



Applications of In-Solution DNA Hybridization Capture at the Center for Conservation and Evolutionary Genetics





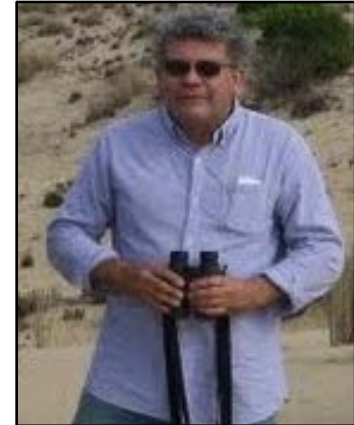
Applications of In-Solution DNA Hybridization Capture at the Center for Conservation and Evolutionary Genetics



CCEG laboratory @NZP



Robert Fleischer



Jesús Maldonado



Applications of In-Solution DNA Hybridization Capture at the Center for Conservation and Evolutionary Genetics

Applications

- Ancient DNA (aDNA)
- Population/Conservation genomics
- Species ID
 - Environmental DNA (eDNA)
 - Disease ecology (pathogen detection)
 - Dietary analysis
- Noninvasive DNA

Molecular Markers

- UCEs
- Mitochondrial genomes
- Custom SNPs
- Specific genes of interest
- Exon capture



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Ancient DNA (aDNA)

Benefits:

- More cost/time efficient than PCR
- Increase proportion of endogenous DNA
- Heterospecific capture possible
- Multiplex multiple samples/dilute probes

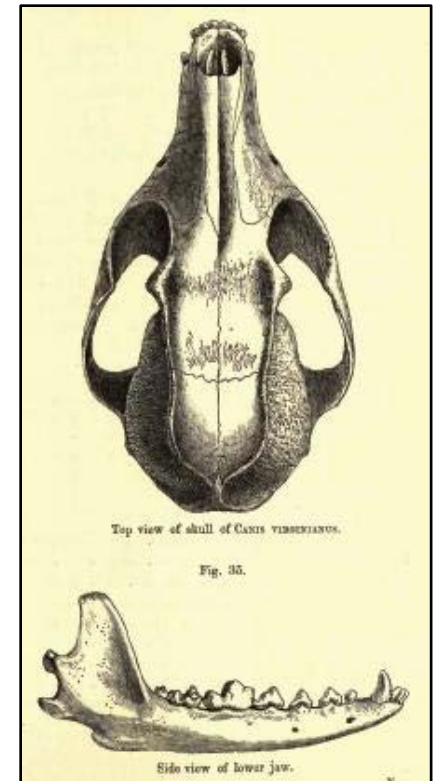




Ancient DNA (aDNA)

