Syrphing the wind: Long-distance seasonal migration in Eupeodes americanus hoverflies in eastern North America

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Co-authors:

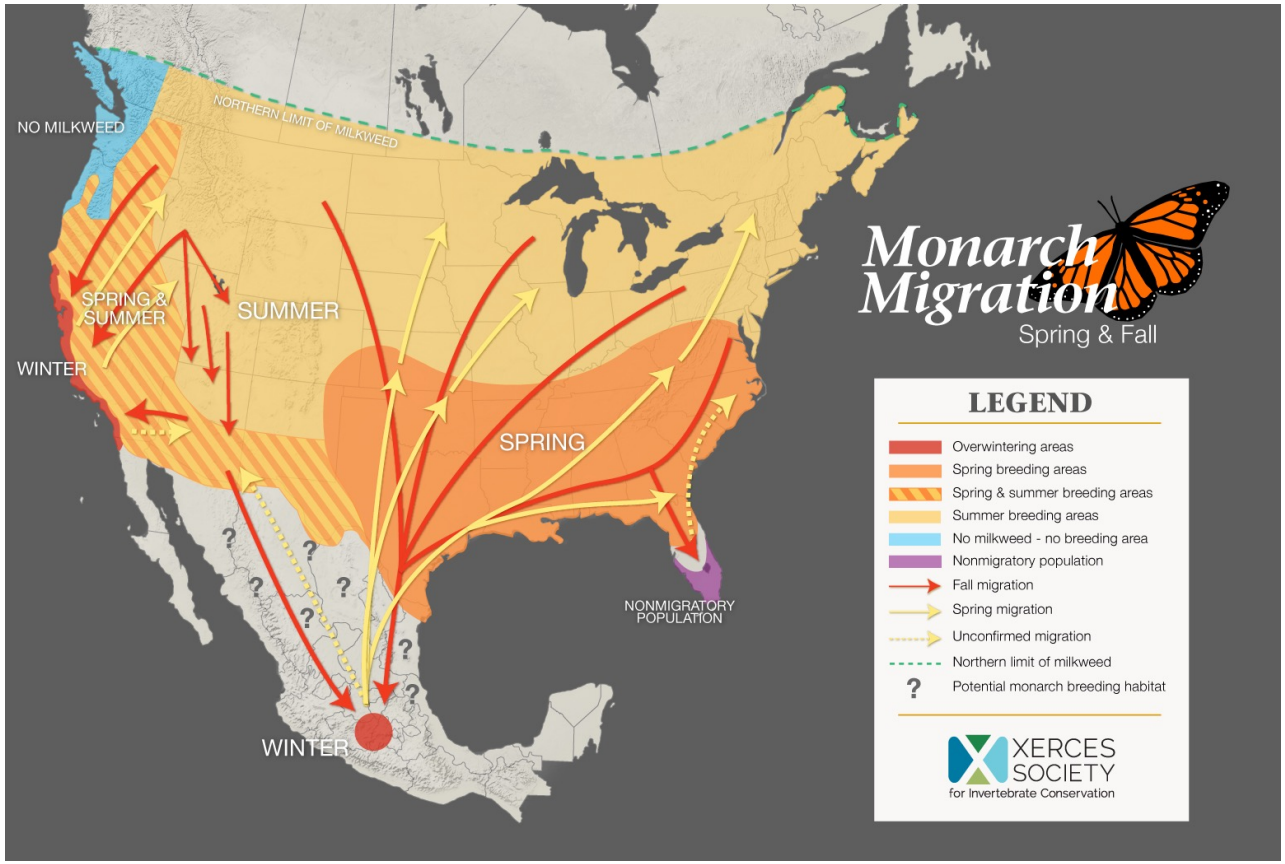
Dr. Pedro Rodrigues, Dr. Kieth Hobson, Dr. Doris Lagos-Kutz, Dr. Bill Snyder

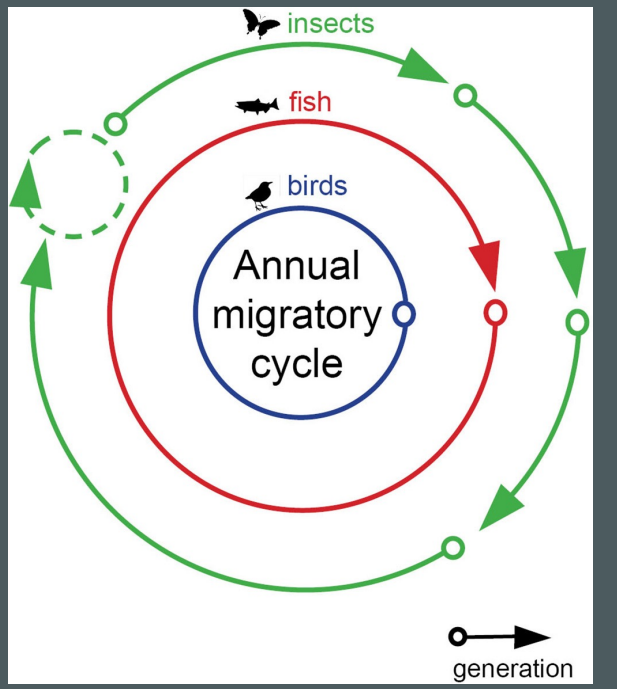
Blue sky: @clemlab

Email: csclem2@ilstu.edu



Insect Migration – what is it?





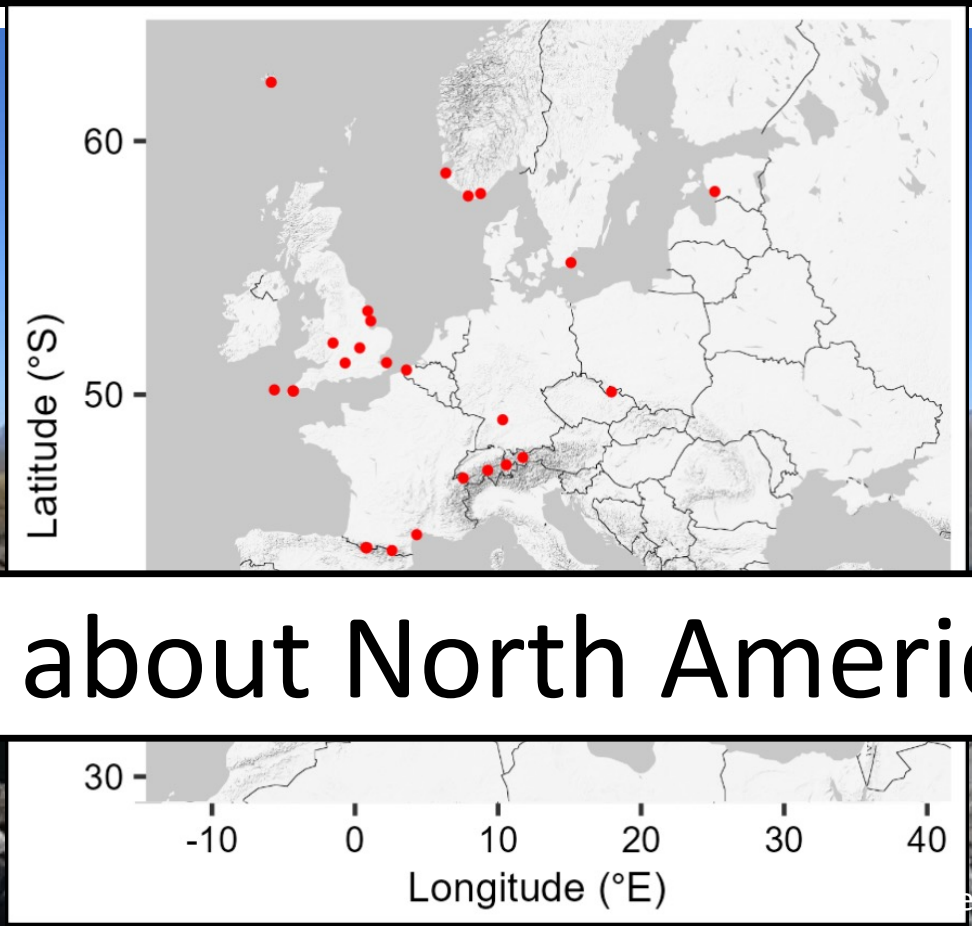
Satterfield et al. 2020, *Front Ecol Environ*

Hover Fly Migration



Episyrphus balteatus







But what about North America?

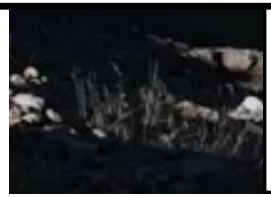
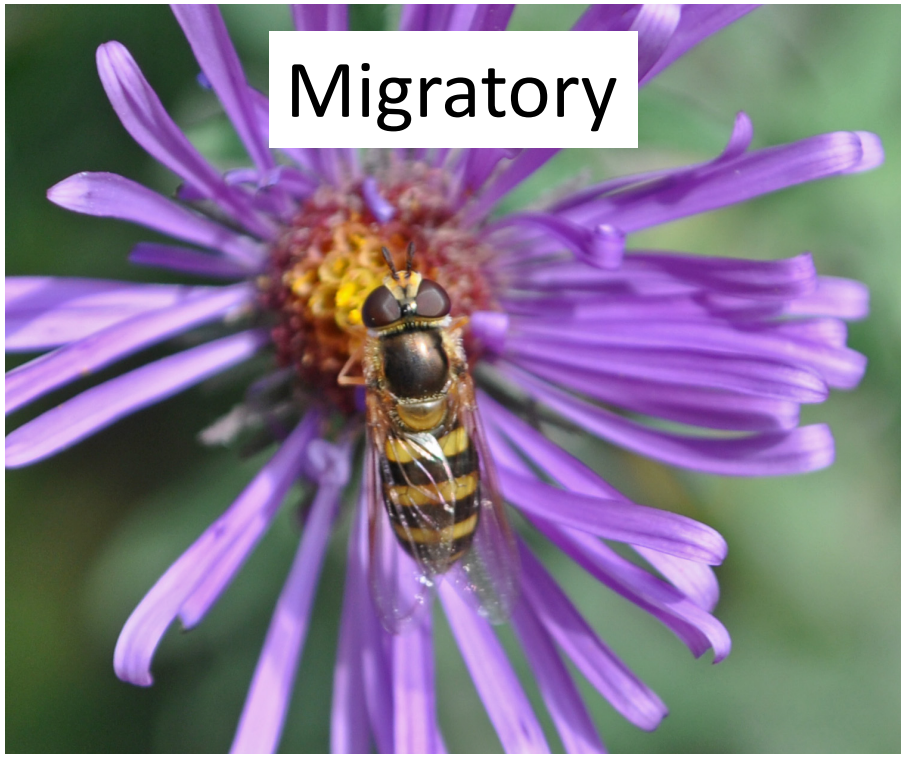


