

Climate change and evolution in the tropics: a genomic perspective

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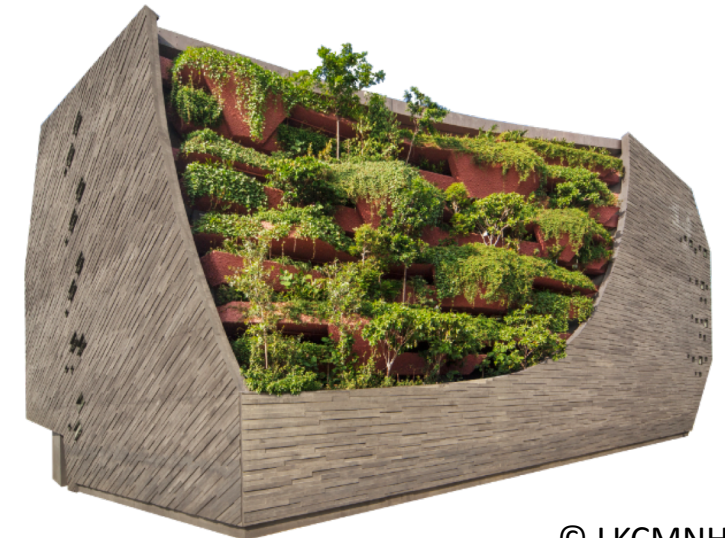
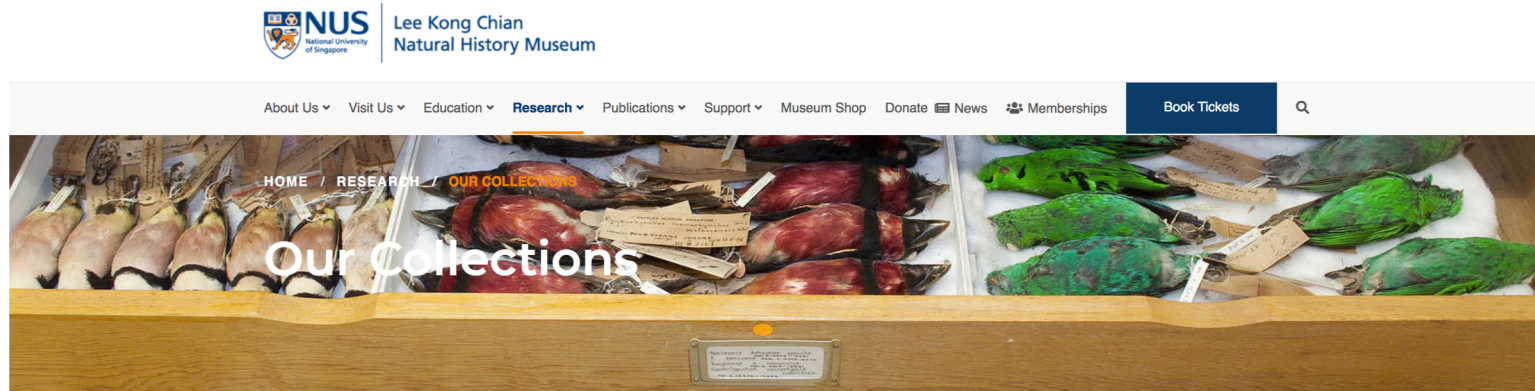


Genomics of non-model organisms: SEABIG (NUS)

- Multiple NGS facilities in Singapore
- Turnover time from sample submission to data is fast – less than a month in many cases
- Historic DNA Genomic facility at NUS
- Rich repertoire of specimens at LKCMNH



© NUS



© LKCMNH

Genome sequencing initiatives at NUS

- Genomics of non-model organisms: SEABIG (NUS)
- WGS
- Population Genomics
- Transcriptomics
- Metagenomics
- Both vertebrates and invertebrates