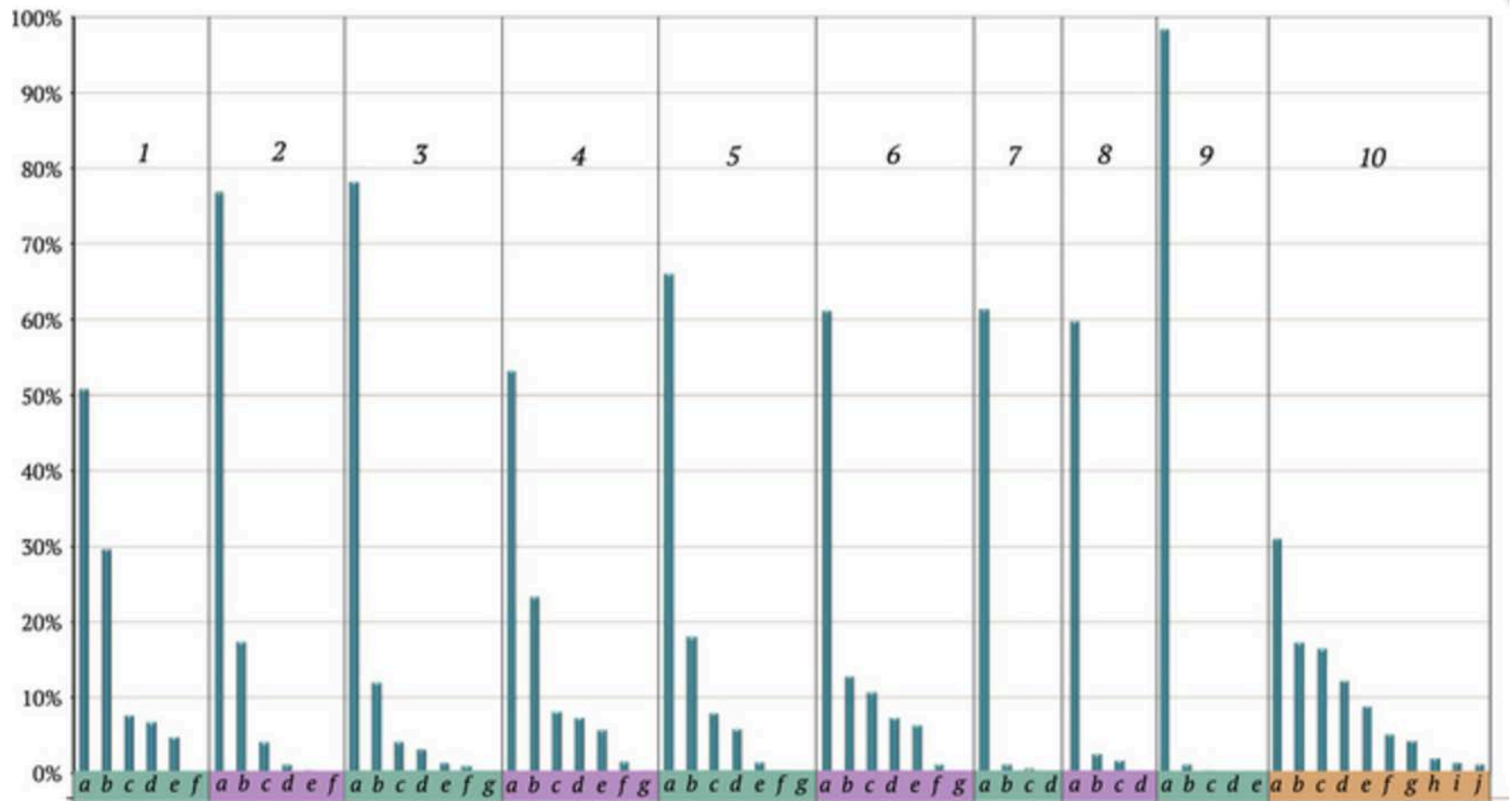
Some considerations for aDNA:

- Minimize contamination (dedicated clean lab)
- Dual indexing recommended
- **Can** optimize multiplex
- Lower hybridization temperature
- Minimize PCR cycles; pool multiple rxns
- Increase sequencing effort





Ancient DNA (aDNA)



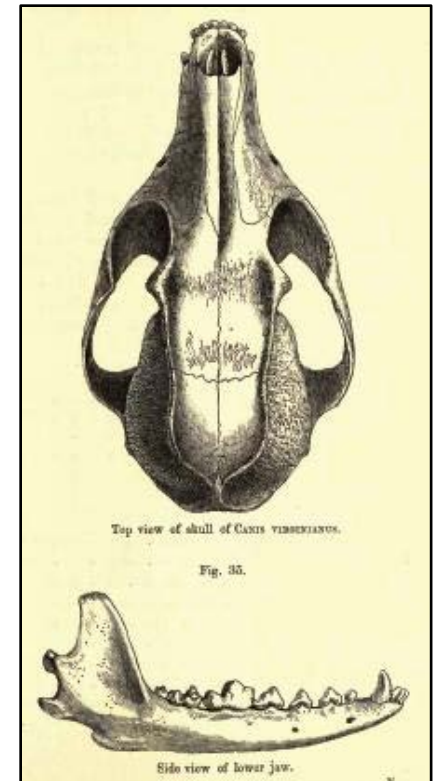
Hawkins et al. (2015) Mol. Ecol. Res.