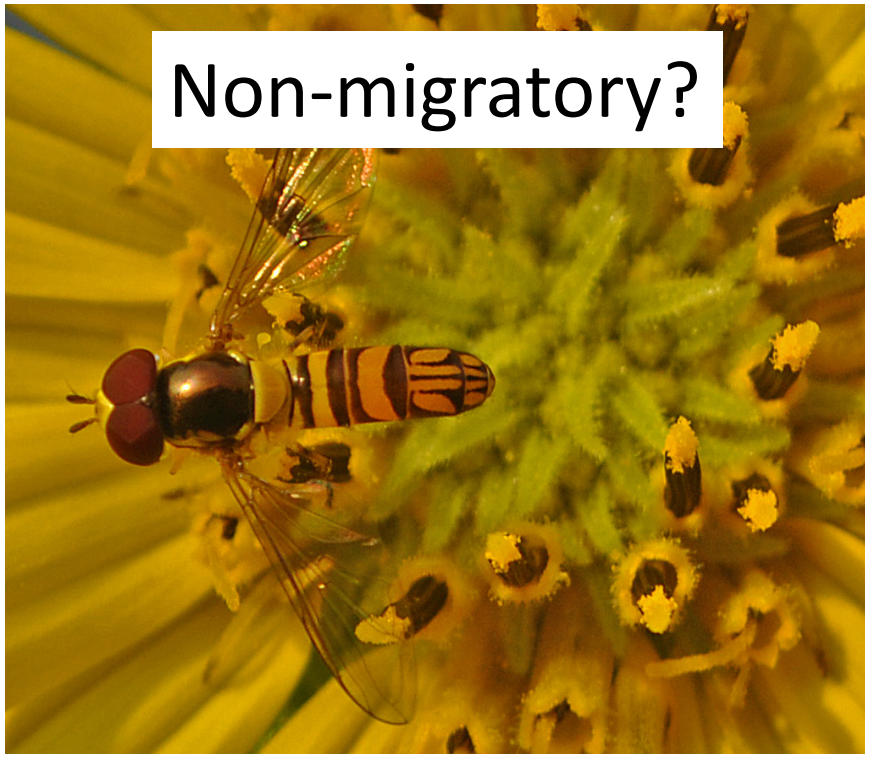
Photo credit: Will Hawkes

Reynolds, Clem et al. 2024, *Ecological Entomology*

The Study System



Eupeodes americanus



Allograpta obliqua

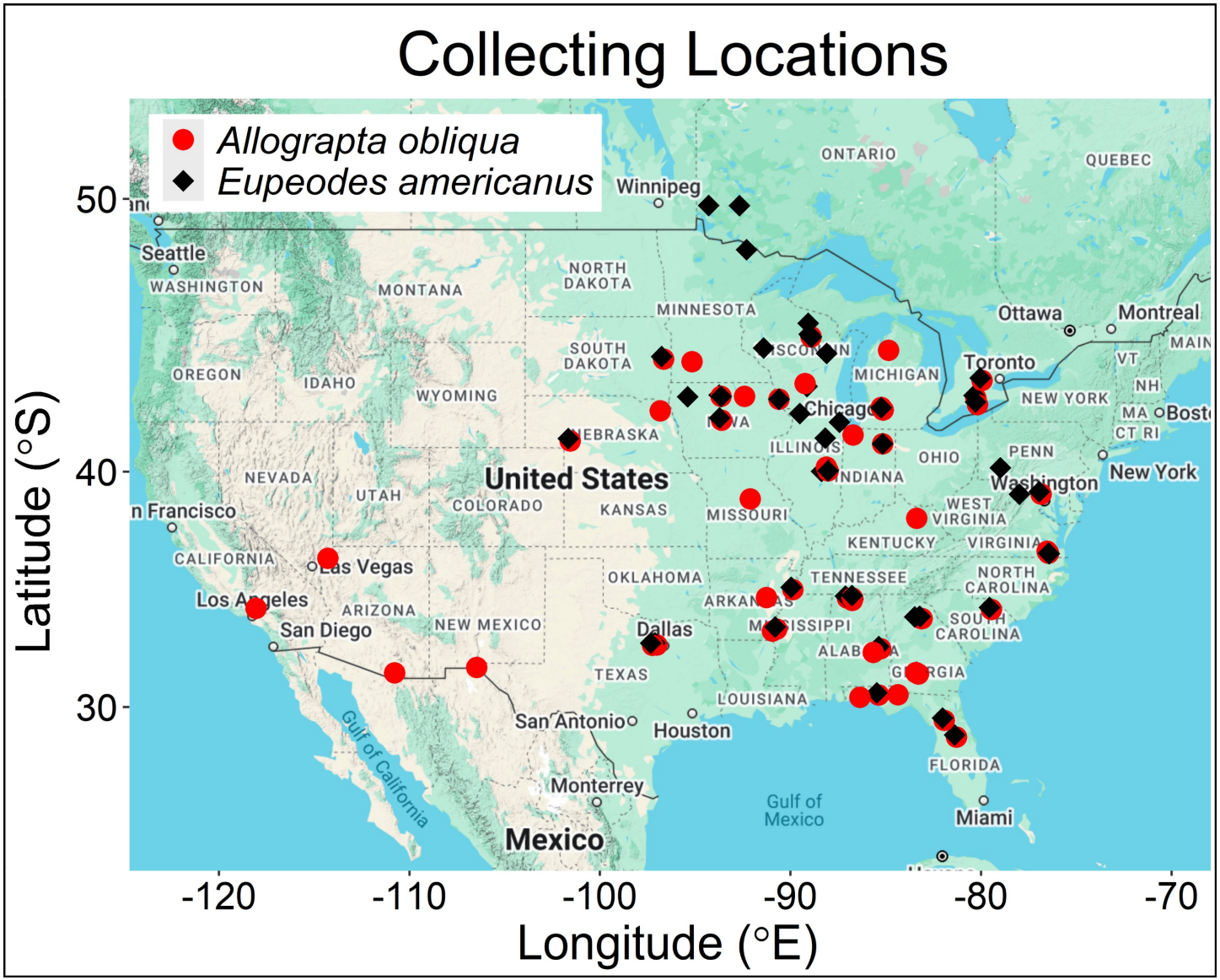
Clem et al. 2022, *Ecological Monographs*

Objectives



1. Use isotope analyses (δ^2H) to model natal origins of individuals collected in the southeastern USA

2. Apply population genomics (RADseq) and microbial community assessments (16S rRNA) to examine population connectivity across North America

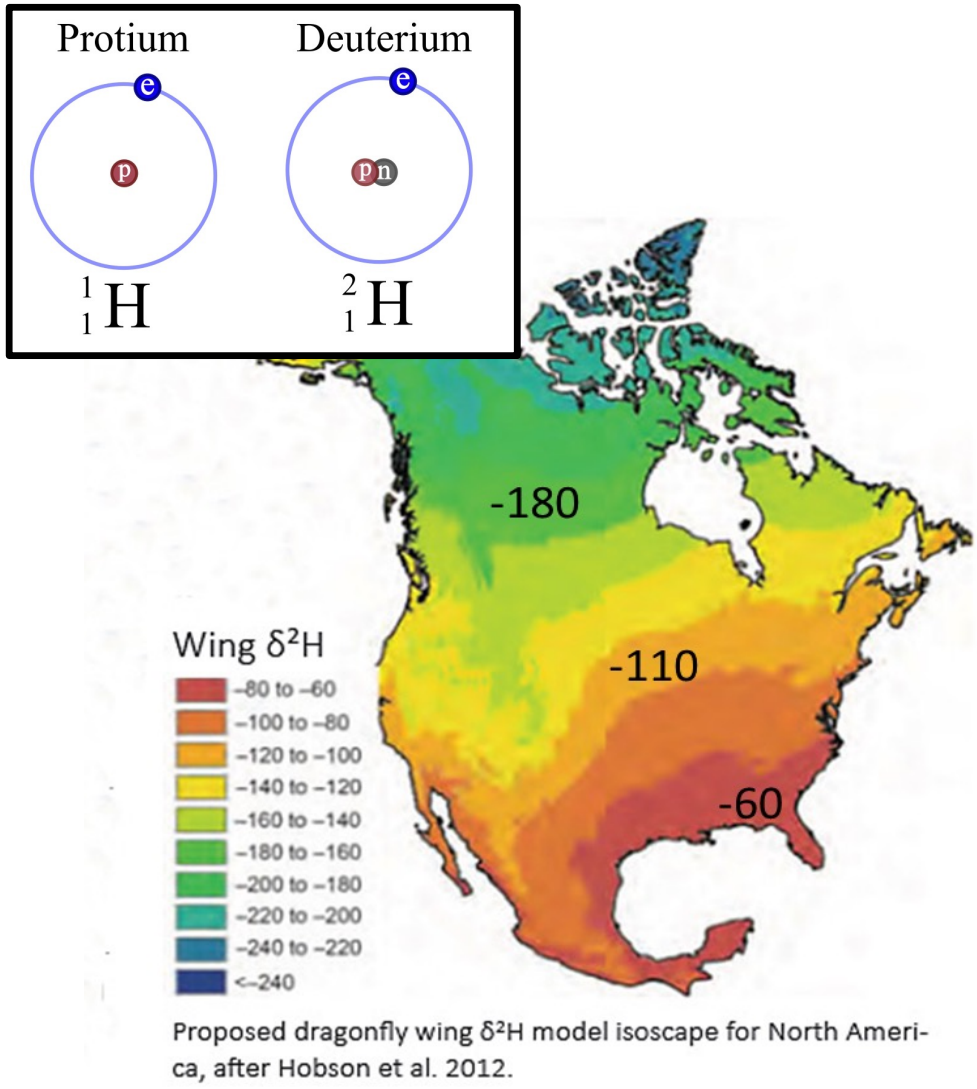


Total specimens:
322 *Allograpta obliqua*
347 *Eupeodes americanus*



Migration and Isotopes

- Hydrogen isotope ratios (δ^2H) vary geographically
- Are permanently fixed in wing and leg chitin after development
- Reflect insect natal origin

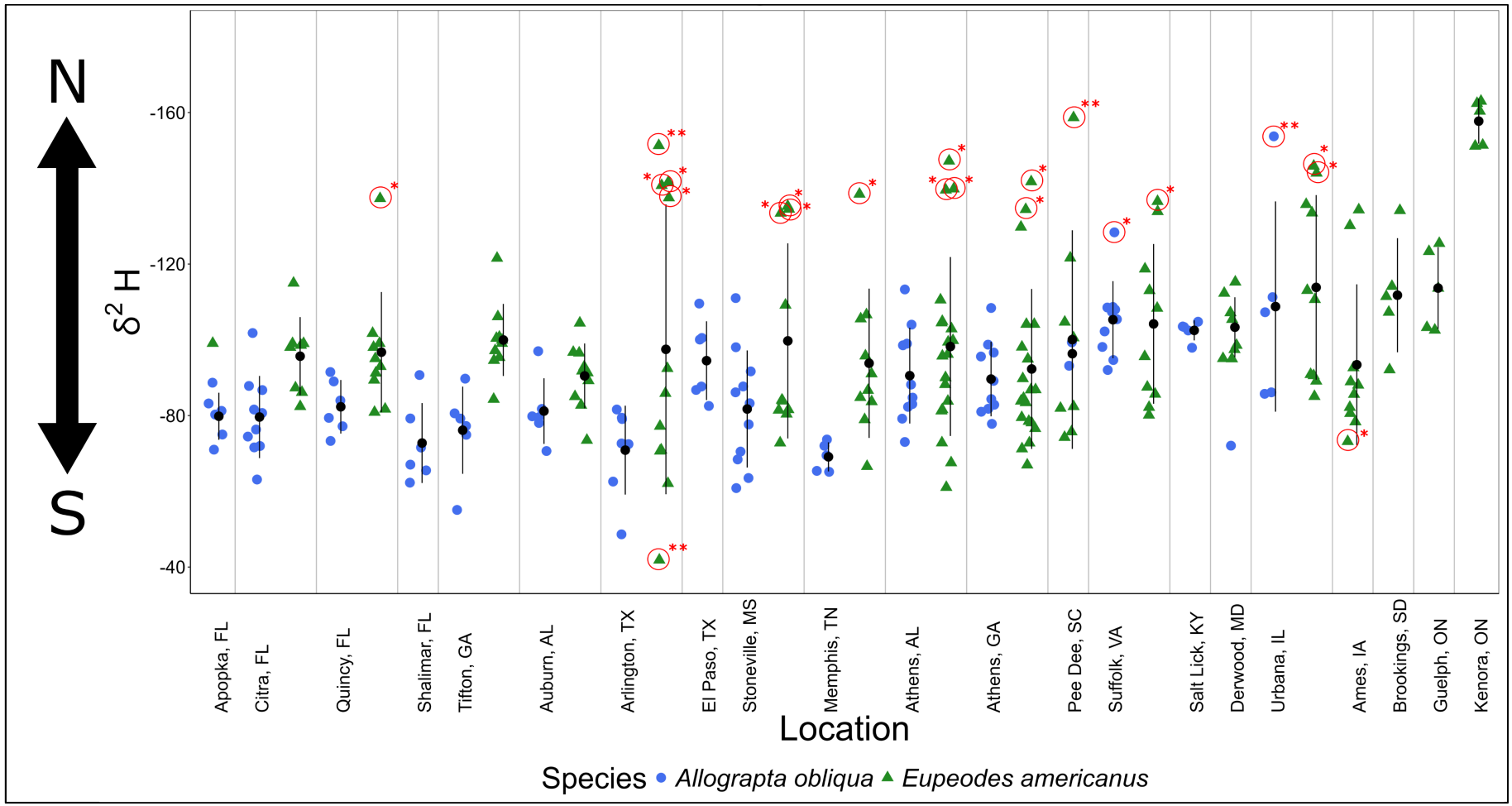


Proposed dragonfly wing δ^2H model isoscape for North America, after Hobson et al. 2012.