Black-capped babbler



Sunda fruit bat



Short-tailed babbler



Siamese crocodile

Assembly, annotation, and comparative methods used

- *de novo* genome assembly, annotation and comparative analysis
 - PLATANUS, MaSuRCA, SOAPdenovo, CLC workbench, Novoplasty, AUGUSTUS, MAKER, BUSCO, CAFE, ETE toolkit, Orthofinder, TOGA, BLASTtoGO, PSMC, etc.
- ddRAD-Seq
 - STACKS, pyRAD, ANGSD, PLINK, MP-EST, ASTRAL, RAxML, fastsimcoal, STRUCTURE, Admixturegraph, etc.
- Target enrichment
 - HybPiper, ANGSD, PLINK, MP-EST, ASTRAL, RAxML, fastsimcoal, Admixturegraph, etc.
- Metagenomics
 - In-house pipeline for metabarcoding (Meier et al. 2015; Srivathsan et al. 2018; Srivathsan et al. 2021)

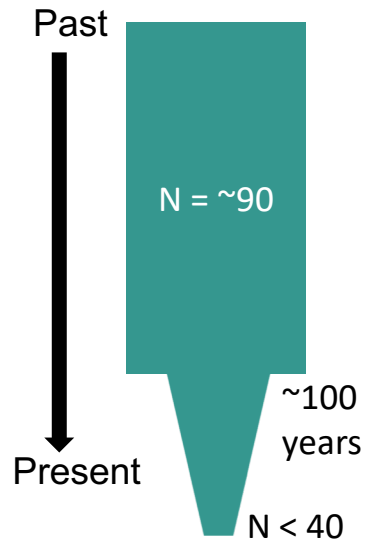
Species history in Conservation: Siamese crocodile