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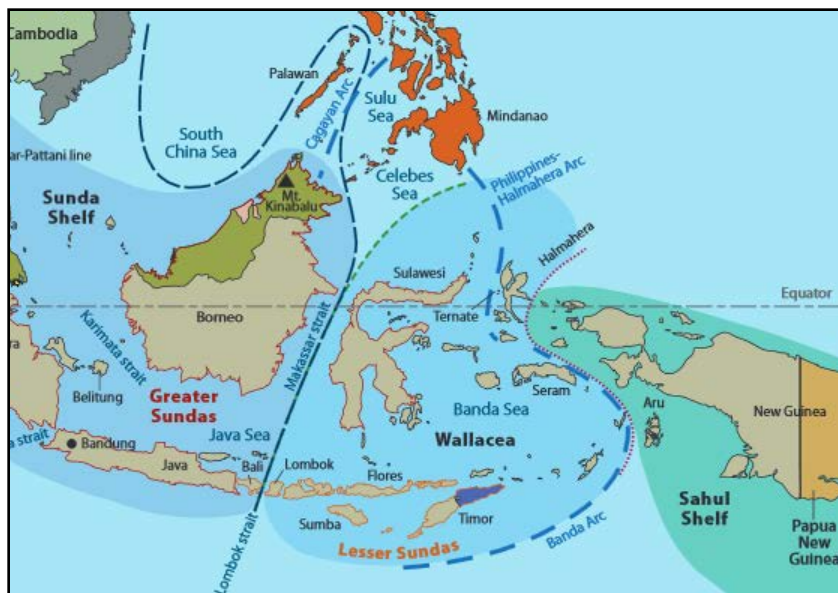
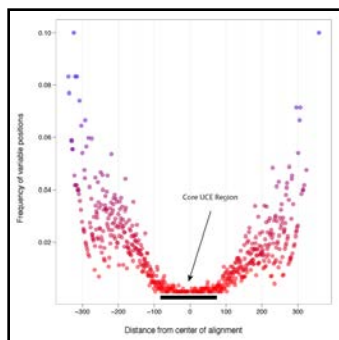




Project: Phylogenomics of the Phalangeridae

Markers: UCEs and Mitogenomes from museum specimens

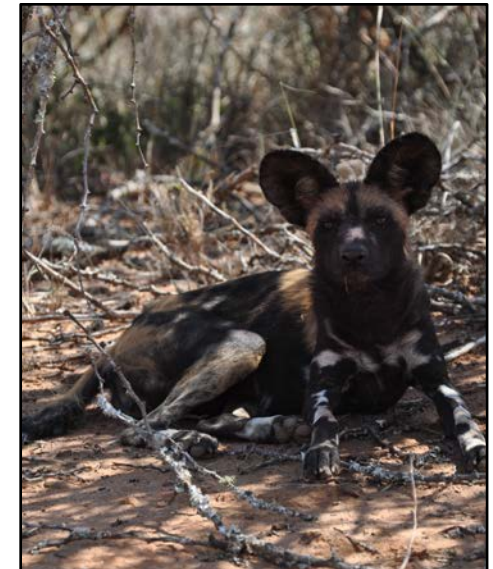
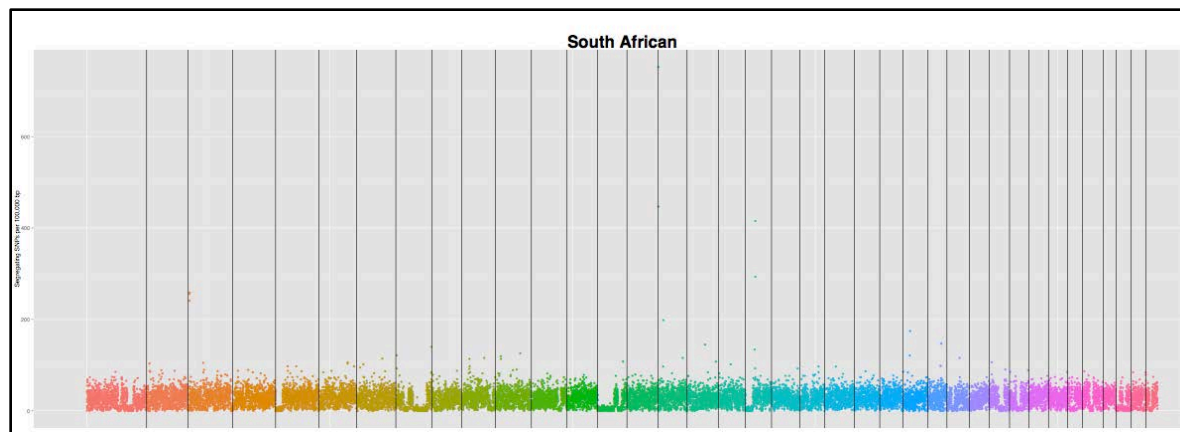
Lillian Parker, Kristofer Helgen, Jesús Maldonado





