Figure S3. Median-joining network showing the relationships among the 266 mtDNA ND2 haplotypes (trimmed to a uniform size of 705bp) sampled in the Gulf Coast/Atlantic clade of the native range and the non-native range. Black dots represent median vectors and connections among haplotypes are single nucleotide mutations unless indicated otherwise (slashes). The size of the pie (haplotype) corresponds to the number of individuals sampled with that haplotype (after trimming).
Figure S4. Structure plots. (A) Second best fit in analysis including all individuals/sampling locations for K=4 clusters. (B) When only locations in the native range were included, best fit for K=3. (C) When only sampling locations in the non-native range, best fit for K=2.

Figure S5. DAPC clustering analysis. Introduced populations (WP-Guam, WP-Saipan, WP-Palau, HI-Hawaii and HI-Oahu) are nested within native locations. For population coding see Table 1.
Figure S6. Test for a pattern of isolation by distance in the native and non-native range. Significant correlation in the native range (Mantel test, $R = 0.45$, $P = 0.001$) but not in the non-native (Mantel test, $R = -0.08875$, $P = 0.46$).