Inform field-based conservation: Captive breeding and reintroductions

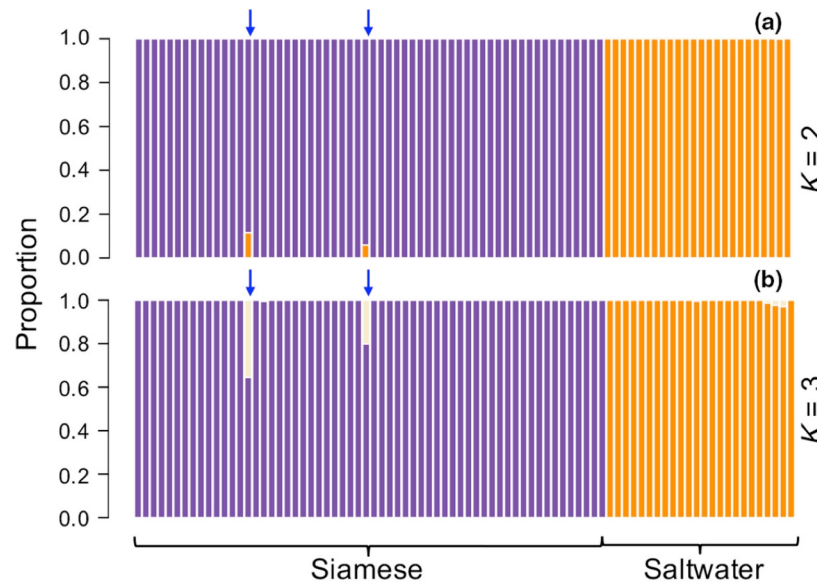
2,067 SNPs ddRAD-Seq



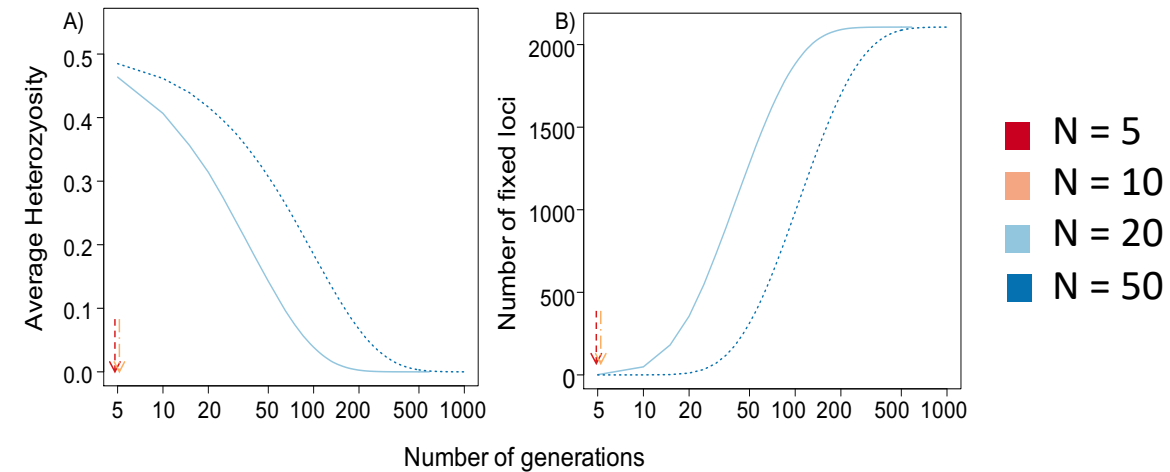
Siamese crocodile



Recent Bottleneck and continuing decline



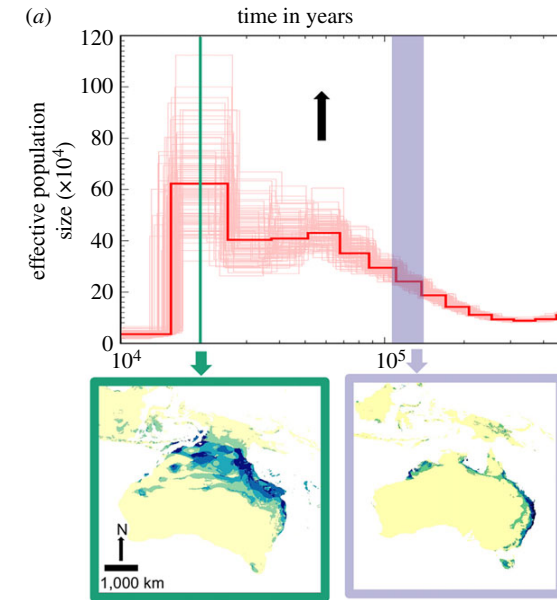
Incidences of ghost introgression possibly with Cuban crocodiles



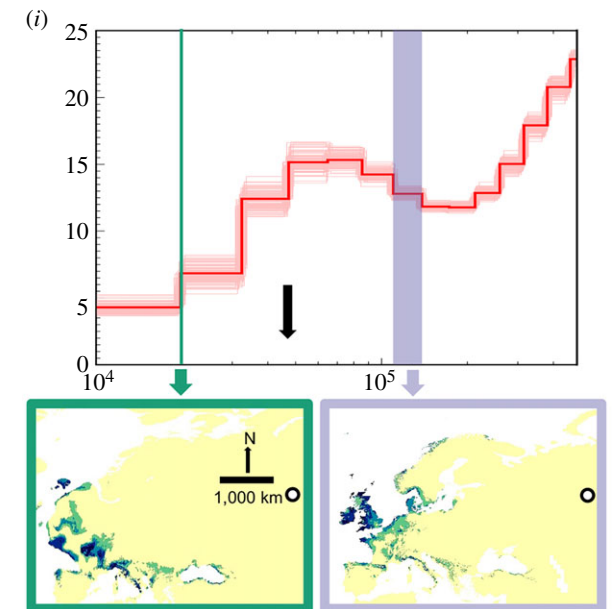
Imminent risk of extinction in the wild

Bat biology dictates species response

- Whole genome analyses of 12 bat genomes using PSMC method
- Frugivores susceptible to global warming
- Large insectivores generally have a low effective population size
- Most bats have entered Holocene with low genetic diversity