Design custom SNPs

- Use **genome reference** to design SNP bait set
 - Use heterozygous sites in single genome or multiple individuals
- Can also design probes from **RADseq data**
- Custom script by Michael Campana (CampanaM@si.edu)



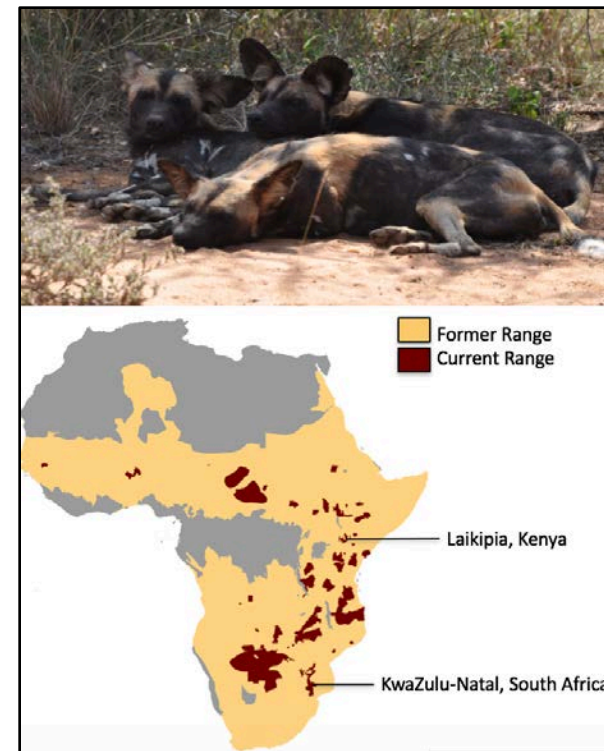


Project: Population Genomics of African Wild Dogs

Markers: Single Nucleotide Polymorphisms

Michael Campana, Robert Fleischer, Kristofer Helgen, et al.

- Sequenced genomes for 2 individuals
- Designed custom SNP baits (~20K) from genome alignment
- 32 extant Kenyan wild dogs
- 17 historic wild dogs





Species Detection

Applications:

- Diet analysis
- Disease ecology (ectoparasite, host and pathogens)
- Environmental DNA (metagenomics)



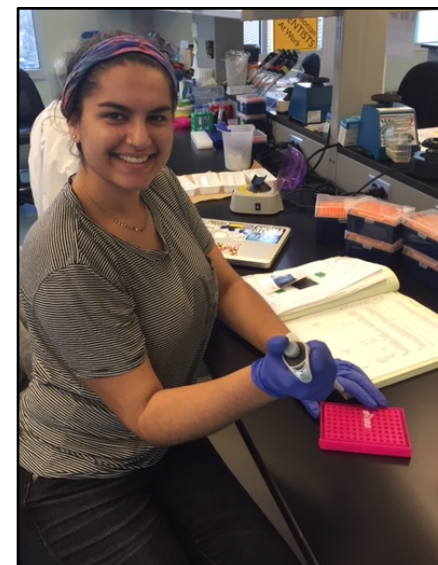
Project: Recreating Paleoecosystems using eDNA from Archeological Sites

Markers: Mitochondrial genes (COI, Cytb)



Sabrina Shirazi, Courtney Hofman, Torben Rick and Jesús Maldonado

- Baits designed from mtDNA sequences of birds and mammals
- Extract DNA from soil at archeological sites
- Applying method to samples from Santa Cruz Island