Hobson et al. 2012, *MEE*

Objective 1

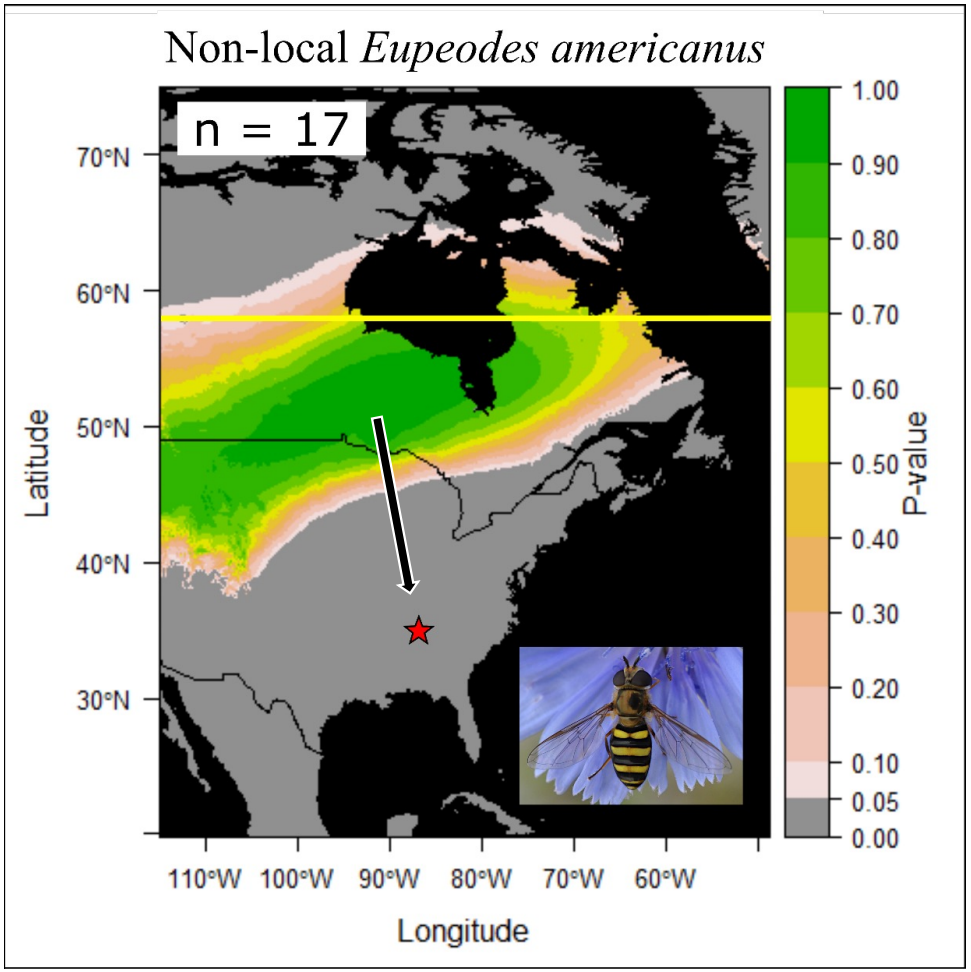
Results: Isotope raw values

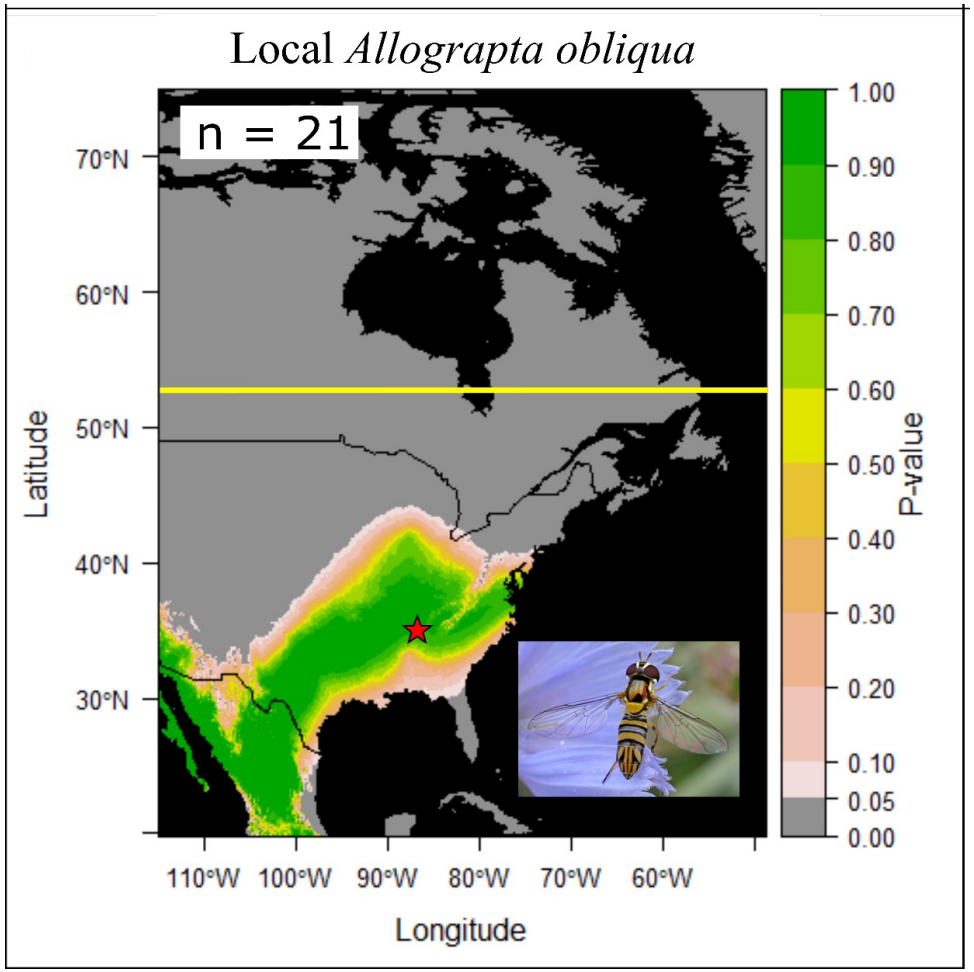


Objective 1

Clem et al. 2026, *in prep*

Results: Natal Origin Assignments





Objective 1

Clem et al. 2023, *Ecography*

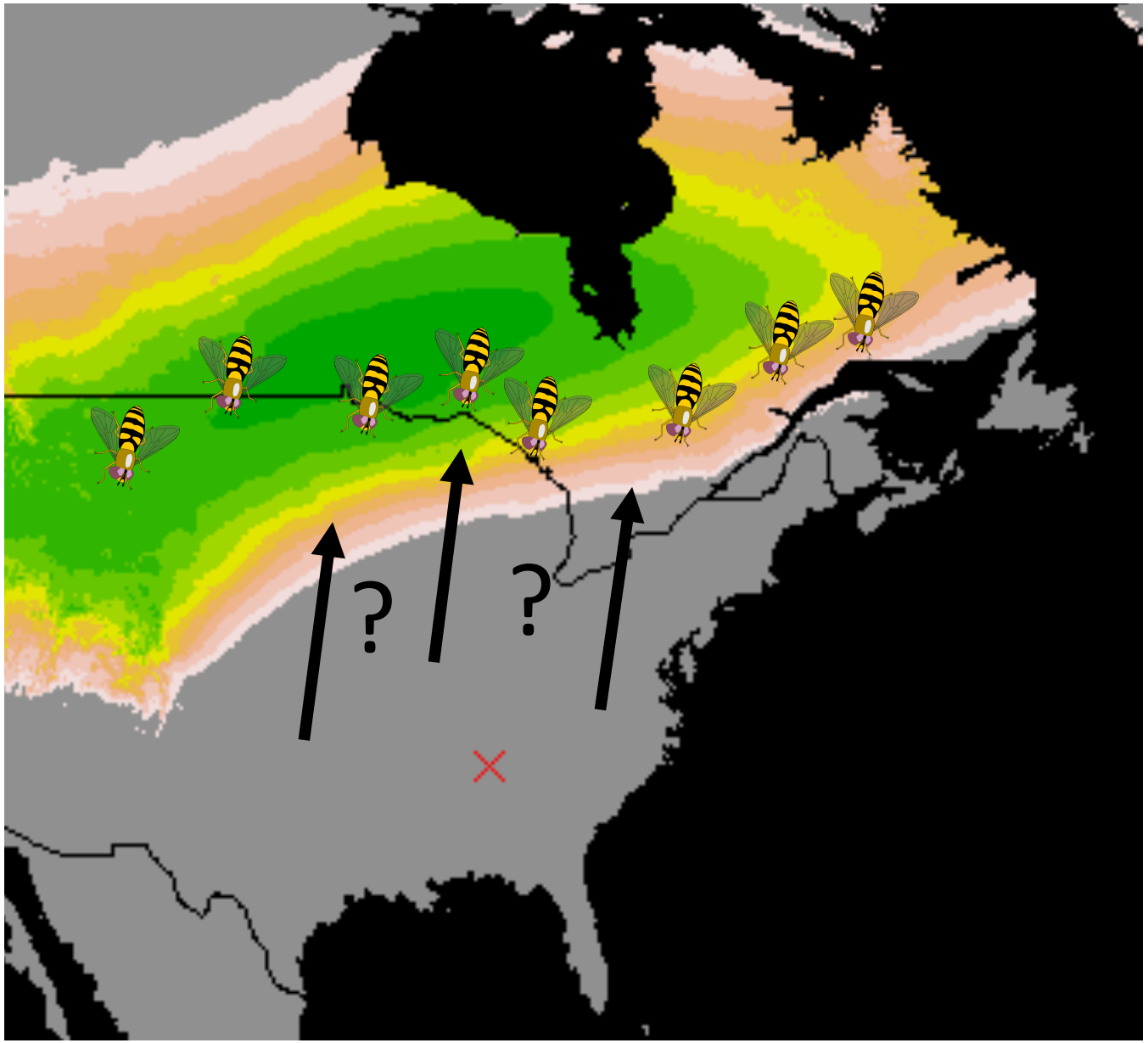
Seasonal migration

June/July

August/ September

October

Spring



Objective 1

Objectives



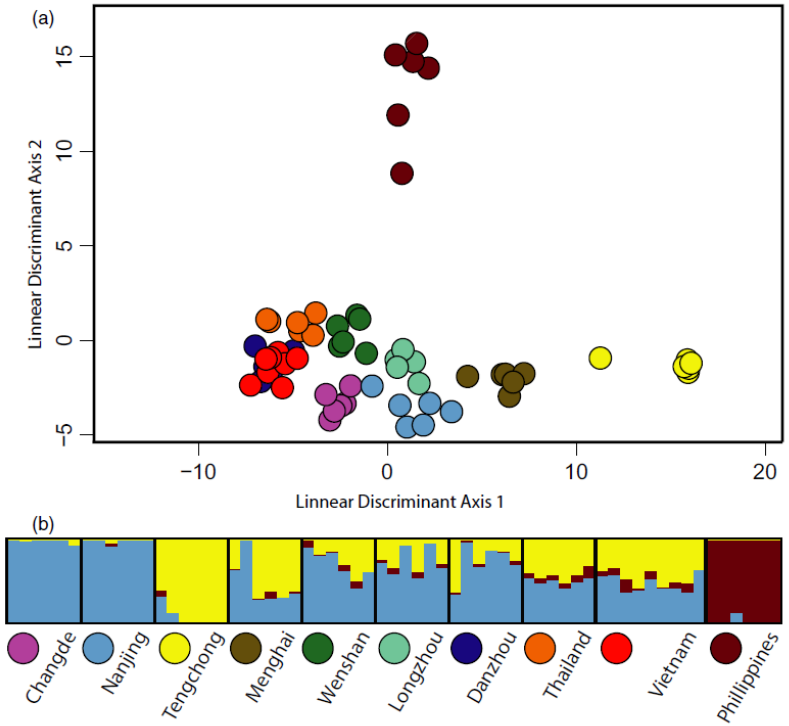
1. Use isotope analyses (δ^2H) to model natal origins of individuals collected in the southeastern USA

2. Apply population genomics (RADseq) and microbial community assessments (16S rRNA) to examine population connectivity across North America



Molecular tools for movement ecology

Population genomics



Hereward et al. 2020, *Evolutionary Applications*

Microbiome assessments



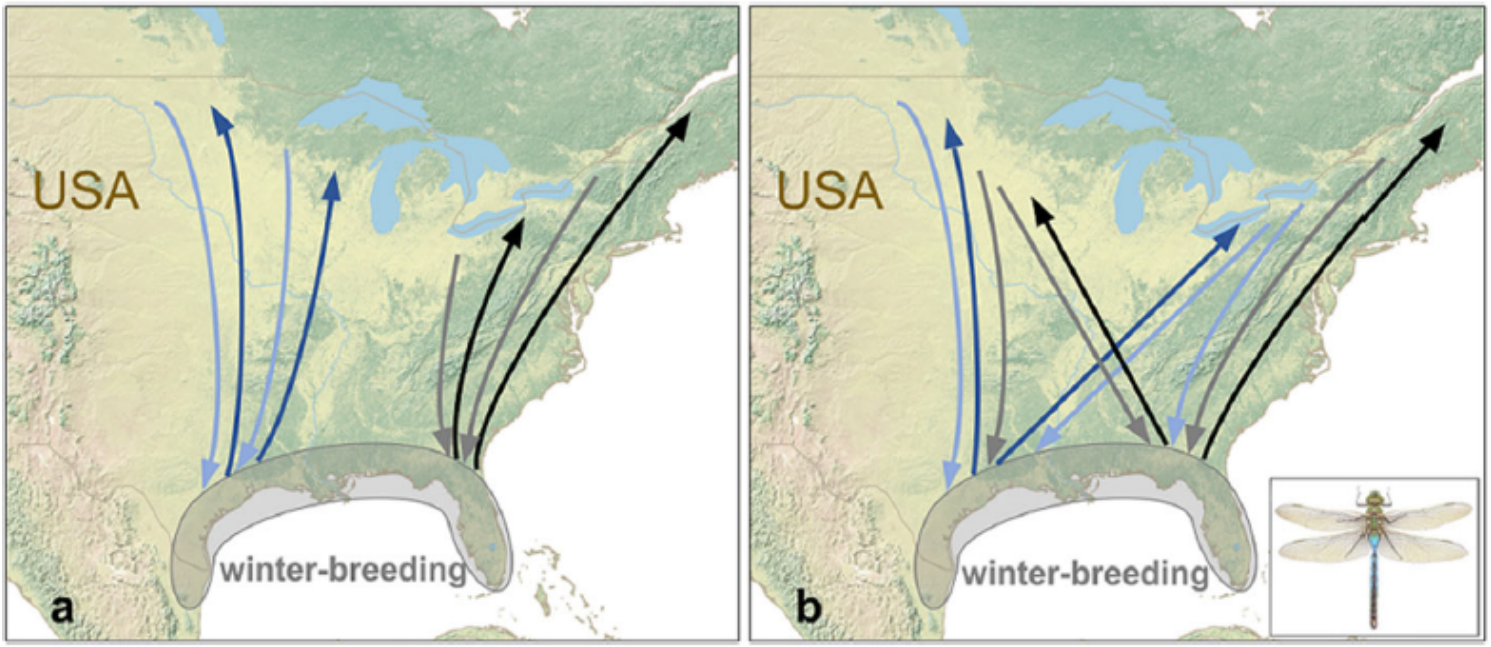
Washington genetic group

Idaho genetic group

Fu et al. 2020 *Evolutionary Applications*

Migratory connectivity

Two scenarios:



