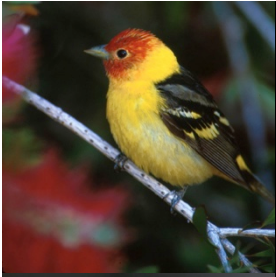


The Bird Genoscape Project

Rachael Bay

Center for Tropical Research,
Institute for the Environment and Sustainability,
University of California, Los Angeles



Bird Genoscape Project:

Where do populations of migratory birds found breeding in North America spend the non-breeding season?

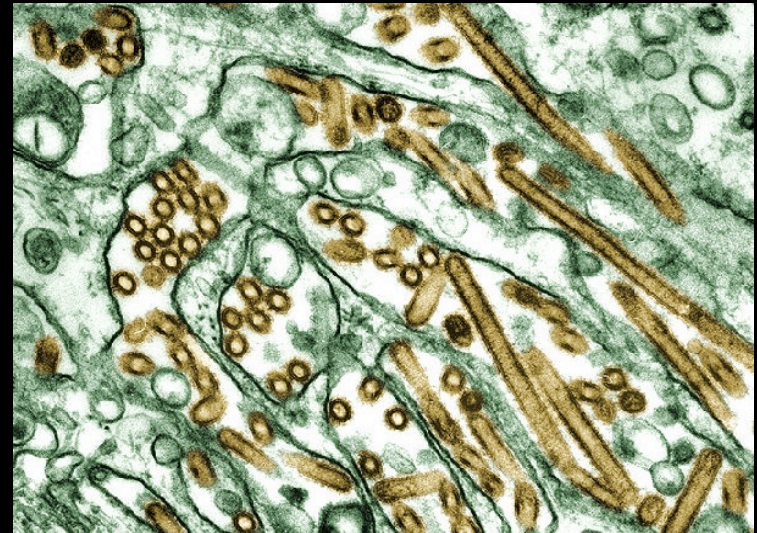
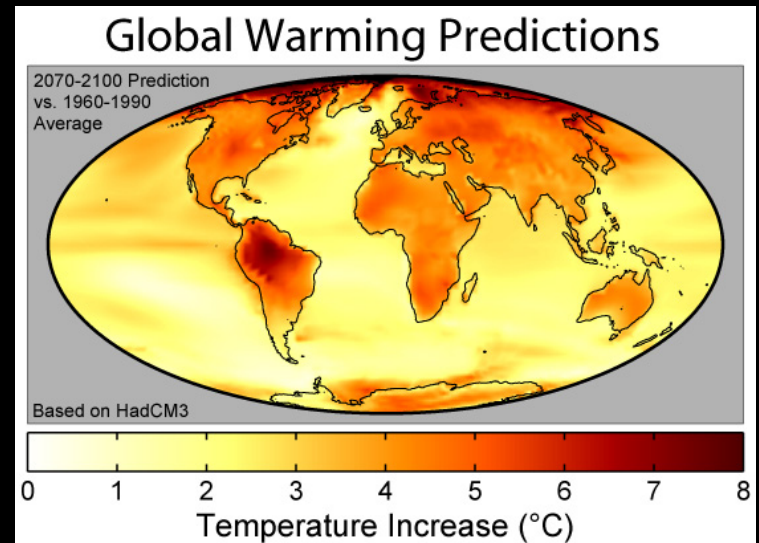


Kristen Ruegg

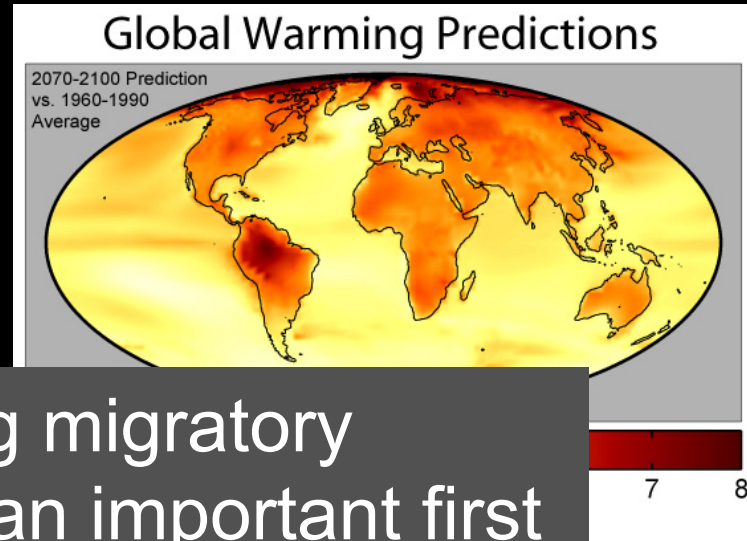


Tom Smith

Stressors across the breeding, wintering and migratory stopover areas



Stressors across the breeding, wintering and migratory stopover areas



Identifying migratory connections is an important first step for developing effective conservation strategies



Past Approaches: Bird Banding

**So, the big question is:
How can we get the information we
need from all the birds we capture,
band, or recover?**

Our Approach: High-Resolution Genetic Tags

Tissue at base of
feather contains
DNA



Identify unique genetic code that allows us to *trace the breeding origin* of migrants captured anywhere along their migratory trajectory

Our Approach: High-Resolution Genetic Tags

Advantages:

1. Information on migration, wintering, and breeding area from **100%** of birds.
2. Feathers can be collected with ***minimal impact.***
3. Can be used to ID individuals subject to ***collisions, poaching*** and ***avian disease.***

How does it work?

Proof of Concept – The Wilson's warbler



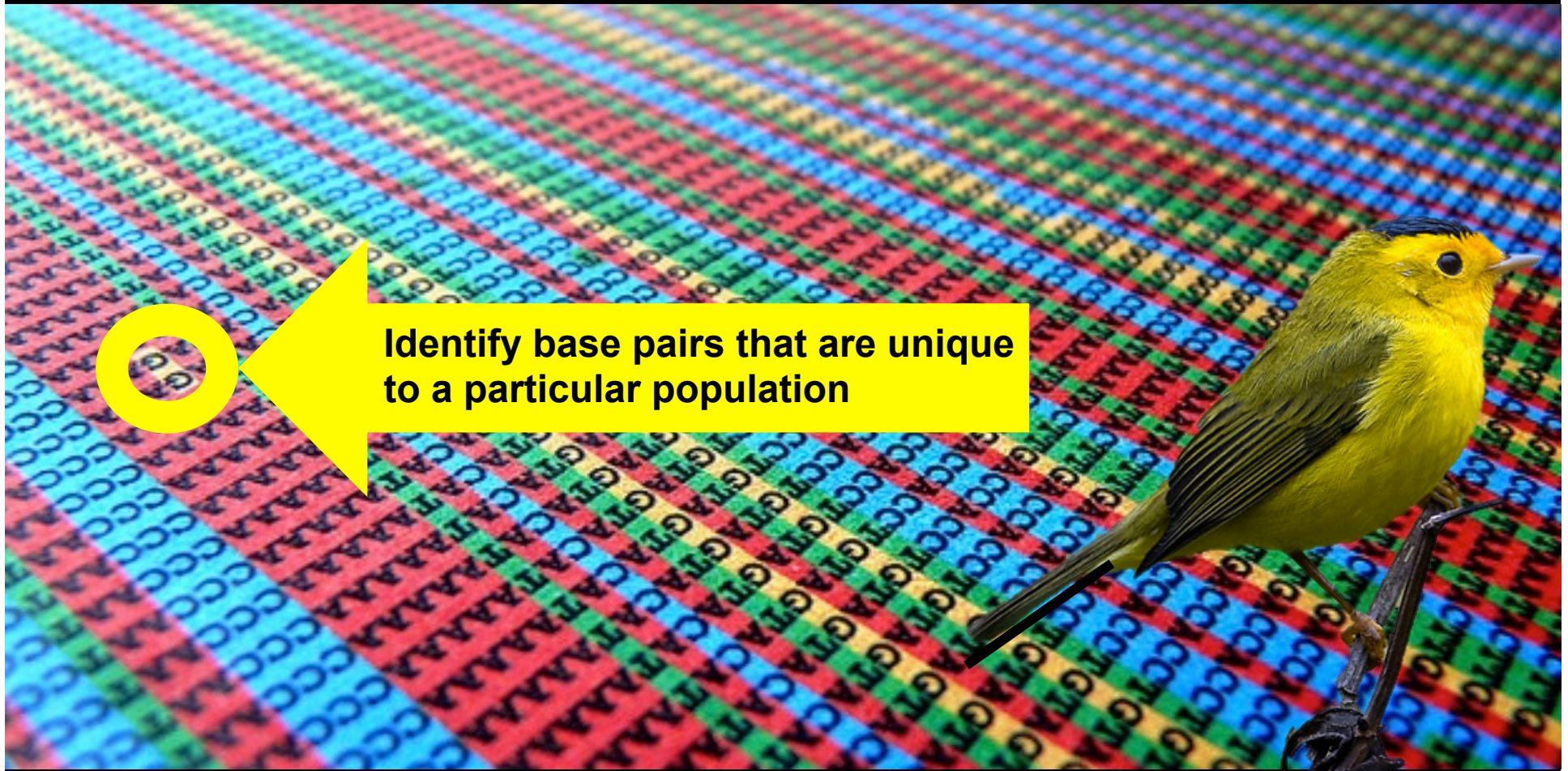
Little was known about *population specific* migration patterns

