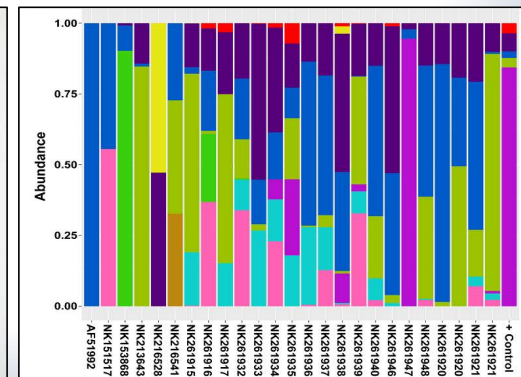
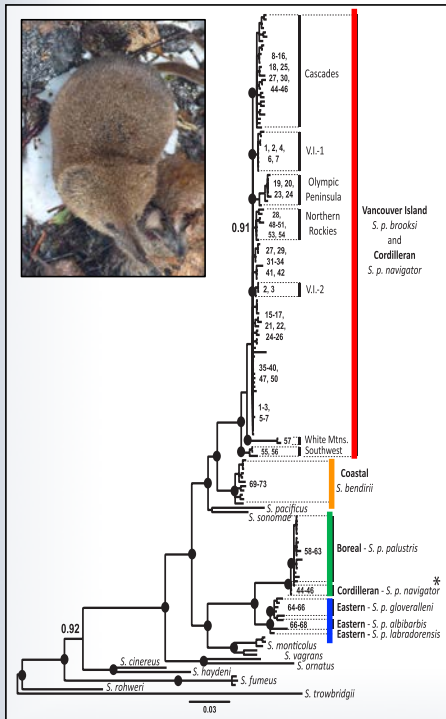




Biodiversity conservation via evolutionary analysis of *common* species: Case studies from North American shrews

Andrew G Hope



Conservation often focuses on rapidly declining,
or critically rare species

- Very expensive
- Often too little, too late...
- May require a "permanent" life-line into the future.



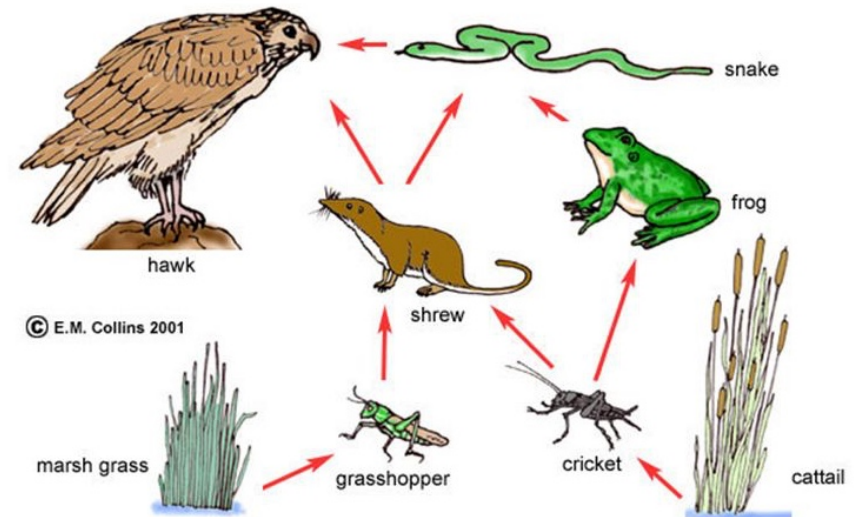
Should we care about imperiled species?
What can they tell us?

- They epitomize the problems:
 - Biodiversity declines can be sudden and fast.
 - We normally know very little about rare taxa.
 - Conserving rare taxa is extremely difficult!
- We should care because:
 - They are indicators of change
 - We don't know what role this species fulfilled
 - We need to understand biodiversity connections!



Benefits of studying common species

- High genetic diversity → high adaptive capacity
- Large populations → easy to work with
- Broad geographic coverage → adapted to regional processes
- Lots of intact ecological connections!
 - High potential to resolve them...

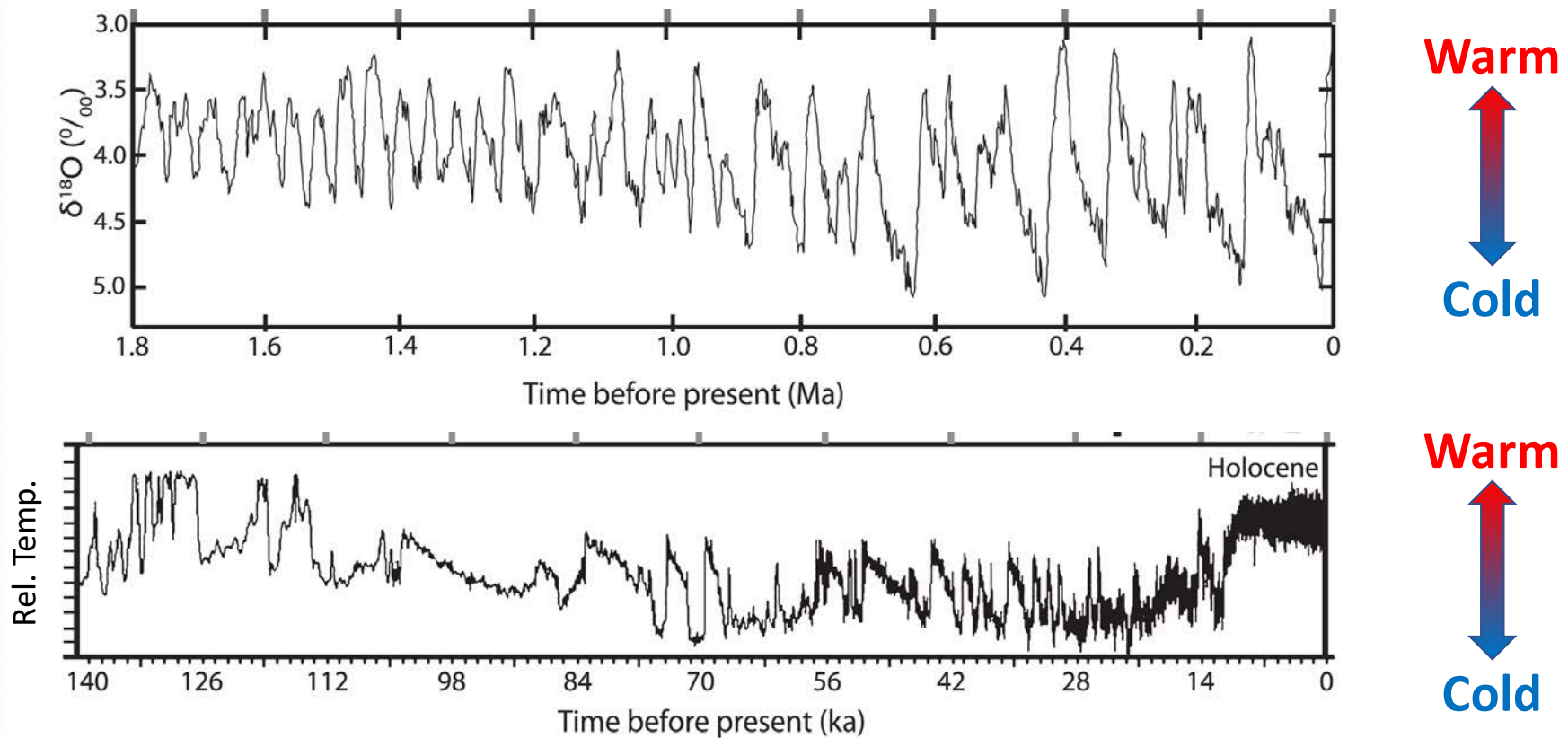


Goals for biodiversity conservation (my view)

1. Define the taxonomy - Phylogeography
 - Describe species and identify distinct lineages
 - Explore evolutionary processes
2. Identify regional centers of diversification
 - Genetic diversity centers/borders over many species?
 - Same spatial/temporal history across species?
 - Regional conservation hotspots?
3. Resolve connections among associated biodiversity
 - Community ecology
 - Hosts and parasites – Co-evolution.

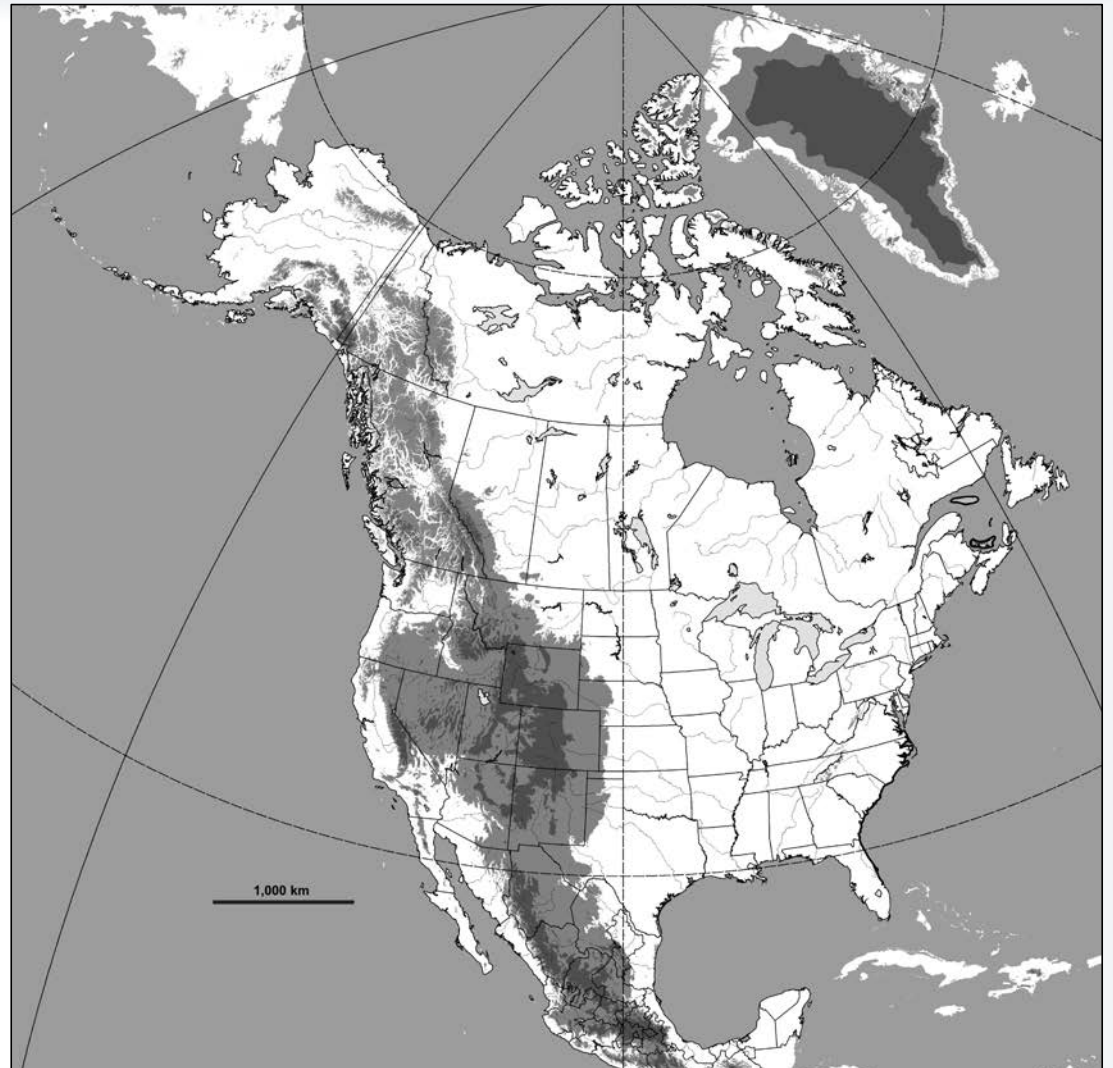
My Study System

Temporal Focus: Quaternary through to present



Spatial Focus:
Northern hemisphere

Current interglacial



Spatial Focus:
Northern hemisphere

Glacial cycle dynamics
e.g., America 20 kyr.



Taxonomic focus: Shrews... common, but cool!



The 19 species of shrews found in Canada.

Shrews, genus *Sorex* ~80 Holarctic species



Resolving generalizable processes of change

- Abundant, ubiquitous
- Tiny, high metabolism, high turnover → rapid evolution
- Insectivorous → complex parasite life cycles

Evolutionary conservation relies on specimens!!



Geo-referenced locality



Ecto & endo parasites



Virus isolates



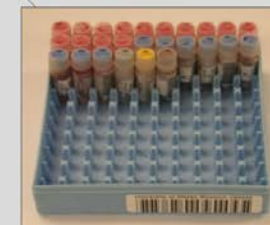
Field notes, ecological data

170 180 190
ATCTCTTGGCTCCAGCATCGATGAAGAACGCA
TCATTAGAGGAAGTAAAGTCGTAAACAGGT
GAATGTCAGAACTTTTAAACACGGATCTCTT
TGTGCTTCGGCGGCGCCGCAAGGGTGCCCG
GGCTTCCCGTGGCAGATCCCAACGCCGGCC
TCTCTTGGCTCCAGCATCGATGAAGAACGCGAG
CAGCATCGATGAAGAACGCGAGAACGCGAT
CGATACCTTCTGAGTGTCTTAGCGAAGTGTCA
CGGATCTCTTGGCTCCAGCATCGATGAAGAAC
ACAAACGGATCTCTTGGCTCCAGCATCGATGAA
CGGATCTCTTGGCTCCAGCATCGATGAAGAAC
GATGAAGAACGCGAGAACGCGATATGTAAT

Genomic data



Publications



Ultrafrozen tissues

Methods

Collect specimens → Sequence genes → Analyze data

- 800 specimens representing all “species”
- Mitogenome sequencing (in progress)
 - Long-range PCR for ~200 samples
- Nuclear reduced representation sequencing (in development)
 - ~4000 gene regions
- Build phylogenetic trees
- Test for signals of selection – adaptation across environments
- Test for hybridization – fitness consequences

Goals for biodiversity conservation

1. Define the taxonomy.

- Describe species and identify distinct lineages
- Explore evolutionary processes

2. Identify regional centers of diversification

- Genetic diversity centers/borders over many species?
- Congruent spatial/temporal history across species?
- Regional conservation hotspots?

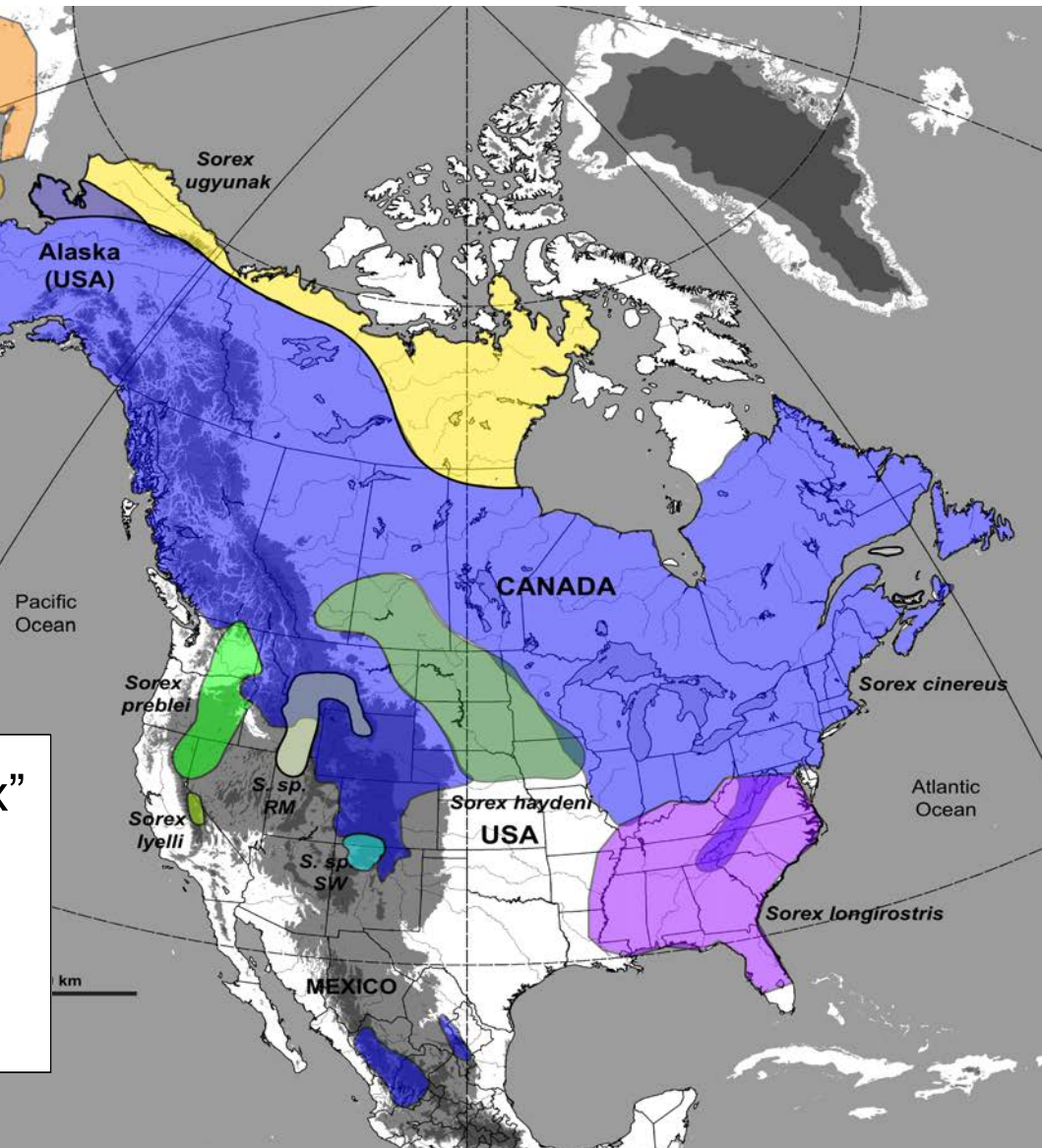
3. Resolve connections among associated biodiversity

- Community ecology
- Hosts and parasites – Co-evolution.