High Connectivity
Low mixing between migratory groups

Low Connectivity
High mixing between migratory groups

Objective 2

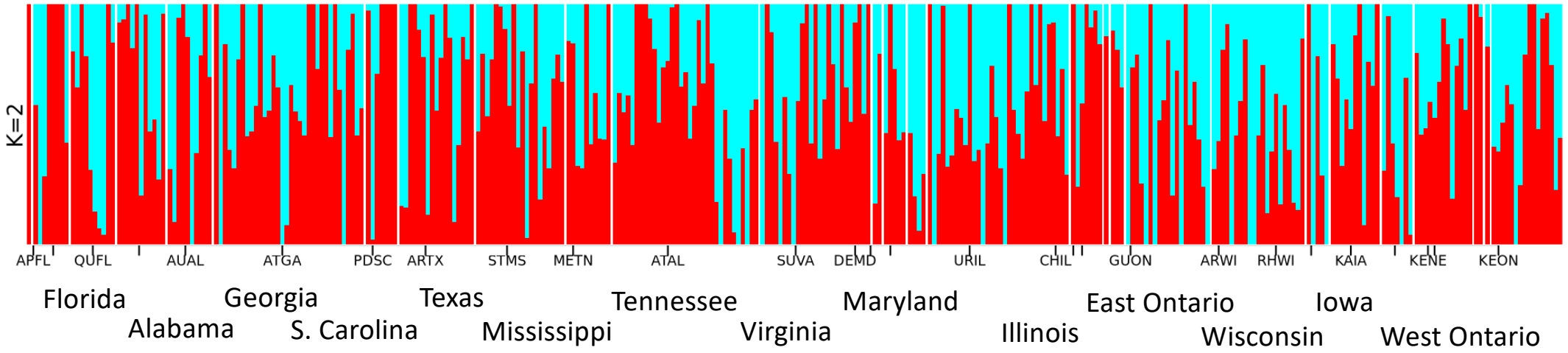
Gao et al. 2020 *Movement Ecology*

Popgen results: *Eupeodes americanus*



ADMIXTURE analysis

Migratory



South → North

Objective 2

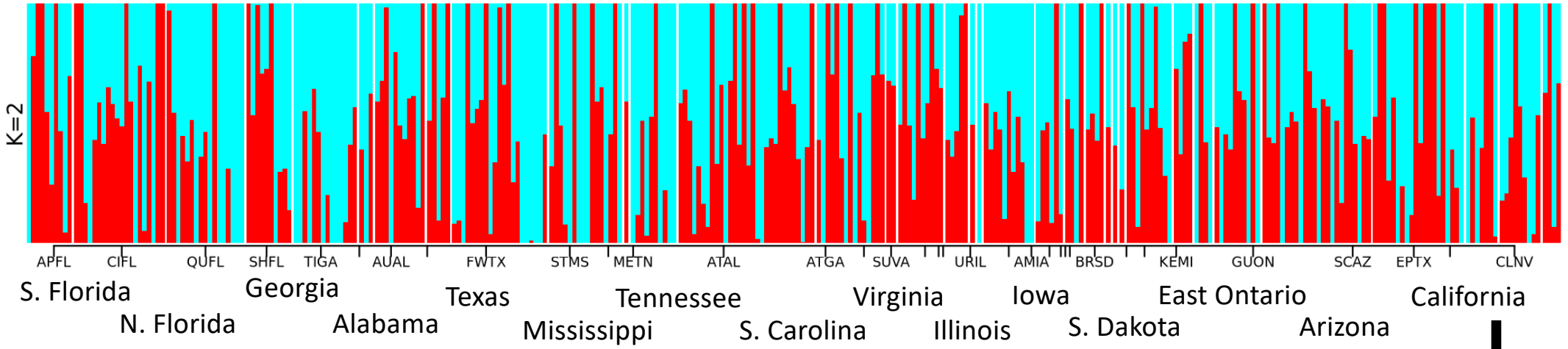
Clem et al. 2026, *in prep*

Popgen results: *Allograpta obliqua*



ADMIXTURE analysis

Non-migratory



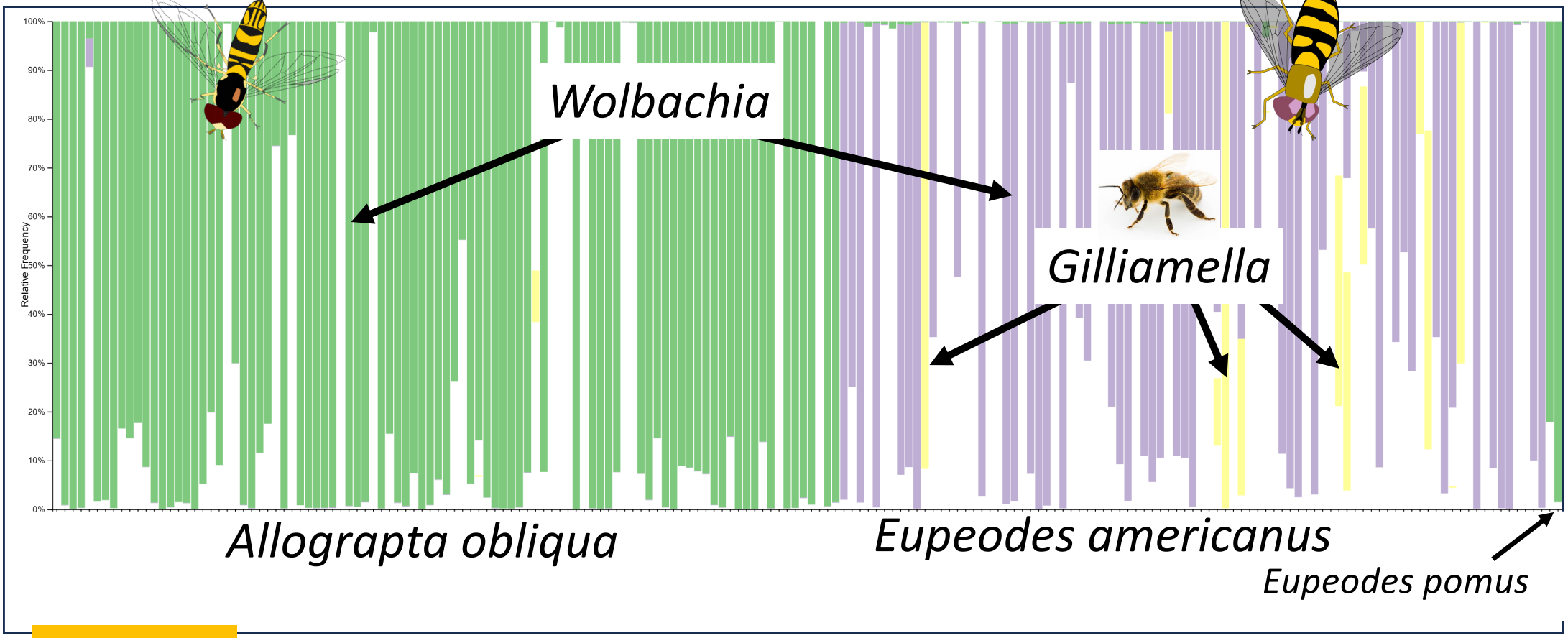
South → North

West

Objective 2

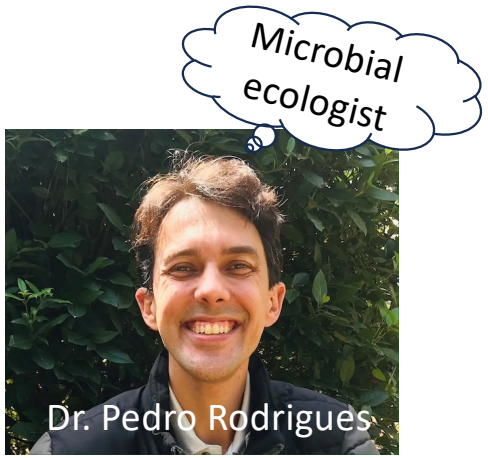
Clem et al. 2026, *in prep*

Results: Microbiomes

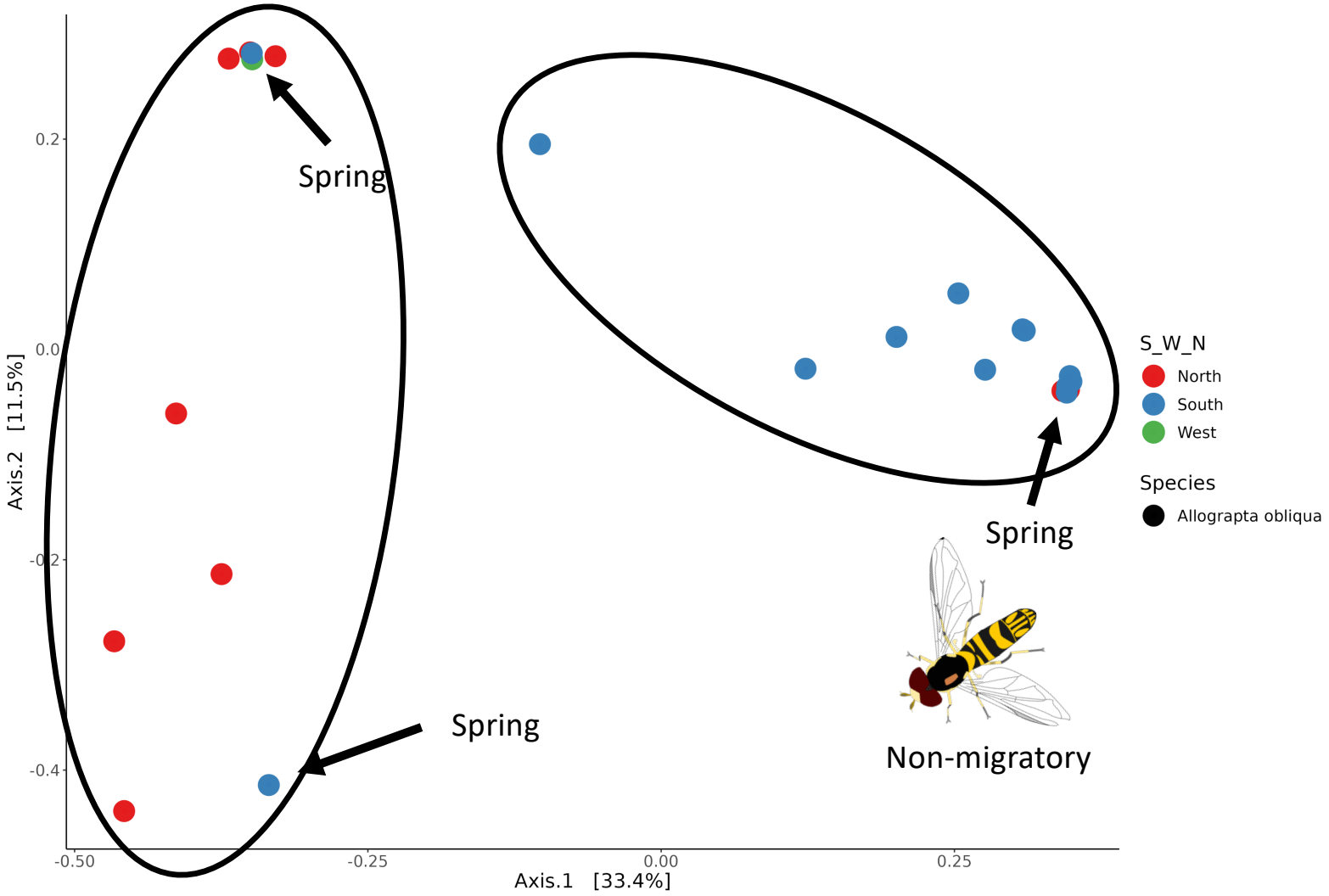


Objective 2

Results: Microbiomes



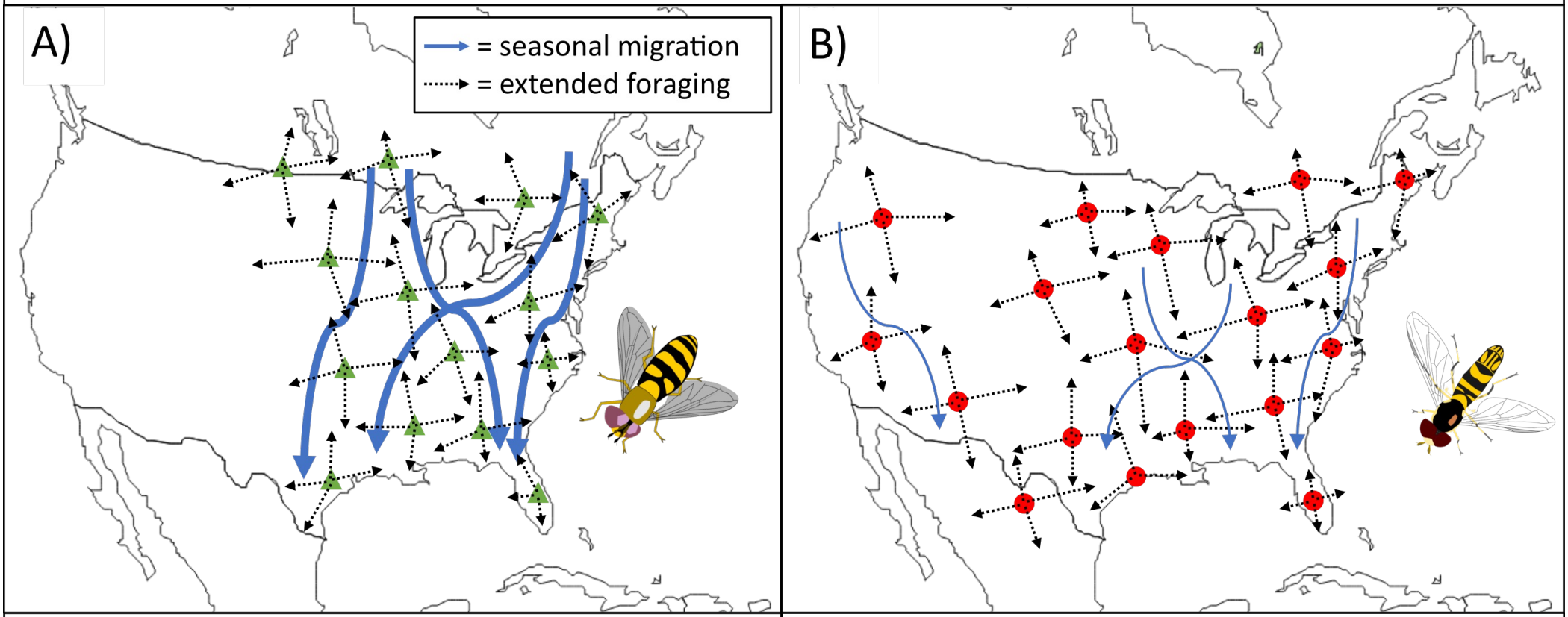
Microbial Ecologist



Objective 2

Clem et al. 2026, *in prep*

Proposed movement characteristics of two North American hover flies

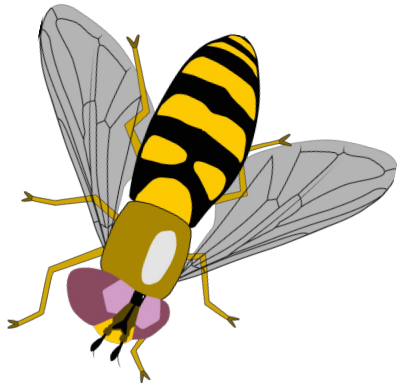


Eupeodes americanus

Allograpta obliqua

Synthesis and future directions

- *Eupeodes americanus* can move 2,000-3,000 km south during autumn migration
- Population genomics and microbiome assessments reveal little structure across North American populations in either species