Wilson's Warbler - Conservation Status

What we need is a *population specific* map of migration flyways

Patterns of declines in the Wilson's warbler are *population specific*

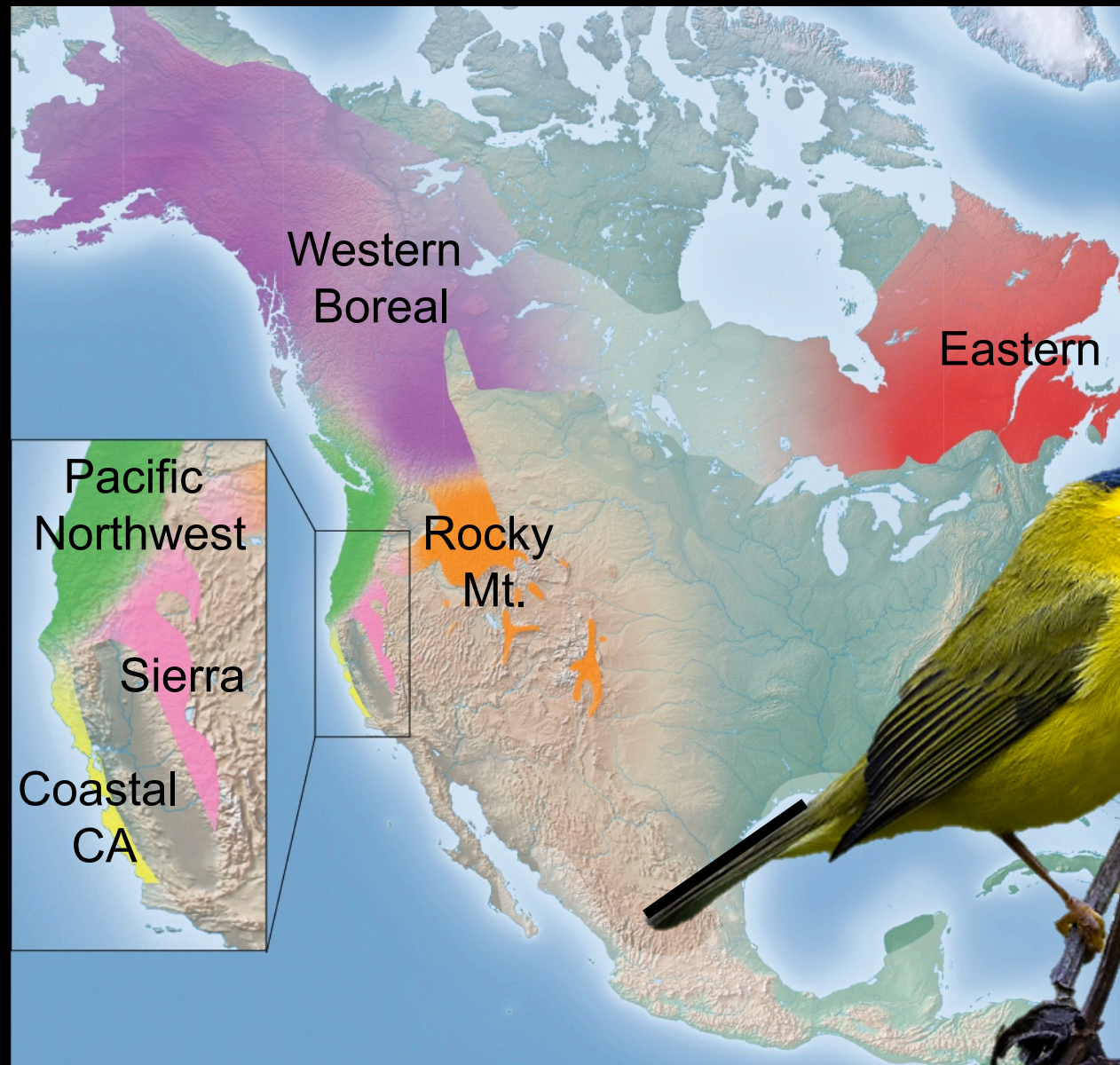
Step 1: Build a Map of Genetic Variation Across Geographic Space



Identify base pairs that are unique to a particular population

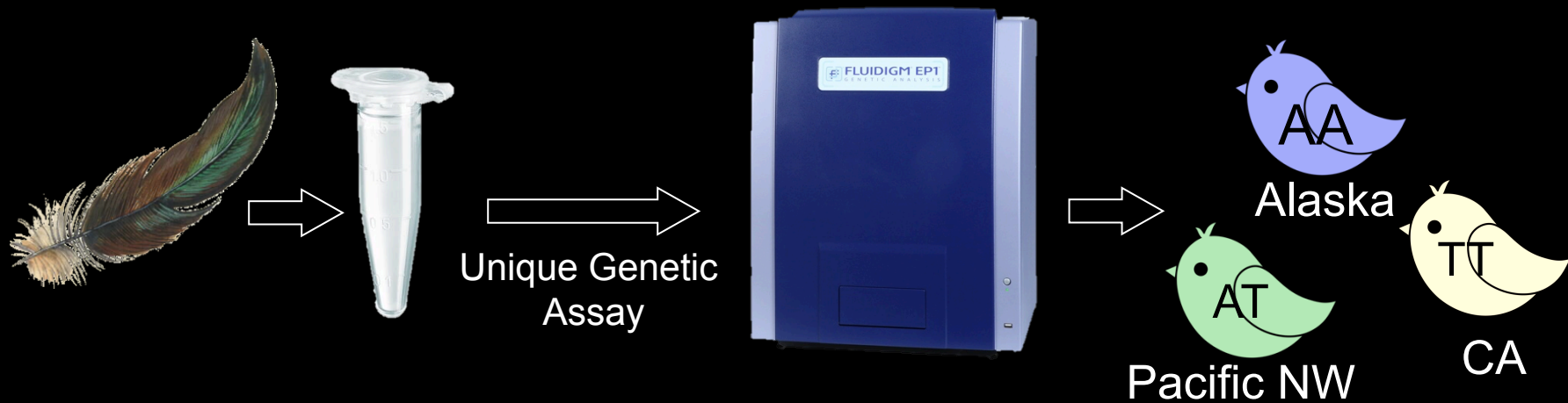
Scan the Genome for Unique Genetic Variants

Step 1: Build a Map of Genetic Variation Across Geographic Space



Ruegg et al.
2014
Mol Ecol

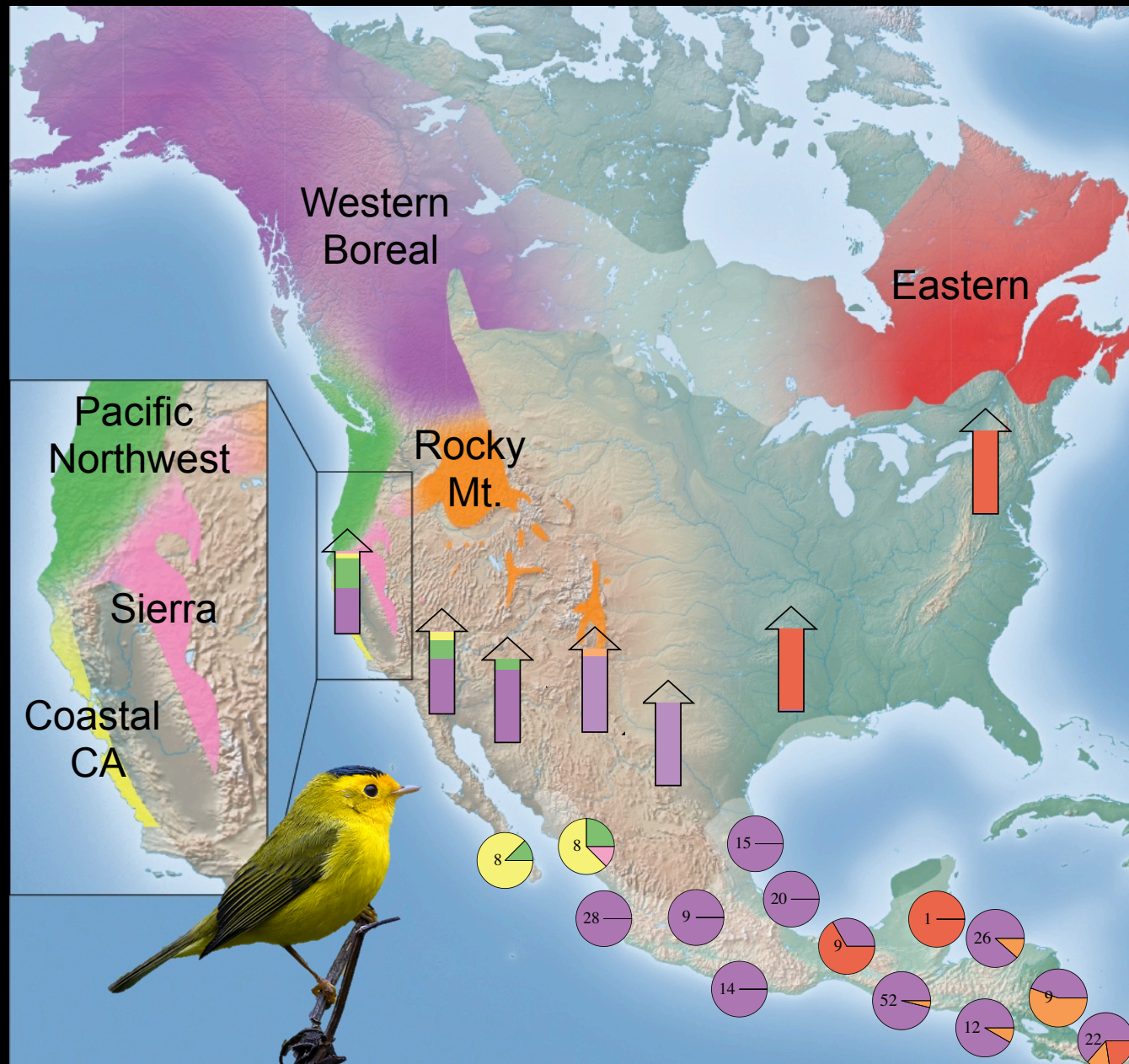
Step 2: Trace the Origin of Migrants using DNA from Feathers



Rapid Feather Screening Pipeline

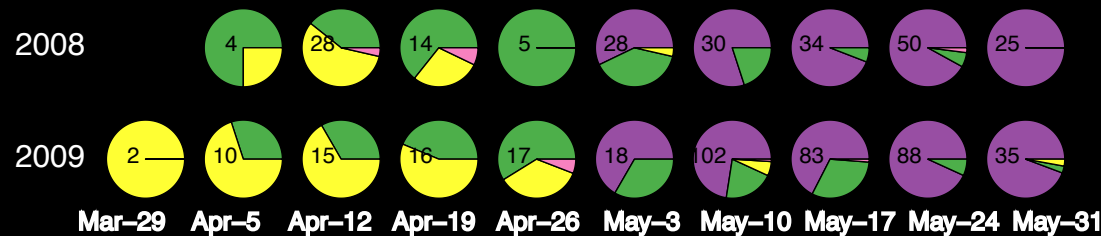
- Can screen **~800 feather samples/week**.
- Works well with **low quantity** and **degraded DNA (97% reliability)**.

