

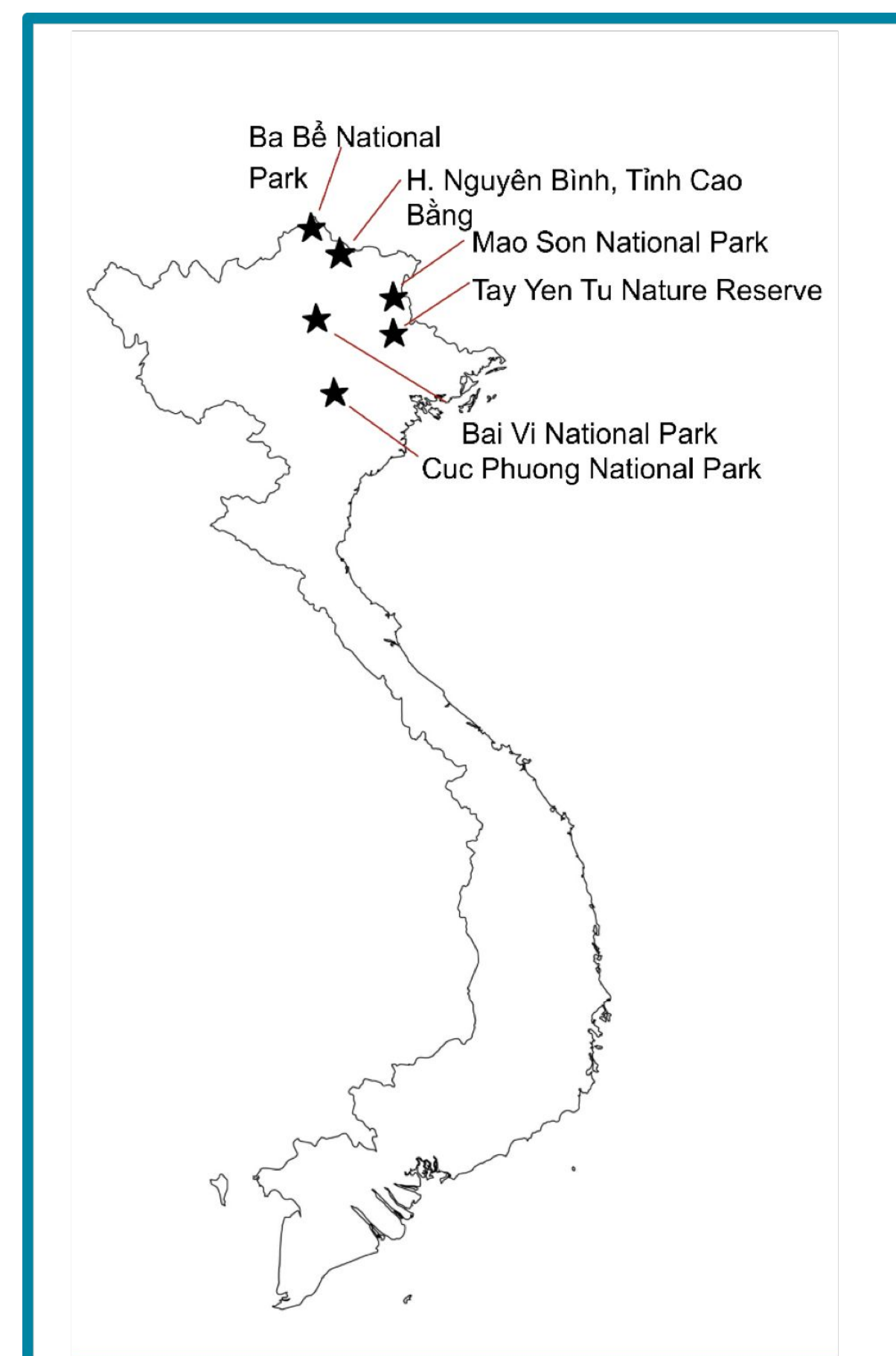


DNA BARCODING OF VIETNAMESE MAYFLIES

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OVERVIEW

The purpose of this project will be to investigate the genetic diversity of mayflies collected in Vietnam during 2016 and 2018 by the Ogden Lab. The generated data will contribute to the Barcoding of Life Data System (BOLD).



METHODS

- DNA Extraction
- PCR Amplification of CO1 Gene
 - Primer Design
- DNA Sequencing
- Submit and analyze at BOLD



RESULTS

Specimen Identifier	GenBank BLASTN Results	% Match	Accession Number
455	Heptageniidae, Paegniodes	92.28%	HM004123.1
460	Heptageniidae Anapos	85.84%	HG935066.1
461	Baetidae, Baetis	83.71%	KY262182.1
465	Heptageniidae, Thalerosphyrus	84.93%	MH108086.1
466	Metretopodidae, Metretopus	87.23%	KJ675306.1
467	Siphlaenigmatidae, Siphlaenigma	86.80%	MF668554.1
469	Ephemeridae, Ephemera	87.99%	MK951659.1

Table 1 - GenBank BLASTN results show the closest match for potential Family and Genus identification.

BACKGROUND

The uniqueness of an organism's DNA allows for species level identification via DNA barcoding. In BOLD there are currently 26,832 records with sequences, forming 2,203 BINs, with specimens from 71 countries, deposited in 83 institutions. However, there is currently no DNA data for Vietnamese Mayflies. Mayflies that were collected will have their DNA sequenced and the data will be contributed to BOLD.



FUNDING

- NSF S-STEM Grant
- NSF EAGER Grant
- UVU URSCA Grant



REFERENCES



CONCLUSION/FUTURE WORK

A GenBank BLASTN result hypothesized the Families and Genera listed in Table 1. For future work more genes (12S, 16S, 18S, 28S, and H3) will be sequenced to increase the identification data. Additionally, increased taxonomic sampling is needed for phylogenetic analysis.