

Genomes of two Extinct-in-the-Wild reptiles from Christmas Island reveal distinct evolutionary histories and conservation insights

Tristram Dodge¹, Katherine Farquharson¹, Claire Ford², Lisa Cavanagh², Kristen Schubert³, Molly Schumer⁴, Katherine Belov¹, and Carolyn J. Hogg¹

¹The University of Sydney

²Taronga Conservation Society Australia

³Parks Australia

⁴Stanford University

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Abstract

Genomics can play important roles in biodiversity conservation, especially for Extinct-in-the-Wild species where genetic factors can influence total extinction risk and probability of successful reintroductions. The Christmas Island blue-tailed skink (*Cryptoblepharus egeriae*) and Lister's gecko (*Lepidodactylus listeri*) are two endemic reptile species that went extinct in the wild shortly after the introduction of a predatory snake. After a decade of management, captive populations have expanded from 66 skinks and 43 geckos to several thousand individuals; however, little is known about patterns of genetic variation in these species. Here, we use PacBio HiFi long-read and Hi-C sequencing to generate contiguous reference genomes for both species, including the XY chromosome pair in the skink. We then analyze patterns of genetic diversity to infer ancient demography and more recent histories of inbreeding. We observe high genome-wide heterozygosity in the blue-tailed skink (0.007) and Lister's gecko (0.005), consistent with large historical population sizes. However, nearly 10% of the skink reference genome falls within long runs of homozygosity (ROH), resulting in homozygosity at all major histocompatibility complex (MHC) loci, whereas we detect only a single ROH in the gecko. We infer from the ROH lengths that related skinks may have established the captive populations. Despite a shared recent extinction in the wild, our results suggest important differences in species' histories and implications for management. We show how reference genomes can provide evolutionary and conservation insights in the absence of resequencing data, and we provide a resource for future population-level and comparative genomic studies in reptiles.

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