Step 3: Map Population Specific Migratory Flyways



Ruegg et al.
2014
Mol Ecol

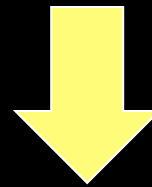
Step 3: Map Population Specific Migratory Flyways



Ruegg et al.
2014
Mol Ecol



**So, the big question was:
How can we get the information
we need from all the birds we
capture, band, or recover?**



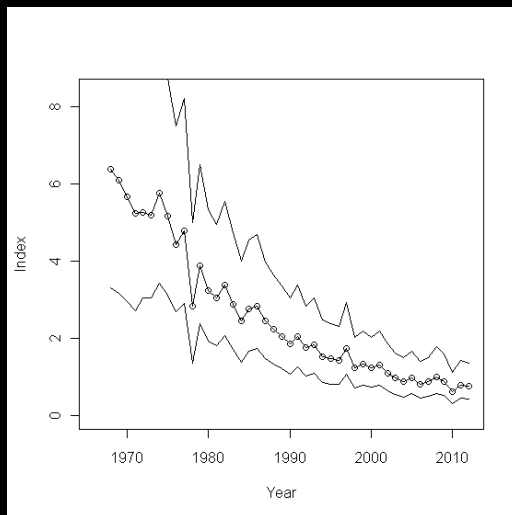
**Answer: Screen feathers using
high-resolution genetic tags**



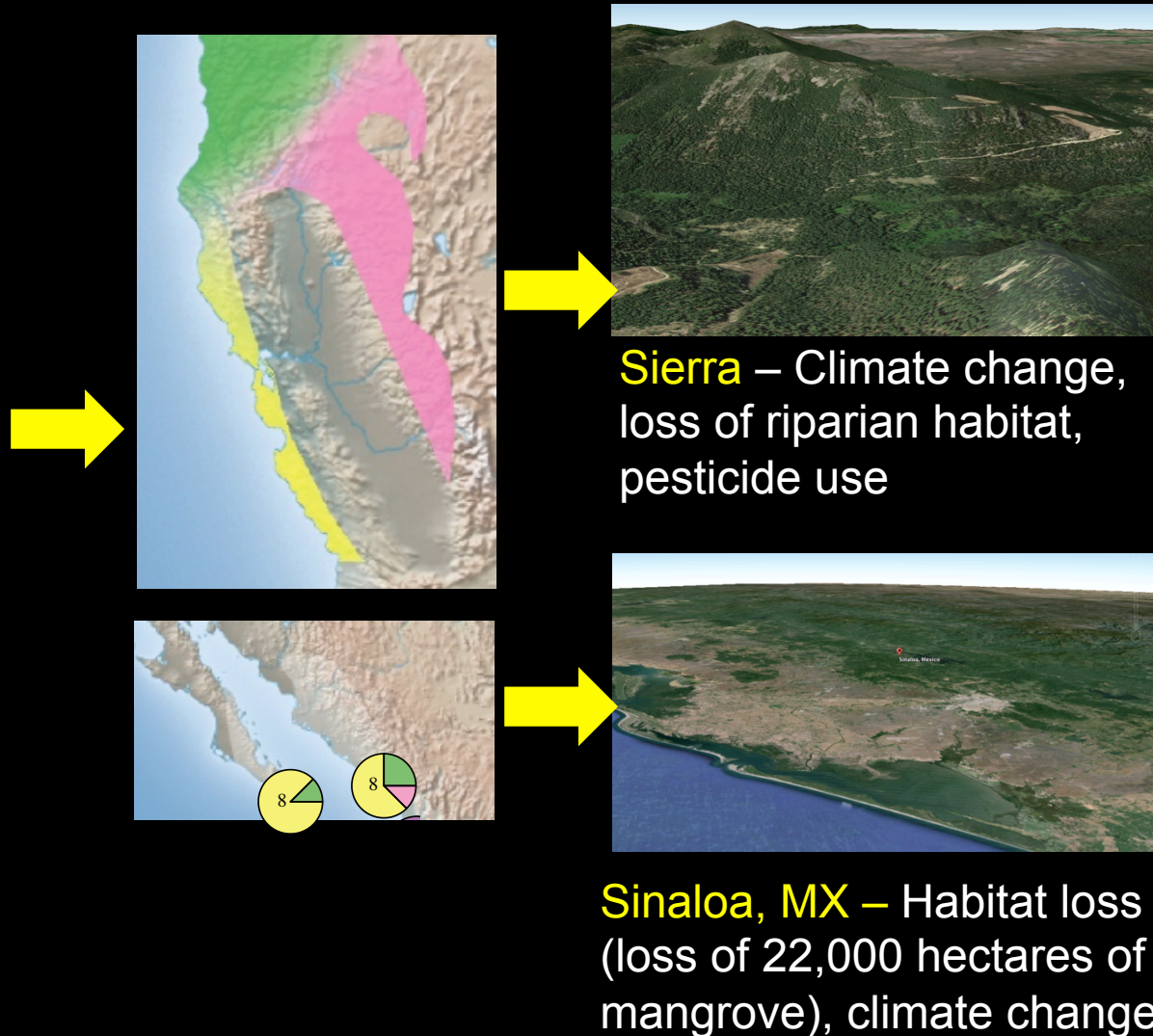
**What can we do with the
resulting information?**

Application: Assess drivers of population trends at regional scales

BBS Data Sierra region

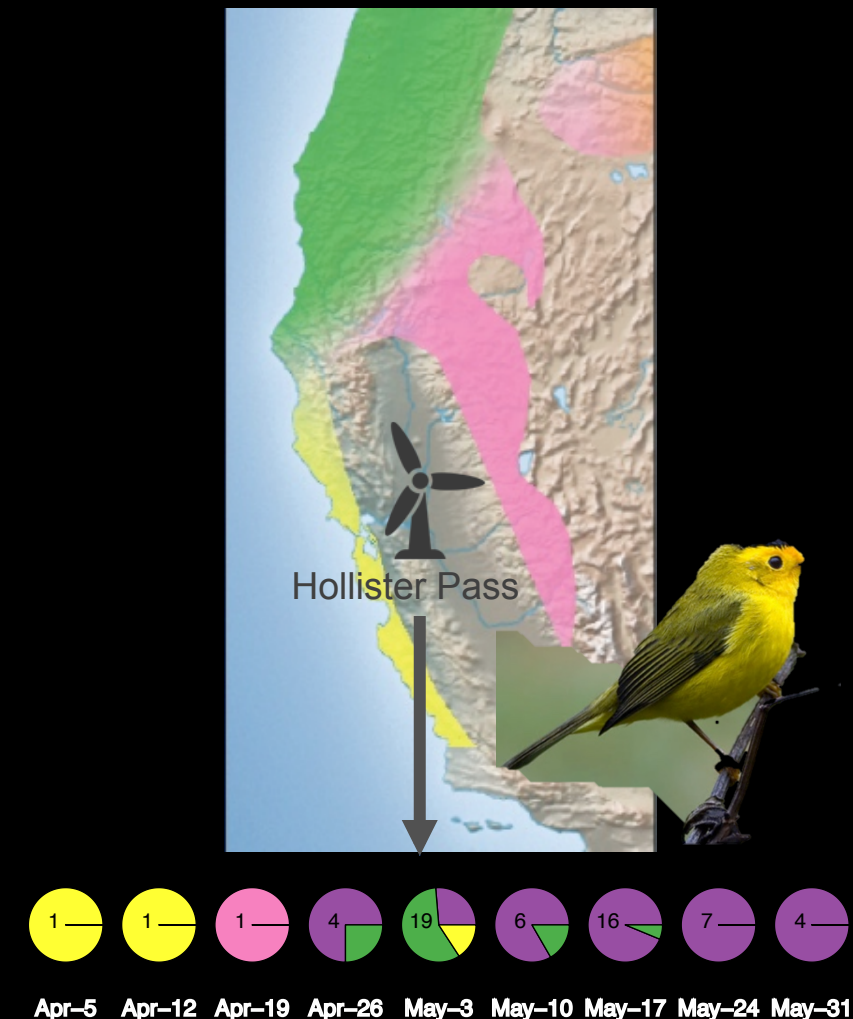


Consistent decline
since 1970's



Application: Siting and mitigation

- Assess if and when vulnerable populations utilize an area.
- Use the timing information to *inform operational mitigation*.
- Can id carcasses to assess *population-level impacts* of collisions.



