

Table S1. Polymerase chain reaction (PCR) and sequencing (Seq.) primers used in this study.

| Locus | Primer Name | Primer Sequence | Direction & Type |
|-------|-----------------------------|----------------------------|----------------------|
| 16S | ⁶ 16sA-L | CGCCTGTTTATCAAAAACAT | forward (PCR & Seq.) |
| 16S | ⁶ 16sB-H | CCGGTCTGAACTCAGATCACGT | reverse (PCR & Seq.) |
| ND2 | ⁴ MetF1 | AAGCTTTCGGGCCCATACC | forward (PCR & Seq.) |
| ND2 | ¹ COIR1 | AGRGTGCCAATGTCTTTGTGRTT | reverse (PCR & Seq.) |
| ND2 | ² TrpR3a | TTTAGGGCTTTGAAGGC | reverse (Seq.) |
| KIF24 | ⁵ KIF24F1 | SAAACGTRTCTCCMAAACGCATCC | forward (PCR & Seq.) |
| KIF24 | ⁷ Kif24R1zebra | GCTGCTGRARCTGGTGATAAAGRCG | reverse (PCR & Seq.) |
| RAG1 | ⁵ RAG1skinkF2 | TTCAAAGTGAGATCGCTTGAAA | forward (PCR & Seq.) |
| RAG1 | ⁵ RAG1skinkR1200 | CCCTTCTCTTTCTCAGCAAAA | reverse (PCR & Seq.) |
| RAG1 | ⁵ RAG1skinkF370 | GCCAAGGTTTTTAAGATTGACG | forward (Seq.) |
| RAG1 | ⁵ RAG1skinkR2 | AACATCACAGCTTGATGAATGG | reverse (Seq.) |
| BRCA2 | ³ Skink984F | AACAGGTAGTCAGTTTGAMTTYACAC | forward (PCR & Seq.) |
| BRCA2 | ³ Skink2315R | RTTGAAGYYTGAATGCYAGGTTTGAC | reverse (PCR & Seq.) |

¹Arevalo, E., Davis, S.K., Sites, J.W., 1994. Mitochondrial DNA sequence divergence and phylogenetic relationships among eight chromosome races of the *Sceloporus grammicus* complex (Phrynosomatidae) in central Mexico. Syst. Biol. 43, 387–418.

²Greenbaum, E., Bauer, A.M., Jackman, T.R., Vences, M., Glaw, F., 2007. A phylogeny of the enigmatic Madagascan geckos of the genus *Uroplatus* (Sauria: Gekkonidae). Zootaxa 1493, 41–51.

³Karin, B.R., Metallinou, M., Weinell, J.L., Jackman, T.R., Bauer, A.M., 2016. Resolving the higher-order phylogenetic relationships of the circumtropical *Mabuya* group (Squamata: Scincidae): an out-of-Asia diversification. Mol. Phylogenet. Evol. 102, 220–232. <http://dx.doi.org/10.1016/j.ympev.2016.05.033>.

⁴Macey, J.R., Larson, A., Ananjeva, N.B., Fang, Z., Papenfuss, T.J., 1997. Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome. Mol. Biol. Evol. 14, 91–104.

⁵Portik, D.M., Bauer, A.M., Jackman, T.R., 2010. The phylogenetic affinities of *Trachylepis sulcata nigra* and the intraspecific evolution of coastal melanism in the western rock skink. Afr. Zool. 45, 147–159. <http://dx.doi.org/10.3377/004.045.0217>.

⁶Simon, C., Frati, F., Beckenbach, A., Crespi, B., Liu, H., Flook, P., 1994. Evolution, weighting, and phylogenetic utility of mitochondrial gene sequences and a compilation of conserved polymerase chain reaction primers. Ann. Entomol. Soc. Am. 87, 651–701. <http://dx.doi.org/10.1093/aesa/87.6.651>.

⁷Skipwith, P.L., Bauer, A.M., Jackman, T.R., Sadlier, R.A., 2016. Old but not ancient: coalescent species tree of New Caledonian geckos reveals recent post-inundation diversification. J. Biogeogr. 43, 1266–1276. <http://dx.doi.org/10.1111/jbi.12719>.