Who's that Pokémoth?
Barcoding Micro-Moths

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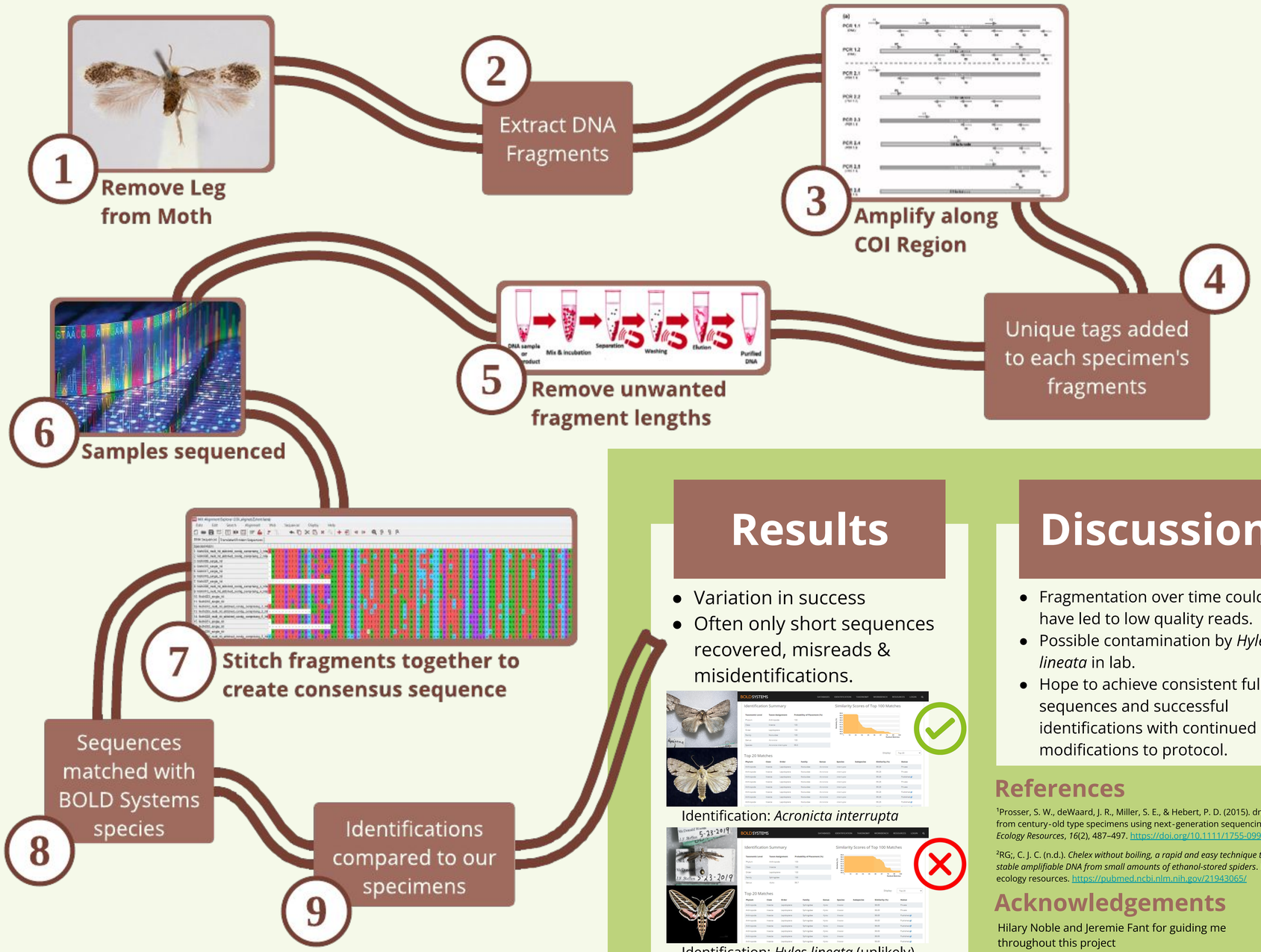
Introduction

- Mcdonald Woods undergoing restoration after severe degradation.
- Surveys of changing biodiversity have continued throughout recovery.
  - Incr. species of moths, Incr. woodland species diversity.
- Often, moths are too small or physically similar to other moths to differentiate species.
- Genetic information can be used to help identify tricky specimens.
  - COI Region, ~658 bp, site w/ low intraspecies diversity & high interspecies diversity.
  - DNA degraded from preservative.

Objective

- Identity the 500+ individuals brought to CBG to species level without destroying the fragile moths.
  - Hope to preserve individual as museum specimens for further comparison to other unidentified moths.

Methods



Results

- Variation in success
- Often only short sequences recovered, misreads & misidentifications.

Identification: *Acronicta interrupta*

Identification: *Hyles lineata* (unlikely)

Discussion

- Fragmentation over time could have led to low quality reads.
- Possible contamination by *Hyles lineata* in lab.
- Hope to achieve consistent full sequences and successful identifications with continued modifications to protocol.

References

[1]Prosser, S. W., deWaard, J. R., Miller, S. E., & Hebert, P. D. (2015). dna barcodes from century-old type specimens using next-generation sequencing. *Molecular Ecology Resources*, *16*(2), 487–497. https://doi.org/10.1111/1755-0998.12474

[2]RG;, C. J. C. (n.d.). *Chelex without boiling, a rapid and easy technique to obtain stable amplifiable DNA from small amounts of ethanol-stored spiders*. Molecular ecology resources. https://pubmed.ncbi.nlm.nih.gov/21943065/

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