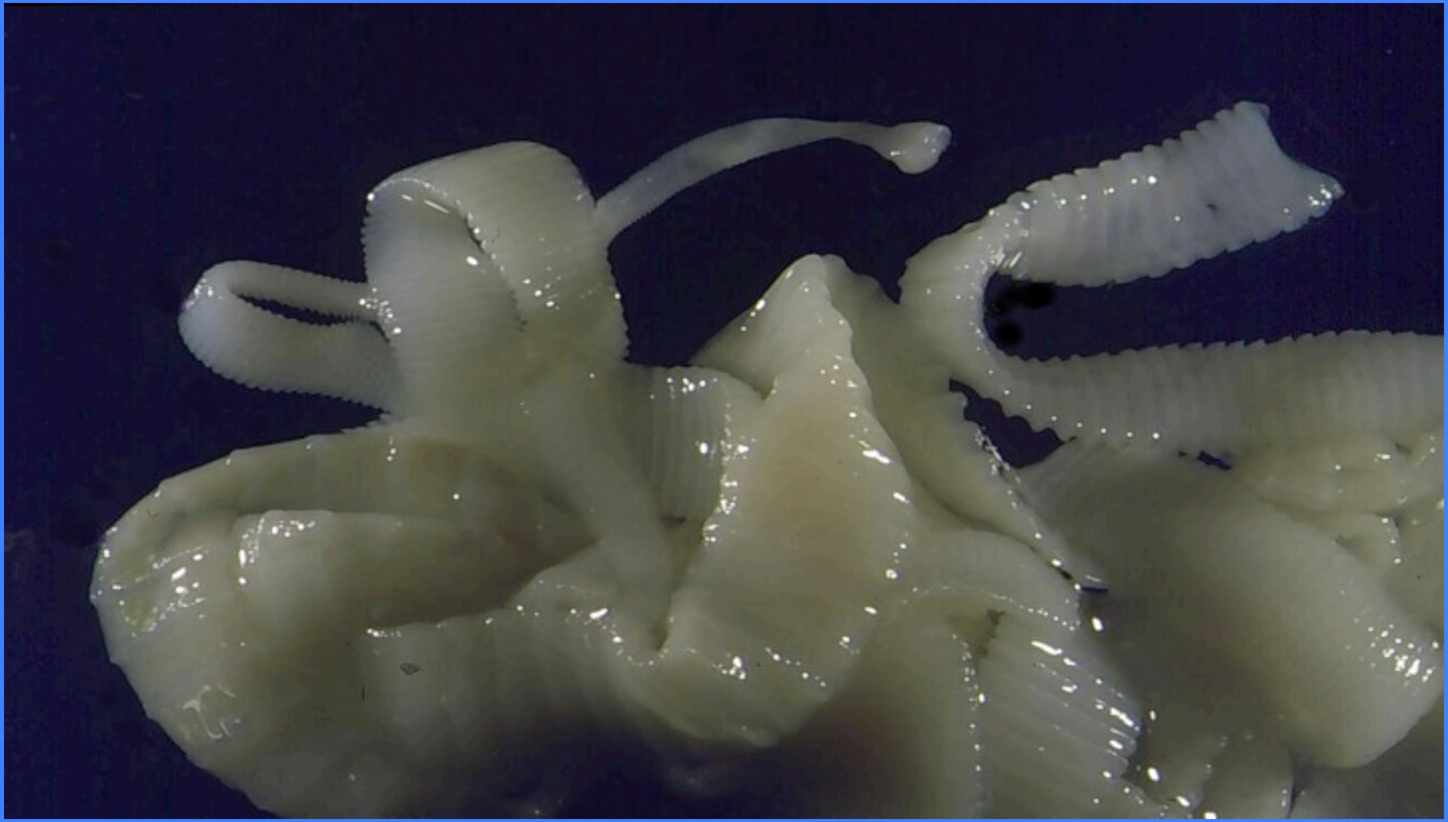
Primary Scientific Infrastructure

Integrated Host/Parasite Collections



Microparasites

Viruses, Blood-borne Protozoans

Macroparasites

Endoparasites

- Nematode
- Cestode
- Trematode

