

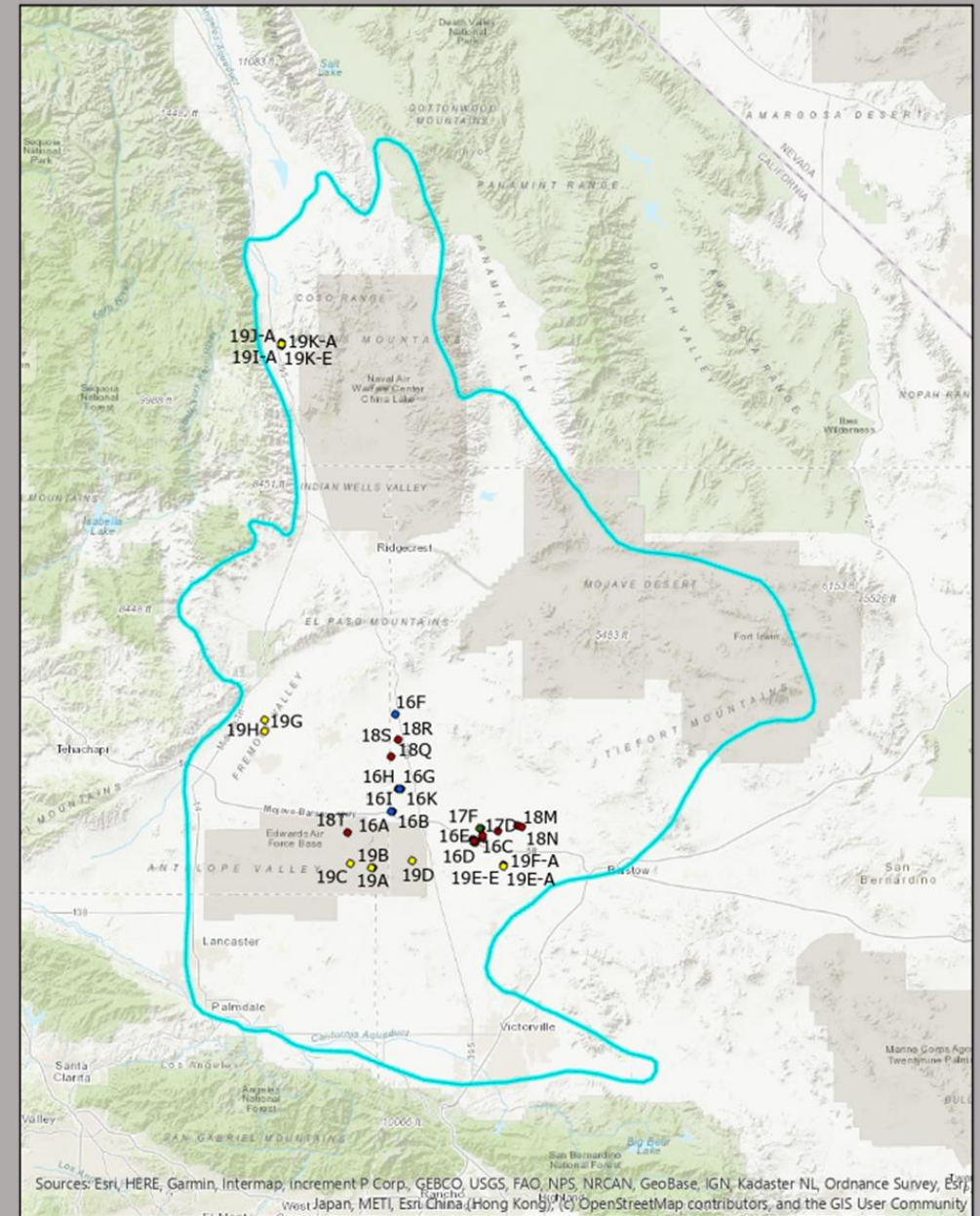


Diet Analysis using Fecal Metabarcoding for MGS: Preliminary Results

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Poop

- Samples from 61 individual MGS
- Focused on Hinkley (now called Harper Lake based on MGS Conservation Strategy) and EAFB/Bowling Alley (now called North of Kramer)
- 20 from EAFB/Bowling Alley from 2016, 2018, 2019
- 35 from Harper Lake from 2016-2019
- 2 from Cal City in 2019
- 6 from Rose Valley in 2019