Our Goal: Map the Migratory Flyways of 50 Species by 2020



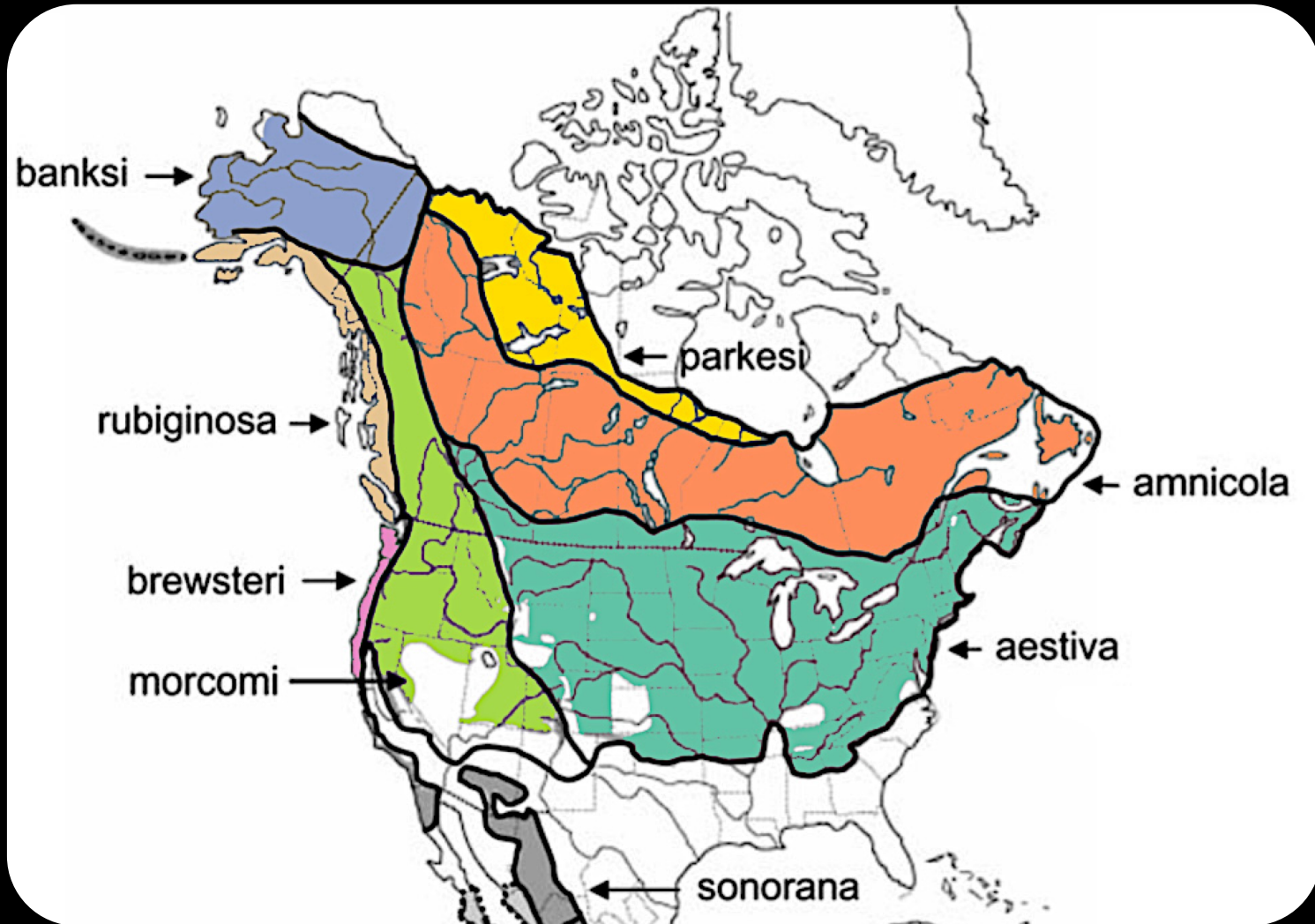
We are 20% of the way there!



Population structure in Yellow Warblers



Do subspecies represent distinct genetic populations?



Genoscape Pipeline

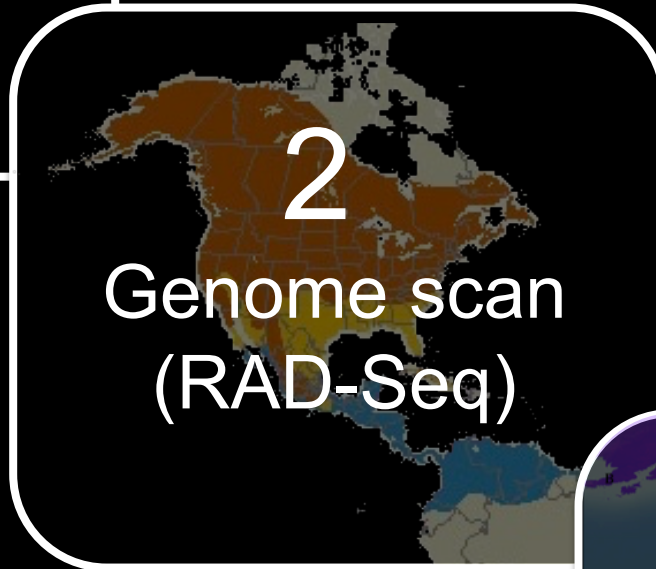
1

Genome Assembly



2

Genome scan
(RAD-Seq)

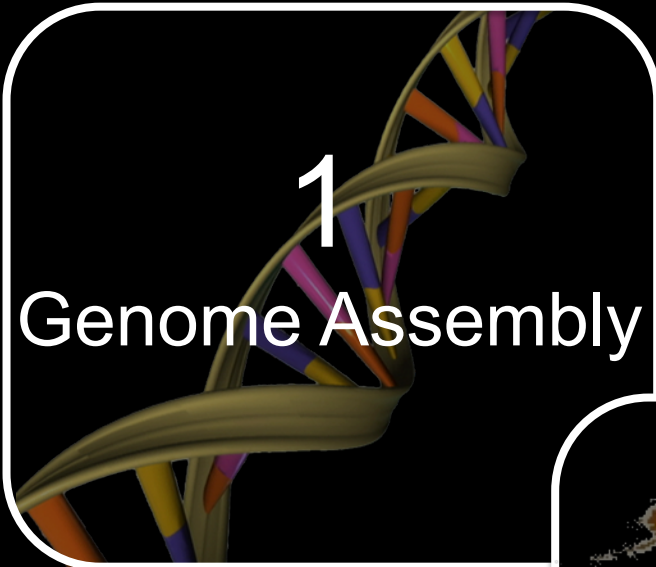


3

96 SNP assay
feather screen

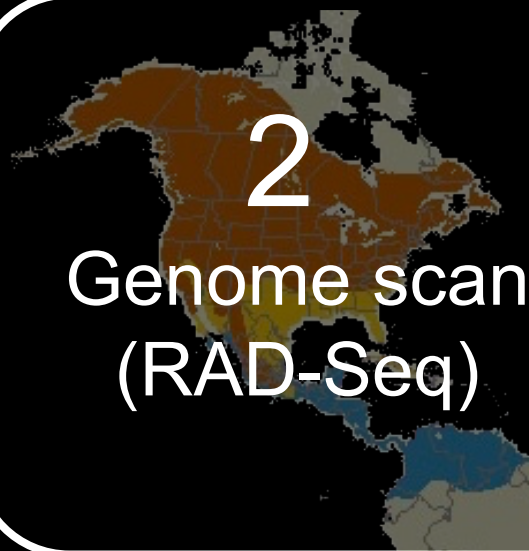


Genoscape Pipeline



1
Genome Assembly

n=1 bird



2
Genome scan
(RAD-Seq)

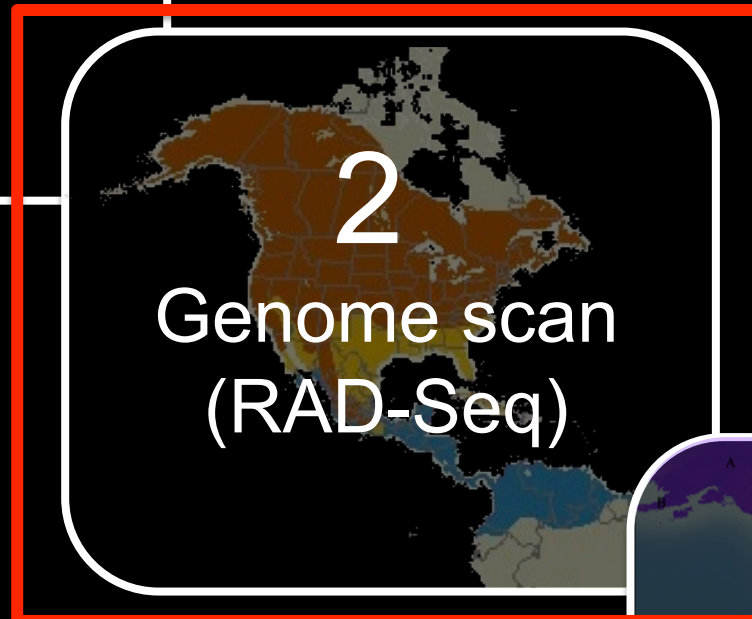
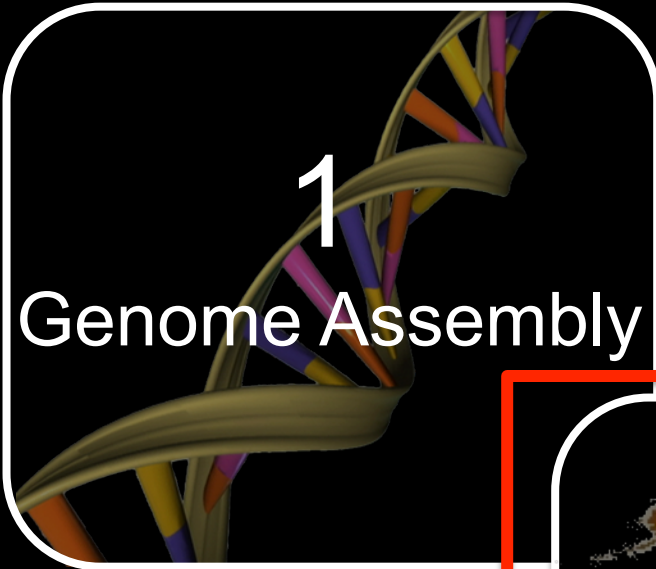
n=~200



