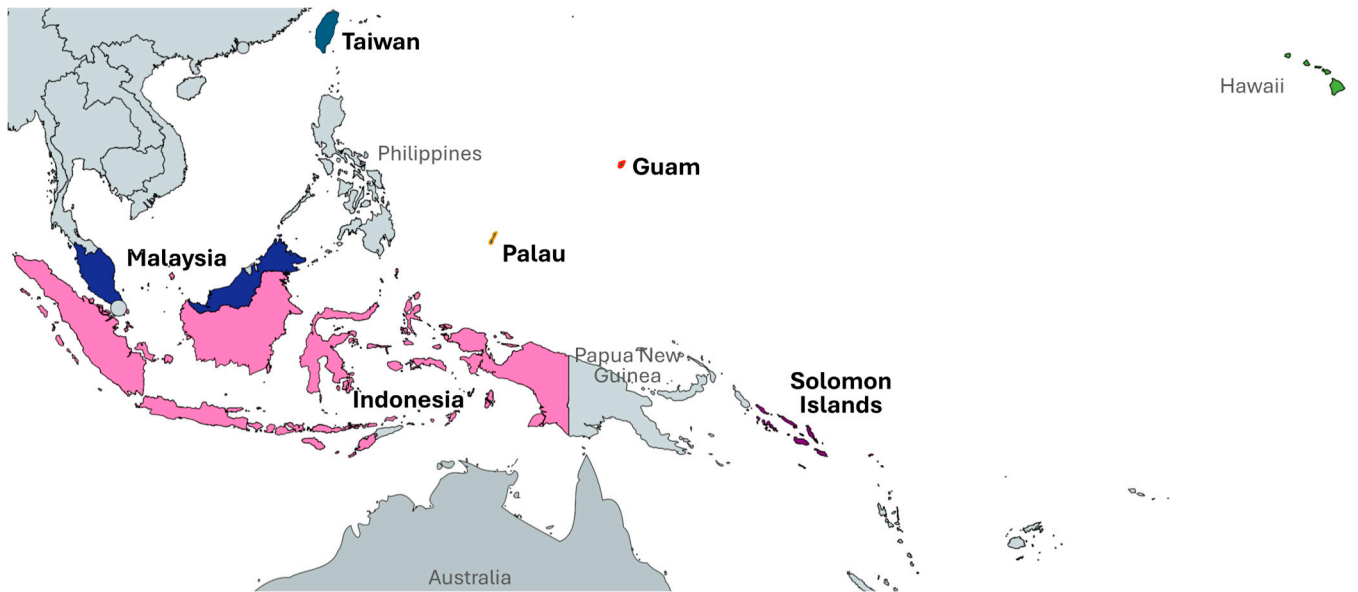


**Table S1.** Pairwise nucleotide comparisons of the full mitochondrial DNA *cytochrome oxidase subunit I* (mtCOI) gene (lower triangle), with the concatenated full ATP6 (*ATP synthase membrane subunit 6*) and full COIII (*cytochrome oxidase subunit III*) genes (top triangle, left and right values, respectively) for *Oryctes rhinoceros* (CRB) individuals.

[illegible]

**Notes:** The individually numbered CRB specimens were associated with the following locations: from Guam (#1-7, including specimen 04-Or5), Solomon Islands (#8), Taiwan (#9), Malaysia (#10-17), Palau (#18-21), Philippines (#22-25), and Indonesia (#26-31). A published draft mitochondrial genome of a related *Oryctes nasicornis* (OK484312) is included, showing a large nucleotide distance against the CRB samples. Red values are pairwise nucleotide identity between Guam CRB specimens. Blue values are CRB individuals from elsewhere with 100% nucleotide identity only for the mtCOI gene (i.e., classified as the CRB-G haplotype described in [35] but with differences in the ATP6 and COIII genes).

**Figure S1.** A map detailing countries (in bold) of *Oryctes rhinoceros* samples featured in the Figure 1 phylogeny. Country names in grey were provided as general reference. Map generated using Mapchart.net with editing in Microsoft PowerPoint for Mac Version 16.87.



**Figure S2.** Phylogeny based on concatenated sequences from the 13 mitogenome protein coding genes of coconut rhinoceros beetle (CRB) *Oryctes rhinoceros* samples as detailed in Table 1. Branch node estimates are shown. Note that the overall topology of the phylogeny with respect to the clades was the same as shown for the partial mitochondrial *ATP6* and *COIII* concatenated sequence phylogeny in Figure 1b and Figure 1c.