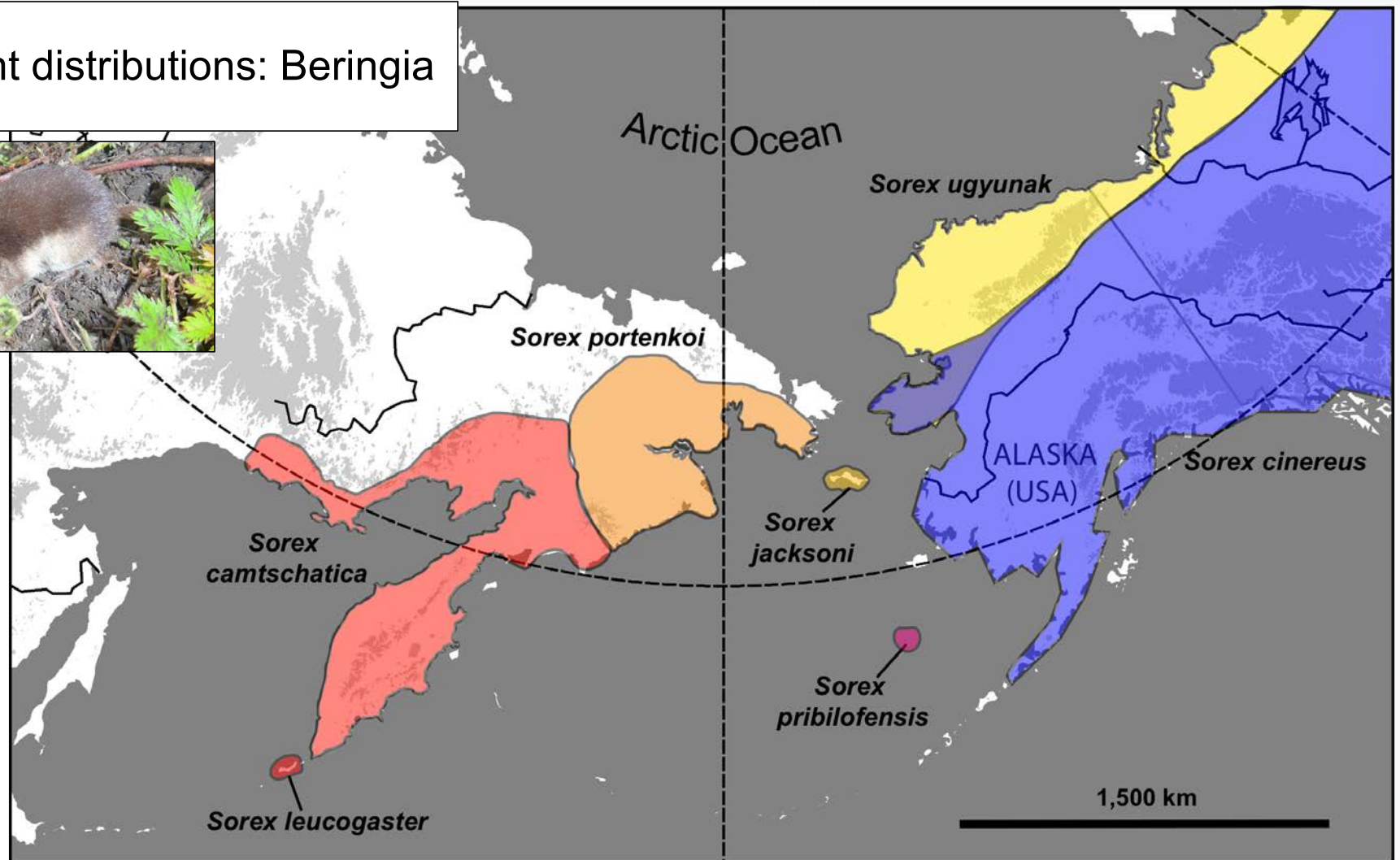


Masked shrew “complex”
13 Species?

Present distributions
North America

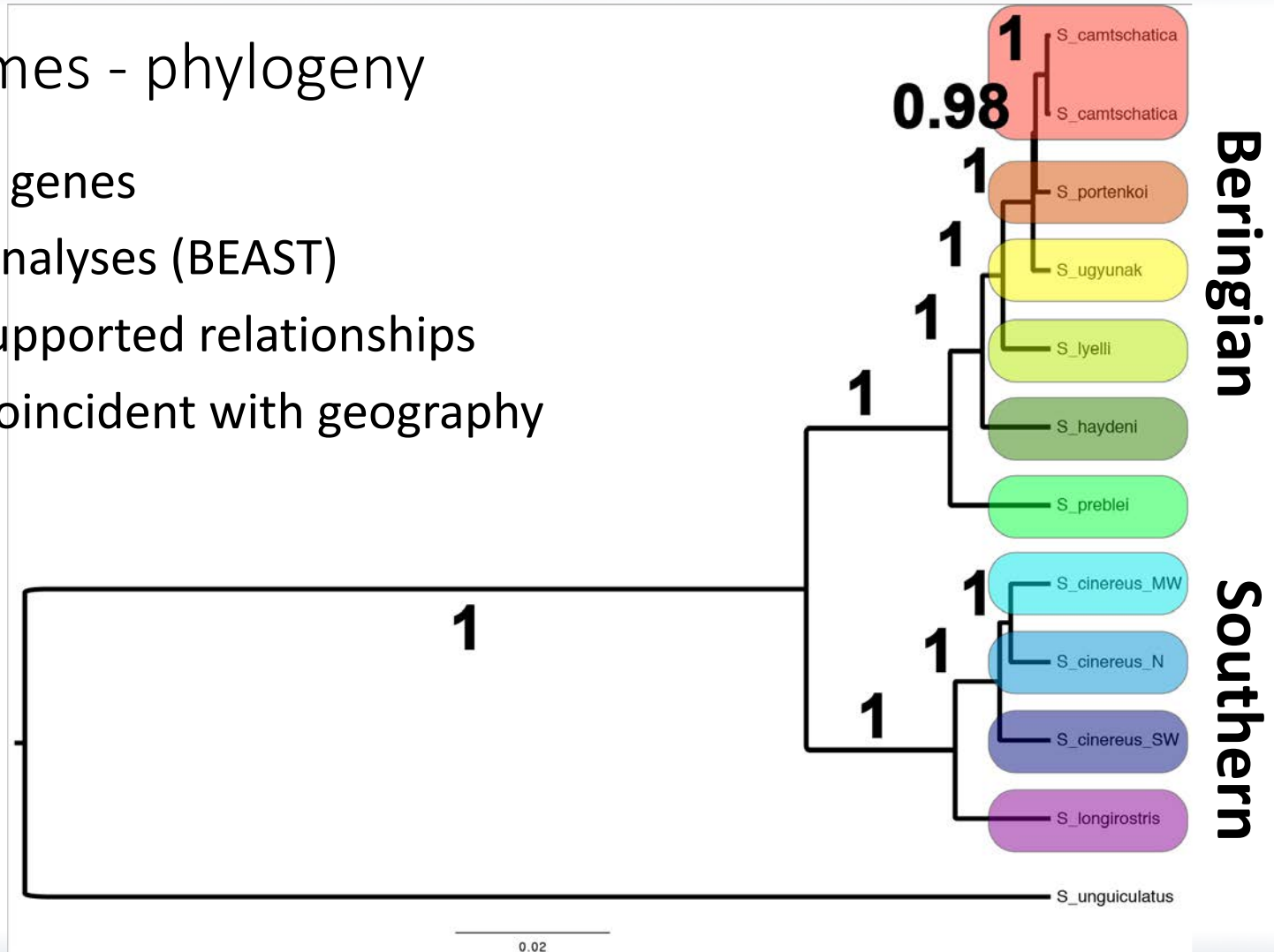


Present distributions: Beringia



Mitogenomes - phylogeny

- All mtDNA genes
- Bayesian analyses (BEAST)
- Strongly supported relationships
- Lineages coincident with geography



Present distributions
North America

Alaska (USA)

Canada

USA

Mexico

Atlantic Ocean

Sorex camtschatica

S. portenkoi

S. ugunak

S. lyelli

S. haydeni

S. preblei

S. cinereus_MW

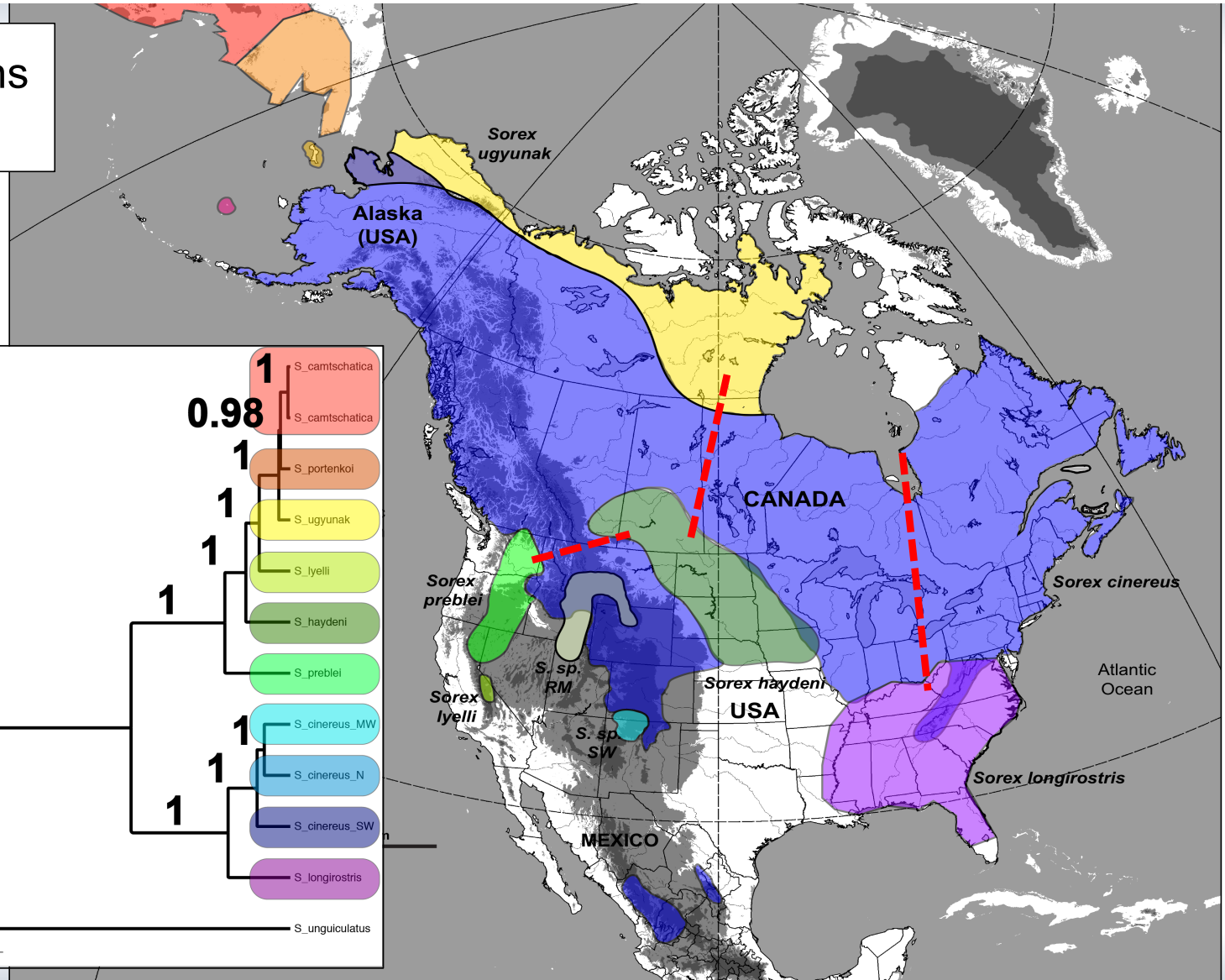
S. cinereus_N

S. cinereus_SW

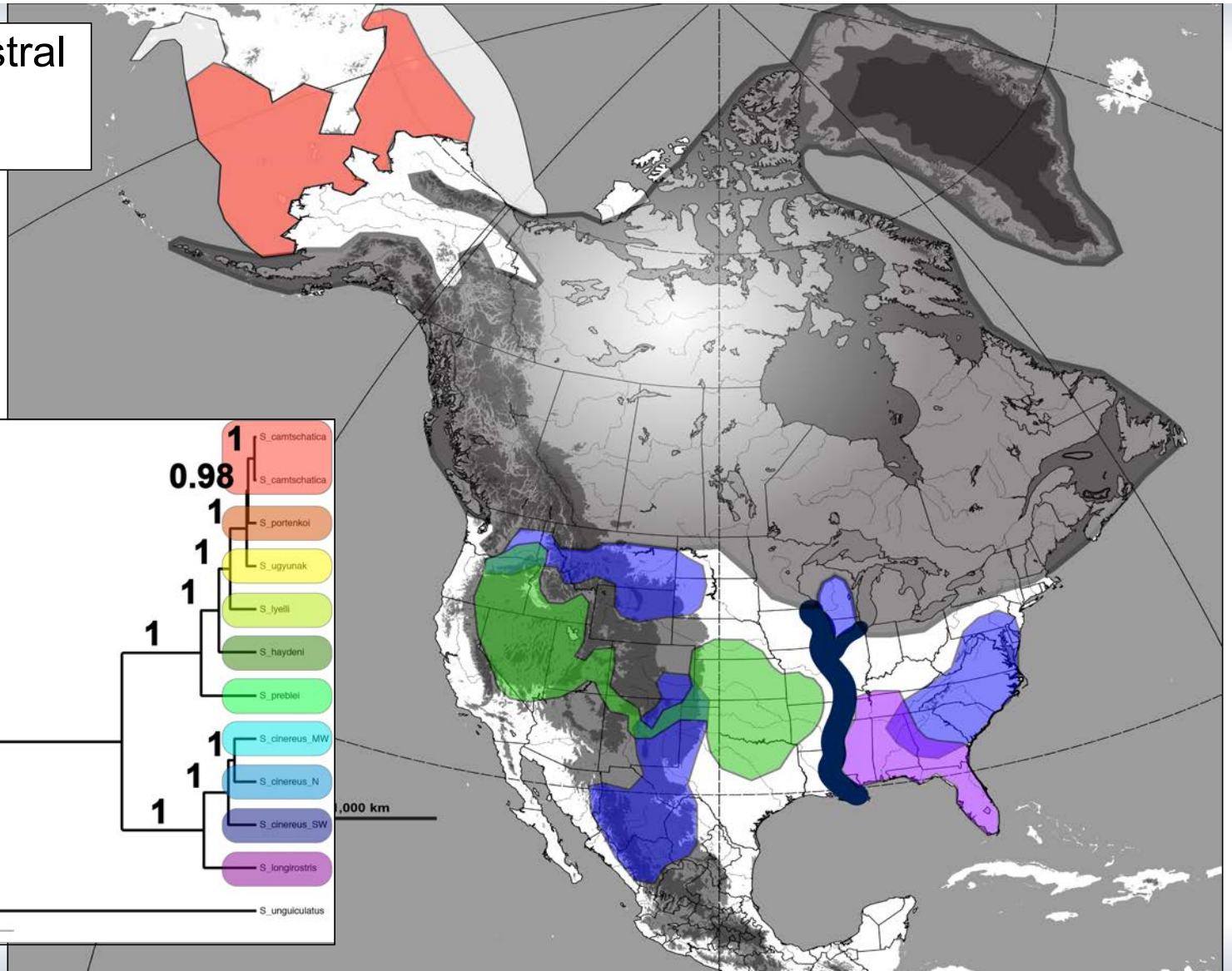
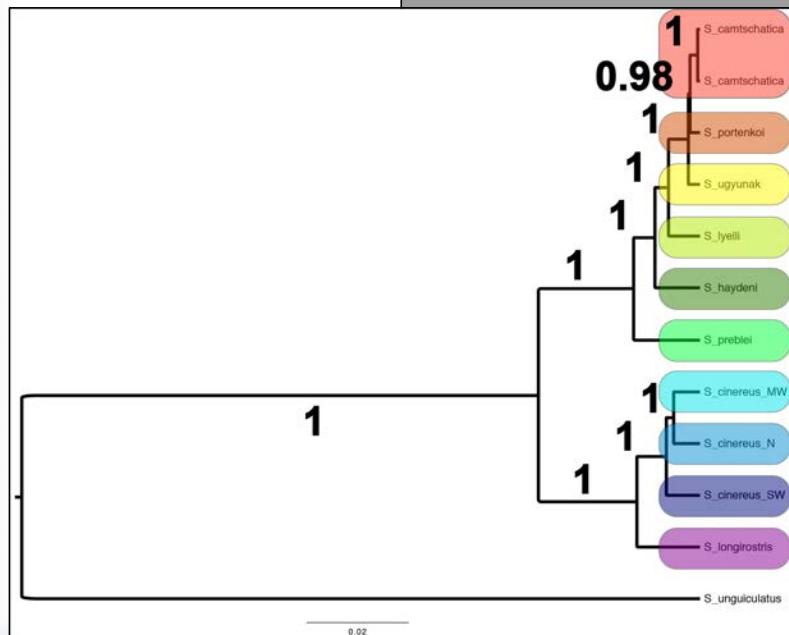
S. longirostris

