Independent introductions and sequential founder events shape genetic differentiation and diversity of the invasive green anole (*Anolis carolinensis*) on Pacific Islands

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**Supporting Information**

**Table S1.** Primer sequences and annealing temperatures (Tm) for the seven microsatellite loci used in our study.

**Table S2.** Sequences used in the phylogenetic analyses.

**Table S3.** Prior distributions of parameter used in DIYABC analyses.

**Table S4.** Matching introduced haplotypes to native locations.

**Table S5.** Posterior probabilities of competing scenarios tested by ABC.

**Table S6.** Population differentiation (F<sub>ST</sub> values) between native and introduced locations.

**Table S7.** Frequencies of private alleles.

**Figure S1.** Graphical representation of colonization scenarios of *Anolis carolinensis* in the Pacific.

**Figure S2.** Bayesian inference phylogenetic tree

**Figure S3.** Median joining network of 226 mtDNA ND2 haplotypes from introduced locations and native location belonging to Gulf-Atlantic clade.

**Figure S4.** Additional structure plots.

**Figure S5.** DAPC analysis plot.

**Figure S6.** Mantel test plots in native and non-native ranges
### Table S1. Primer sequences and annealing temperatures (Tm) for the seven microsatellite loci used in our study.

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### Table S2. Previously published and newly collected sequences used in the phylogenetic analyses. Haplotype code is shown only for sequences used in the network analyses.

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Table S3. Prior distributions of the historical, demographic and mutation parameters used in ABC analyses. Effective population sizes (N) are expressed in number of diploid individuals and times of events (t) in numbers of generations going back to the past.

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<th>Interpretation</th>
<th>Parameter</th>
<th>Prior distribution</th>
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<td>Effective size in native population</td>
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<td>Uniform [10;10000]</td>
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<tr>
<td>Effective size in introduced population</td>
<td>N2</td>
<td>Uniform [10;1000]</td>
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<td>Effective size in unsampled population</td>
<td>N3</td>
<td>Uniform [10;1000]</td>
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<td>Bottleneck event duration</td>
<td>db</td>
<td>Uniform [1;5]</td>
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<td>Effective population size of founders</td>
<td>N_F</td>
<td>Uniform [1;50]</td>
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<tr>
<td>Introduction time</td>
<td>t</td>
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*Introduction time (in generations) is based on historical data on date of introduction for each population and assuming one-year generation time for A. carolinensis.

Table S4. A comparison matching haplotypes sampled in the non-native range to their identical or most similar haplotypes from native-range locations.

<table>
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<tr>
<th>Introduced Haplotypes*</th>
<th>Identical native Haplotype</th>
<th>Nearest native haplotype#</th>
<th>Location(s)</th>
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<td>LA_H18, H21, H25, H26, H46, H47, TX_H13-20, H23-24, H26-27</td>
<td>LA (Thibodaux, Sherburne WMA, Killian, Jay, Springfield), TX (Brownsville, Orange, Wood County, Camp Tyler, Houston)</td>
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<td>H1_H2</td>
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</table>

* Identical introduced haplotypes after trimming (to 705bp) for the network analysis are shown in parenthesis.
# Based on position on Network (Figure S3).
Table S5. Posterior probabilities of competing scenarios tested by ABC. The selected scenario was the one with the significantly highest posterior probability value (logistic regression approach) and with the 95% confidence interval (CI) not overlapping with the 95% CI of any other compared scenario. (A) First set of analyses to distinguish between three scenarios (independent colonization, stepping-stone colonization or unsampled source). (B) For populations were stepping-stone colonization was selected in (A) a new set of scenarios were tested to identify the specific source. (C) Two scenarios where tested for the Japanese populations.

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<td></td>
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<td>Stepping-stone colonization</td>
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* Approximate date of introduction or first documentation
Table S6. Population differentiation based on pairwise $Fst$ values. Non-significant values are indicated in bold.

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Table S7. Frequencies (F) of the most common and private alleles (Pₐ) across introduced populations and the frequency of these alleles across sampling locations in the native range.