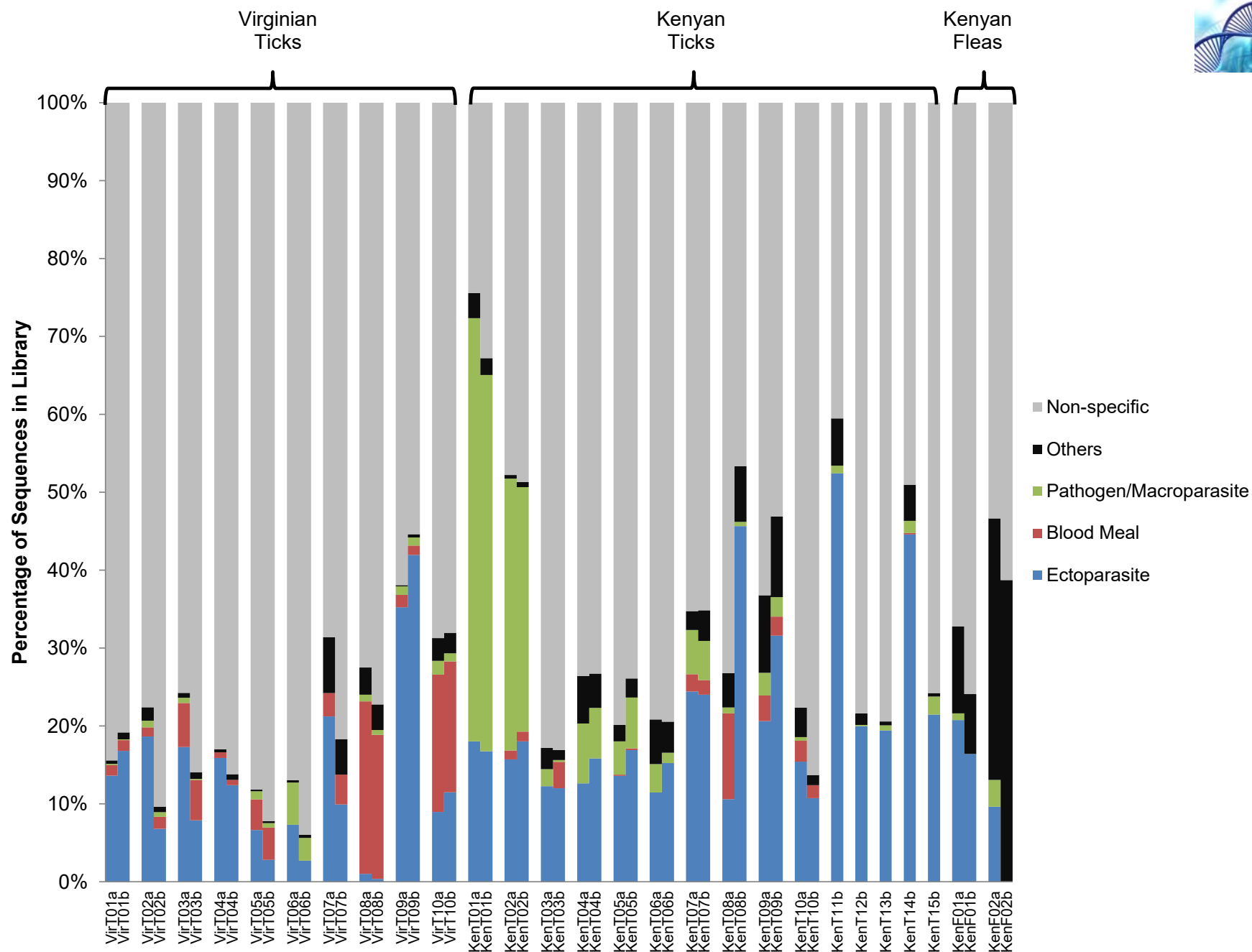
Project: EctoBaits

Markers: Published genes for species ID

Michael Campana, Lauren Henson, Jesús Maldonado, Robert Fleisher et al.

- DNA extracted from ectoparasite
- Probe set with baits for **ectoparasite, blood meal, and pathogen**
- Metagenomic analysis
- Applications for disease ecology







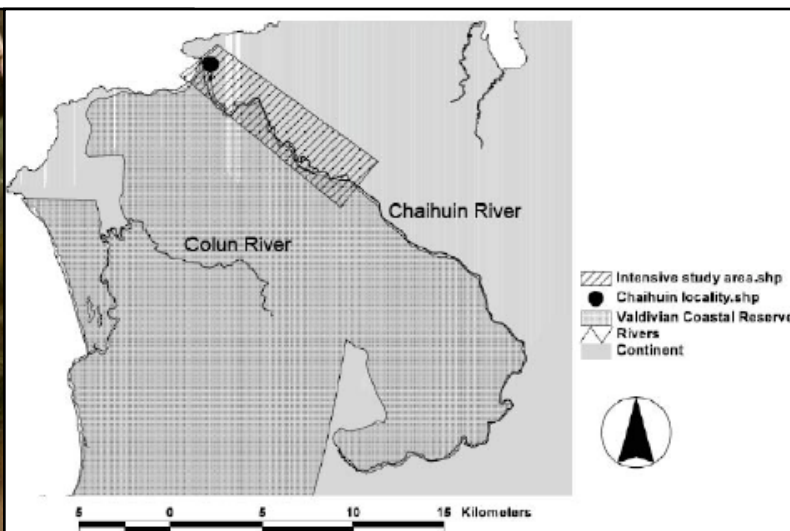
Project: Assessing the impact of invasive mink on Southern river otters in Chile (Noninvasive DNA)

Markers: Mitochondrial genomes



Lilly Parker, Jesús Maldonado, et al.