Plants

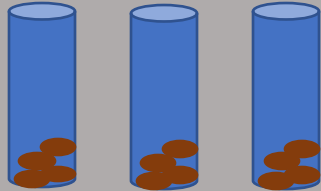


- Have to determine what plants we think they're eating
- Barbara & Erica (mostly Barbara) put together a list of possible plants from informal surveys in March & from other reports across the range
- Cody checked which plants are available in DNA barcode databases
- Obtained field samples or herbarium samples to sequence missing plants

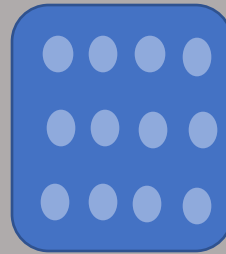
Pipettes

Sample Preparation

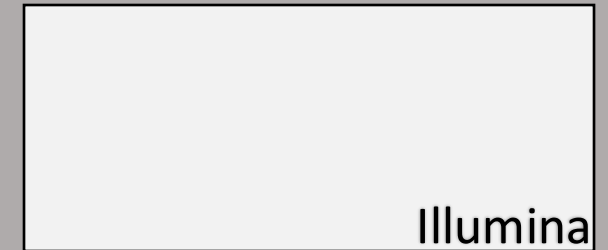
1) Buffer & Filter Samples



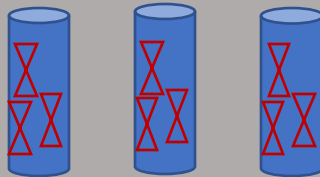
3) DNA Clean Up



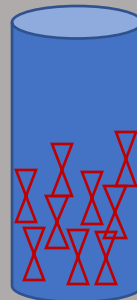
5) Sequencing



2) Cut out ITS2 region and amplify



4) Quantification & Normalization



5) Bioinformatics

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AATGCGCTTAACG  
TATGCGCTTTACG  
ATTGCGCTTAACG  
ATTCCGCTTAAGG
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Sources of Error in Fecal Metabarcoding