3
96 SNP assay
feather screen

n=~3000

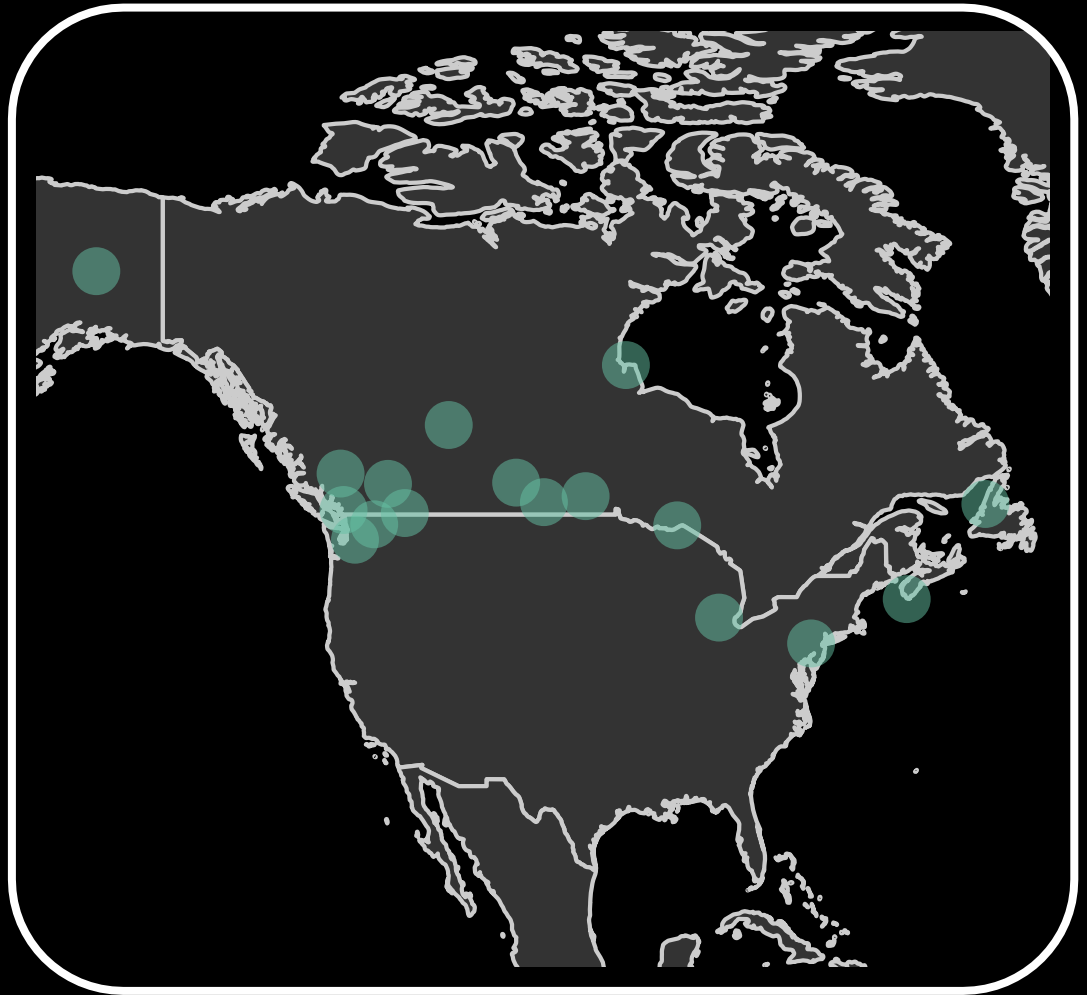
Genoscape Pipeline



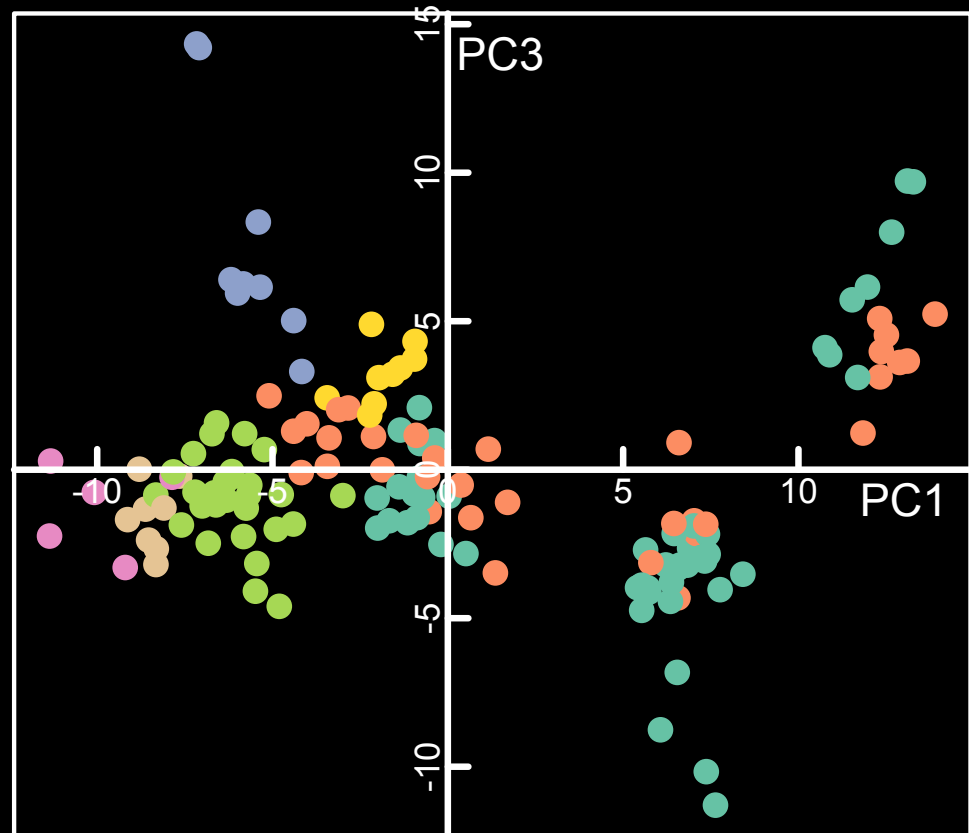
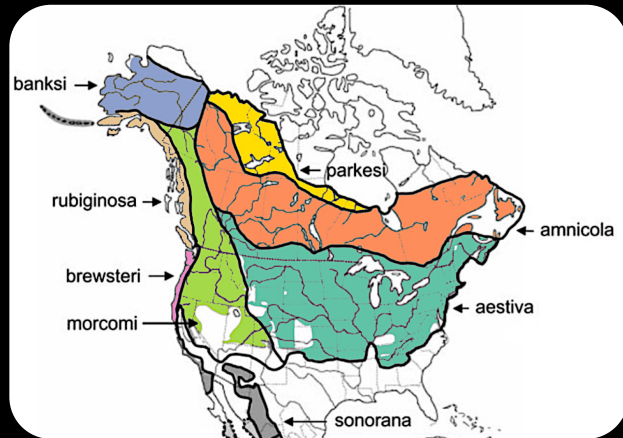
2

Genome scan (RAD-Seq)

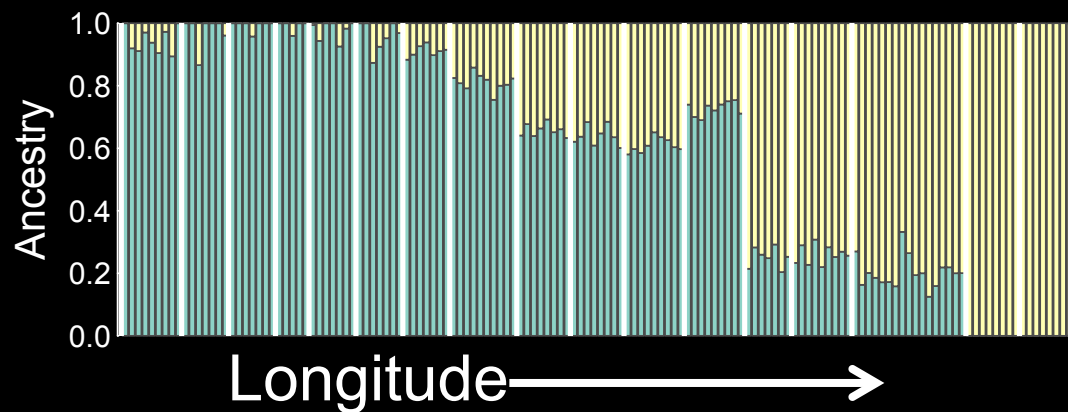
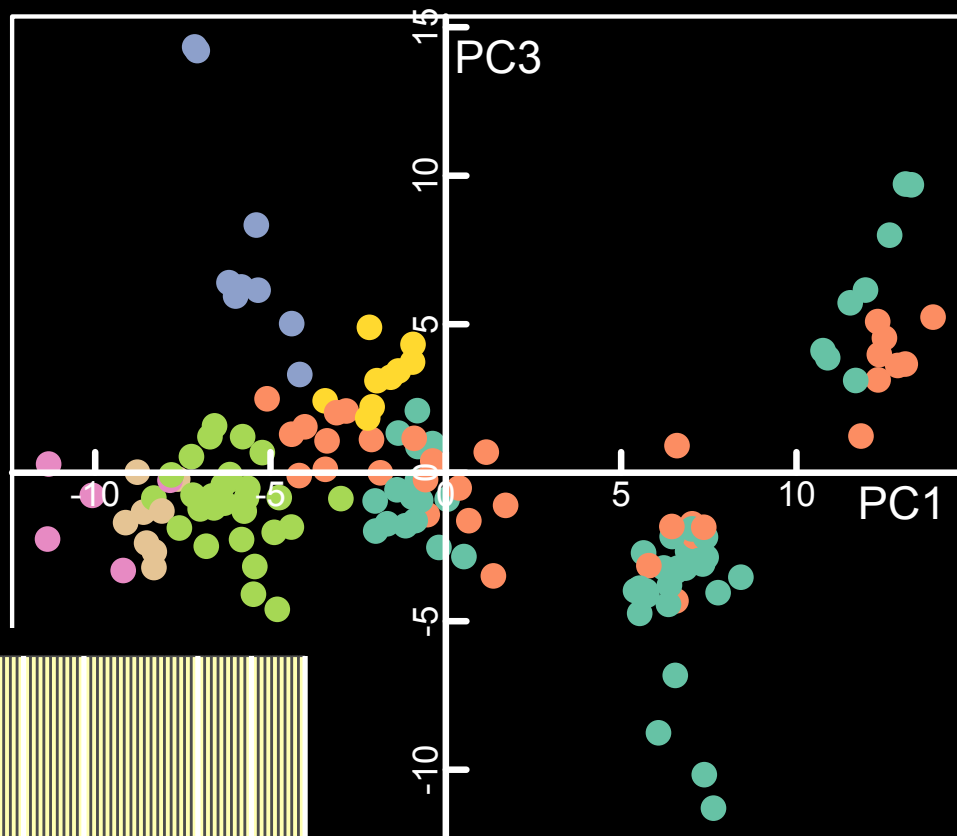
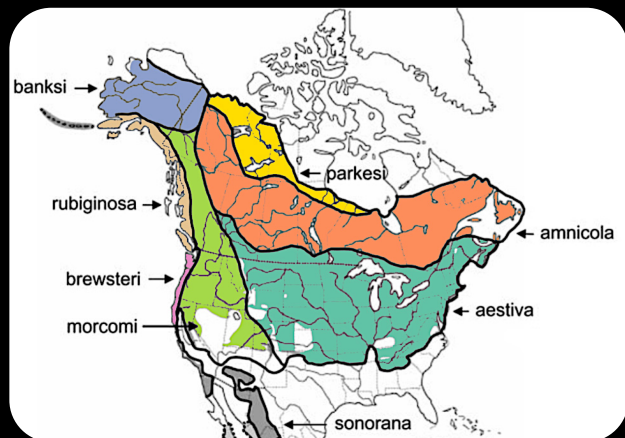
- 192 individuals
- 17 locations
- 7 subspecies
- 492,000 SNPs