- Introduced mink and endangered otter, habitat overlap
- Designing baits to capture mitochondrial genomes for all *Lontra* species
- Apply capture technique to DNA extracted from scats





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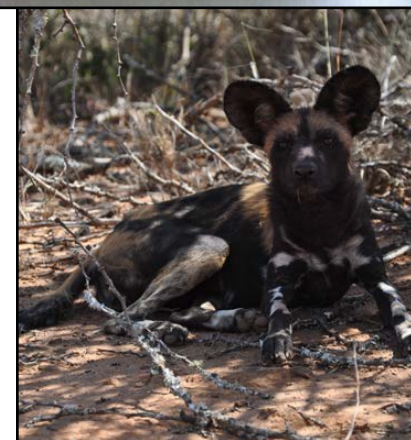
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Applications

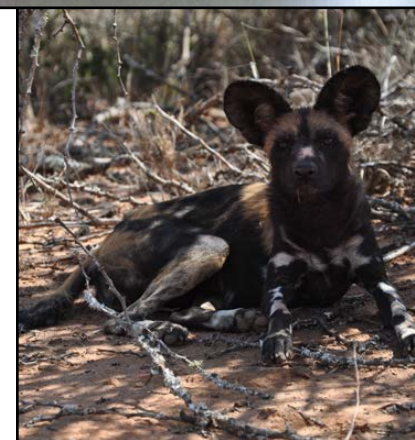
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Thank you! Questions?



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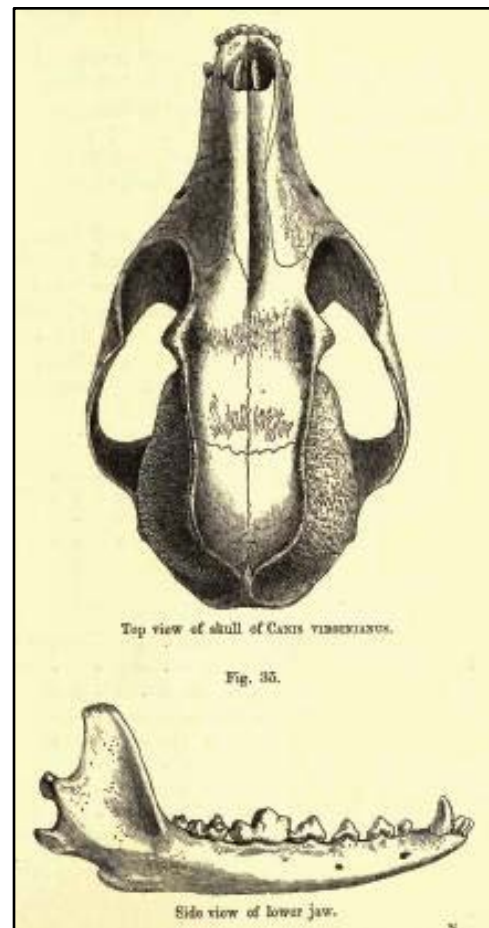


Project: Phylogenomics of *Urocyon cinereoargenteus*

Markers: UCEs and Mitogenomes from museum specimens

Susette Castañeda Rico and Jesús Maldonado

- Range from southern Canada to Venezuela and Colombia
- 16 described subspecies
- Sample 7 subspecies and investigate history in Mexico and Central America





Project: Conservation genomics of the Mariana crow

Markers: Single Nucleotide Polymorphisms

Nandadevi Cortes-Rodriguez, Michael Campana, Robert Fleischer

- Mariana Crow found only on Guam and Rota Islands
- Conservation concern: threatened by loss of habitat and predation by brown tree snake
- Designed custom SNPs from *de novo* assembled genome
- Capture & sequence SNPs from many individuals
- Genetic diversity, population structure, sex ratios, N_e