Pteropus alecto 🍌

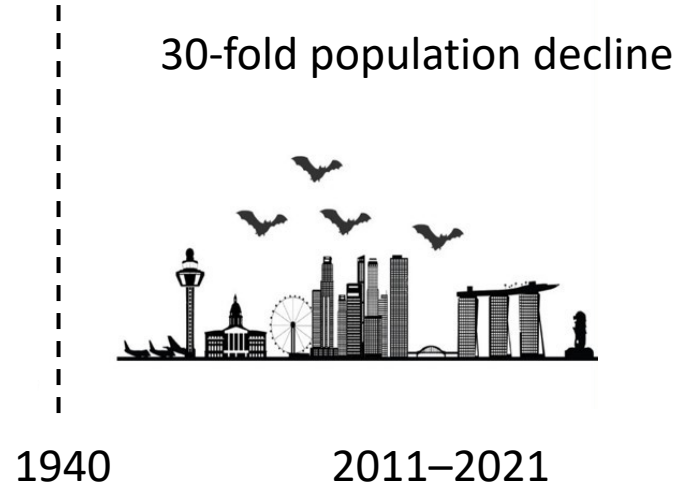
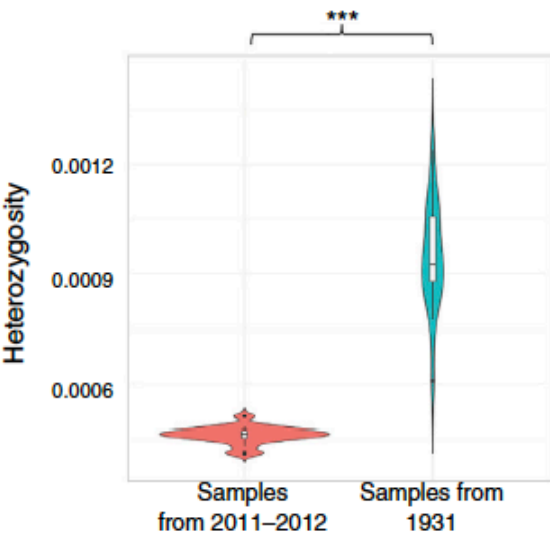