S. unguiculatus

0.02

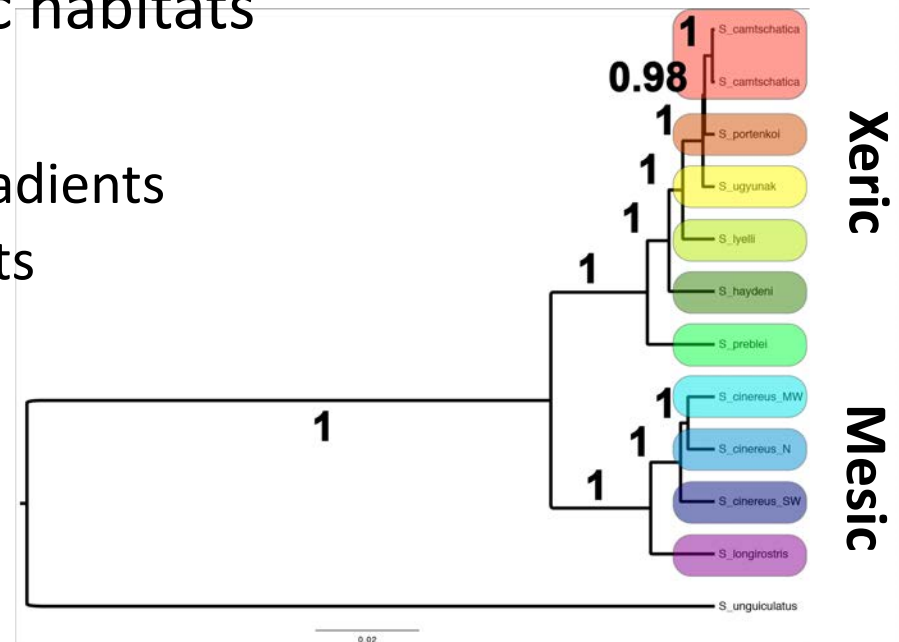


Hypothetical ancestral
distributions
20,000 yrs ago



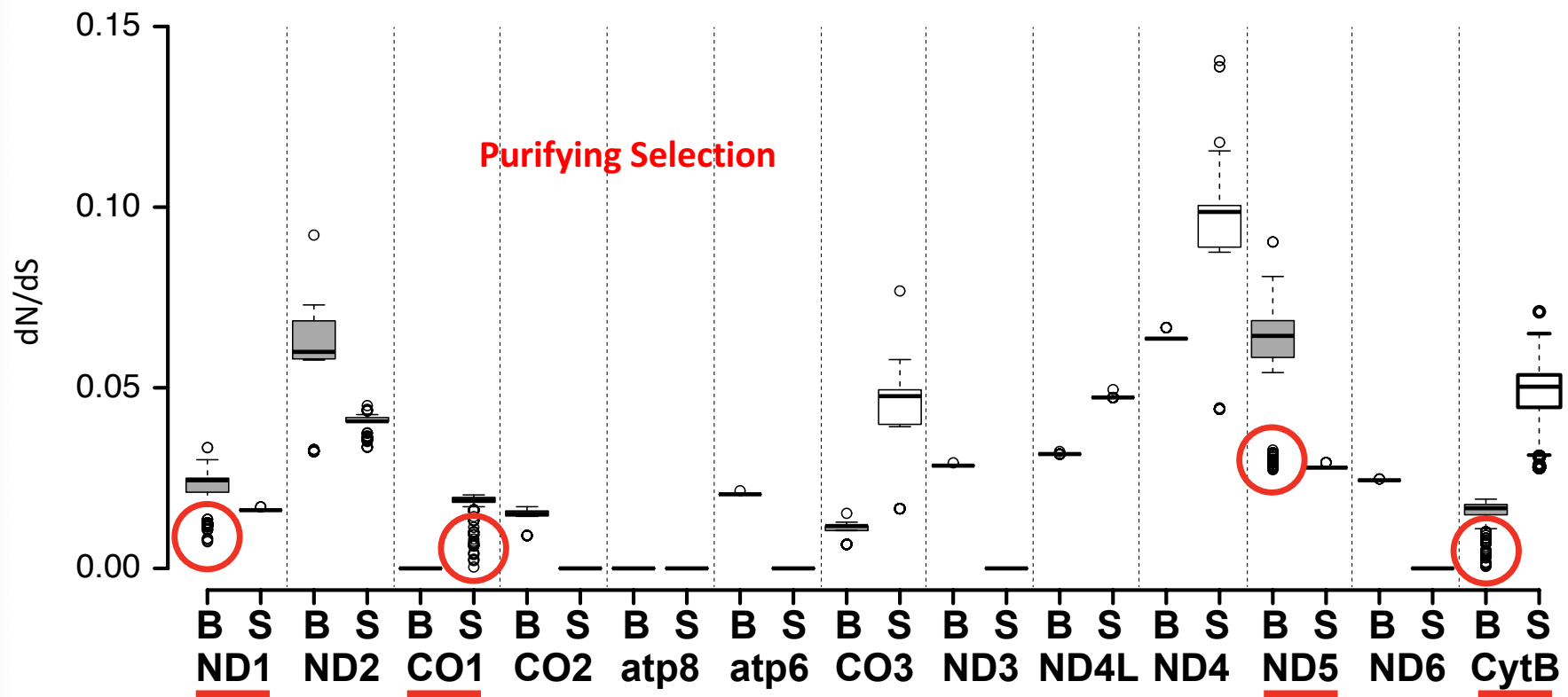
Mitogenomes – adaptation to local environments

- Masked shrews - extremely high metabolism
- Two major clades - mesic or xeric habitats
- Expectations:
 - selection across environmental gradients
 - intensified in harsher environments
 - purifying or diversifying selection
 - reflects demographic history

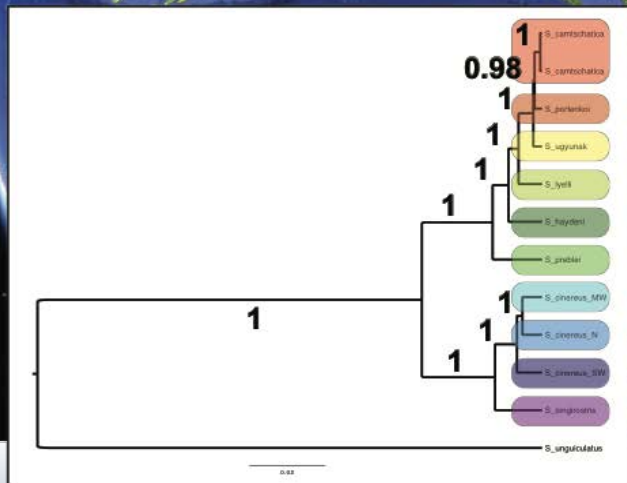


Mitogenomes - adaptation

- REL (random effects likelihood) tests
- dN/dS ratios



Mitogenomes to nuclear genomes...

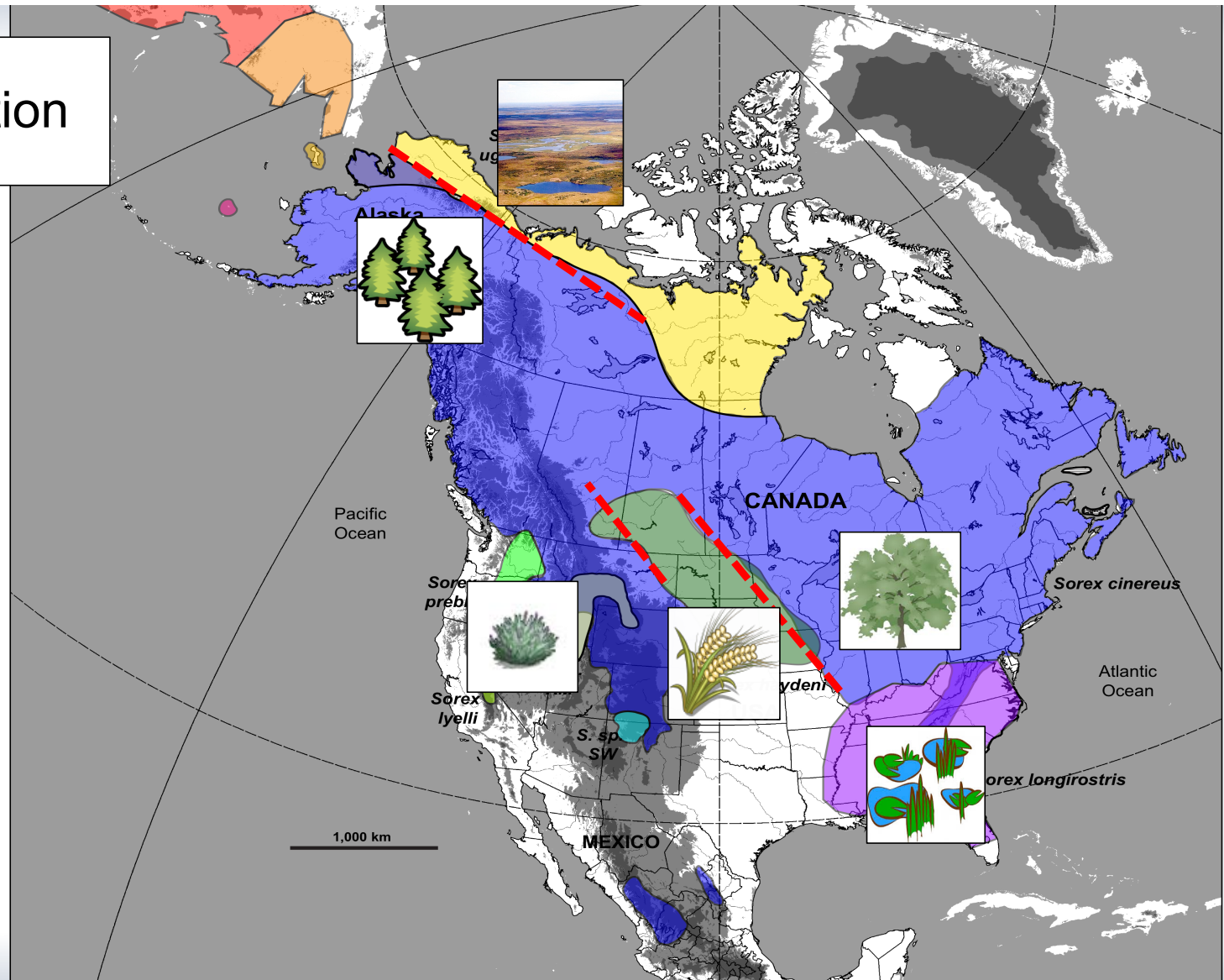


of State Geographer
2016 Google
andsat / Copernicus
A, U.S. Navy, NGA, GEBCO

Google Earth

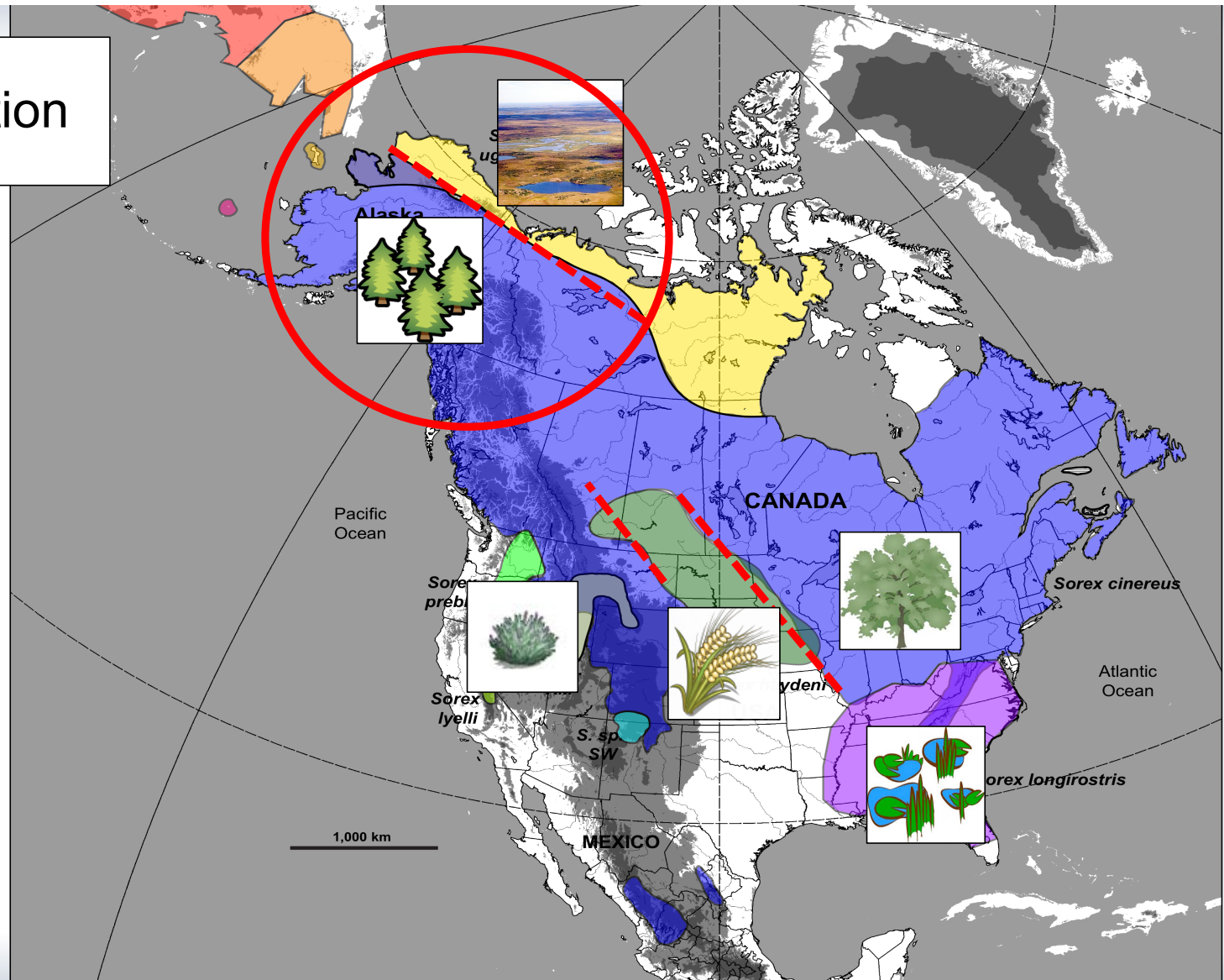
Shrew Hybridization

- Complexity:
 - Evolutionary
 - Geographic
 - Ecological
 - Temporal
- Species-pump mechanism?



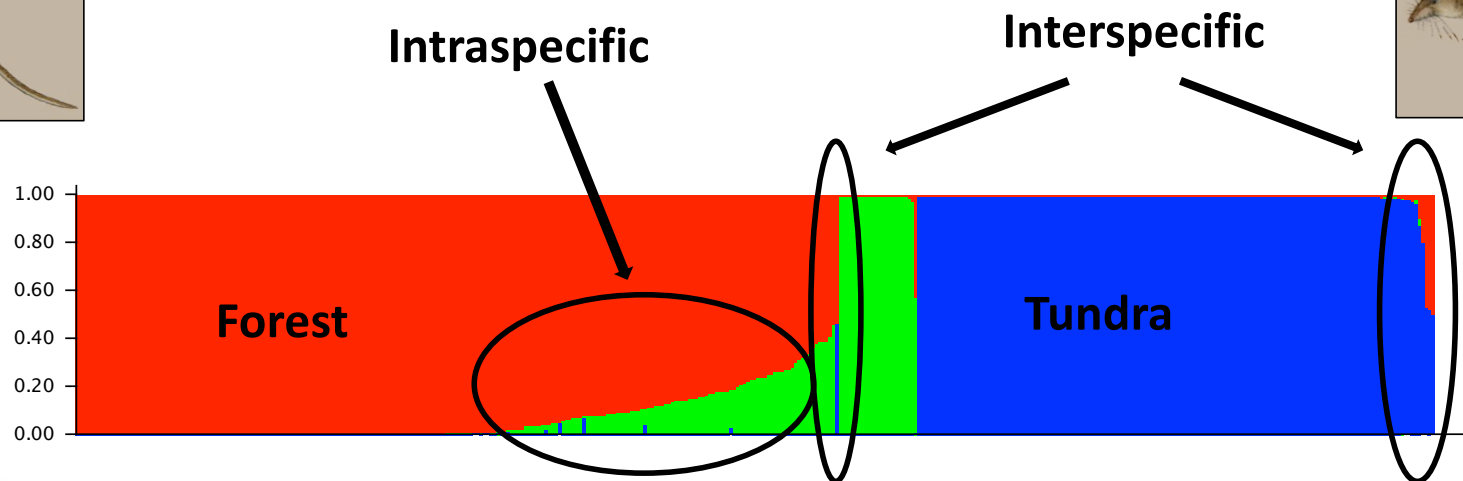
Shrew Hybridization

- Complexity:
 - Evolutionary
 - Geographic
 - Ecological
 - Temporal
- Species-pump mechanism?



