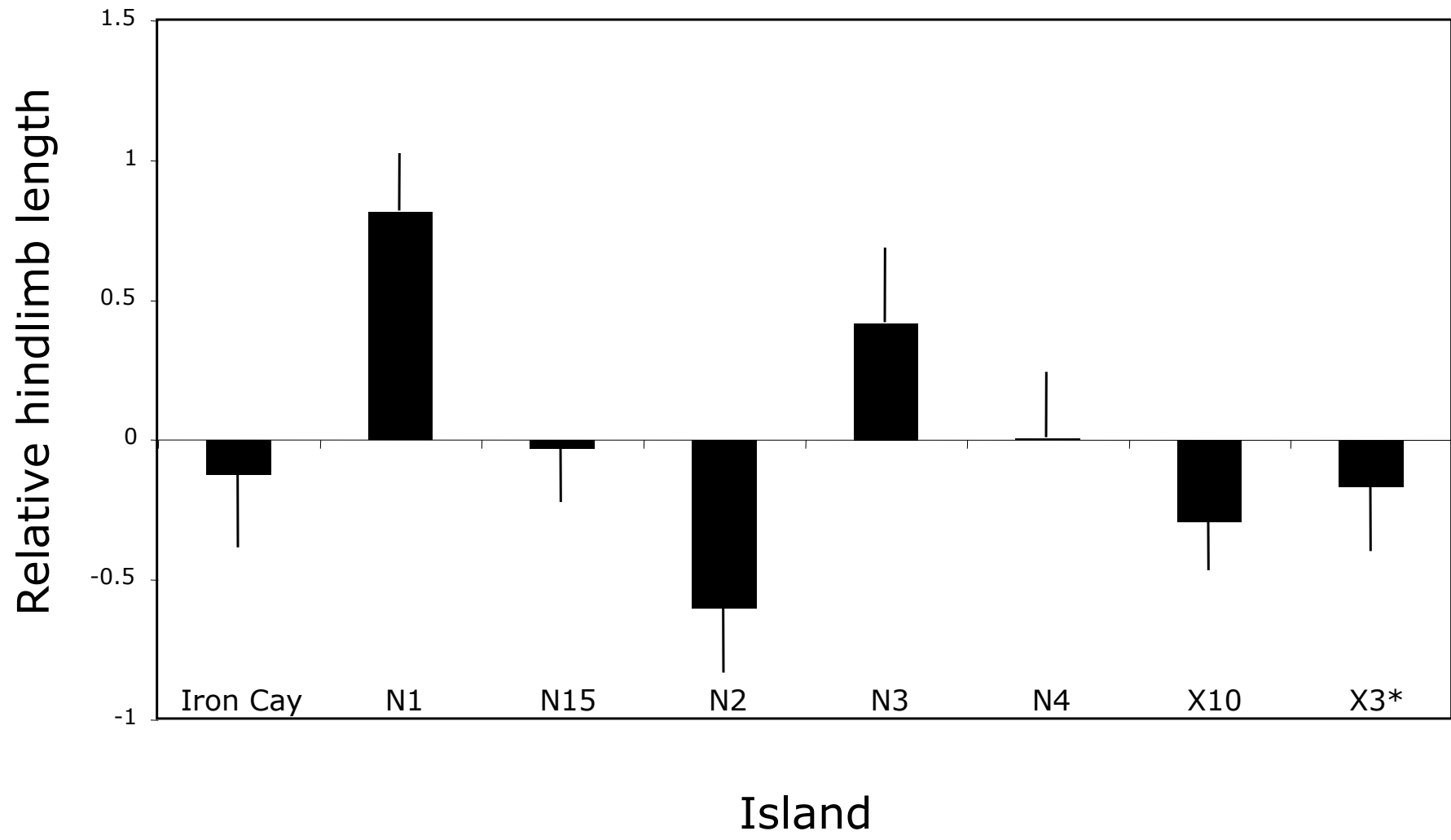
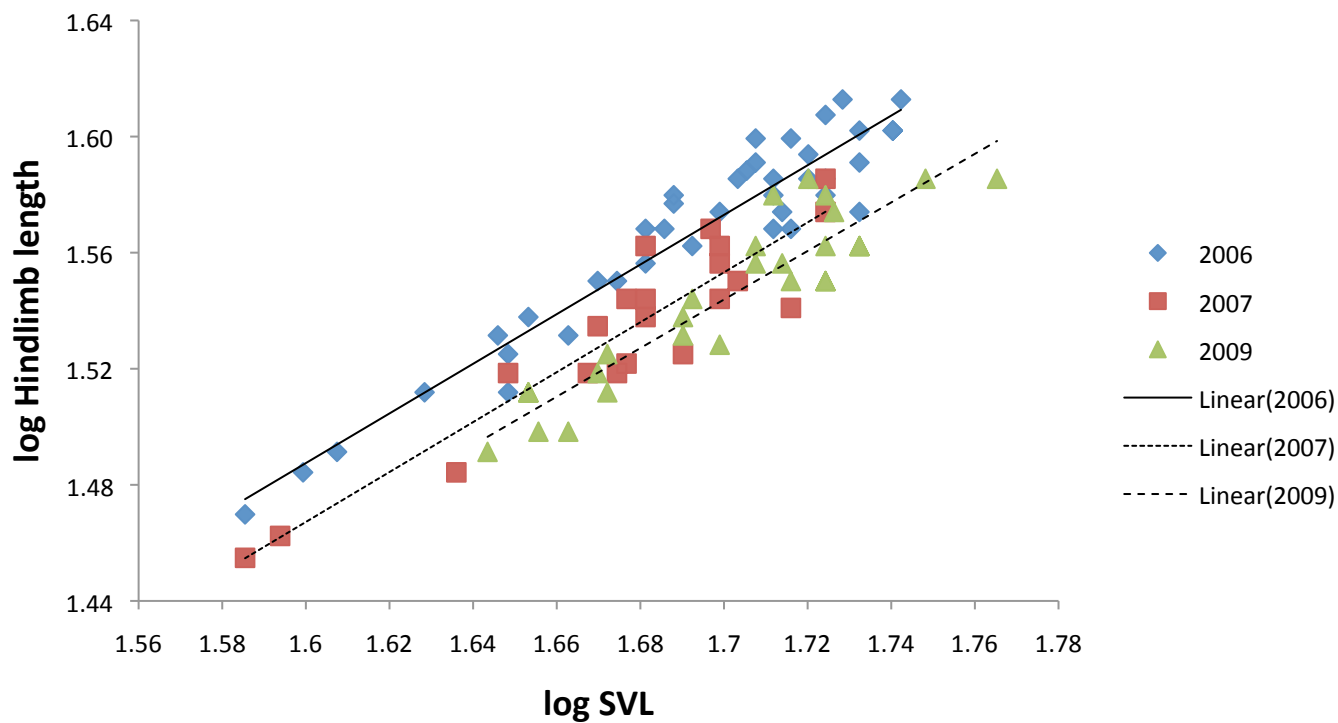