Myotis brandtii 🦋

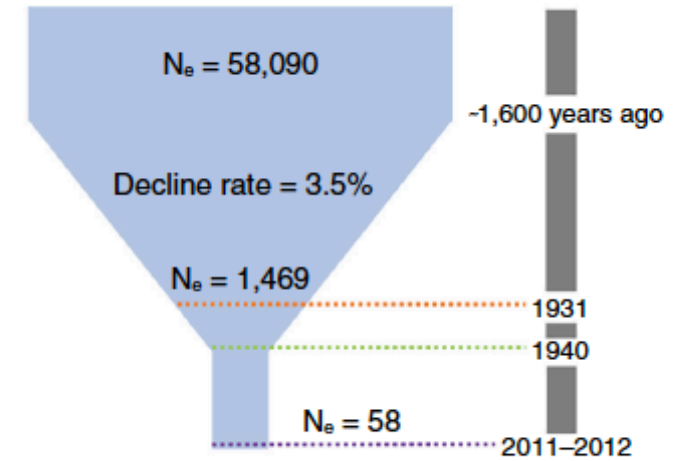
Anthropocene decline in common species



Sunda fruit bat

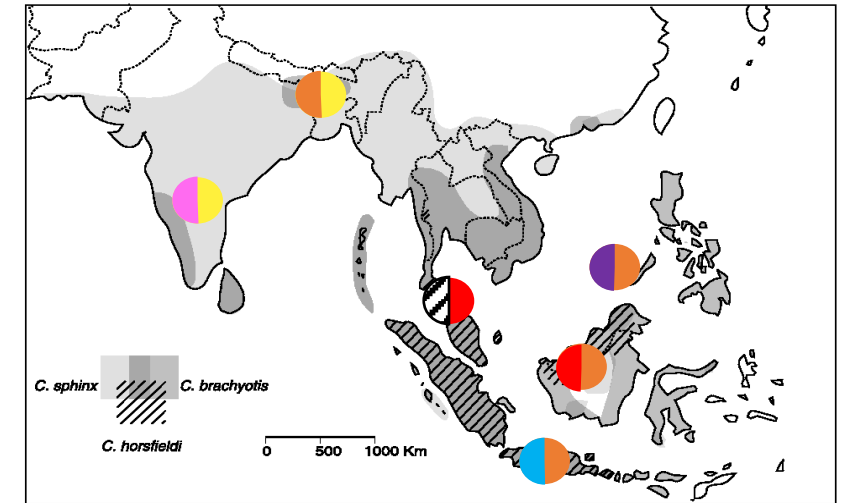
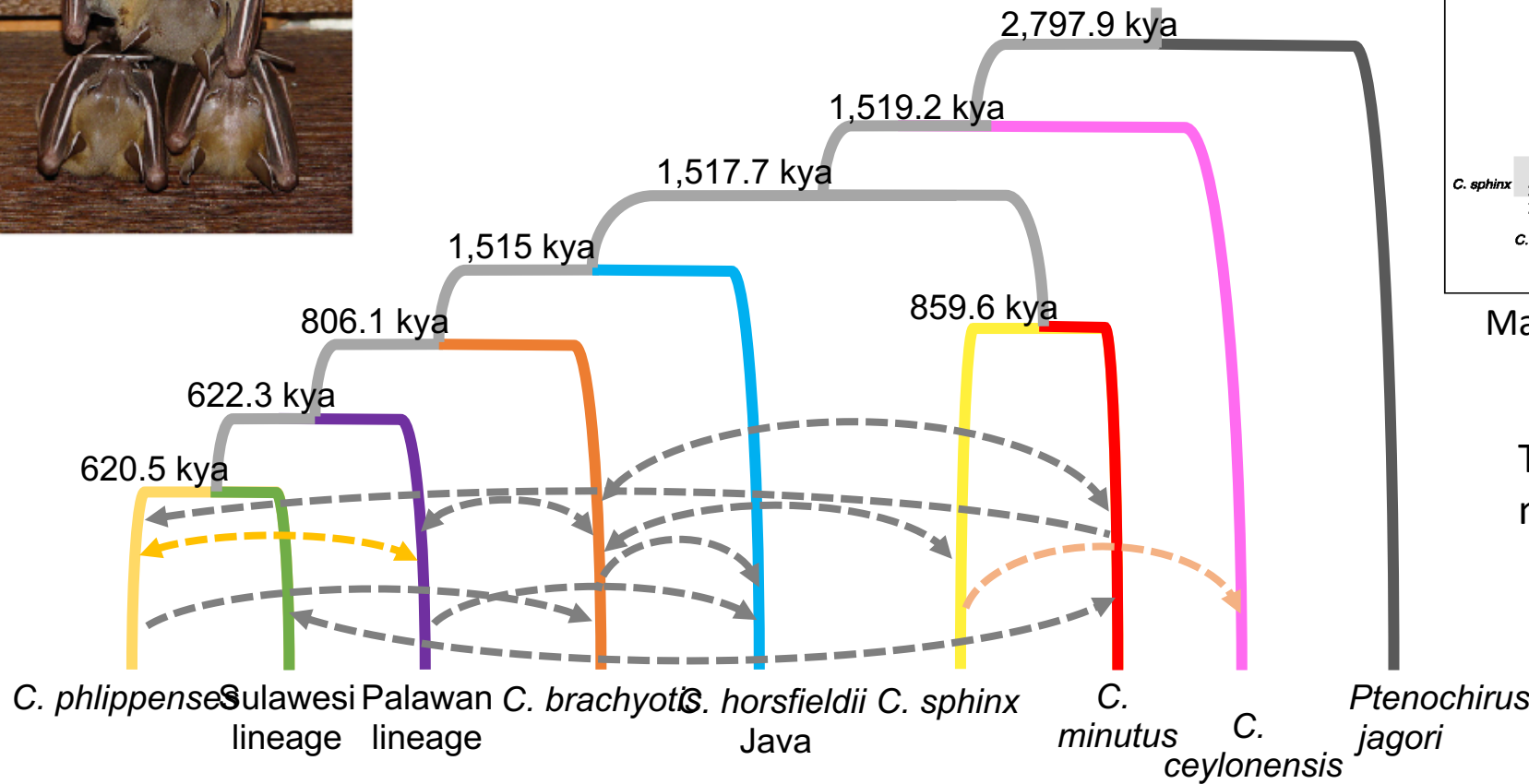


30-fold population decline



Target enrichment, 1184 loci, ~1.5 million base pairs of DNA

Widespread introgression across islands



Map modified from Campbell et al. 2004

Target enrichment, 1184 loci, ~1.5 million base pairs of DNA

G-PhoCS: 482 unlinked, neutral, non-recombining loci, ~600,000 bp of DNA sequence; only mean value denoted in the figure

Challenges and solutions

- Major challenge: procuring samples from other countries.
- Solutions:
 - Using historic samples from museum collections
 - Improve exchange of samples between research institutes across participating nations.

Thank you