Shrew Hybridization

- Shotgun sequencing (MiSeq) to develop >20 microsatellites
- Rigorous sampling across boreal-tundra contact zone
 - Forest shrew vs. tundra shrew
 - ~400 archived specimens



Goals for biodiversity conservation

1. Define the taxonomy.

- Describe species and identify distinct lineages
- Explore evolutionary processes

2. Identify regional centers of diversification

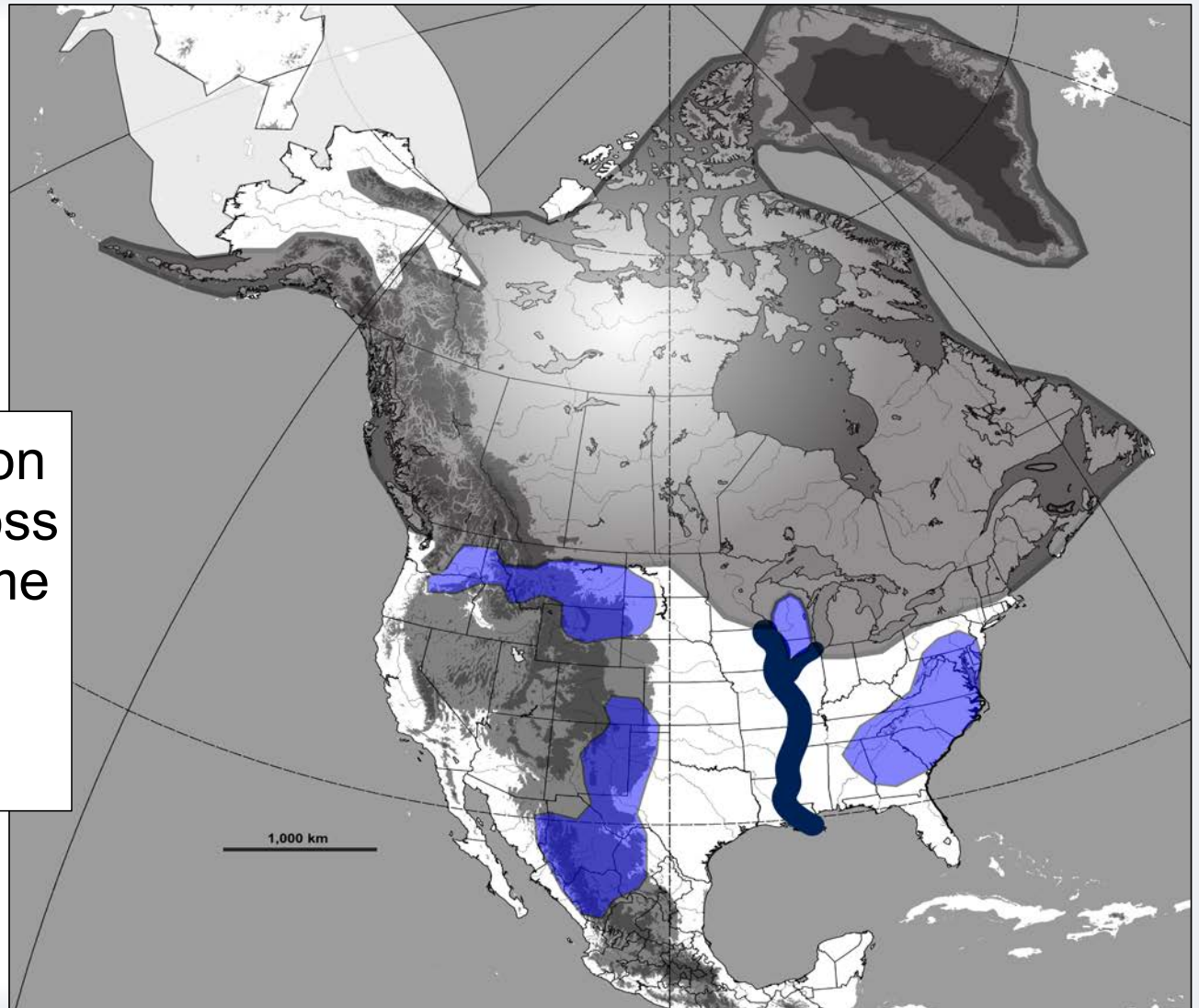
- Genetic diversity centers/borders over many species?
- Congruent spatial/temporal history across species?
- Regional conservation hotspots?

3. Resolve connections among associated biodiversity

- Community ecology
- Hosts and parasites – Co-evolution.
- Host specificity, host switching

Process of diversification
may be repeatable across
species and through time

Regional centers for
masked shrews?

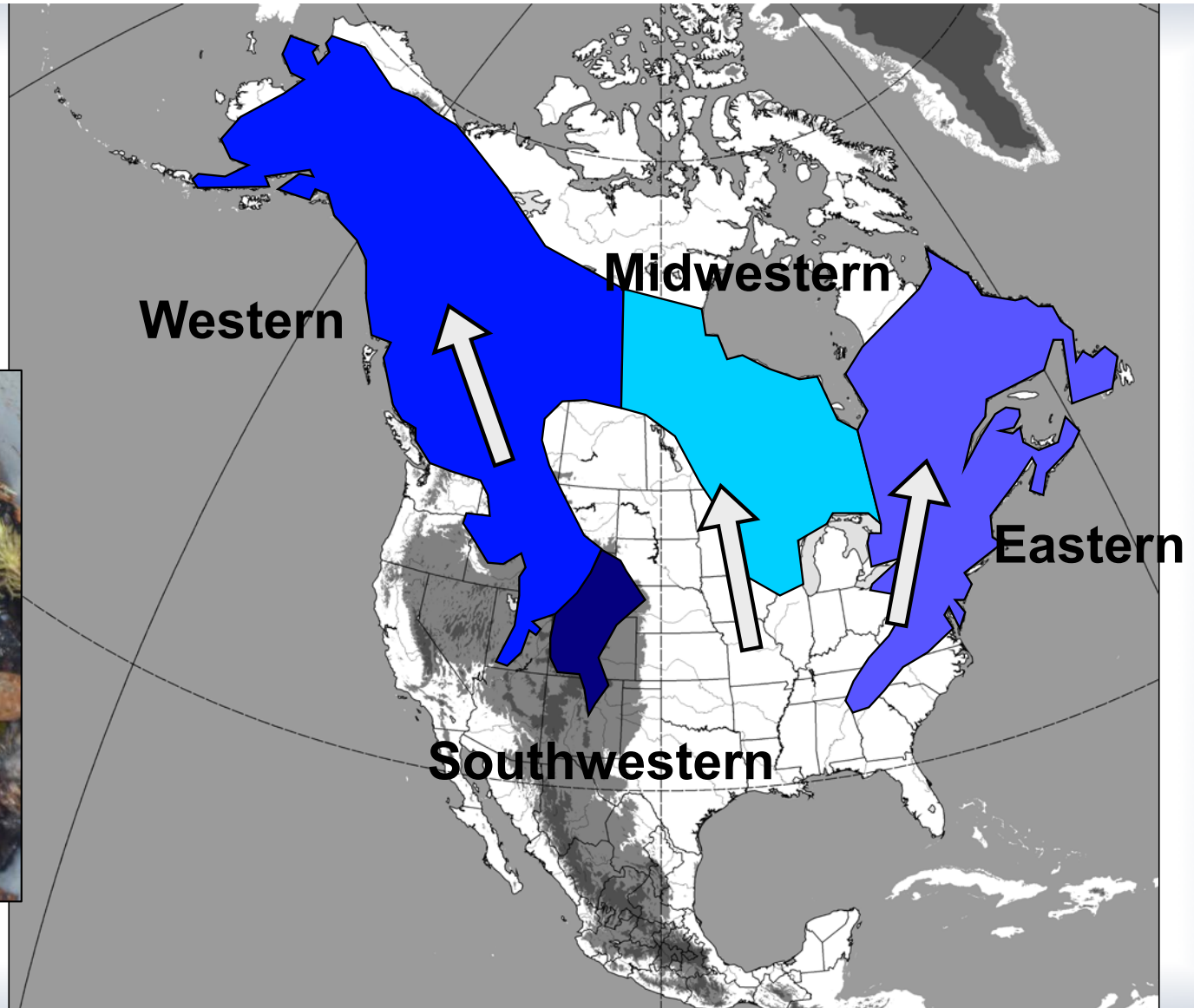


Masked shrews

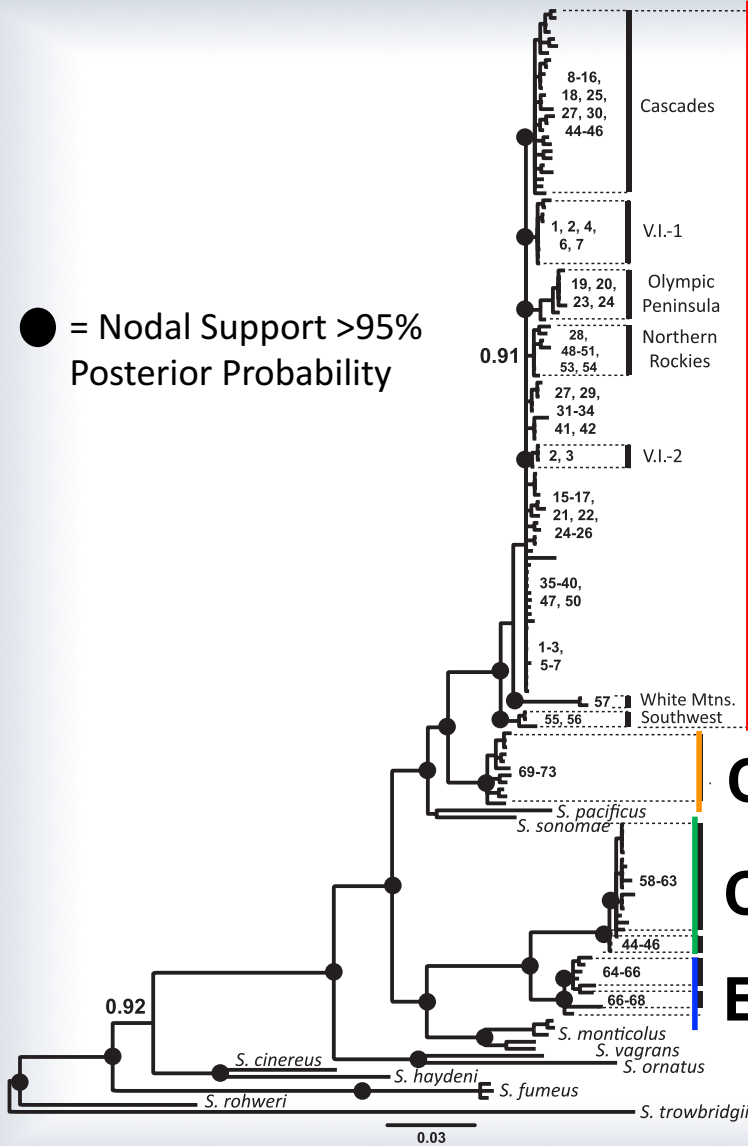
- Four lineages
- All intra-specific
- Recent!



Hope et al. 2012, *Mol. Phylogenet. Evol.*



● = Nodal Support >95%
Posterior Probability



Western

Coastal
Central
Eastern

Other species with same
distribution



Water shrew (*Sorex palustris*)