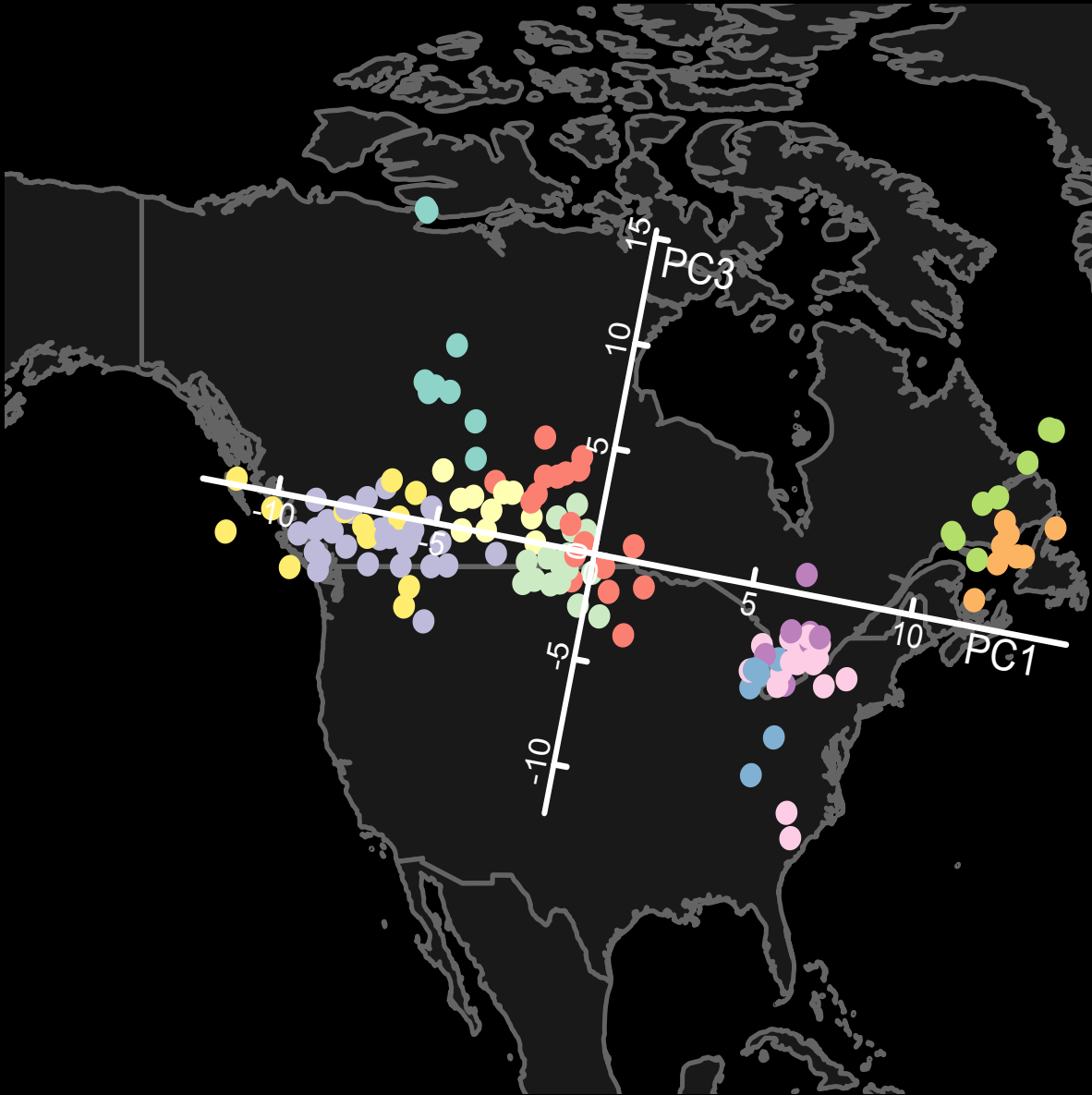
No major splits between subspecies



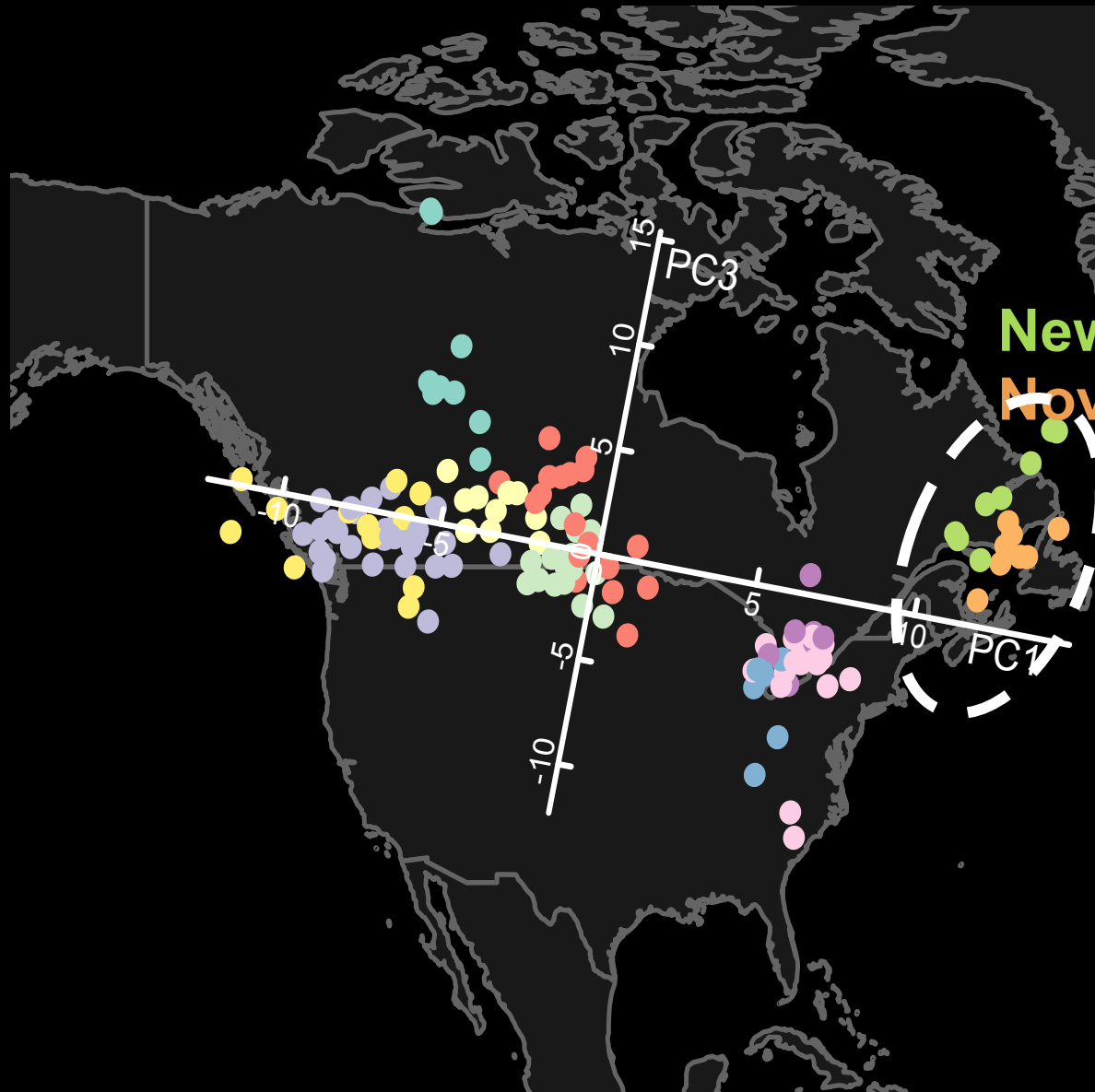
No major splits between subspecies



Isolation by distance

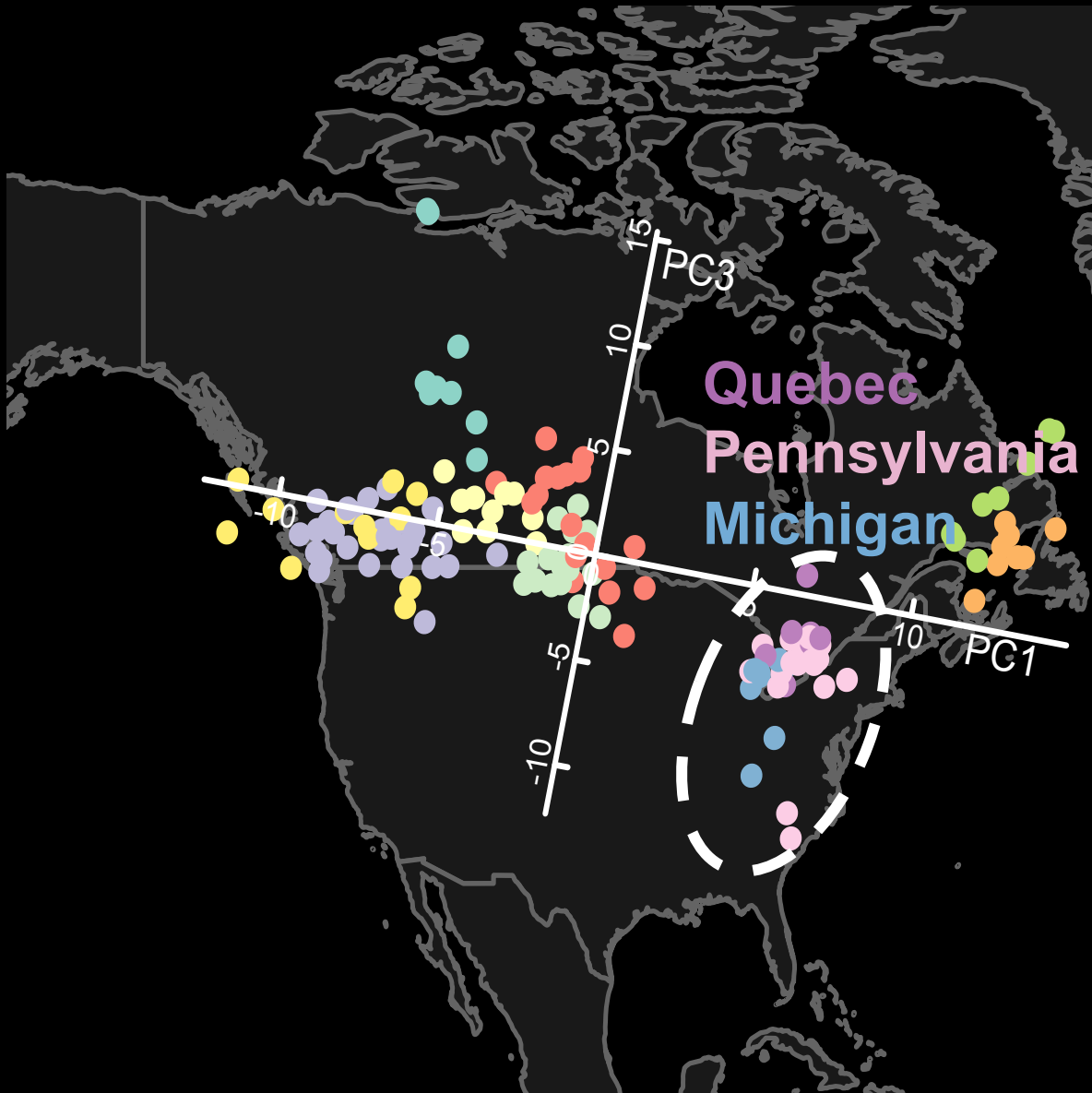


Isolation by distance