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Frequency of the private allele in native populations

| SLA | - | - | 0.03 | 0.03 | 0.03 | - | - | - | - | - | 0.03 | - | - | - | - |
| NLA | - | 0.02 | 0.07 | 0.05 | 0.13 | - | 0.02 | - | - | - | - | - | 0.08 | - | - |
| TYTX | - | - | 0.03 | - | 0.03 | - | - | - | - | - | - | - | 0.06 | - | - |
| CCTX | 0.02 | 0.02 | - | 0.21 | - | - | - | - | 0.07 | - | - | - | - | - | - |
| AR | - | - | - | 0.02 | - | - | - | 0.03 | - | - | 0.02 | - | - | - | - |
| ETN | 0.14 | 0.06 | 0.04 | 0.04 | 0.04 | 0.02 | - | 0.06 | - | - | 0.02 | 0.02 | - | 0.08 | - | - |
| GA | - | 0.15 | - | 0.04 | 0.04 | 0.02 | 0.06 | 0.02 | 0.06 | - | 0.06 | - | 0.06 | - | - | - |
| NFL | 0.08 | 0.03 | - | 0.05 | 0.02 | - | - | - | 0.03 | 0.02 | - | 0.05 | - | - | - |
| BRTX | 0.15 | - | - | - | 0.15 | - | - | 0.05 | - | - | 0.10 | - | - | - | 0.05 |
| MFL | 0.07 | 0.07 | - | 0.03 | - | - | - | 0.26 | 0.07 | - | - | 0.26 | - | - | 0.47 |
| WTN | - | 0.17 | 0.26 | - | 0.12 | - | 0.05 | 0.03 | 0.03 | - | - | - | 0.17 | - | 0.45 |
| ORTX | - | - | 0.02 | 0.03 | - | - | - | 0.05 | - | - | 0.02 | - | 0.02 | - | 0.02 |
| AL | - | 0.15 | 0.09 | 0.09 | 0.17 | - | 0.09 | - | 0.08 | - | 0.02 | - | 0.05 | - | - | - |
| SC | - | 0.27 | 0.02 | - | 0.04 | 0.02 | 0.02 | - | 0.02 | - | 0.02 | - | 0.02 | - | - | - |
| NC | - | 0.05 | 0.02 | 0.02 | 0.20 | - | 0.02 | - | 0.05 | - | - | - | 0.12 | - | - | - |
| SEFL | 0.08 | 0.26 | - | 0.05 | 0.03 | - | 0.02 | 0.11 | 0.03 | - | 0.31 | 0.02 | 0.03 | - | 0.06 |
| SWFL | 0.16 | 0.03 | - | 0.06 | - | 0.03 | - | - | 0.22 | - | 0.06 | - | - | - | - |
| NWFL | 0.02 | 0.02 | - | 0.09 | 0.03 | - | - | - | 0.03 | - | - | 0.09 | - | - | - |
| MS | - | - | 0.03 | 0.03 | 0.07 | - | 0.05 | - | 0.03 | - | 0.05 | - | - | - | - |

* Frequency of the most common allele for the specific locus in introduced populations
** Frequency of the private allele in introduced populations
Figure S1. Graphical representation of possible colonization scenarios of *Anolis carolinensis* in the Pacific as tested using DIYABC. Set (a), represents two scenarios testing for the source of the stepping-stone colonization to Palau (Pa), either from Oahu (Oa) or Guam (Gu). Set (b) represents three scenarios testing for the stepping-stone colonization for Hawaii and Saipan (both represented with X) from established populations in the non-native range. Last set (c) represents two scenarios testing for the colonization pattern in Japanese Islands. Populations on Hahajima and Anijima (both represented with JP2) were tested against a source in the non-native range (Chichijima, JP1) and an unknown source location (Un). The thin red line indicates a reduction in the effective population size due to a bottleneck event following the introduction and t1, t2 and t3 represent time (in generations).
Figure S2. Bayesian inference phylogenetic tree. Haplotypes from introduced locations (Japanese Islands; red, Hawaiian Islands; green and Western Pacific Islands; orange) all belong to the Gulf-Atlantic clade.