- These movements likely have massive ecological and economic implications: pollination, biological control, energy transfer, etc.



Acknowledgments

Co-authors

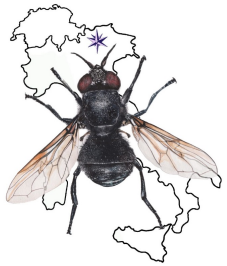
Dr. Bill Snyder (postdoc mentor)
Dr. Pedro Rodrigues (microbial ecologist)
Dr. Keith Hobson (isotope ecologist)
Dr. Doris Lagos-Kutz (Midwest suction trap network)

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Collaborators

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USDA NIFA

NORTH CENTRAL SARE
Sustainable Agriculture Research & Education

EWD fellowships
2019-67011-29504
2021-67034-35132

Award No.
2016-38640-25381

Figure 2

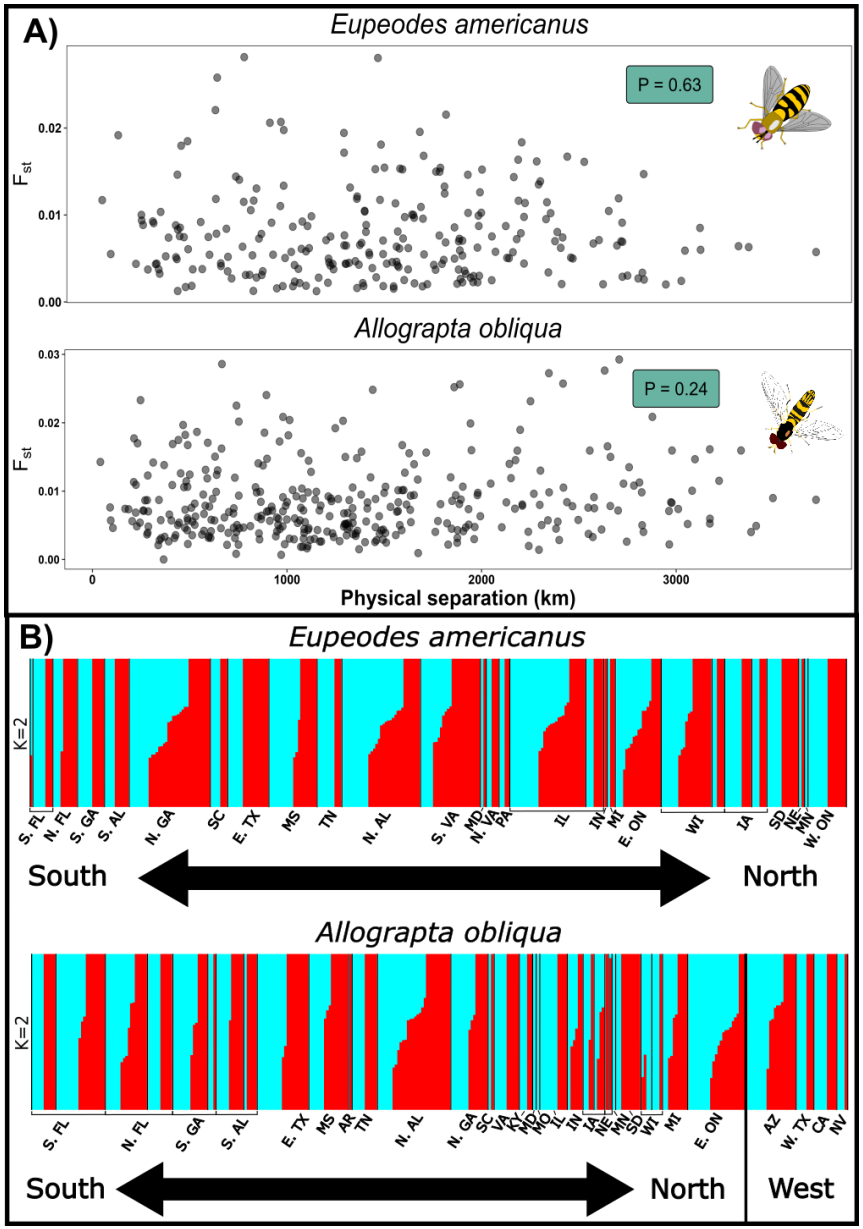

A)
Eupeodes americanus
P = 0.63
Fst
0.02
0.01
0.00
Allograpta obliqua
P = 0.24
0.03
0.02
0.01
0.00
0
1000
2000
3000
Physical separation (km)
B)
Eupeodes americanus
K=2
S. FL
N. FL
S. GA
S. AL
N. GA
SC
E. TX
MS
TN
N. AL
S. VA
MD
N. VA
PA
IL
IN
MI
E. ON
WI
IA
SD
NE
MN
W. ON
South
North
Allograpta obliqua
K=2
S. FL
N. FL
S. GA
S. AL
E. TX
MS
AR
TN
N. AL
N. GA
SC
VA
KY
MD
MO
IL
IN
IA
NE
MN
SD
WI
MI
E. ON
AZ
W. TX
CA
NV
South
North
West

Figure 3

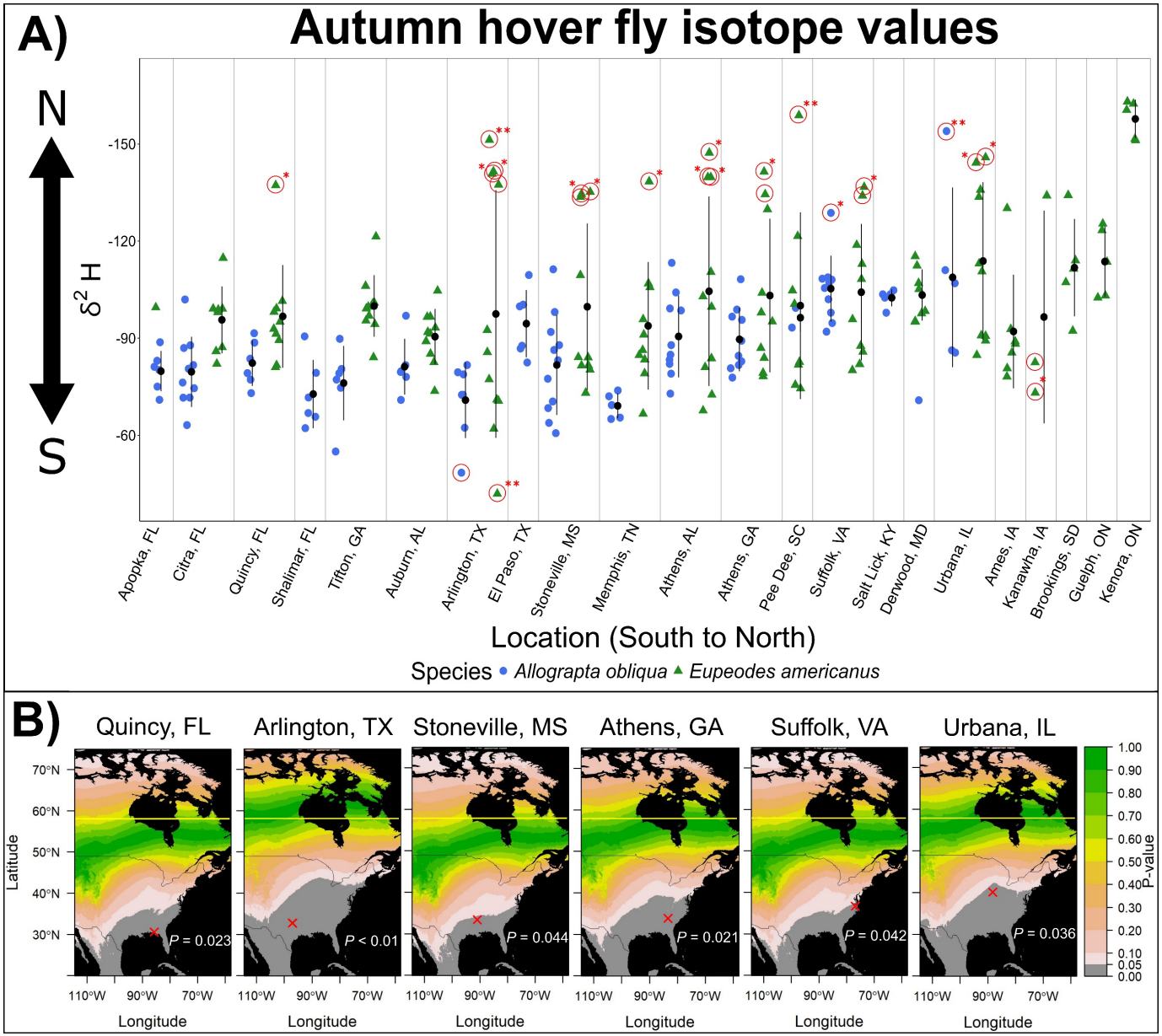
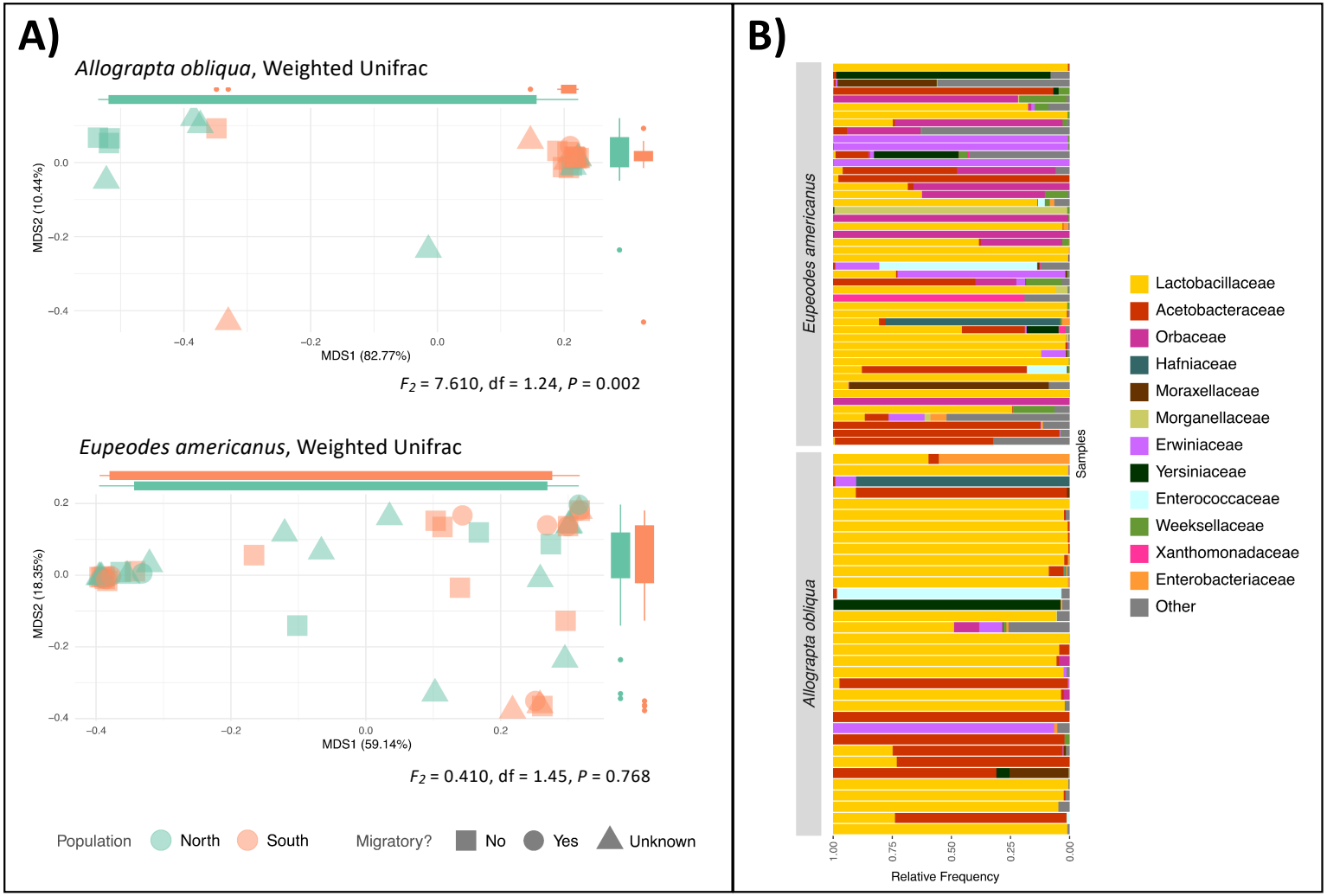
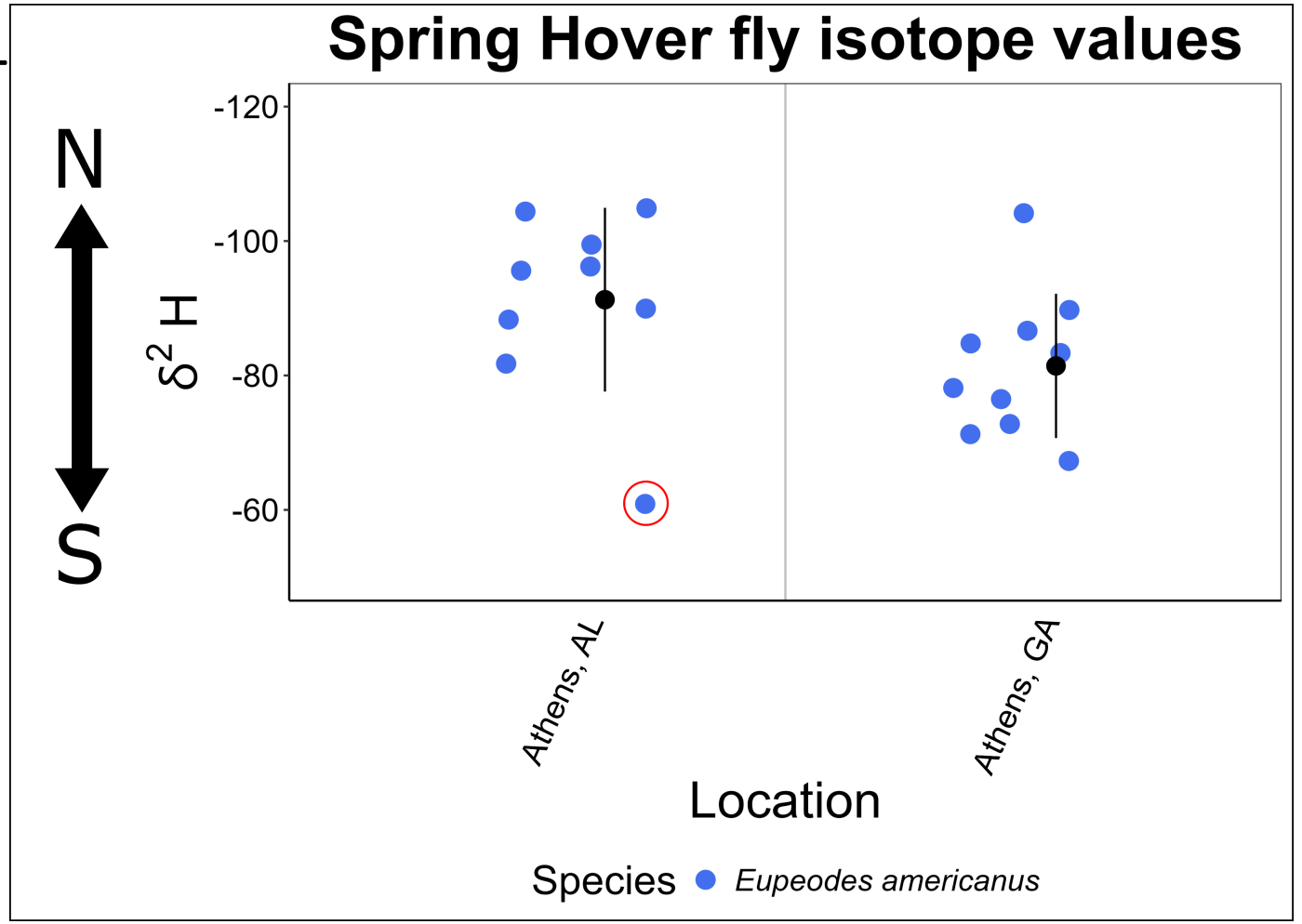