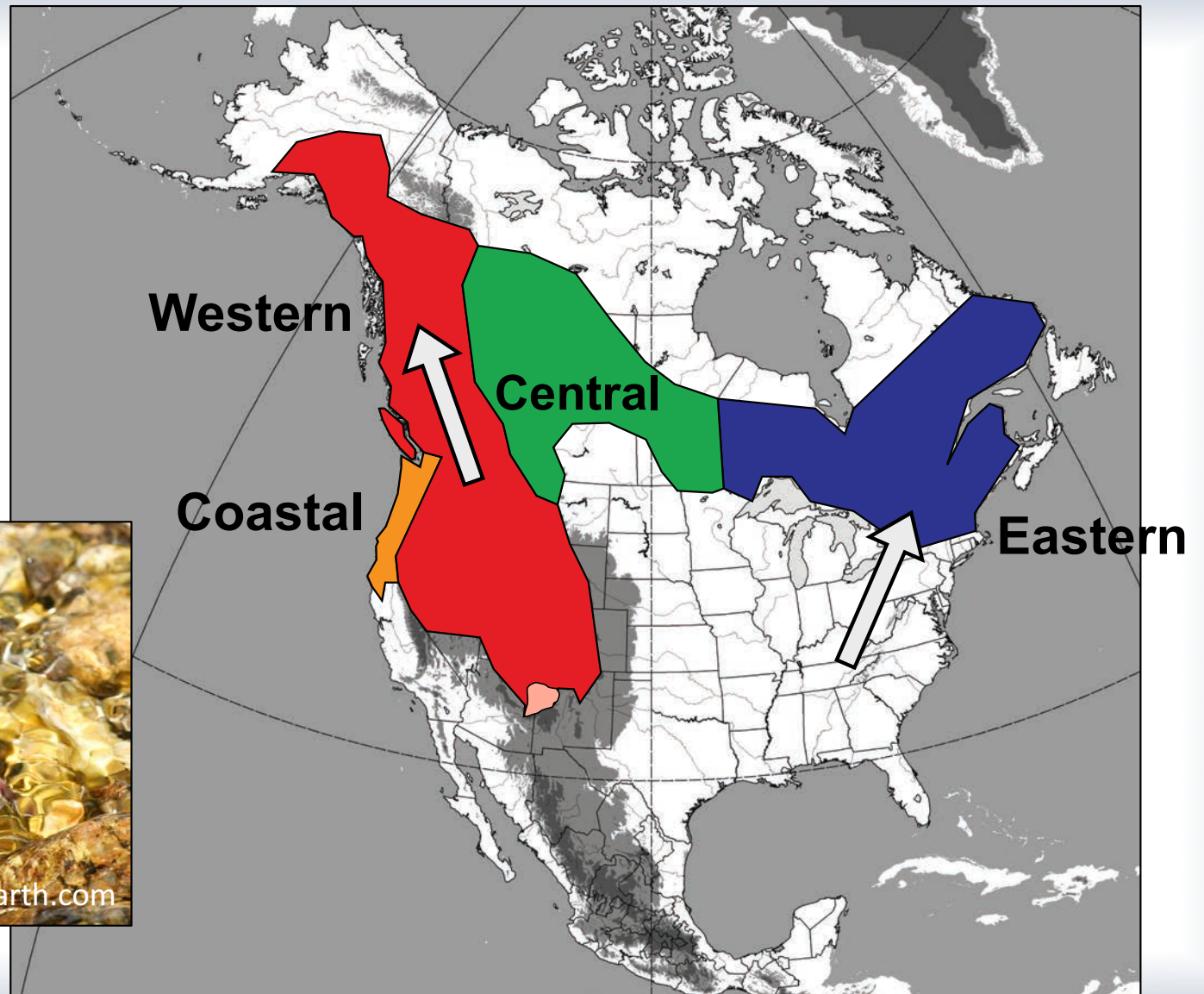
Hope et al. 2014; *J. Mamm.*

Water shrews

- Four species
- Deep divergence



Hope et al. 2014, *J. Mamm.*



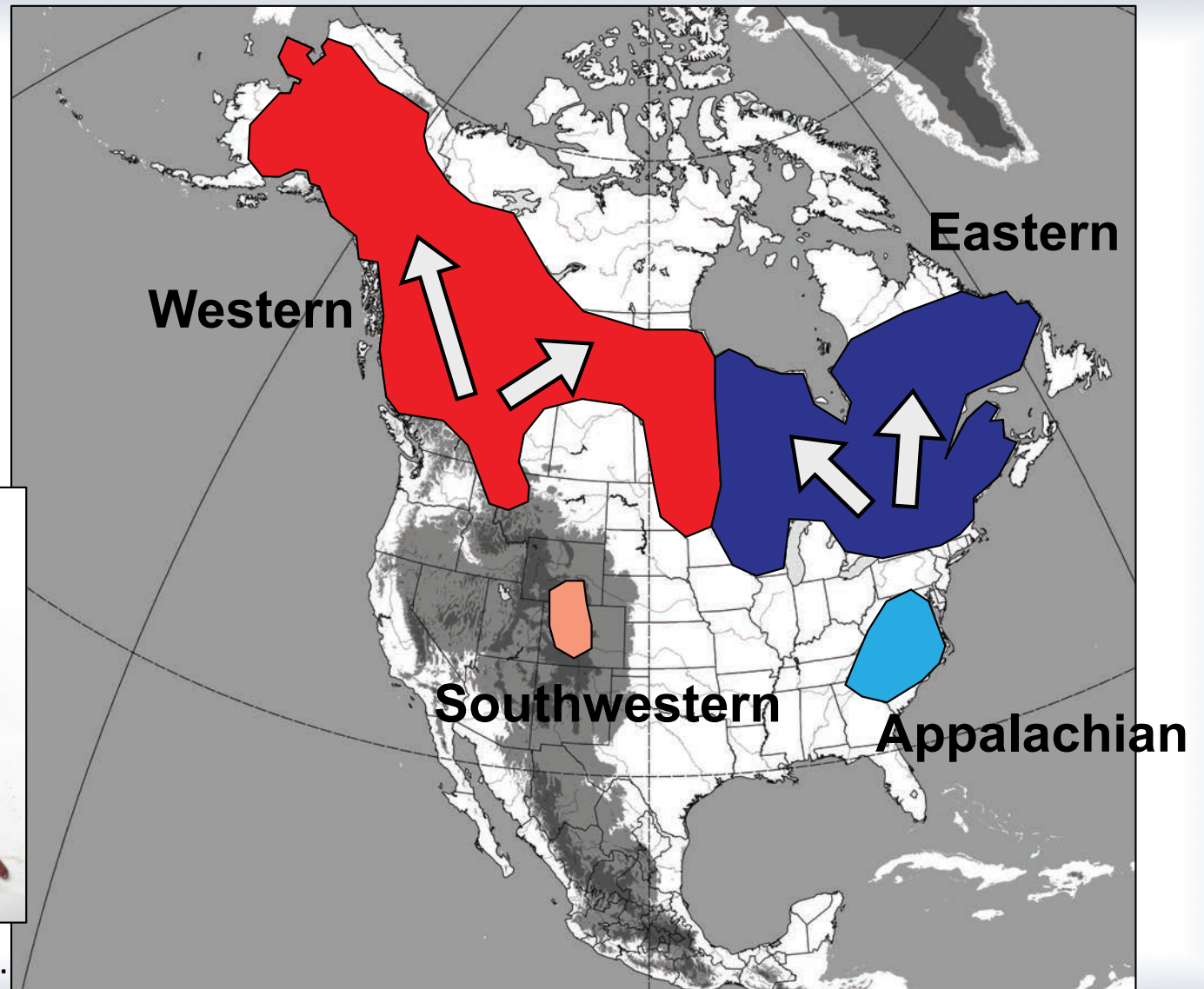
Pygmy shrews

- Two species
- Each with intra-specific lineages
- Intermediate

Ryan Stephens



Hope et al. *In Prep for J. Mamm.*

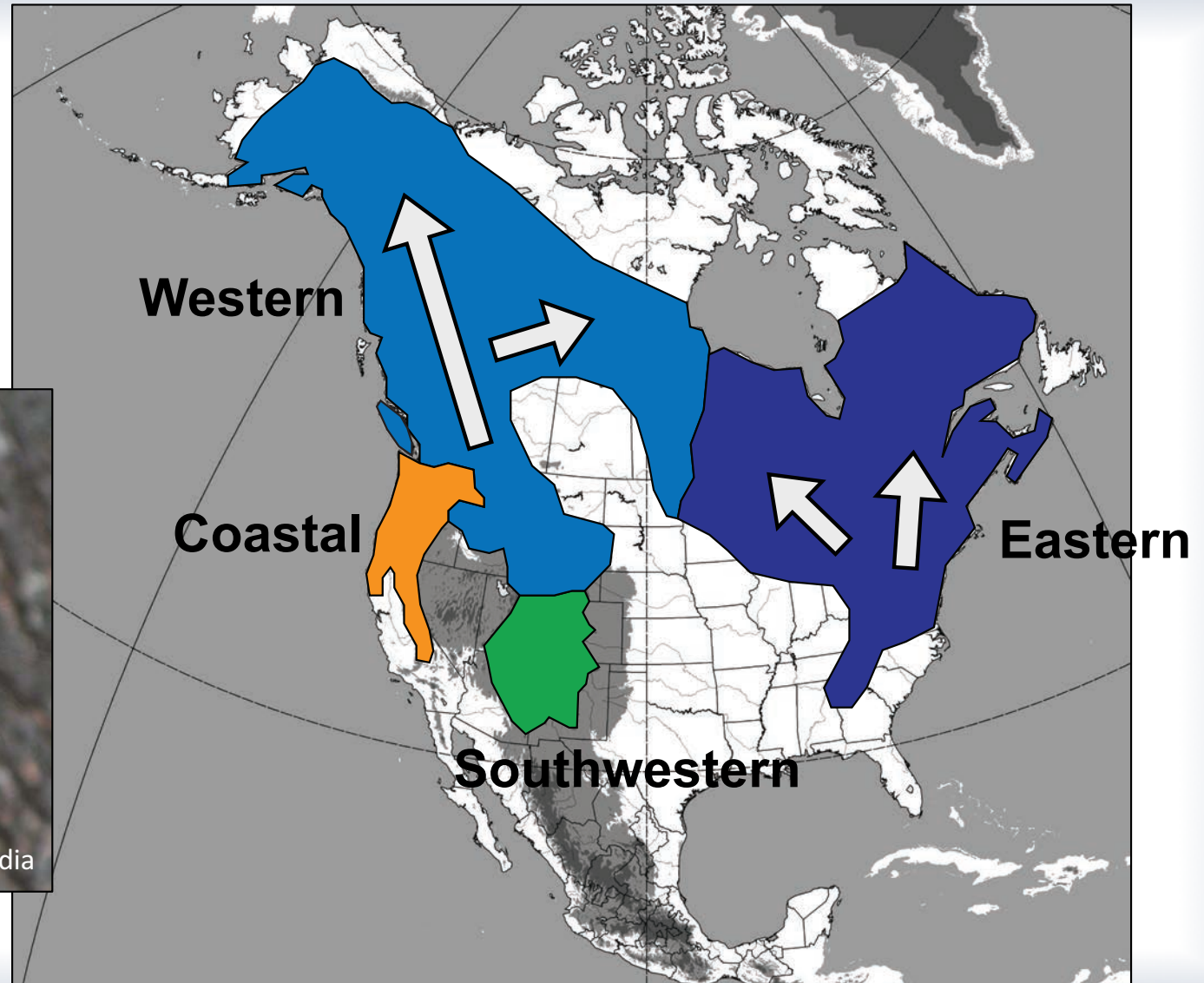


Red squirrels

- Three species
- Both deep and recent divergence



Hope et al. 2016, *Mol. Phylogenet. Evol.*

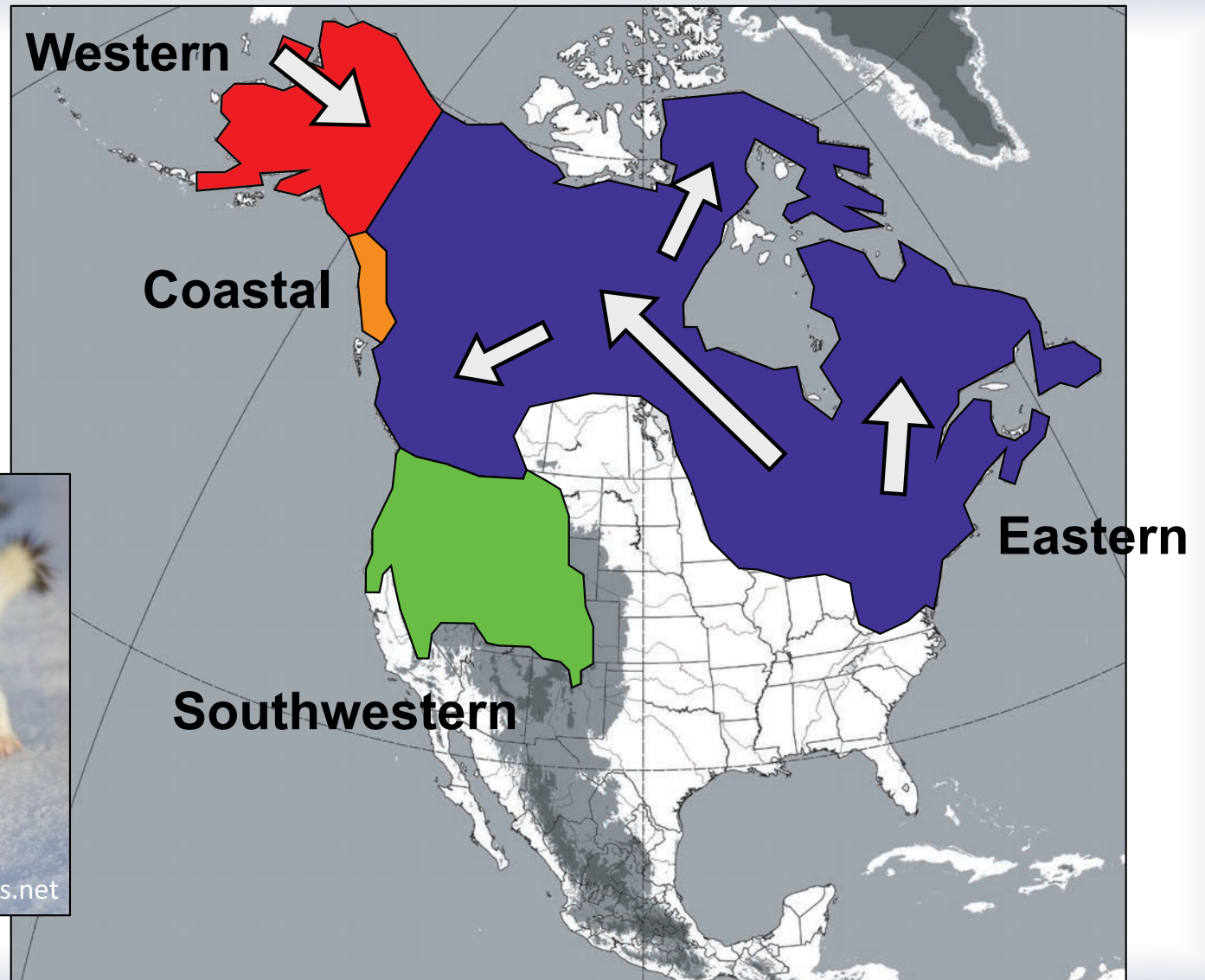


Ermine

- Four species
- Both deep and recent



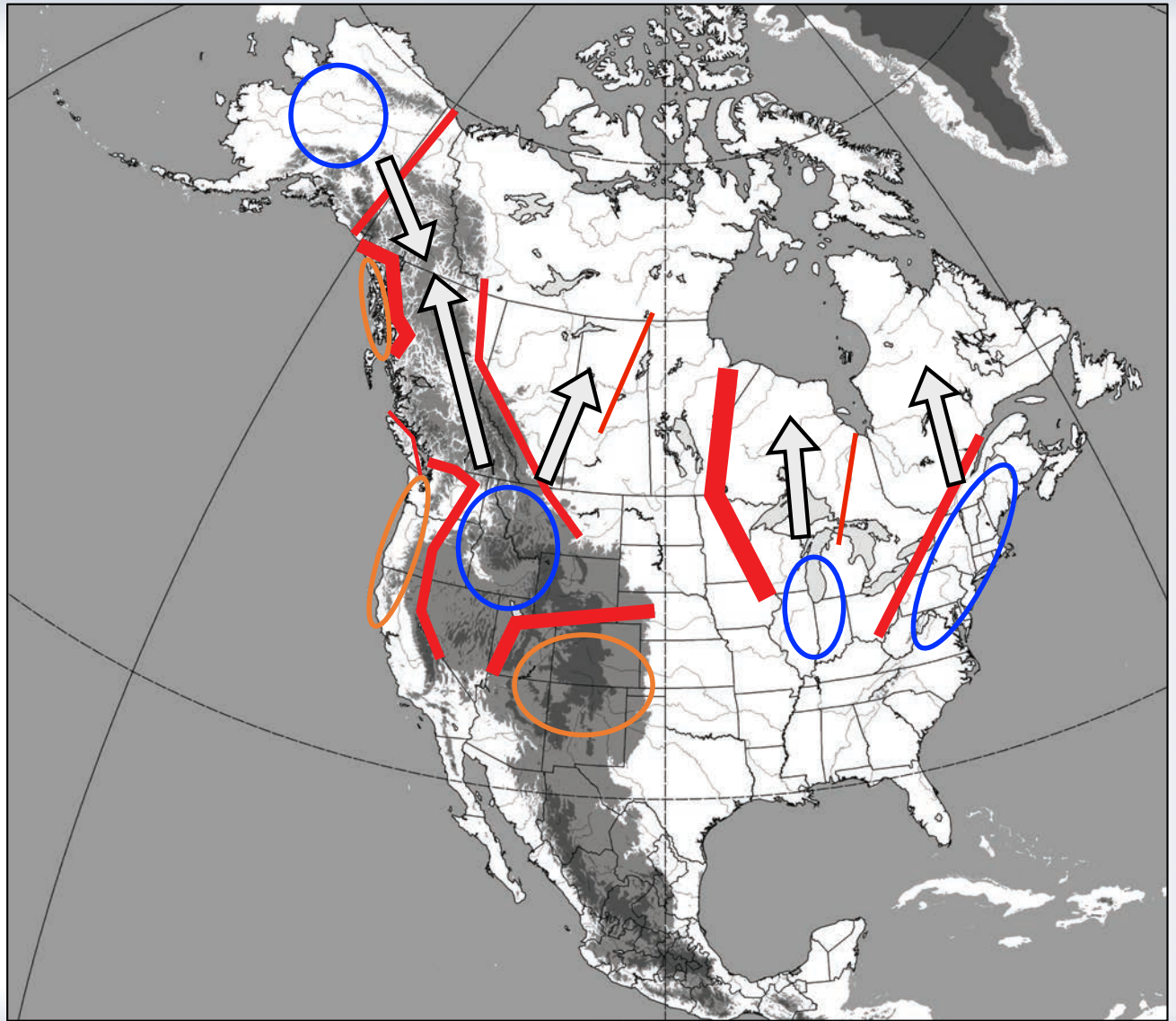
7wallpapers.net



Dawson et al. 2014, *J. Biogeog.*

Suture Zones

- Multiple areas of contact
- Regionally endemic communities
- Stable regions: high diversity
- Recolonized regions: low diversity
- Pseudocongruence of spatial/temporal diversification.



Goals for biodiversity conservation

1. Define the taxonomy.

- Describe species and identify distinct lineages
- Explore evolutionary processes

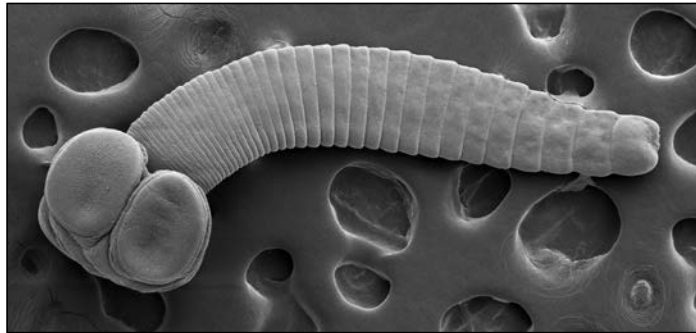
2. Identify regional centers of diversification

- Genetic diversity centers/borders over many species?
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- Regional conservation hotspots?

3. Resolve connections among associated biodiversity

- Community ecology
- Hosts and parasites – Co-evolution.
- Host specificity, host switching

Interdependent communities



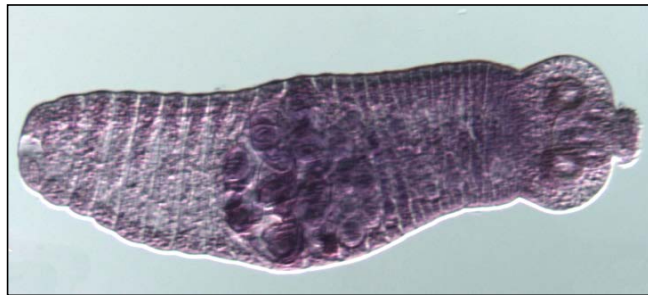
New Genus



Lineolepis sp.



Mathevolepis sp.



Urocystis sp. n.



Staphylocystoides asketus

Shrew endoparasites - helminths

- Highly diverse with complex life cycles
- Woefully underexplored!

Tkach et al.
in prep (x3)

Parasite/microbiome biodiversity

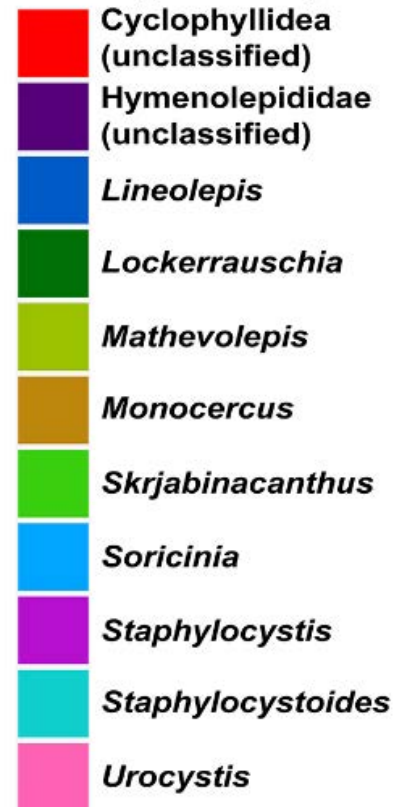
- Metagenomics
 - MiSeq



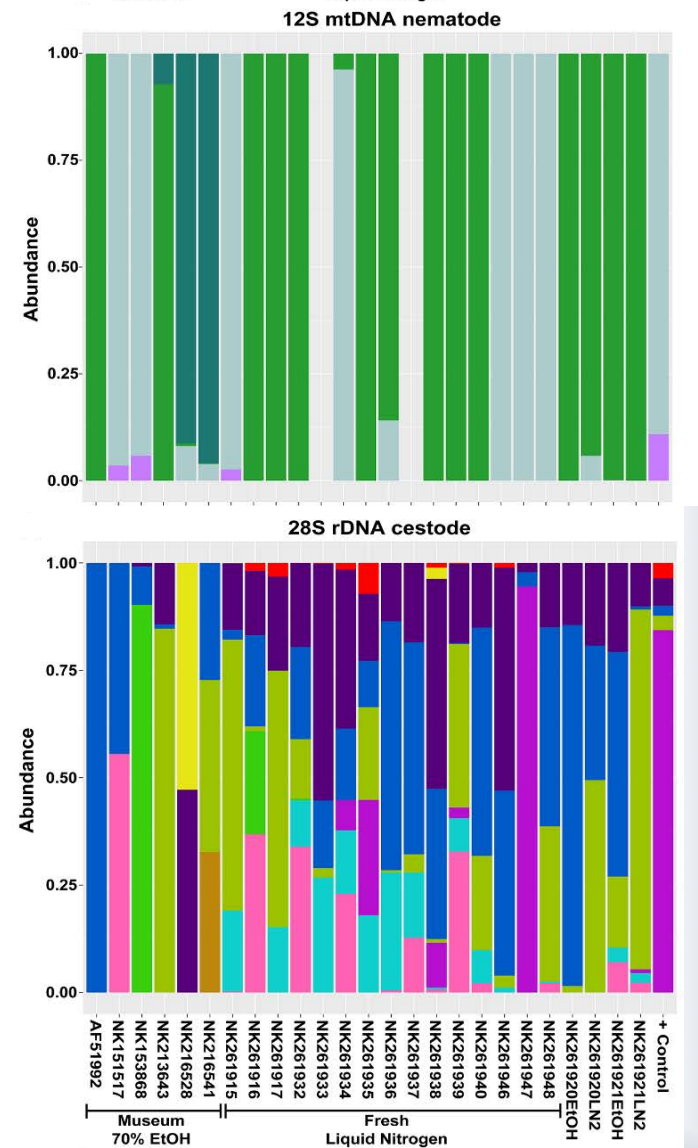
Georgia Southern University

Greiman et al. In Press, *Int.J.Parasit.*

Taxon (16S+28S)