Fig. S4

### Males



### Females

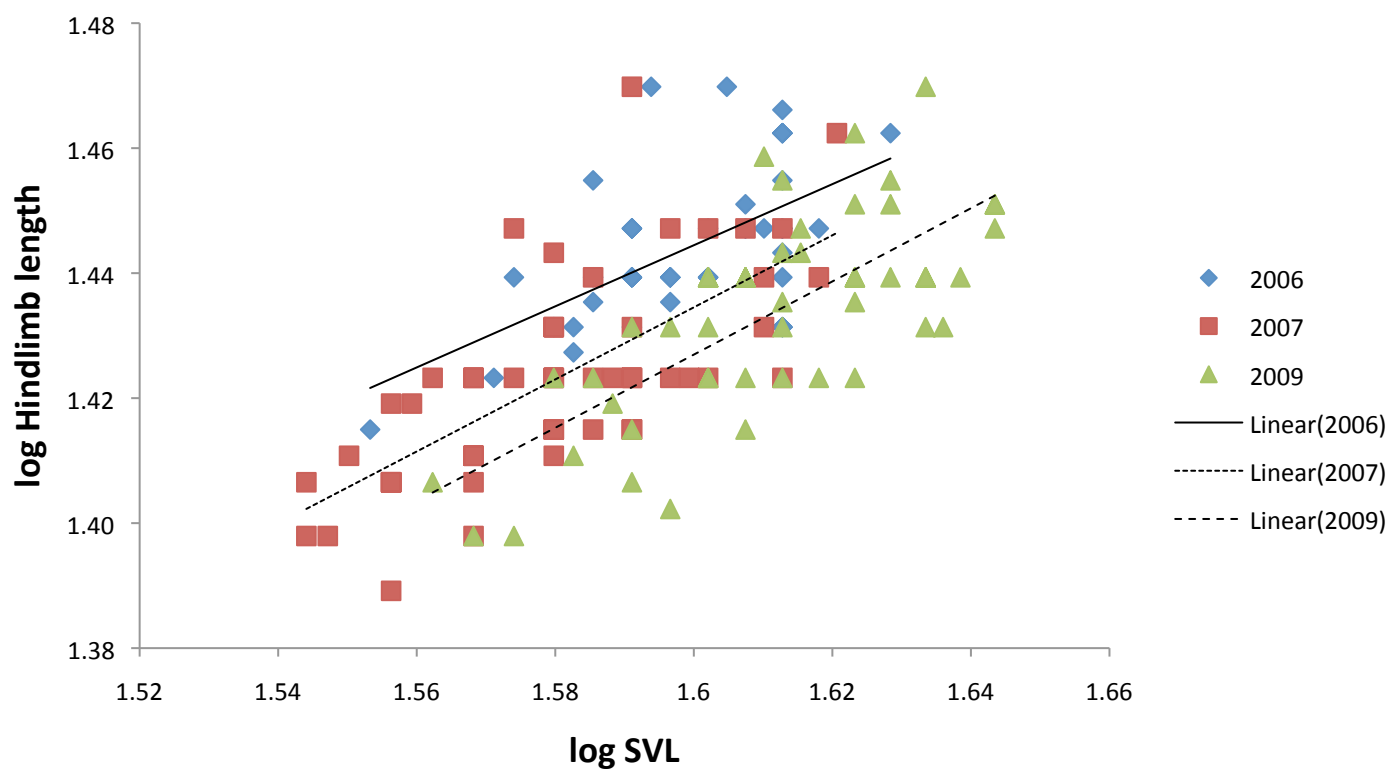