A)
Autumn hover fly isotope values
N
S
δ^2H
-150
-120
-90
-60
Apopka, FL
Citra, FL
Quincy, FL
Shalimar, FL
Tifton, GA
Auburn, AL
Arlington, TX
El Paso, TX
Stoneville, MS
Memphis, TN
Athens, AL
Athens, GA
Pee Dee, SC
Suffolk, VA
Salt Lick, KY
Derwood, MD
Urbana, IL
Ames, IA
Kanawha, IA
Brookings, SD
Guelph, ON
Kenora, ON
Location (South to North)
Species Allograpta obliqua Eupeodes americanus
B)
Quincy, FL
Arlington, TX
Stoneville, MS
Athens, GA
Suffolk, VA
Urbana, IL
Latitude
70°N
60°N
50°N
40°N
30°N
P = 0.023
P < 0.01
P = 0.044
P = 0.021
P = 0.042
P = 0.036
110°W
90°W
70°W
Longitude
P-value
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.05
0.00

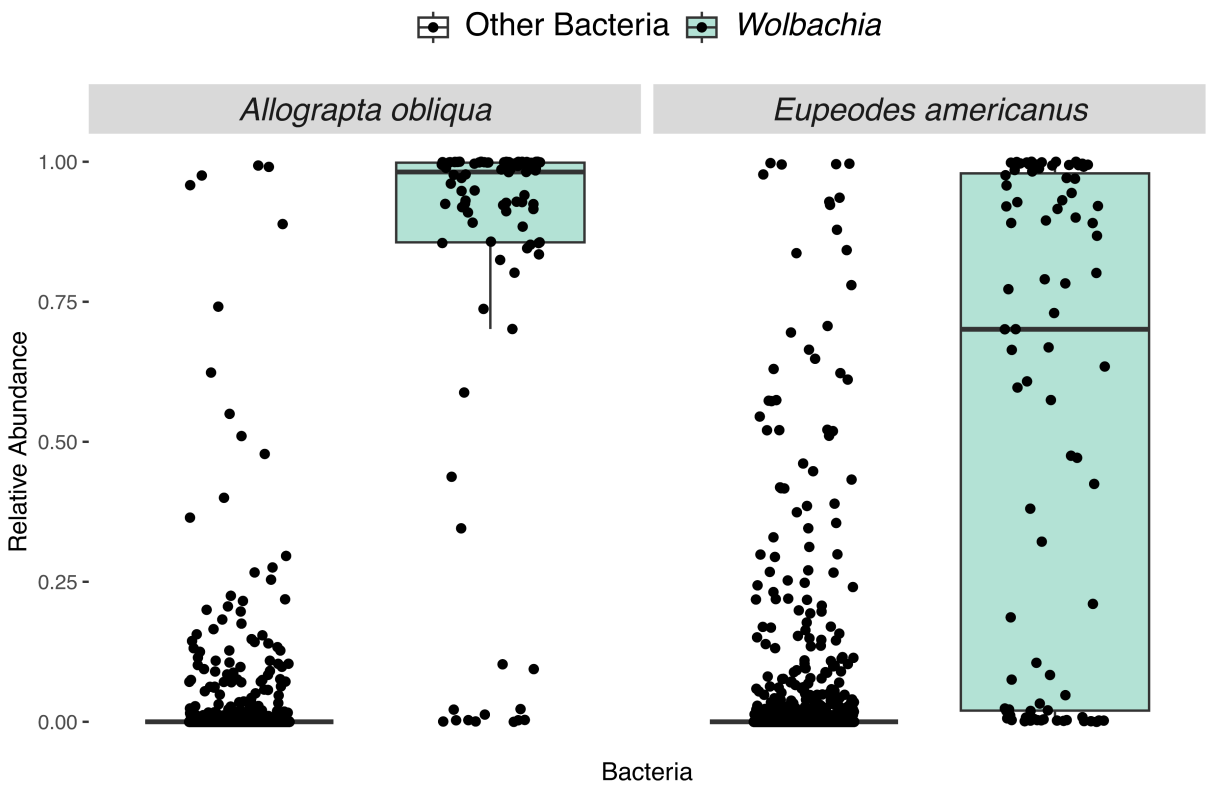
Figure 4


A)
Allograpta obliqua, Weighted Unifrac
MDS2 (10.44%)
MDS1 (82.77%)
F2 = 7.610, df = 1.24, P = 0.002
Eupeodes americanus, Weighted Unifrac
MDS2 (18.35%)
MDS1 (59.14%)
F2 = 0.410, df = 1.45, P = 0.768
Population North South
Migratory? No Yes Unknown
B)
Eupeodes americanus
Allograpta obliqua
Samples
Relative Frequency
Lactobacillaceae
Acetobacteraceae
Orbaceae
Hafniaceae
Moraxellaceae
Morganellaceae
Erwiniaceae
Yersiniaceae
Enterococcaceae
Weeksellaceae
Xanthomonadaceae
Enterobacteriaceae
Other

