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
Genome sequencing initiatives at NUS

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

Photos courtesy Simon J Tonge, Ayuwat Jearwattanakanok, Natthaphat Chotjuckdikul, JackF
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

Recent Bottleneck and continuing decline

Incidences of ghost introgression possibly with Cuban crocodiles

Imminent risk of extinction in the wild

Chattopadhyay et al. 2019, Molecular Ecology
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
Anthropocene decline in common species

Chattopadhyay et al. 2019, Current Biology

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

Sunda fruit bat
Widespread introgression across islands

C. phippenses
Sulawesi lineage
620.5 kya
622.3 kya
1,515 kya
806.1 kya
622.3 kya
C. horsfieldii
Java
1,517.7 kya
859.6 kya
2,797.9 kya
1,519.2 kya
C. sphinx
859.6 kya
1,517.7 kya
1,519.2 kya
1,515 kya
G-PhoCS: 482 unlinked, neutral, non-recombining loci, ~600,000 bp of DNA sequence; only mean value denoted in the figure

C. brachyotis
Palawan lineage
1,517.7 kya
859.6 kya
2,797.9 kya
1,519.2 kya
C. minutus
Ceylonensis

1,515 kya
859.6 kya
2,797.9 kya
1,519.2 kya
C. sphinx
859.6 kya
1,517.7 kya
1,519.2 kya
1,515 kya
G-PhoCS: 482 unlinked, neutral, non-recombining loci, ~600,000 bp of DNA sequence; only mean value denoted in the figure

Map modified from Campbell et al. 2004

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