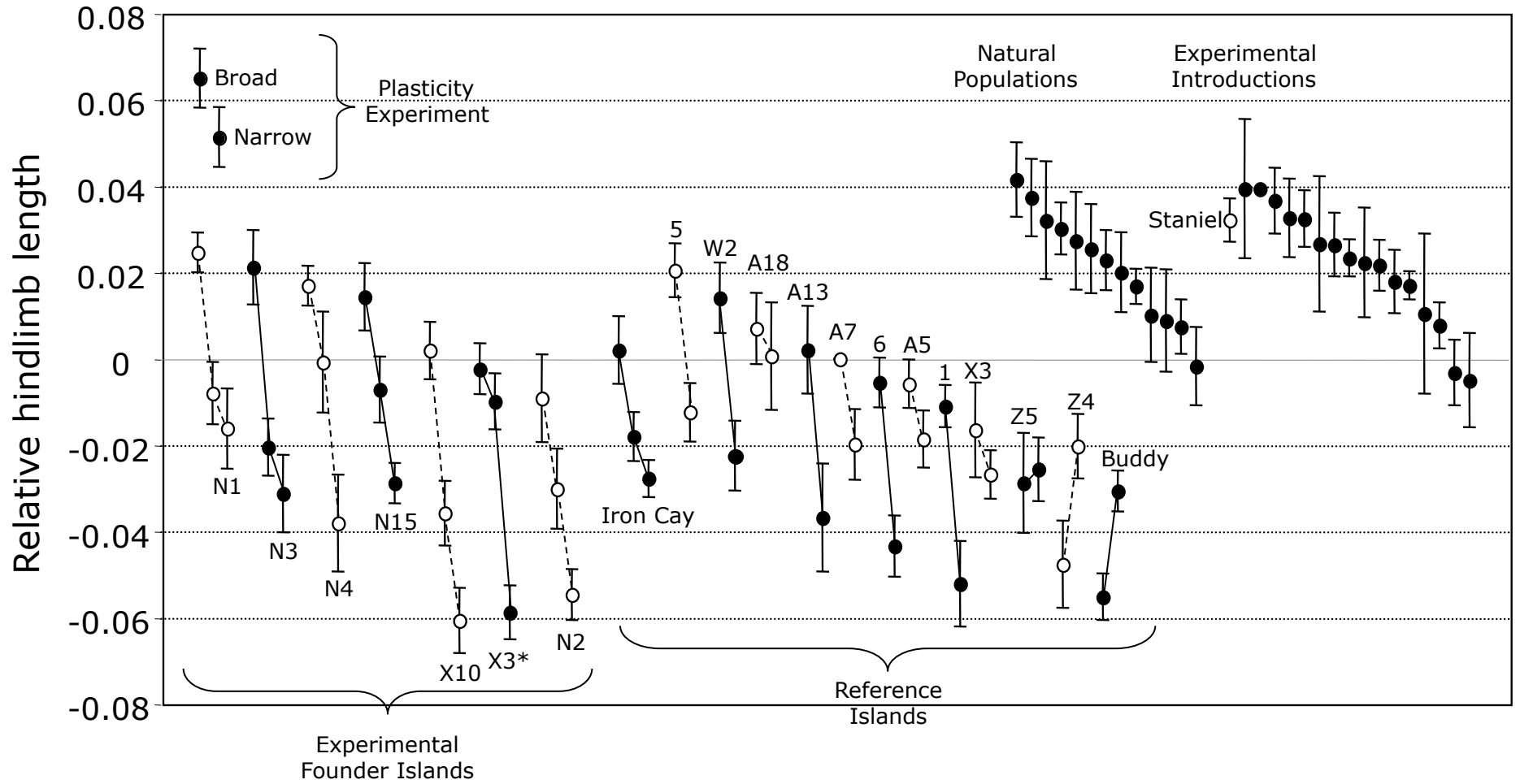


Fig. S5





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