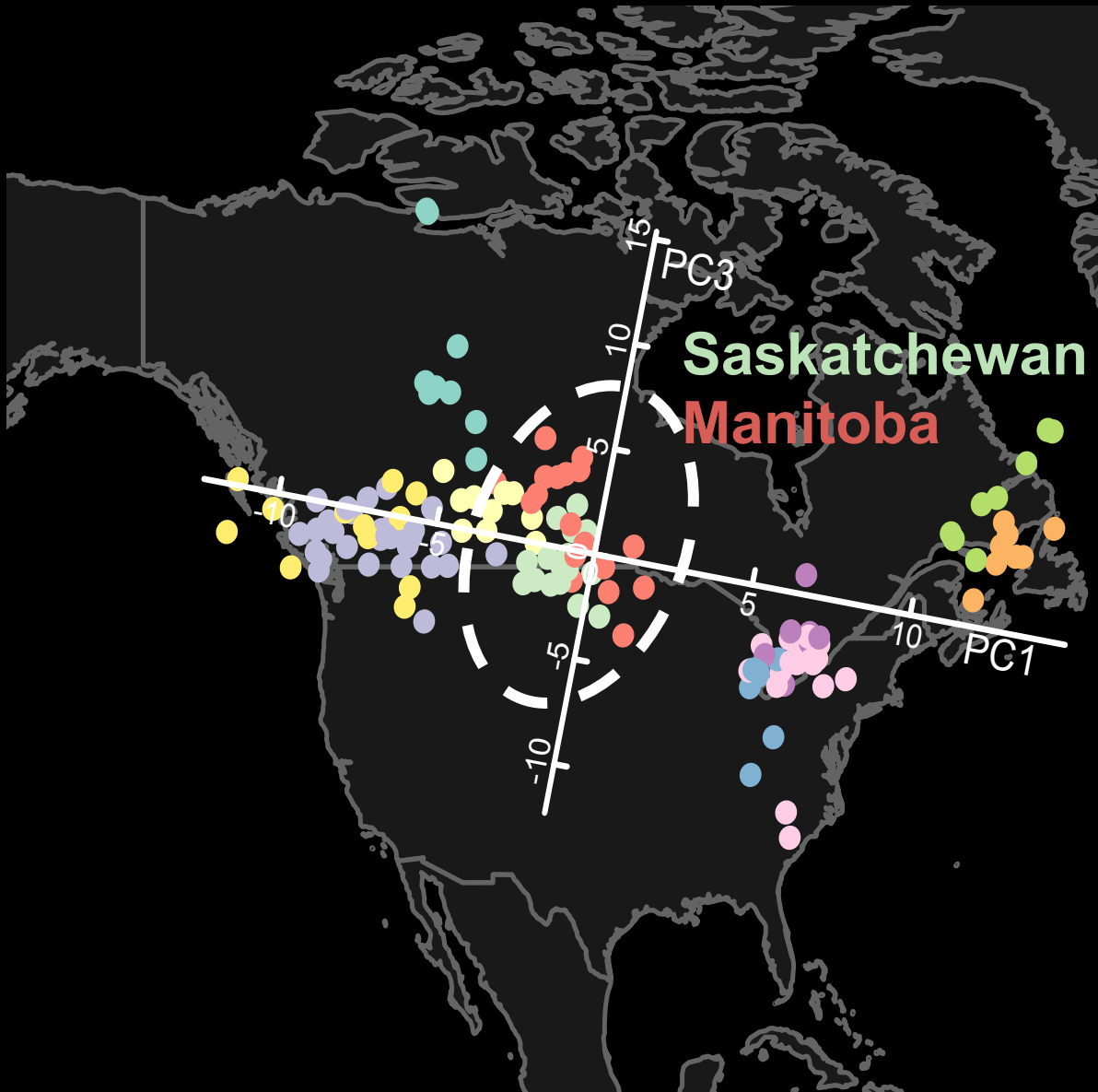


Newfoundland
Nova Scotia

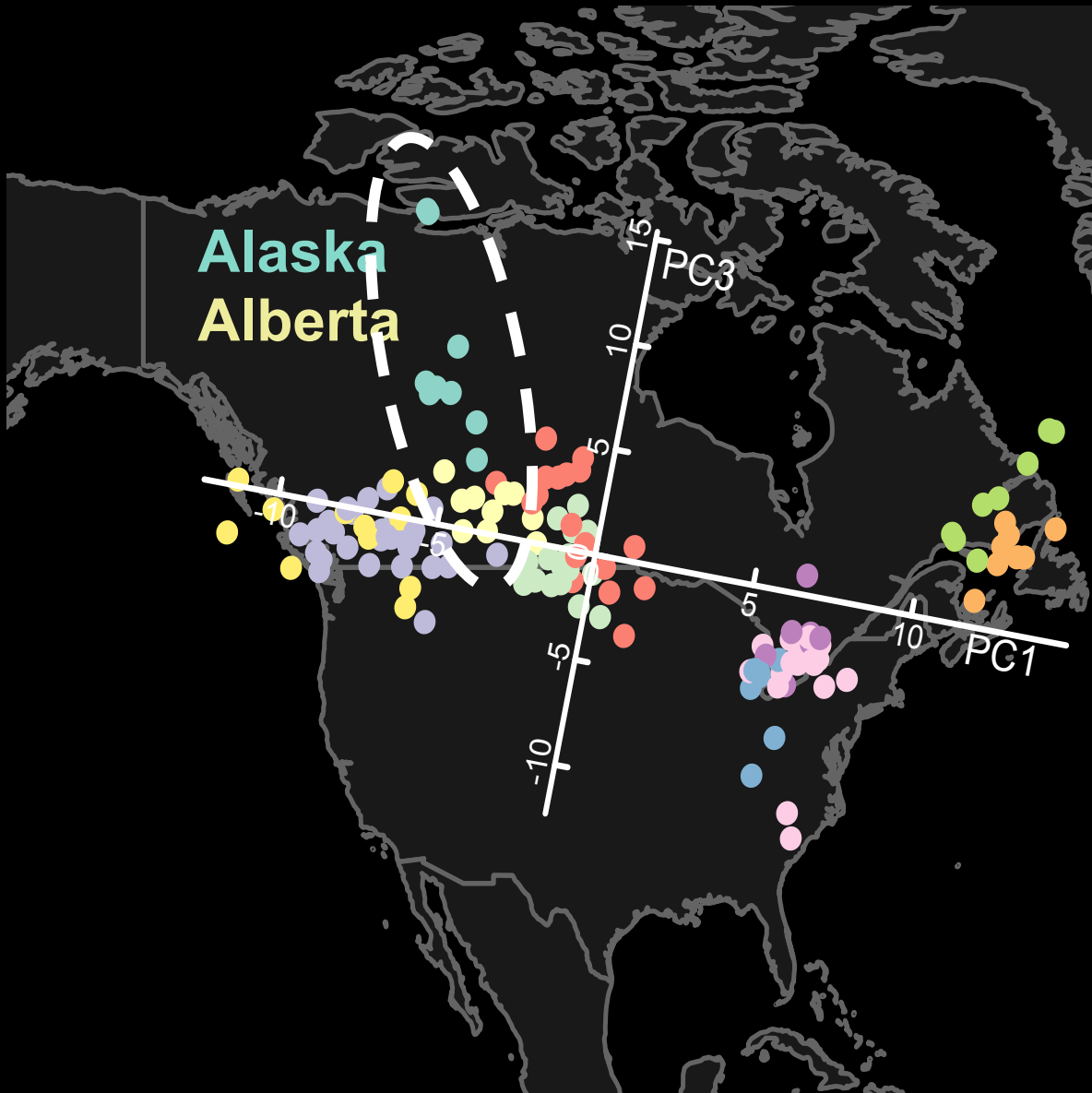
Isolation by distance



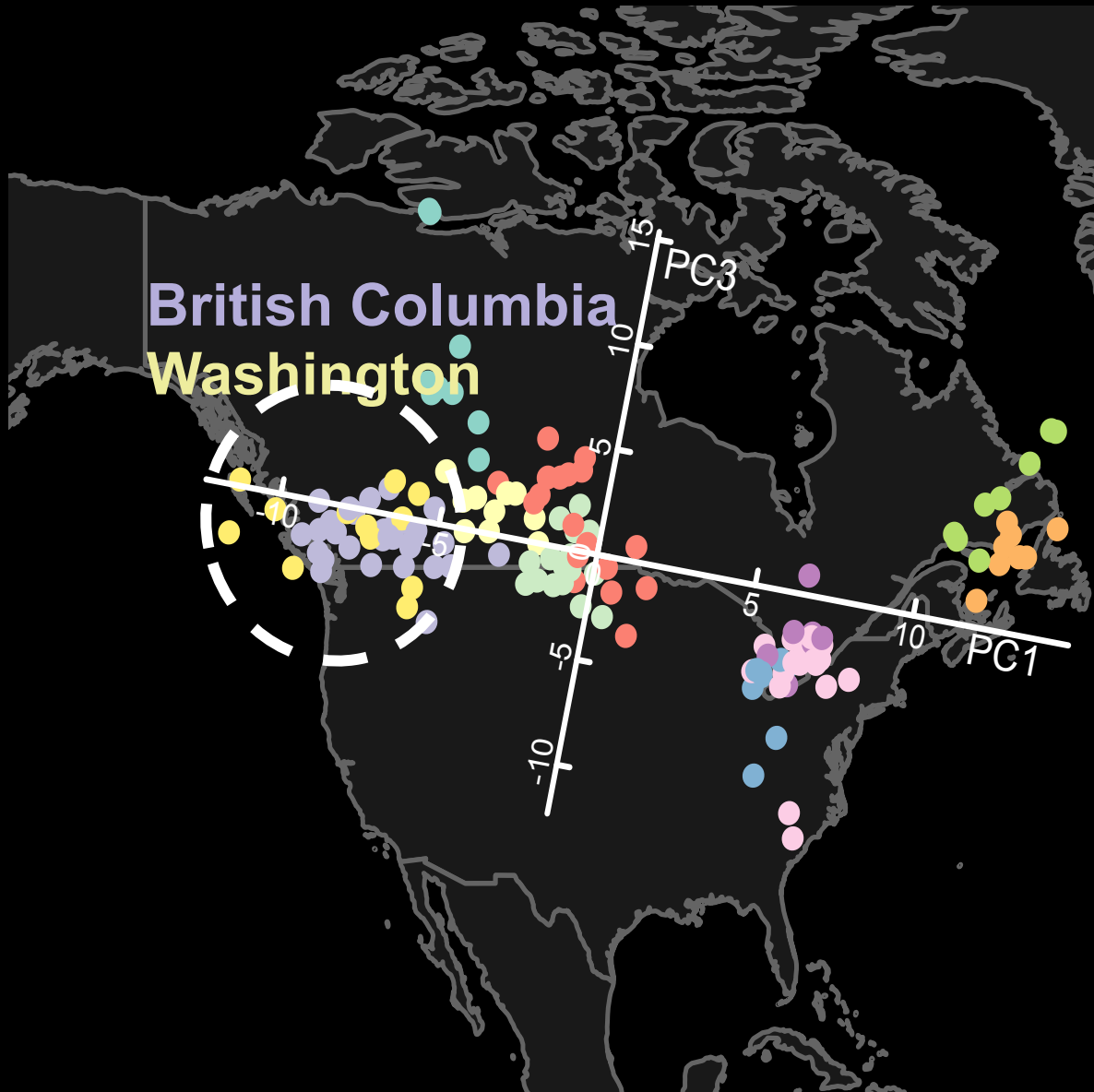
Isolation by distance



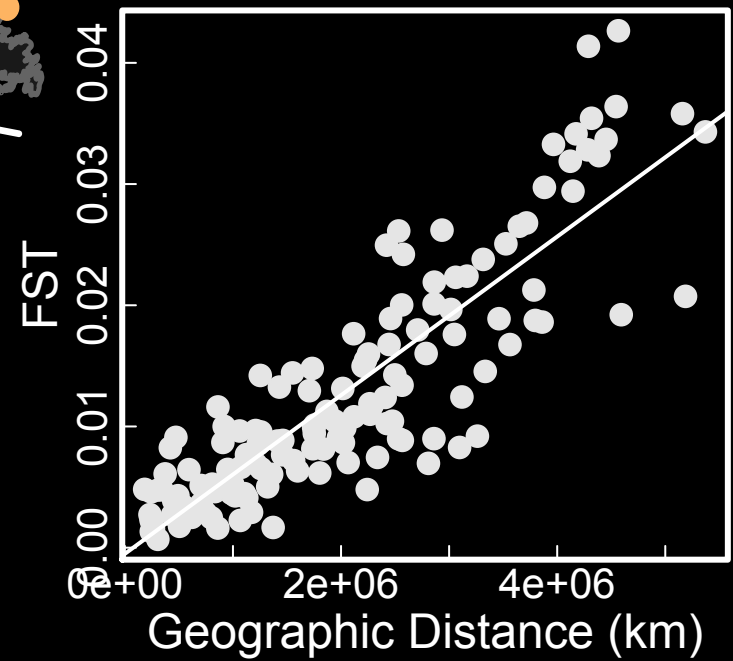
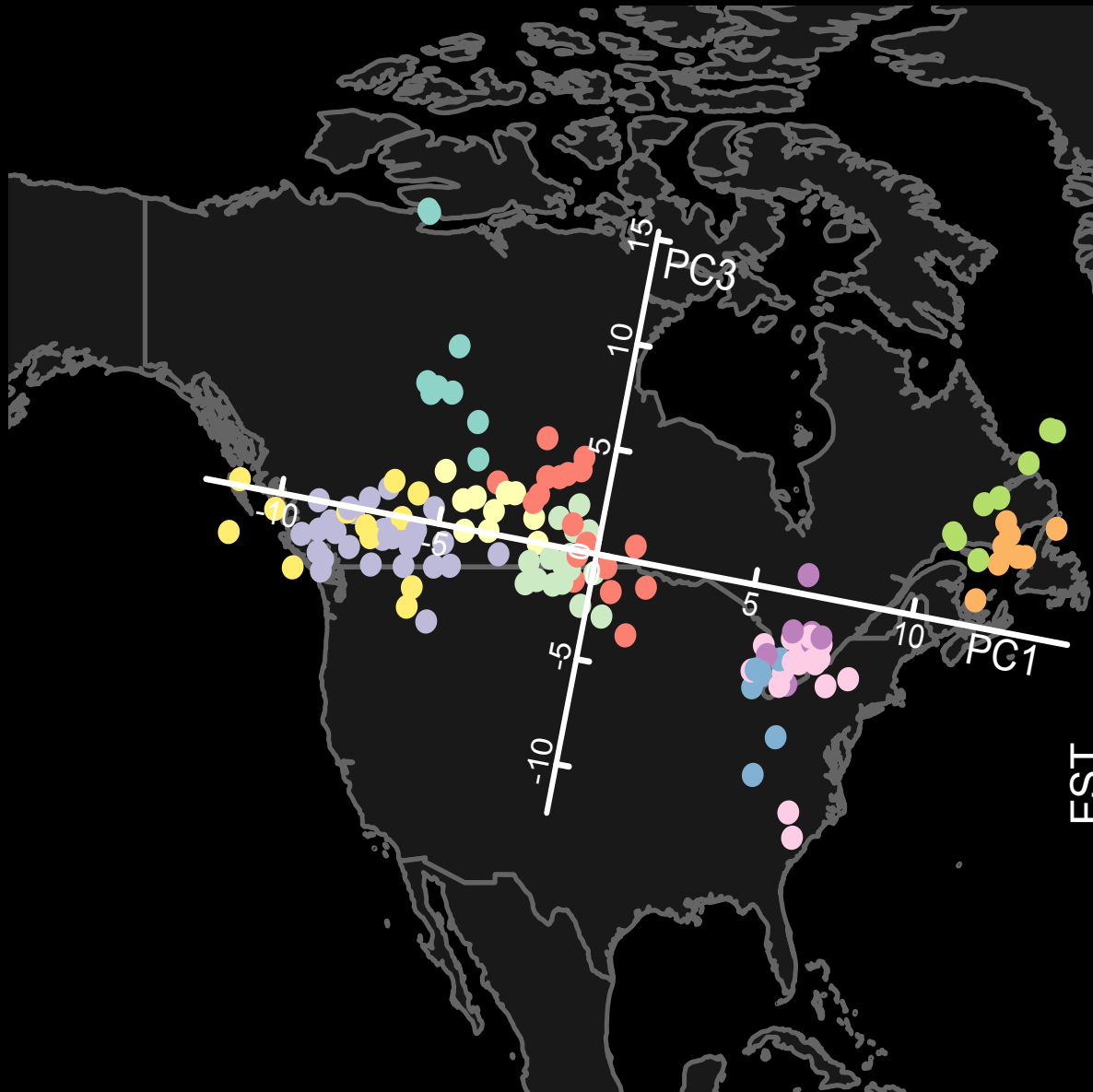