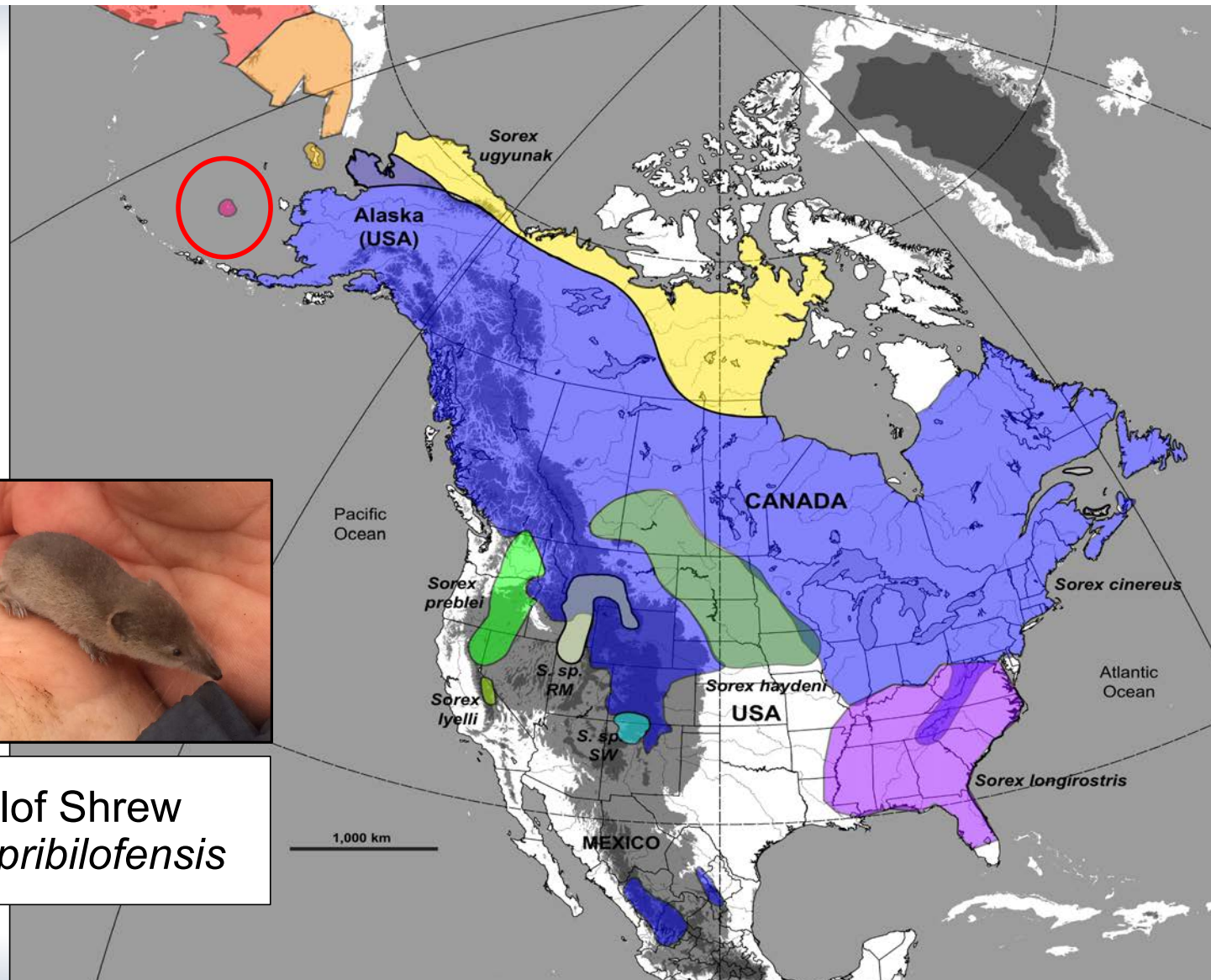


Taxon (12S)



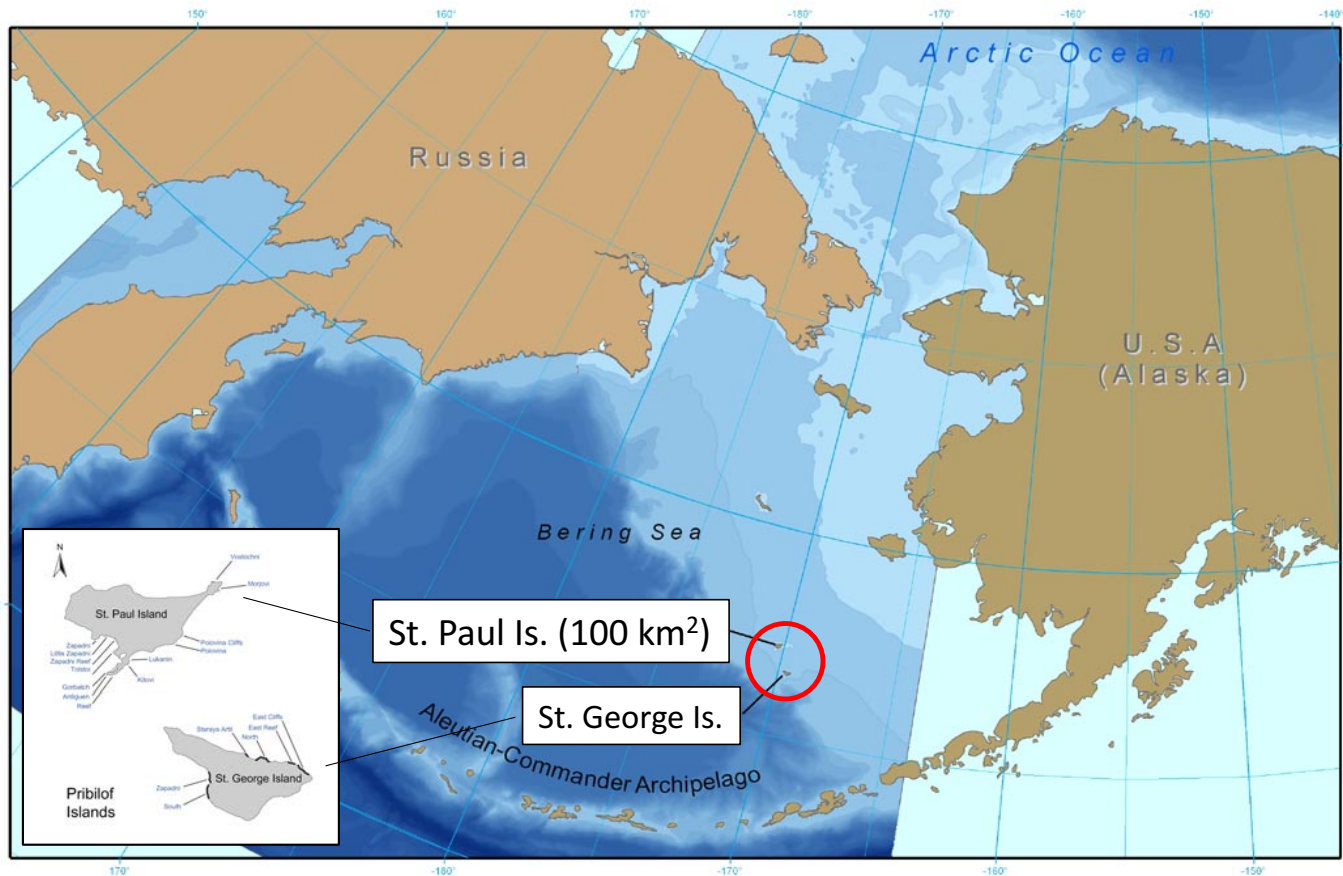


Pribilof Shrew
Sorex pribilofensis



St. Paul Island, Alaska.





Source: ESRI Data & Maps (Countries),
U.S. Geologic Survey (Bathymetry)

Beringia and the Pribilof Islands



The Last Glacial Period

Predictions for island biodiversity

1. Low species richness – faunal relaxation
 - Species interdependence → cascades (more extreme in north)
 - Low host richness → low parasite richness
2. Low genetic diversity
 - Small populations → periodic bottlenecks
 - Loss of diversity through rapid fixation of alleles (purging)
 - Lowered fitness?
3. High endemism
 - Divergence following fragmentation (high drift)
4. Host parasite evolutionary concordance?

Mammals of St. Paul Island



Mammals of St. Paul Island



Obtained 22 frozen
shrews from Aleut
Community on St. Paul

Predictions for island biodiversity

1. Low species richness – faunal relaxation

- Species interdependence → cascades
- Low host richness → low parasite richness

2. Low genetic diversity

- Small populations → periodic bottlenecks
- Loss of diversity through rapid fixation of alleles (purging)
- Lowered fitness

3. High endemism

- Divergence following fragmentation (high drift)

4. Host parasite evolutionary concordance?

Results – parasite diversity

- Very low Richness - 2 species of endoparasite
 - Cestode – *Lineolepis pribilofensis*
 - Trematode – *Maritrema* sp. → **Normally in birds!!**
- Very high parasite loads
 - Multiple hundreds of worms per shrew



Karpenko and
Dokuchaev 2012

Predictions for island biodiversity

1. Low species richness – faunal relaxation

- Species interdependence → cascades
- Low host richness → low parasite richness

2. Low genetic diversity

- Small populations → periodic bottlenecks
- Loss of diversity through rapid fixation of alleles (purging)
- Lowered fitness

3. High endemism

- Divergence following fragmentation (high drift)

4. Host parasite evolutionary concordance?

Results – shrew genetic diversity

- Cytochrome b gene (1140bp) for 22 shrews
- Virtually no genetic variability on St. Paul.

Table 1. Genetic diversity among shrews for Cyt b.

Species	Pi	Hd
<i>Sorex pribilofensis</i>	0.0001	0.22
<i>Sorex cinereus</i> (AK)	0.0039	0.95
<i>Sorex cinereus</i> (Southwest)	0.0059	0.89
<i>Sorex portenkoi</i> (Siberia)	0.0005	0.51
<i>Sorex jacksoni</i> (St. Lawrence Is.)	0.0016	0.52
<i>Sorex haydeni</i> (Mid-west)	0.0031	0.86
<i>Sorex preblei</i> (West)	0.0014	0.85

Predictions for island biodiversity

1. Low species richness – faunal relaxation

- Species interdependence → cascades
- Low host richness → low parasite richness

2. Low genetic diversity

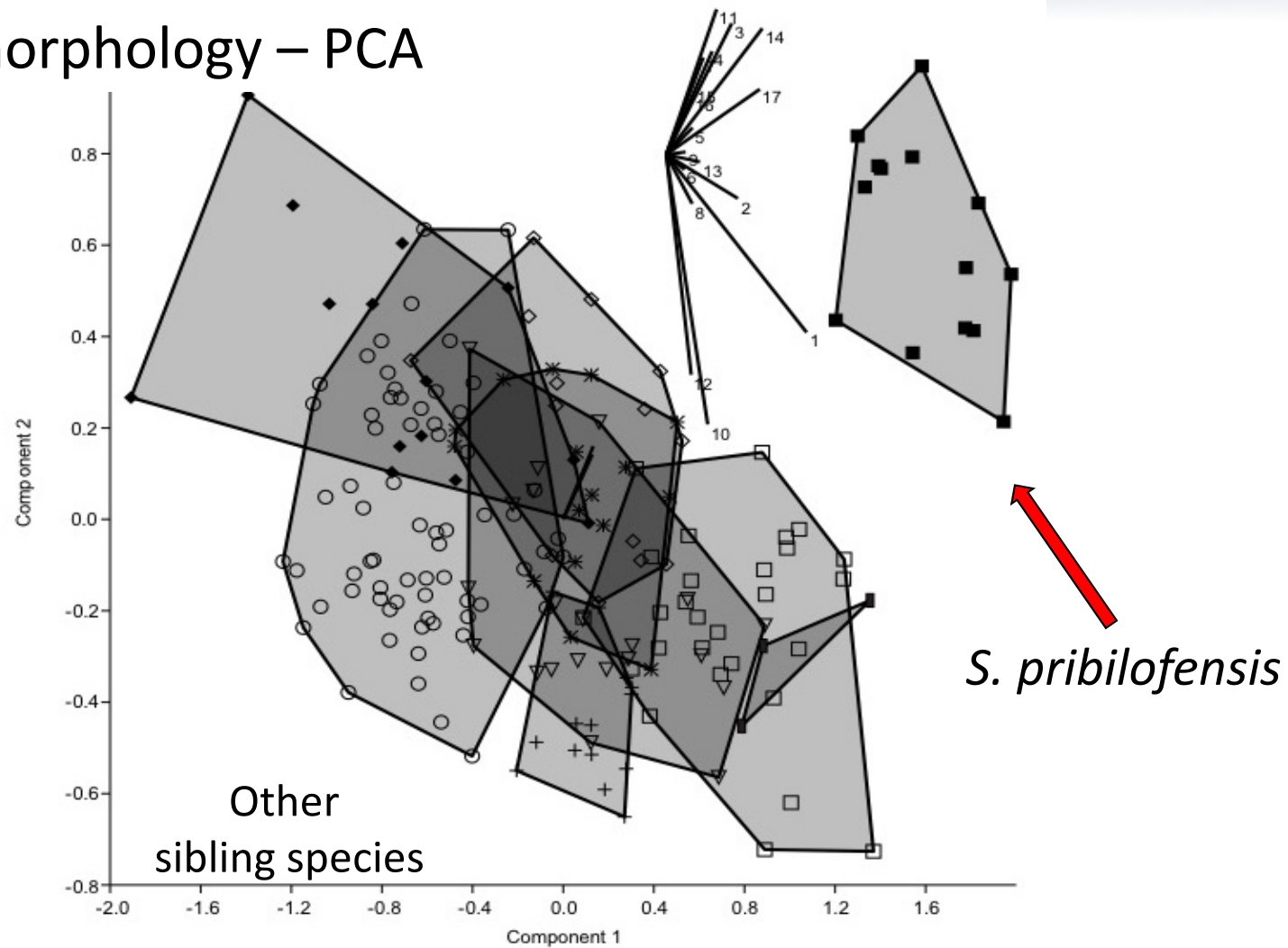
- Small populations → periodic bottlenecks
- Loss of diversity through rapid fixation of alleles

3. High endemism

- Divergence following fragmentation (high drift)

4. Host parasite evolutionary concordance?

Shrew morphology – PCA



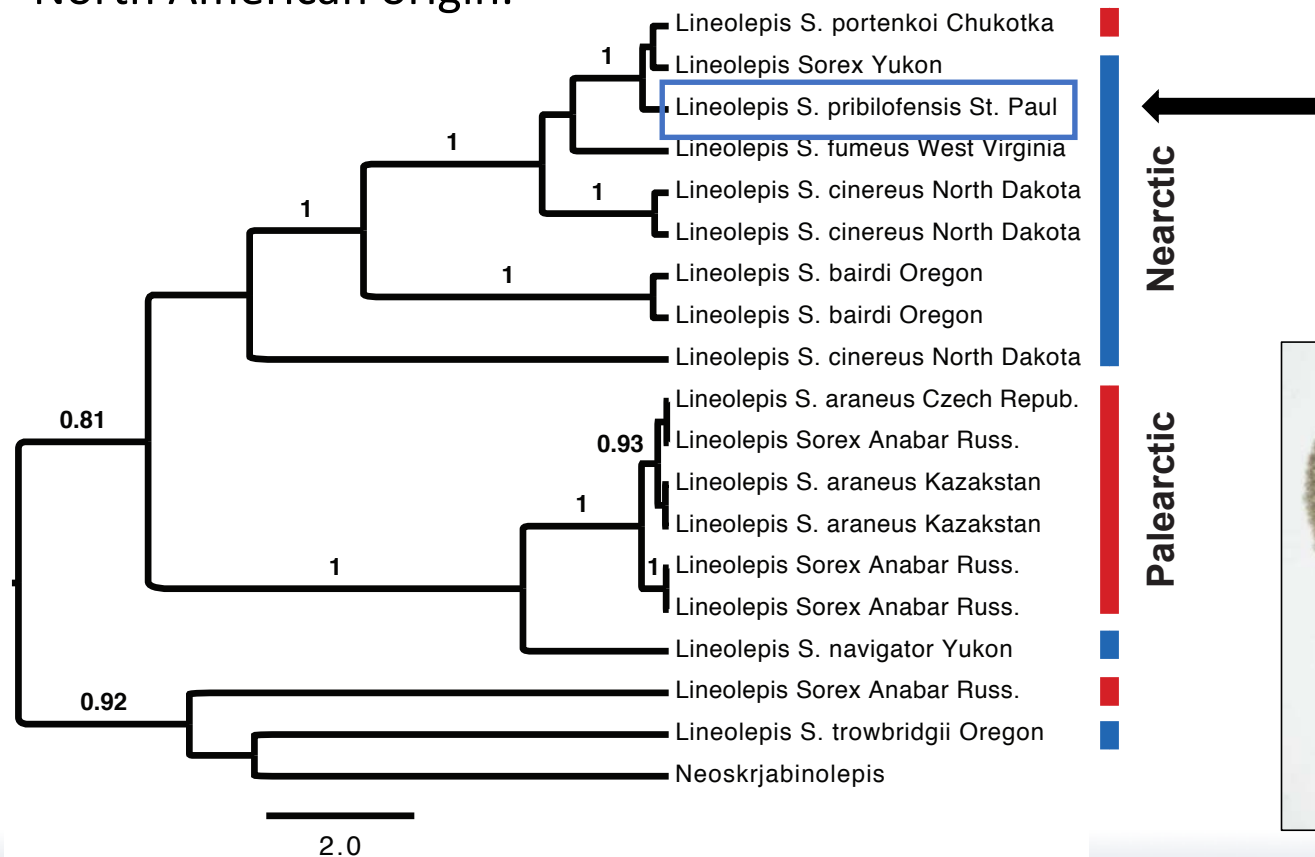
Hope et al. *in prep*

Predictions for island biodiversity

1. Low species richness – faunal relaxation
 - Species interdependence → cascades
 - Low host richness → low parasite richness
2. Low genetic diversity – population demography
 - Small populations → periodic bottlenecks
 - Loss of diversity through rapid fixation of alleles
3. High endemism
 - Divergence following fragmentation
 - Reflected by phylogeographic histories
4. Host parasite evolutionary concordance?