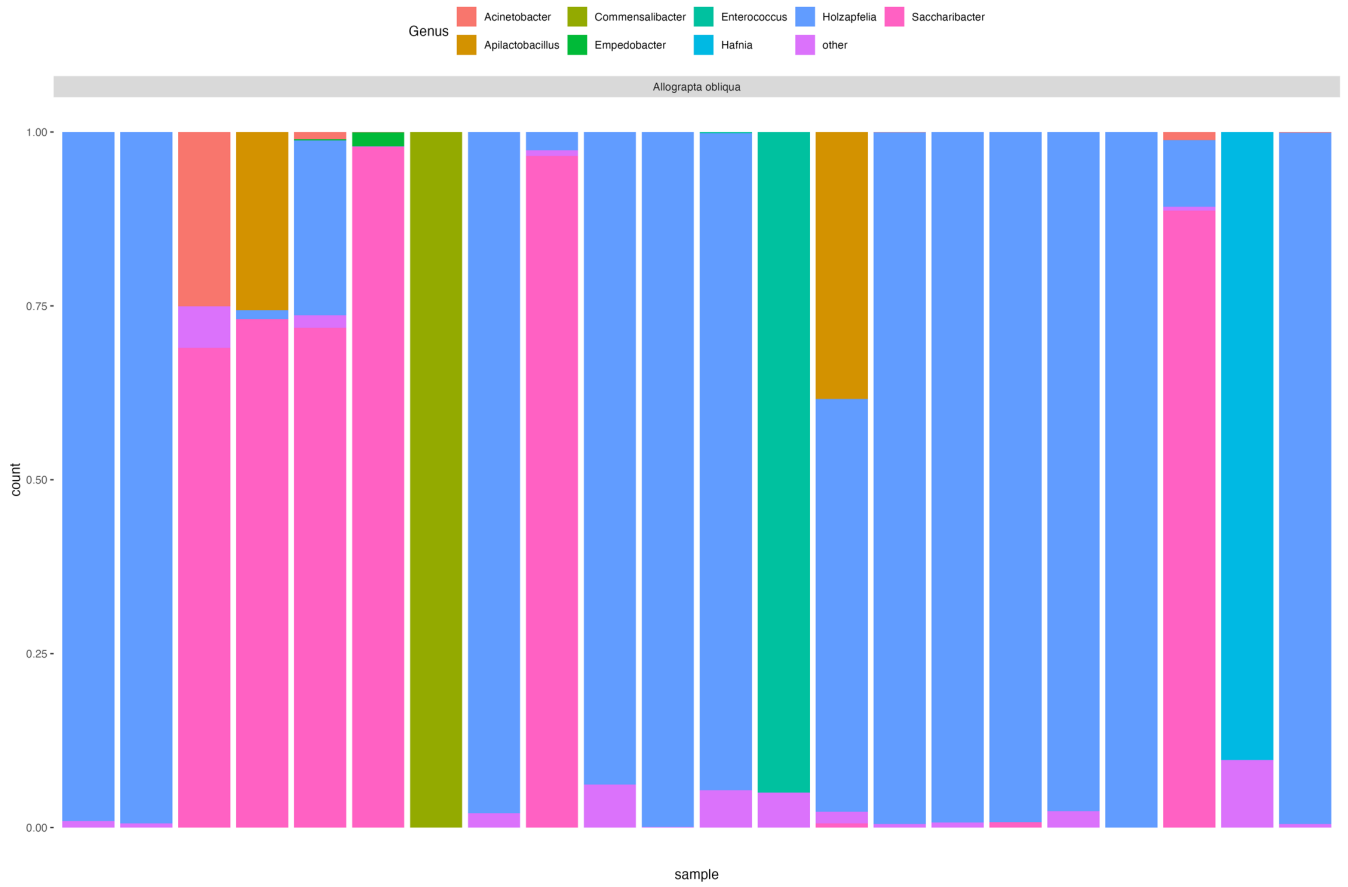
Suppl. Figure 1



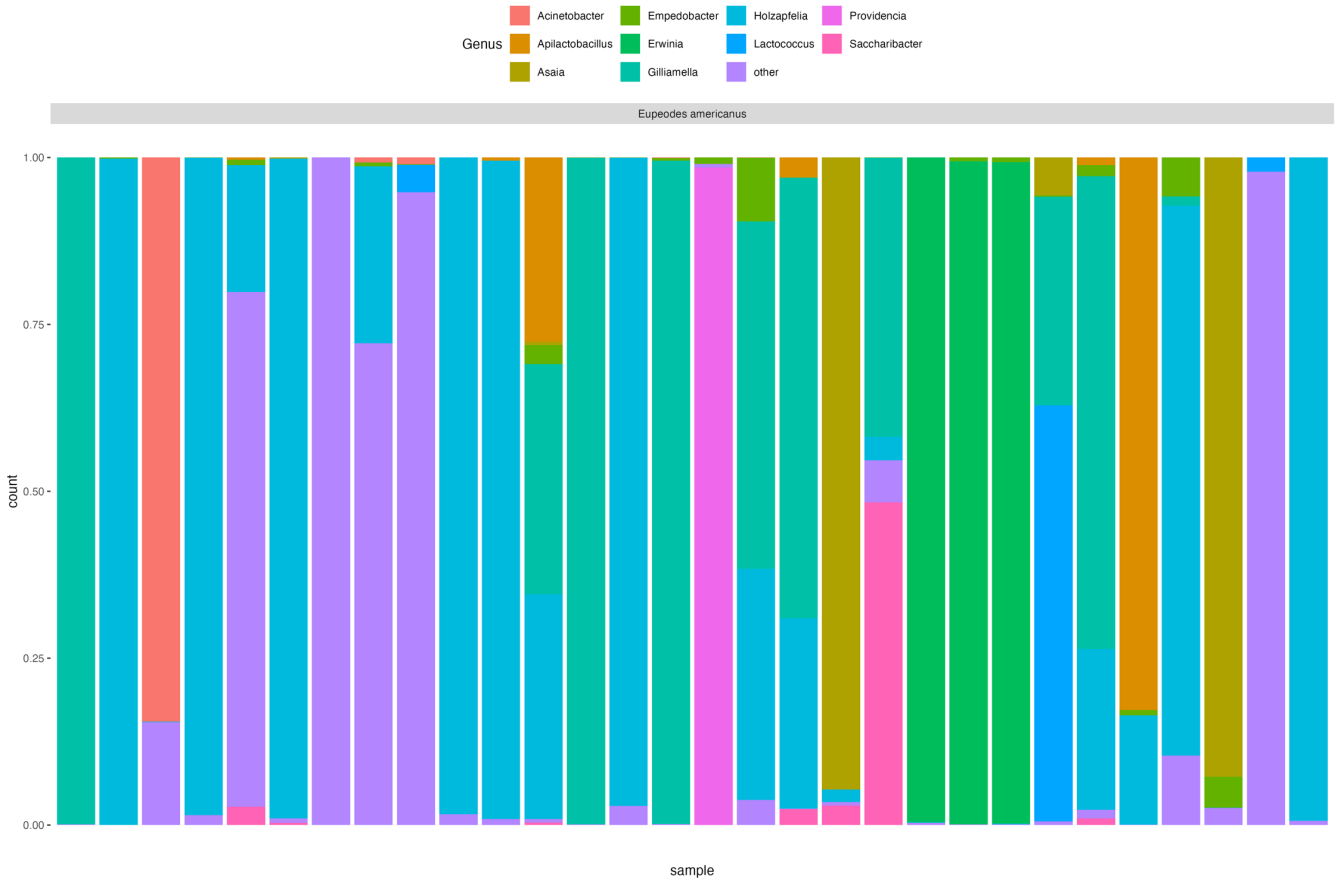
Suppl. Figure 2



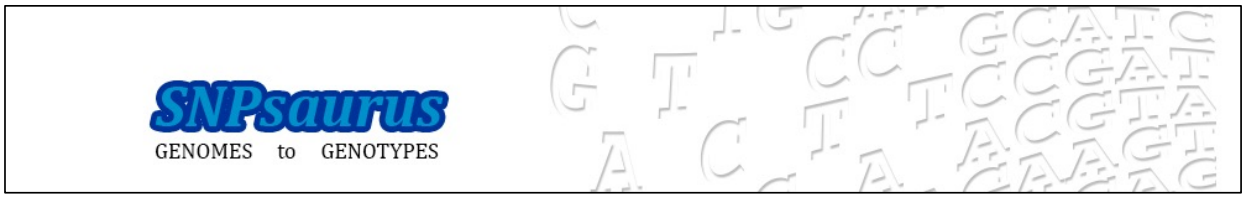
Suppl. Figure 3



Suppl. Figure 4



Methods



Population genomics

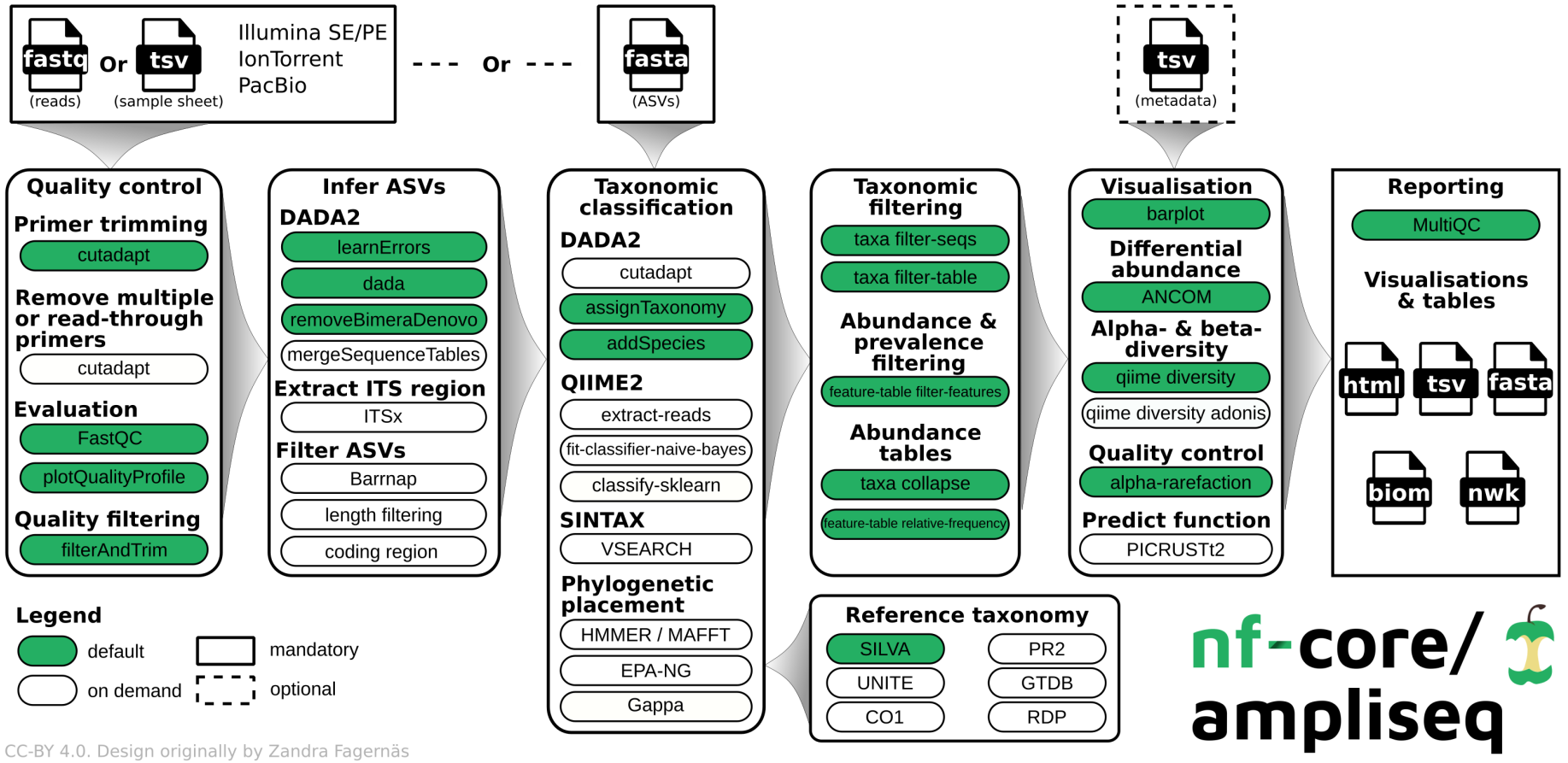
- nextRAD processing (SNPsaurus)
- Illumina sequencing, Oxford Nanopore reference genomes
- Number of SNPs in dataset
  - 8,981 for *Allograpta obliqua*
  - 9,692 for *Eupeodes americanus*



Microbiome assessment

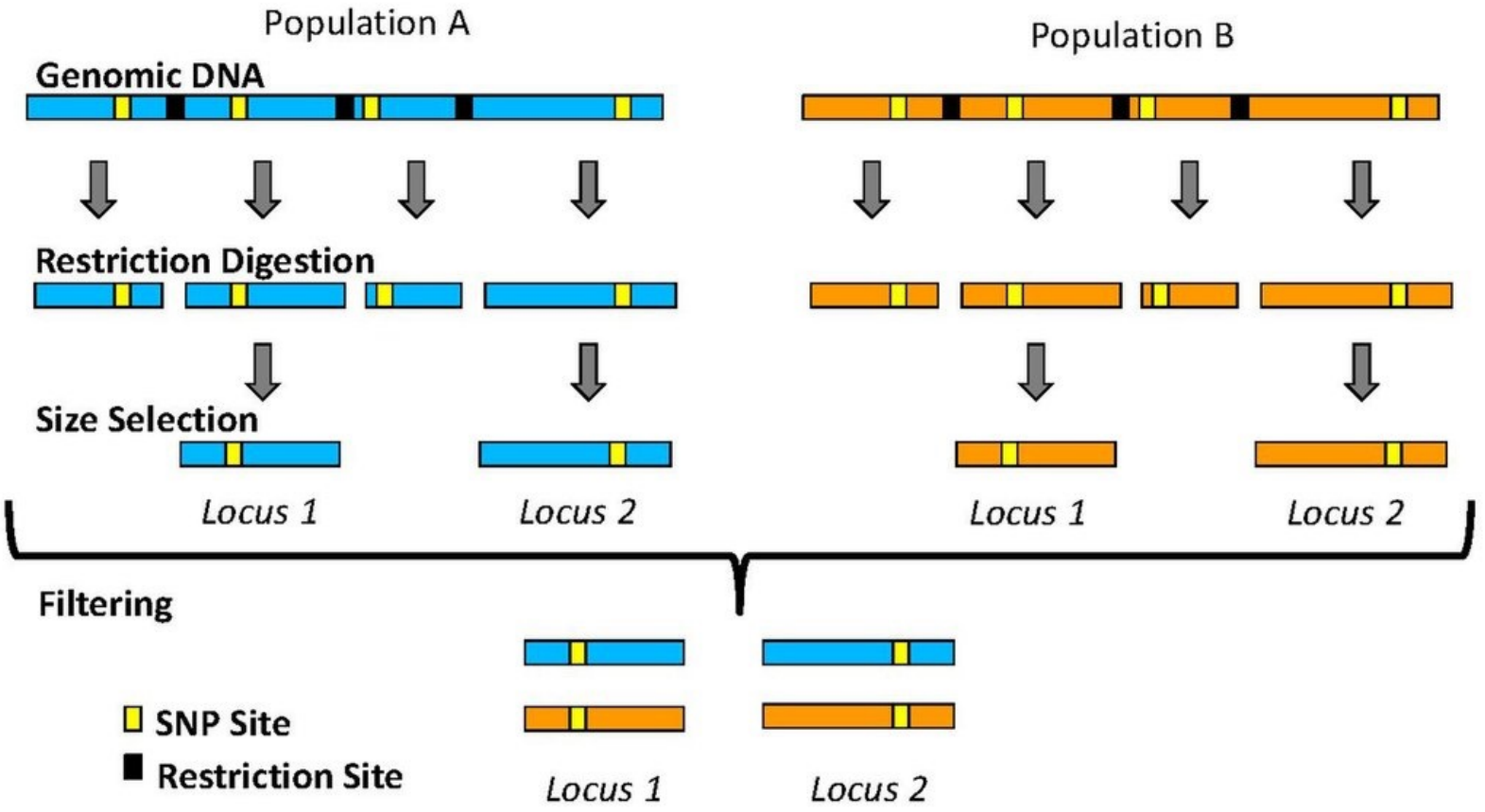
- Whole body DNA extraction, surface sterilization
- 16S rRNA sequencing
- DADA2 processing, Silva reference taxonomy
- Qiime2 data analysis