Isolation by distance



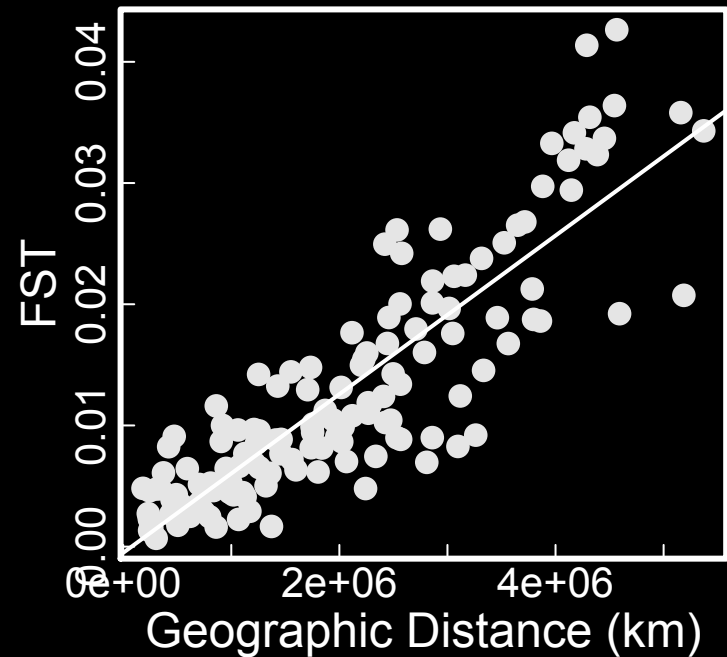
Isolation by distance



Isolation by distance



Conclusion: no strong splits
between subspecies, but genetics
strongly reflect geography



Thank you to our funders:



And several anonymous donors