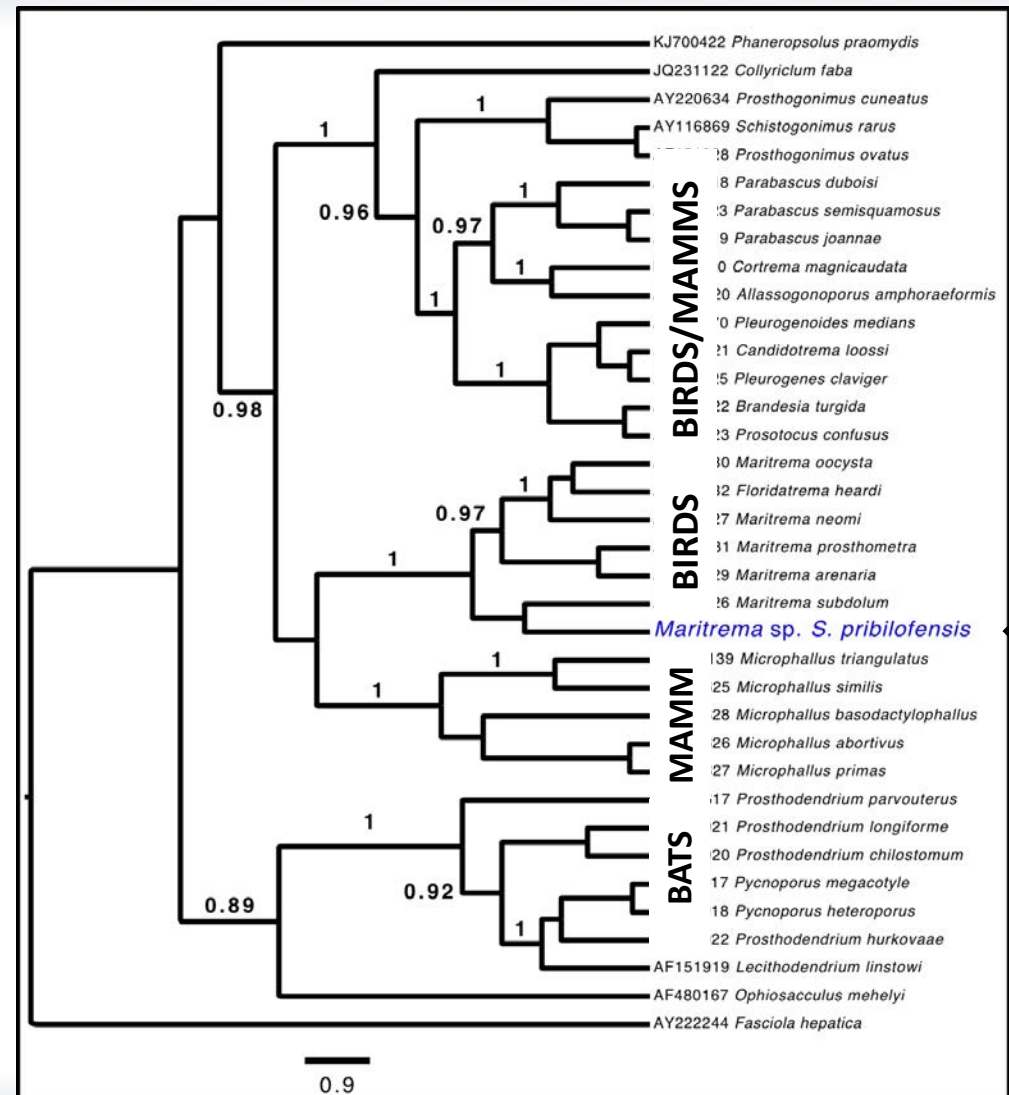
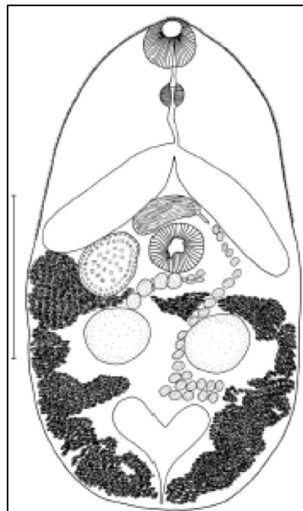
Results – co-evolution?

- Shrew cestode with North American origin.

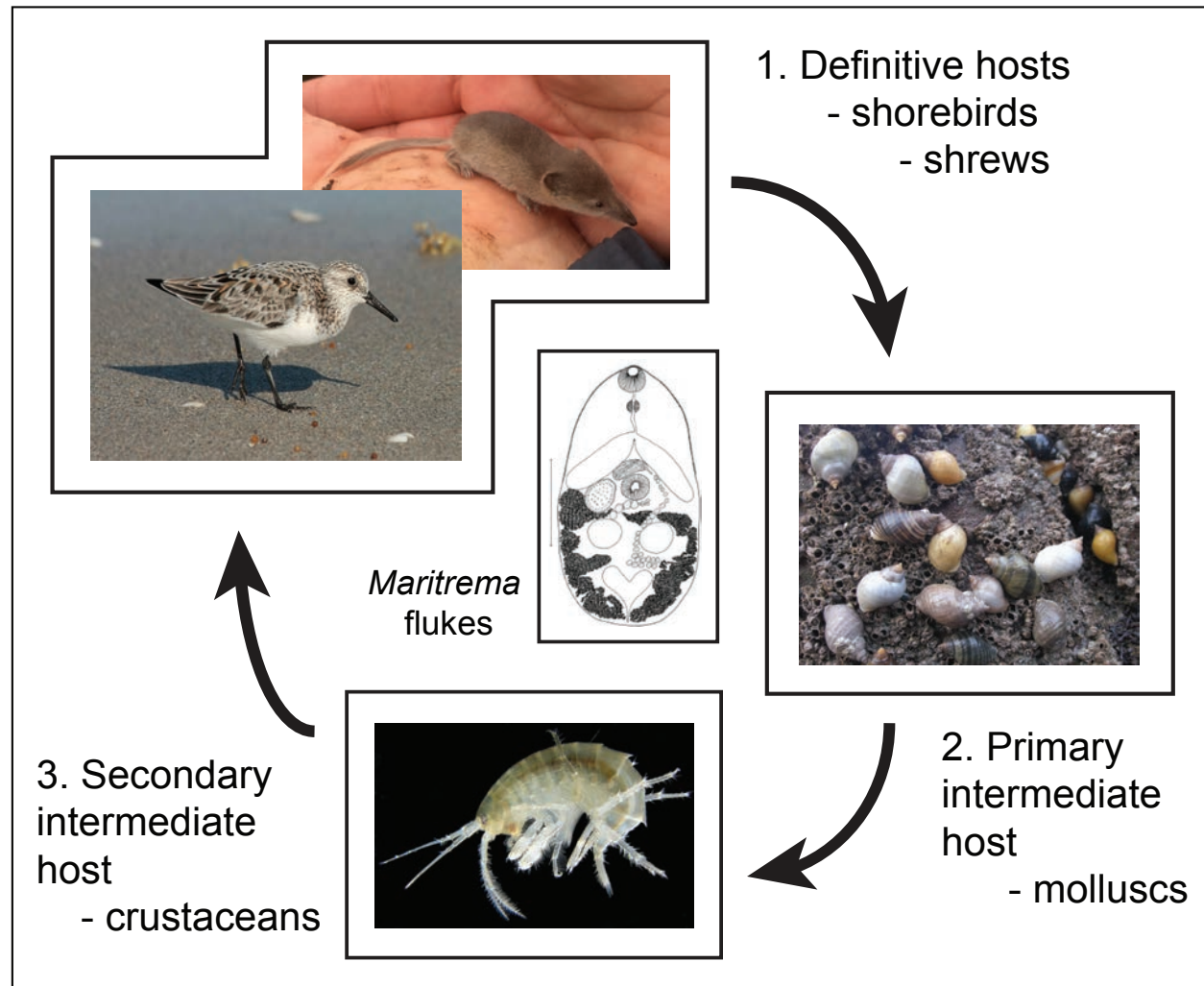


Results – co-evolution?

- Shrew trematode normally parasitizes birds!



Natural History



Implications

1. Host switching and emerging disease
 - Bird to mammalian
 - Marine to terrestrial
 - Intercontinental movement
2. Low parasite diversity
 - High parasite loads
 - “Missing biodiversity” dynamics
3. Low shrew genetic diversity
 - Loss of adaptive capacity
 - Future environmental impacts (raised sea levels!)

Conclusions

- Common species provide windows into ecosystem function
 - Surrogates for rare species
 - Economical
 - Well-represented in museums
 - Often broad geographic focus
 - Resolve regional processes
 - Document connections among species



Thanks To:

Main Collaborators:

- Joseph A Cook – UNM
- Vasyl V Tkach – UND
- John R Demboski – DMNS
- Sandra L Talbot – USGS
- Stephen Greiman – GSU

All Collaborators.

All Student Volunteers.

All Field Crews.

Funding Agencies:

- NSF
- USGS Alaska Science Center
- USFWS
- Aleut Community of St. Paul
- American Society of Mammalogists



Masked shrew “complex”

- 13 closely related species, but...
 - Unresolved genetic relationships
- Very Broad Distributions
 - Selection across environmental gradients?
- Multiple contact zones
 - Hybridization?



Biodiversity conservation...

Conservation of rare species – the “norm”

[CITATION] Survey for the Peñasco least chipmunk (*Tamias minimus atristriatus*) in the Lincoln National Forest with notes on rodent community assemblages

[AG Hope, JK Frey](#) - Final report submitted to Lincoln National Forest ..., 2000

★ 77 Cited by 6 Related articles

2000



2017

Conservation Plan for the Peñasco Least Chipmunk (*Tamias minimus atristriatus*)

Submitted To:

U.S. Fish & Wildlife Service
New Mexico Ecological Services Field Office
2105 Osuna Rd. NE
Albuquerque, NM 87113

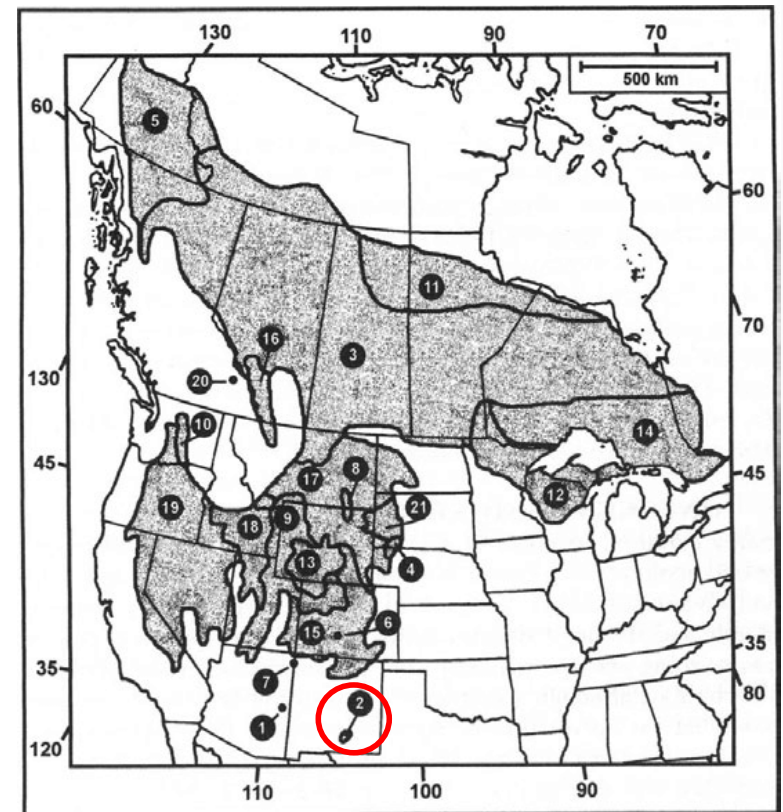
Submitted By:

Andrew G Hope, Ph.D.
Division of Biology
116 Ackert Hall
Kansas State University
Manhattan, KS 66506



Facts:

- 1900's – very common
- 1930's – very common
- **1960's – very uncommon**
- 1980 – virtually gone – 2 specimens found
- 2000 – virtually gone – 2 specimens found
- 2013 – virtually gone – 2 specimens found
- 2016 – petition for listing under the ESA...



Causes of decline?

- Genetic issues with small populations
- Human land practices – grazing, logging, fire suppression
- Drought – 1950's
- Disease – plague
- Competition
- Hybridization
- All extremely difficult to investigate because this population is virtually gone.

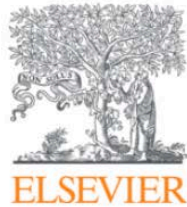


Why should we care about this chipmunk?

- It epitomizes problems:
 - Biodiversity declines can be sudden and fast.
 - Conserving rare taxa is extremely difficult!
 - We normally know very little about rare taxa.
- We should care because:
 - We don't know what role this species fulfilled
 - Indicators of change
 - Need to understand biodiversity connections!!



Biodiversity conservation **via evolutionary analysis...**



Global Ecology and Conservation

Volume 2, December 2014, Pages 81-87

open access



Original research article

Do species conservation assessments capture genetic diversity?

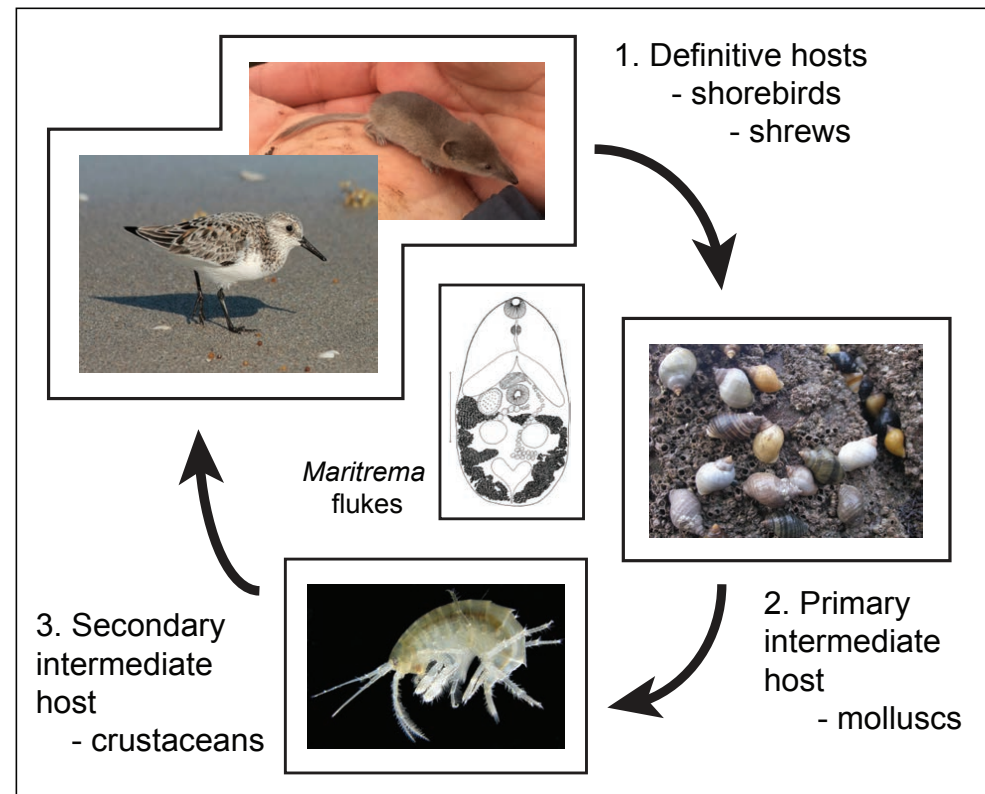
Malin C. Rivers ^{a, b}  , Neil A. Brummitt ^c, Eimear Nic Lughadha ^b, Thomas R. Meagher ^a

Paraphrasing: “A survey of papers published over the past decade found 8897 papers on the topic “IUCN Red List (population and range size)”, and 5505 on “Conservation Genetics”; only 18 (<1%) of these papers included both these topics...”

Message: integrating among scientific disciplines is of critical importance for improving biodiversity conservation.

Why is integration among disciplines important?

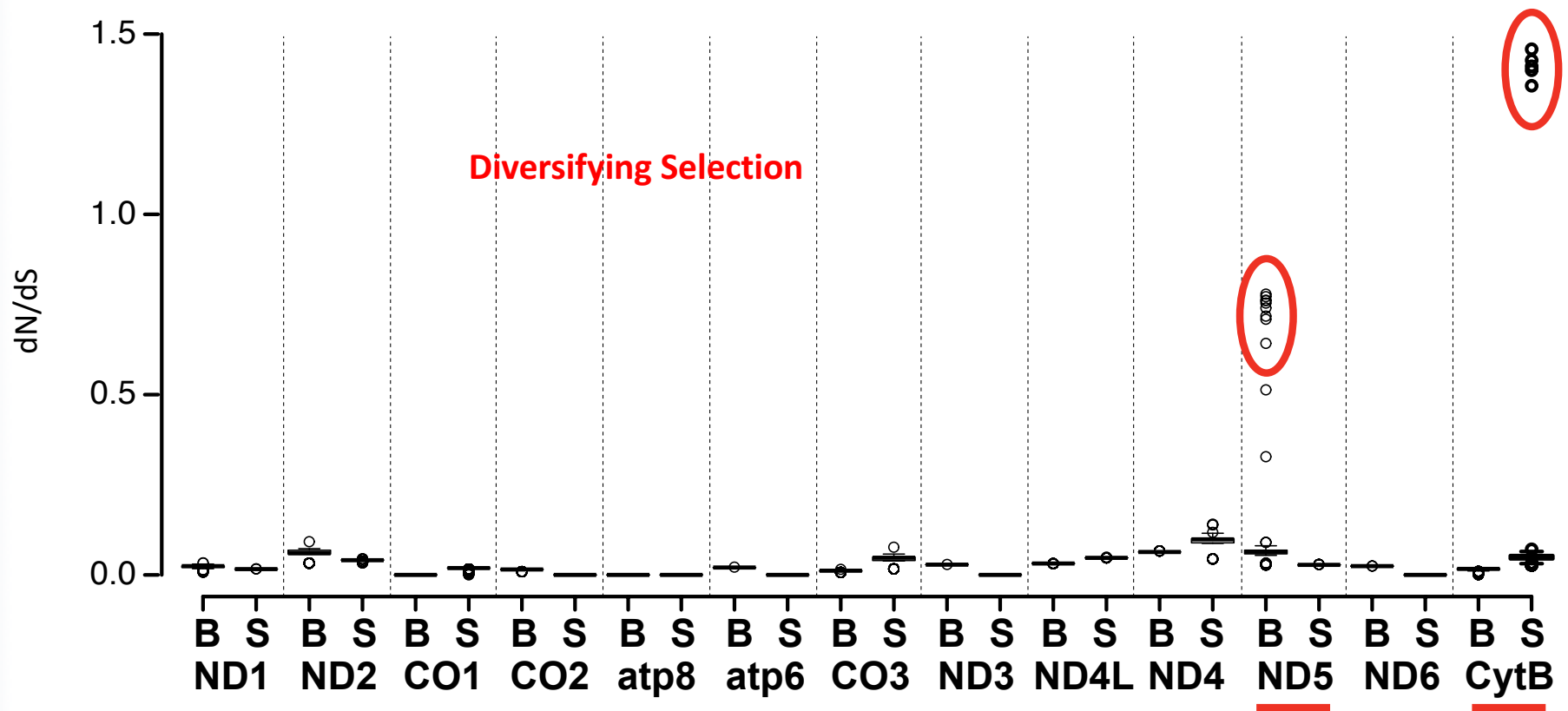
- Maintaining functional ecological systems into the future will benefit from an understanding of both historical and contemporary evolutionary processes that influence fundamental connections among biodiversity.