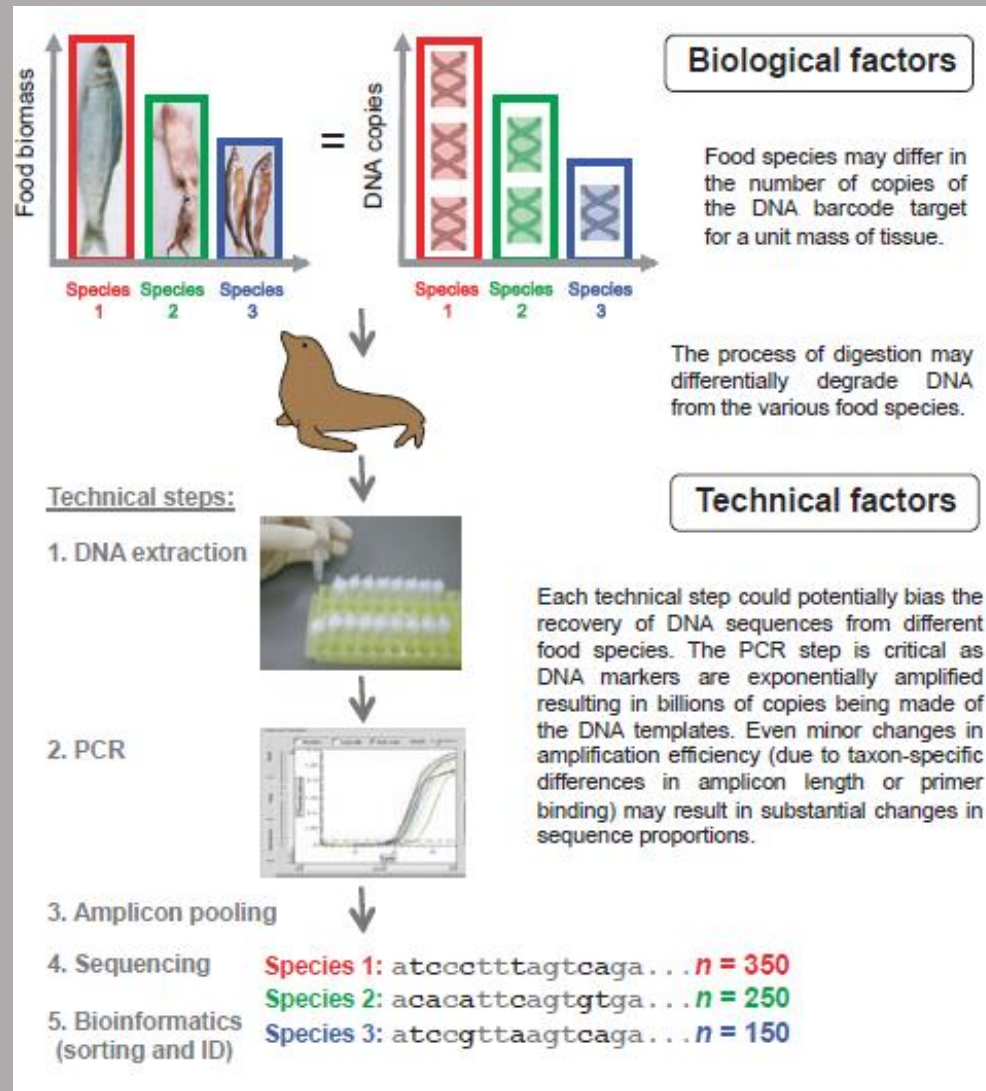


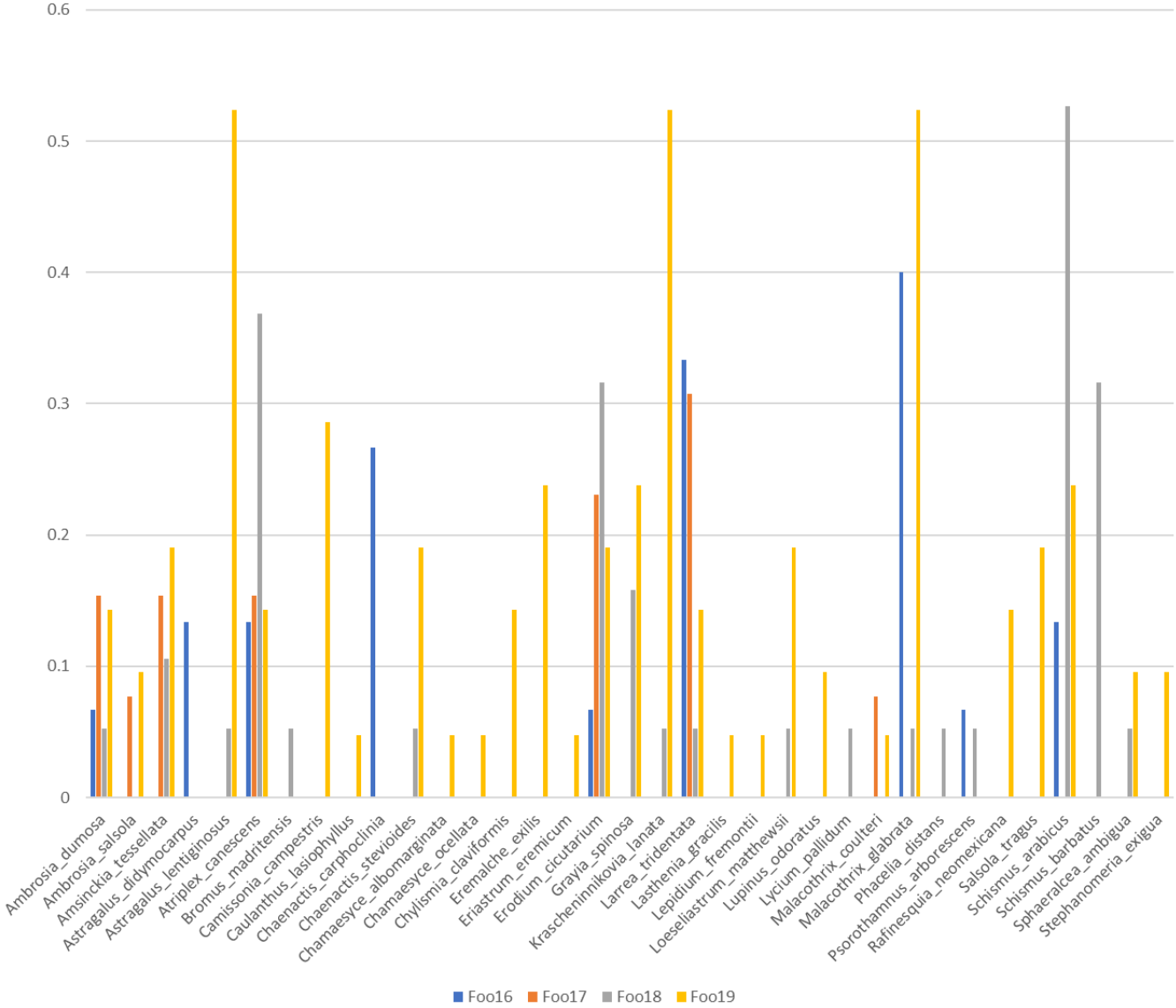
Figure 3 from Pompanon et al. 2012

Results: Fecal Sample Collection

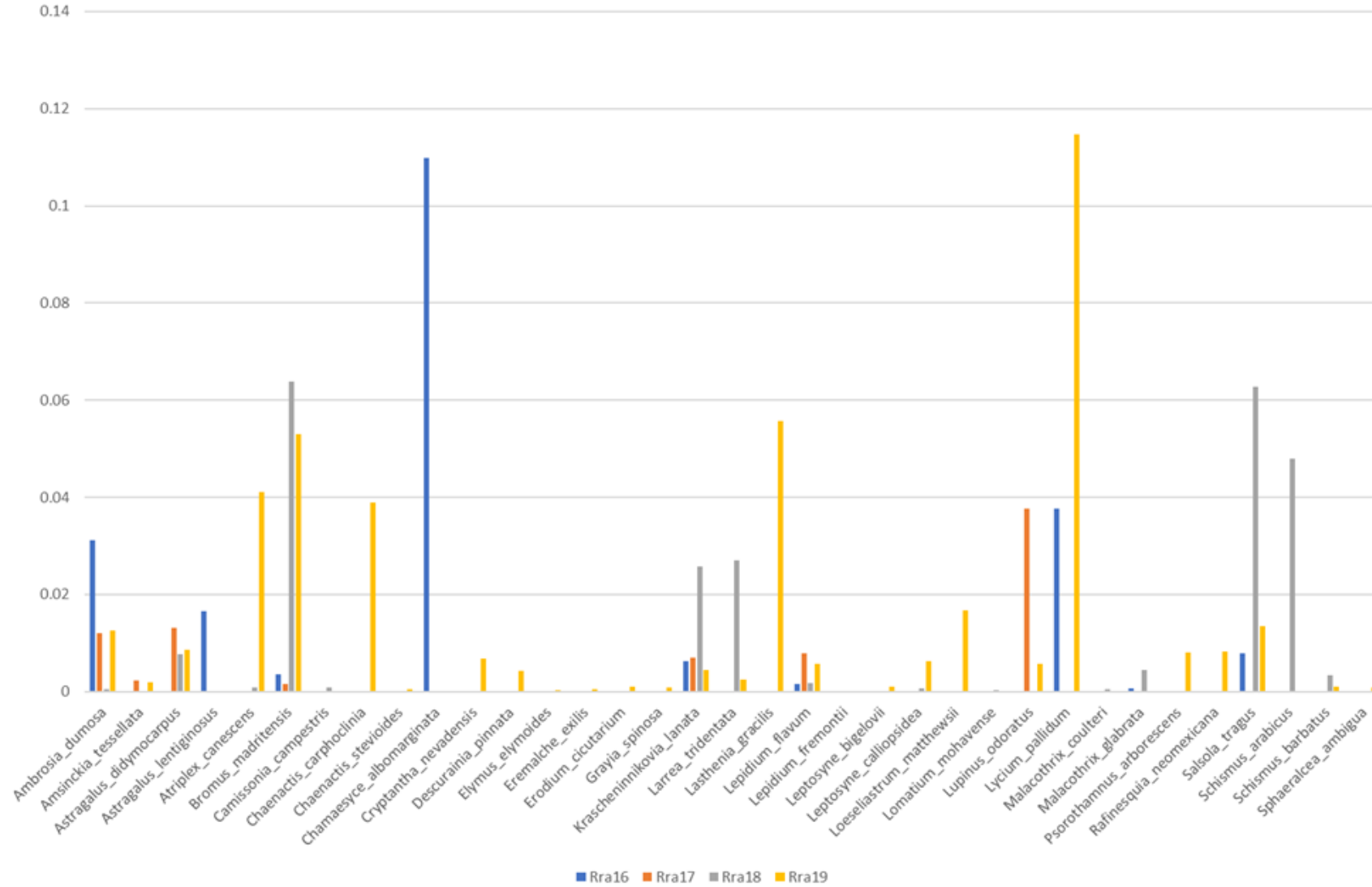
- A lot of the DNA was degraded or difficult to identify
- 8 pairs of ethanol/air dried for comparison from 2019

	Success Rate	Proportion Plant DNA	Species Richness
Air Dried	62.5%	0.46	25
Ethanol	100%	0.63	29

Frequency Of Occurrence



Relative Read Abundance



Dry vs. Wet

- Analysis of Similarity (how similar are groups to each other?)

Dry Samples (N = 16)

Wet Samples (N = 25)

Analysis of similarity = 0.1304

There is some difference between dry and wet years in relative read abundance of certain diet items