Objective 2

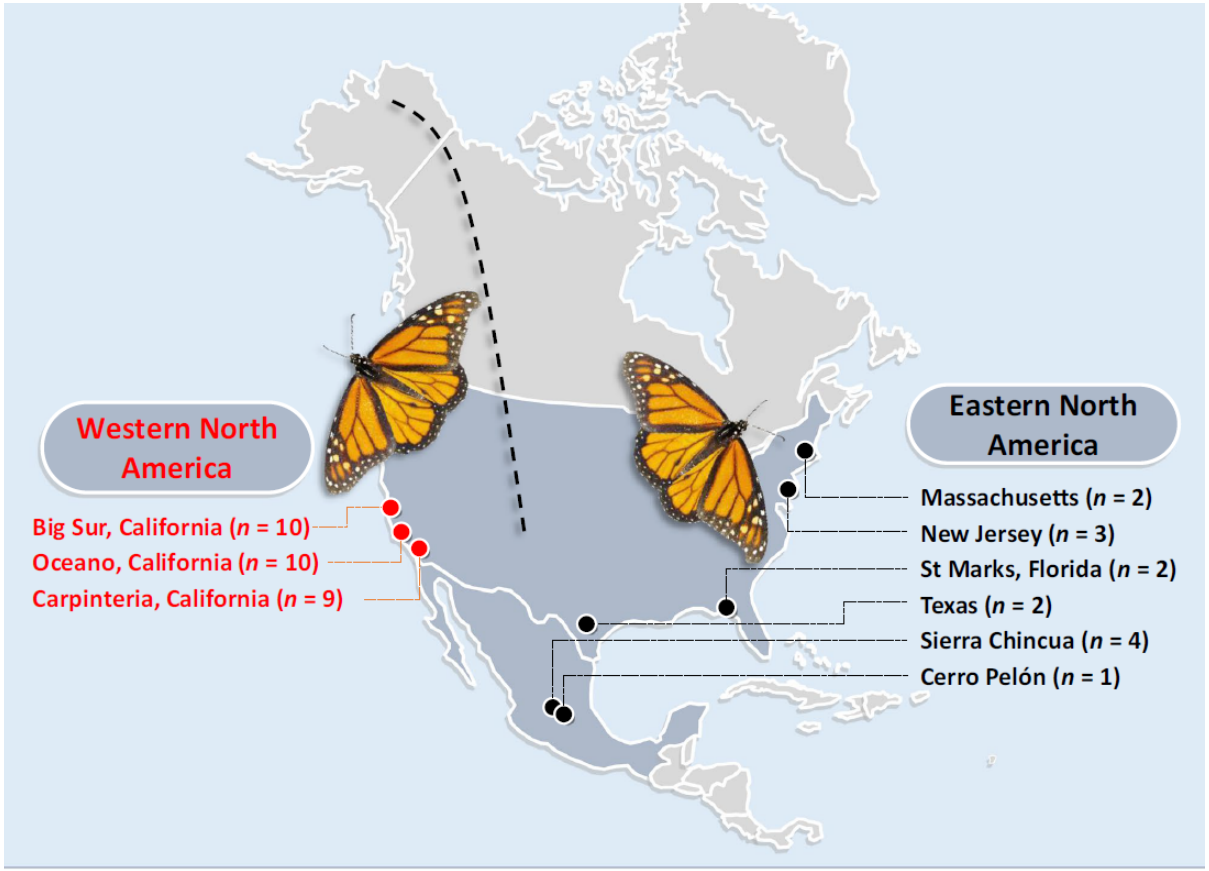


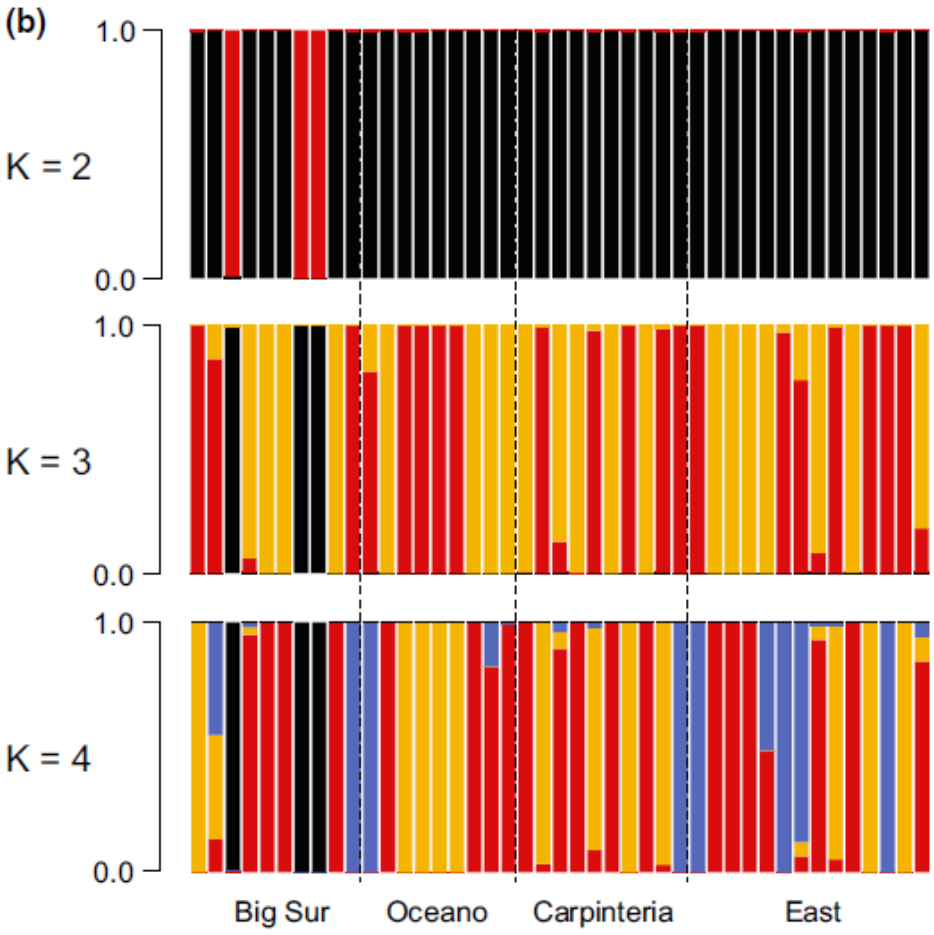
CC-BY 4.0. Design originally by Zandra Fagernäs

Restriction-site Associate DNA Sequencing (RADseq)



Population genomics

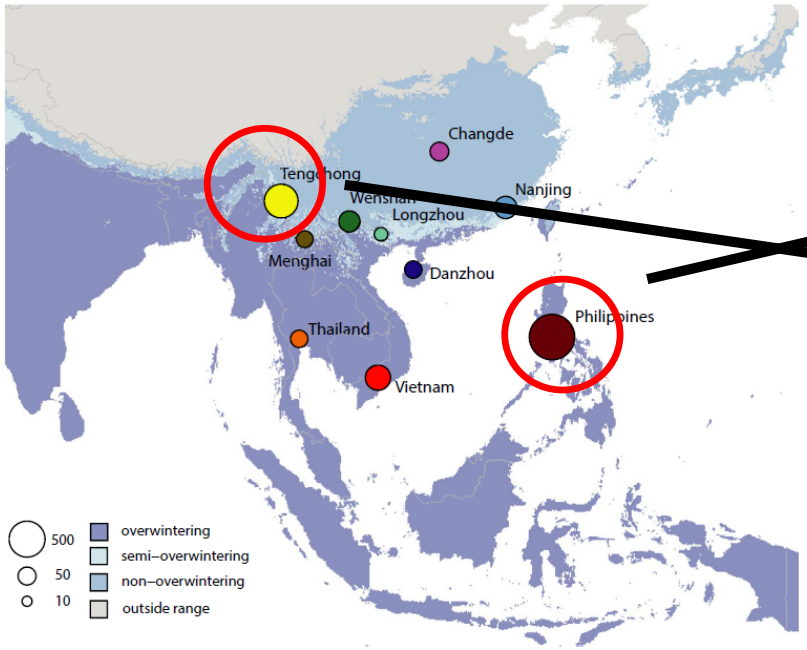


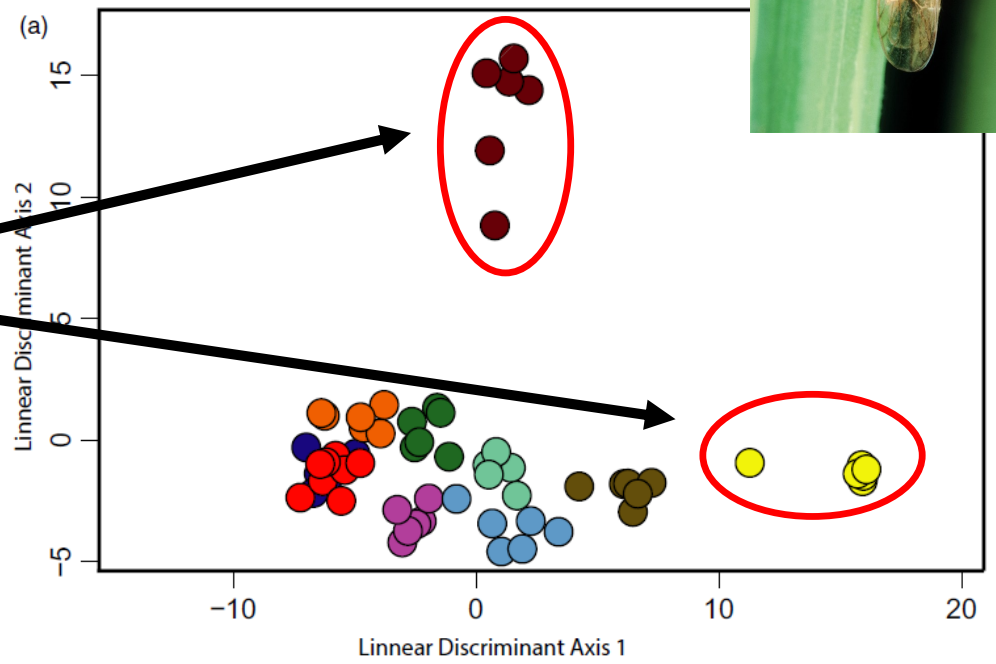


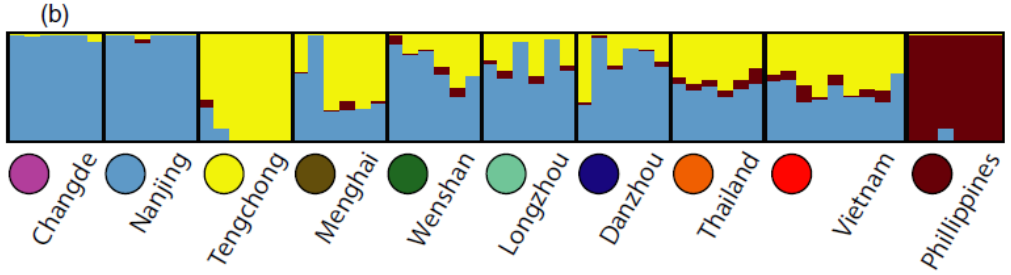
Talla et al. 2020 *Molecular Ecology*

Population genomics and migration





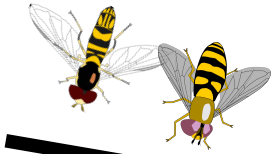




Hereward et al. 2020, *Evolutionary Applications*

RADseq Methods

SNPsaurus
GENOMES to GENOTYPES



DNA Extraction

DNA fragmentation and conversion to nextRAD libraries

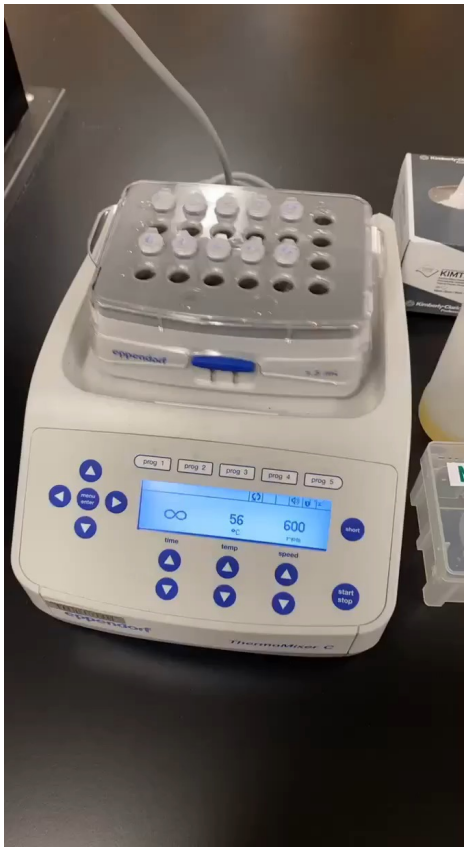
Illumina sequencing

Mapped to Reference Genome (Oxford Nanopore)

SNP calling

Data filtering

Visualization



Total SNPs *Allograpta obliqua*: **8,981**
Total SNPs *Eupeodes americanus*: **9,692**

Methods: Microbiome Assessment

- Whole body DNA extraction
- Surface sterilization
- 16S rRNA sequencing
- Ampliseq pipeline
- DADA2 processing, Silva reference taxonomy