Biodiversity conservation via evolutionary
analysis **of *common* species!**

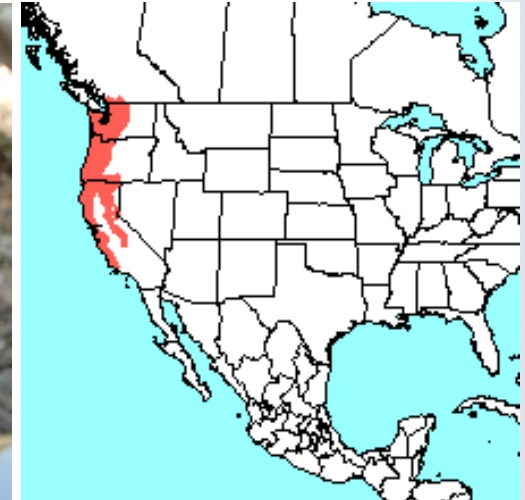
Mitogenomes - selection

- Zoomed Out...
- Positive Selection in 2 genes



Biggest Threat??

- New biotic associations!
 - New parasite-host relationship
 - New intermediate hosts on island
 - New parasite-environment relationship
 - Ecological fitting
- Terrestrial community reorganization
 - Possible ecological release for snails
 - Vacant niche space and/or lack of competition
- Ecosystem (in)stability
 - Shift in shrew population dynamics?
- Other threats to island?
 - Additional species introductions
 - Rats
 - Other shrews!



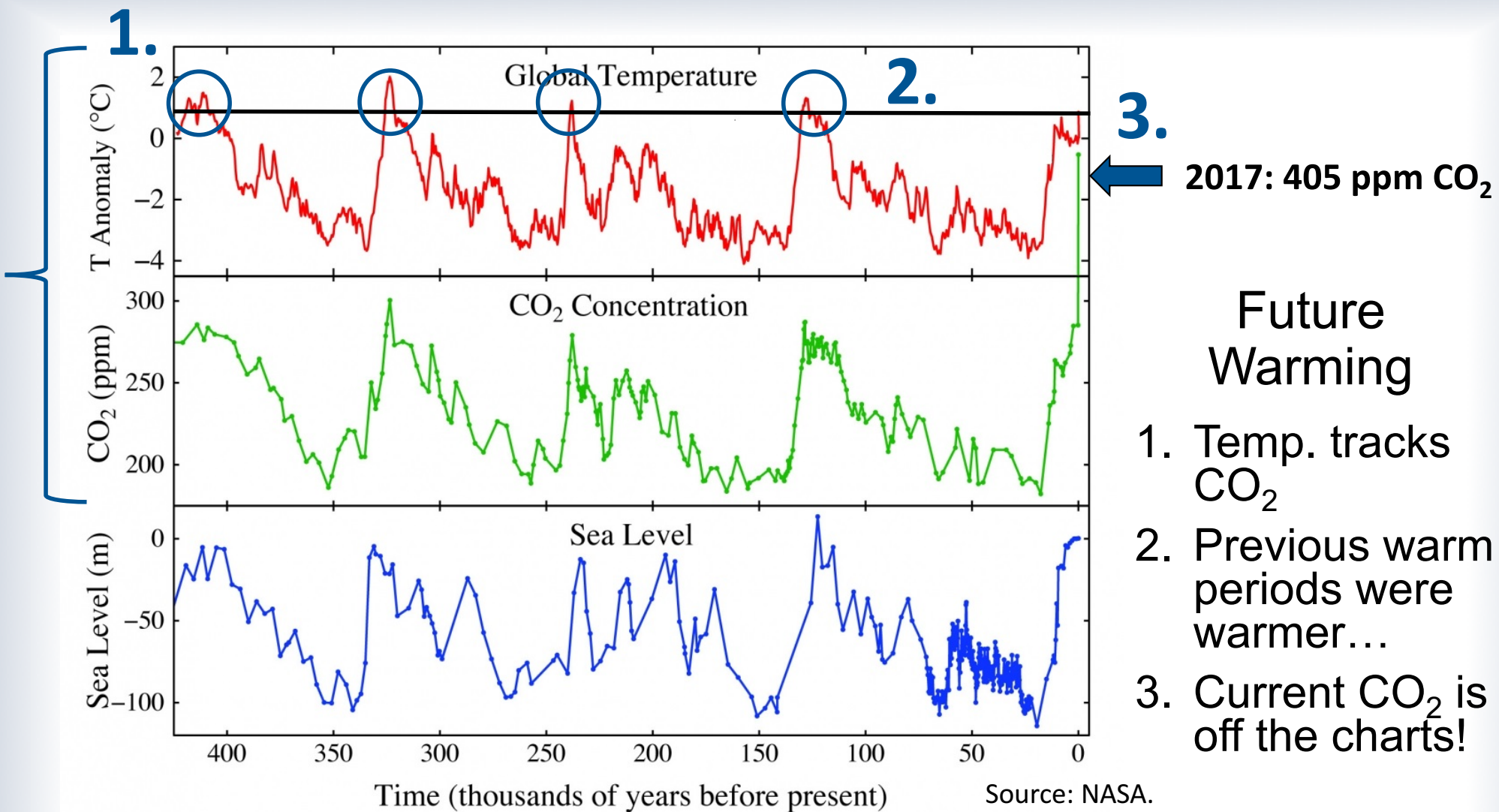
Field collection





Variation in Intestinal Biodiversity

- Metagenomic methods – 12S, 16S, 28S; MiSeq
 - Spatial gradients across host contact zones
 - In-situ temporal change using museum specimens
- Parasite (helminths)
 - Biodiversity discovery
 - Host-parasite co-evolution?
- Microbiomes
 - The next step...

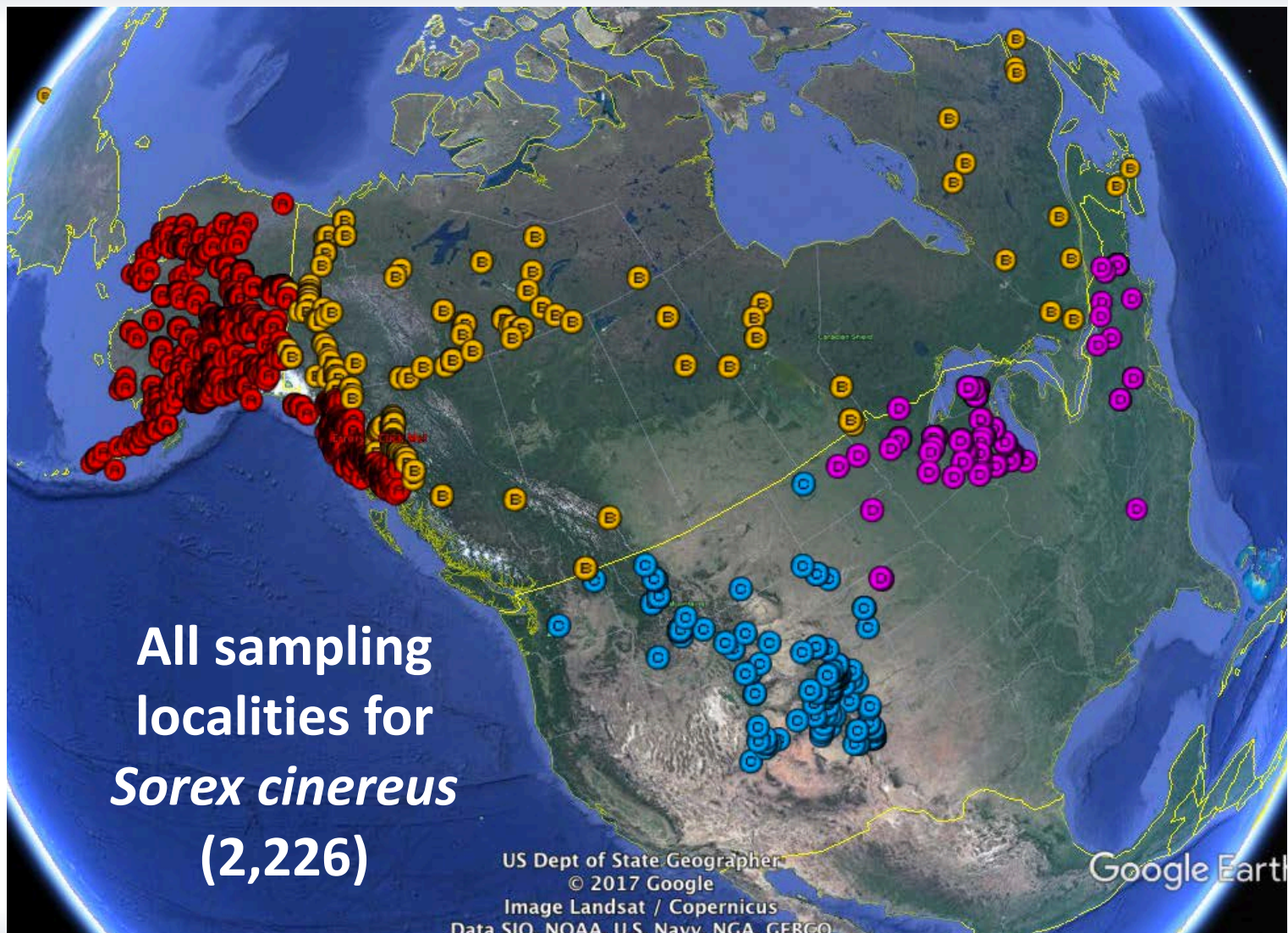


e.g. Sorex cinereus sampling
(parentheses indicate average numbers per locality)

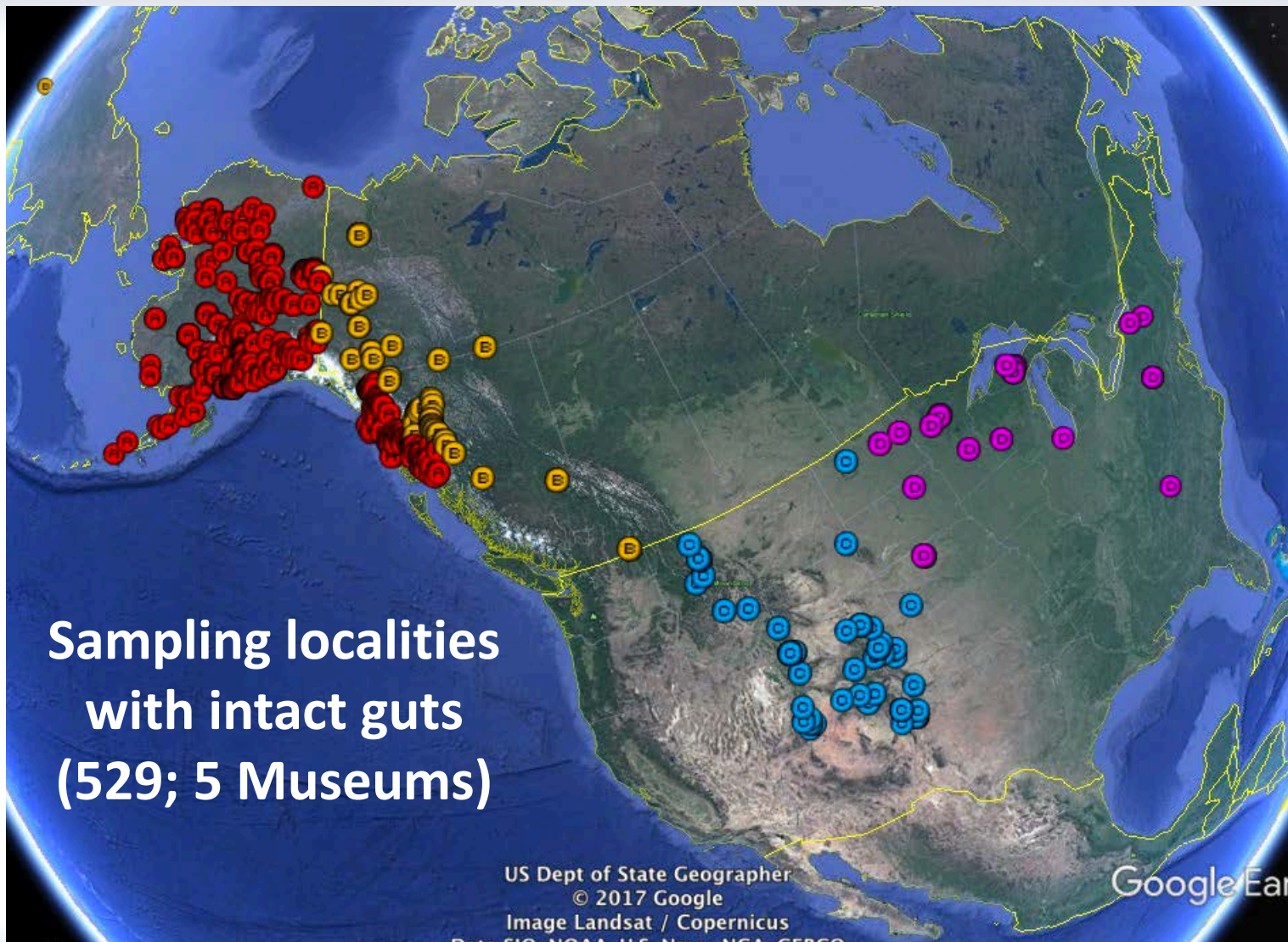


Region	Localities	Total samples	Samples w/ tissues	Samples w/ endoparasites
Alaska	1,391	13,108 (9.4)	11,371 (8.2)	4,687 (3.4)
Canada	291	1,452 (4.9)	905 (3.1)	535 (1.8)
Western US	239	986 (4.1)	445 (1.9)	282 (1.2)
Eastern US	305	1,459 (4.8)	887 (2.9)	172 (0.6)

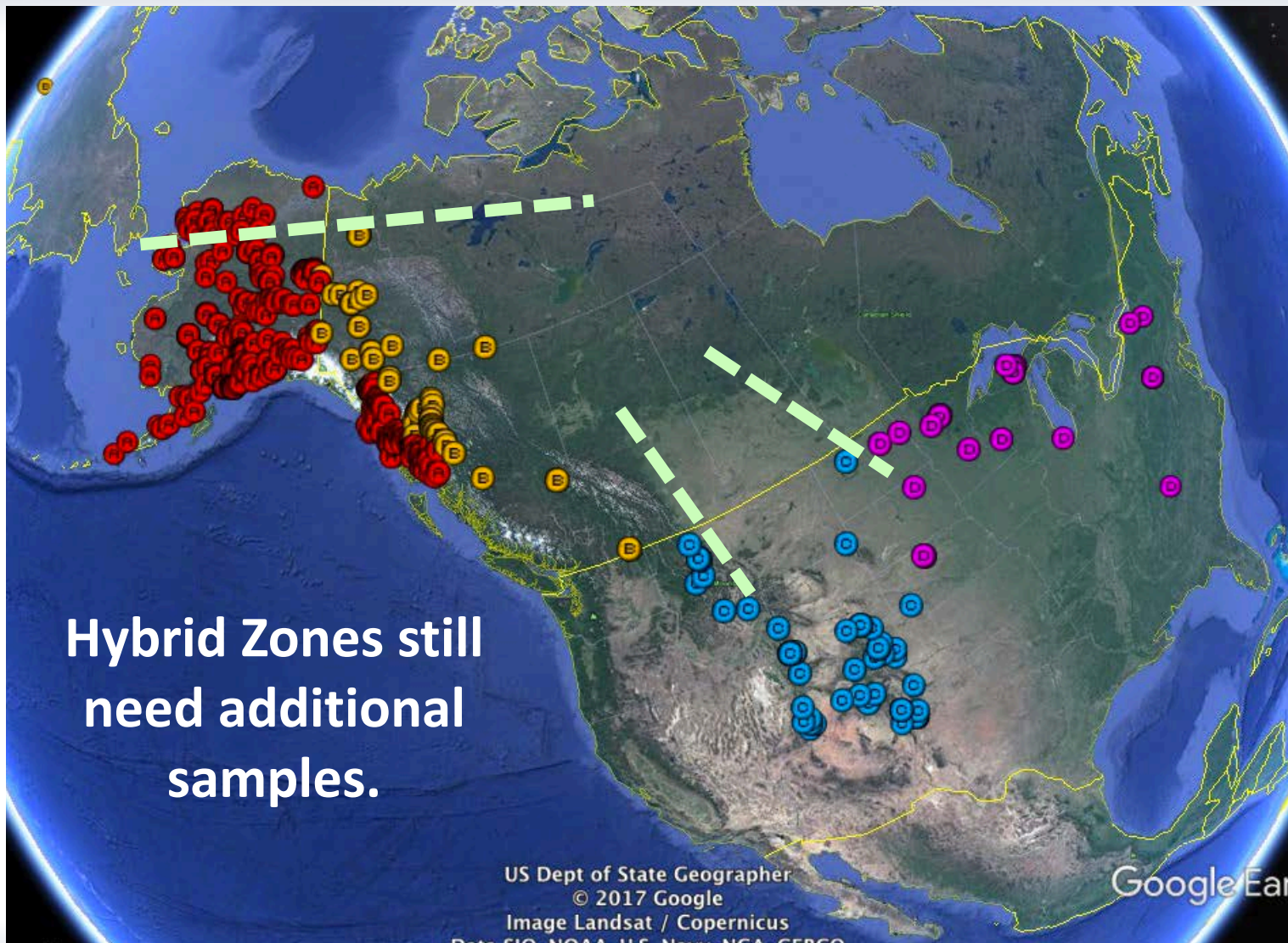
All sampling
localities for
Sorex cinereus
(2,226)



**Sampling localities
with intact guts
(529; 5 Museums)**



**Hybrid Zones still
need additional
samples.**



Summary

- Genomic methods allow for highly integrated eco-evolutionary framework
 - Hybridization, speciation, co-evolution, community assembly
- Combined host-parasite analyses provide greater resolution of generalizable landscape processes
- Understanding interdependency among species...
 - Requires extensive diagnosis of existing biodiversity
 - Requires temporally deep, spatially broad, site intensive, and taxonomically comprehensive sampling

Thanks!

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- Beringian Co-evolution Project
Numerous Field Crews!!



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