Ectoparasites

- Mites--ácaro
- Ticks--garrapatas
- Fleas-pulgas

Hantavirus

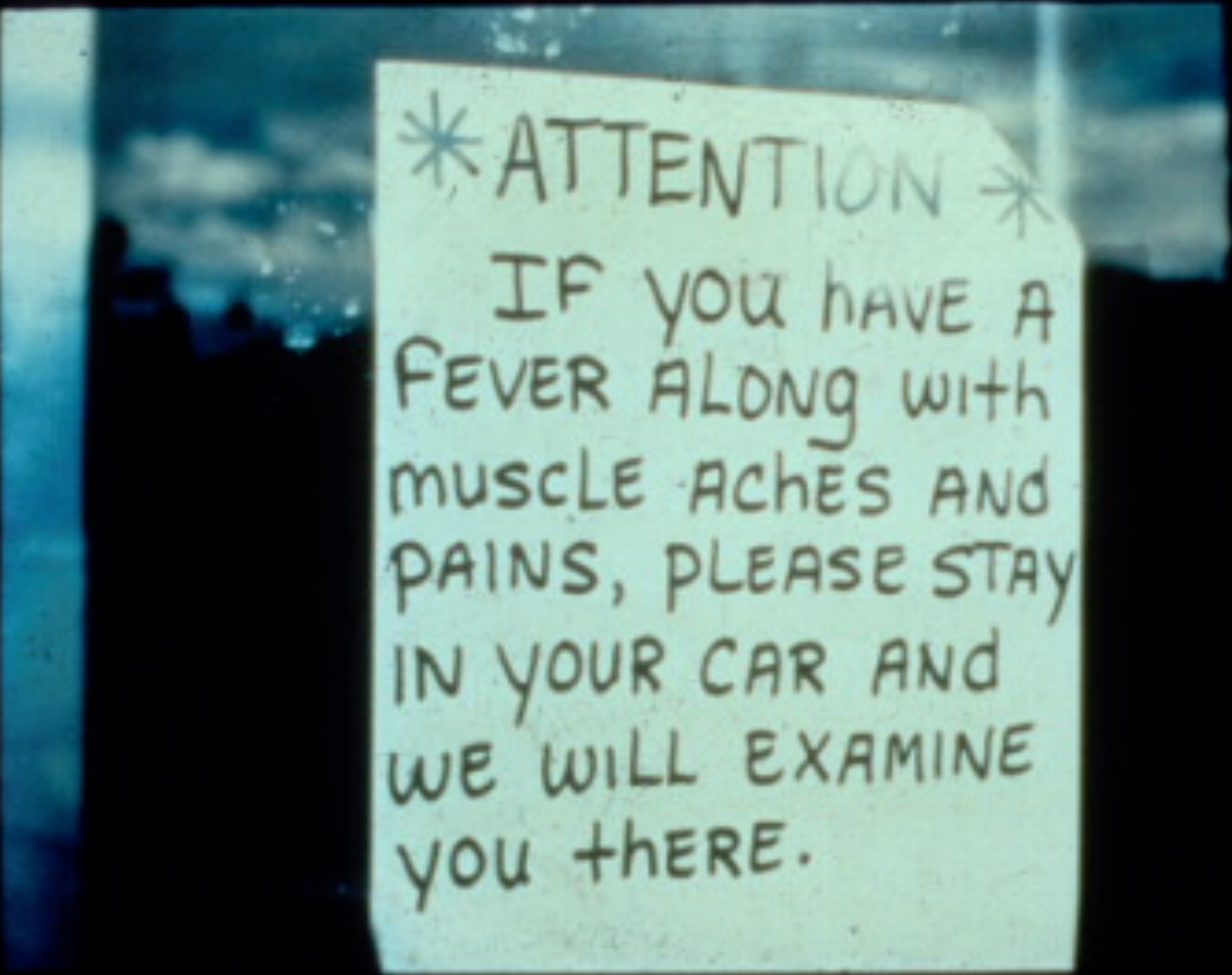
Until 1993, one hantavirus was known from the Americas.

Prospect Hill, Maryland

Hantavirus

In 1993

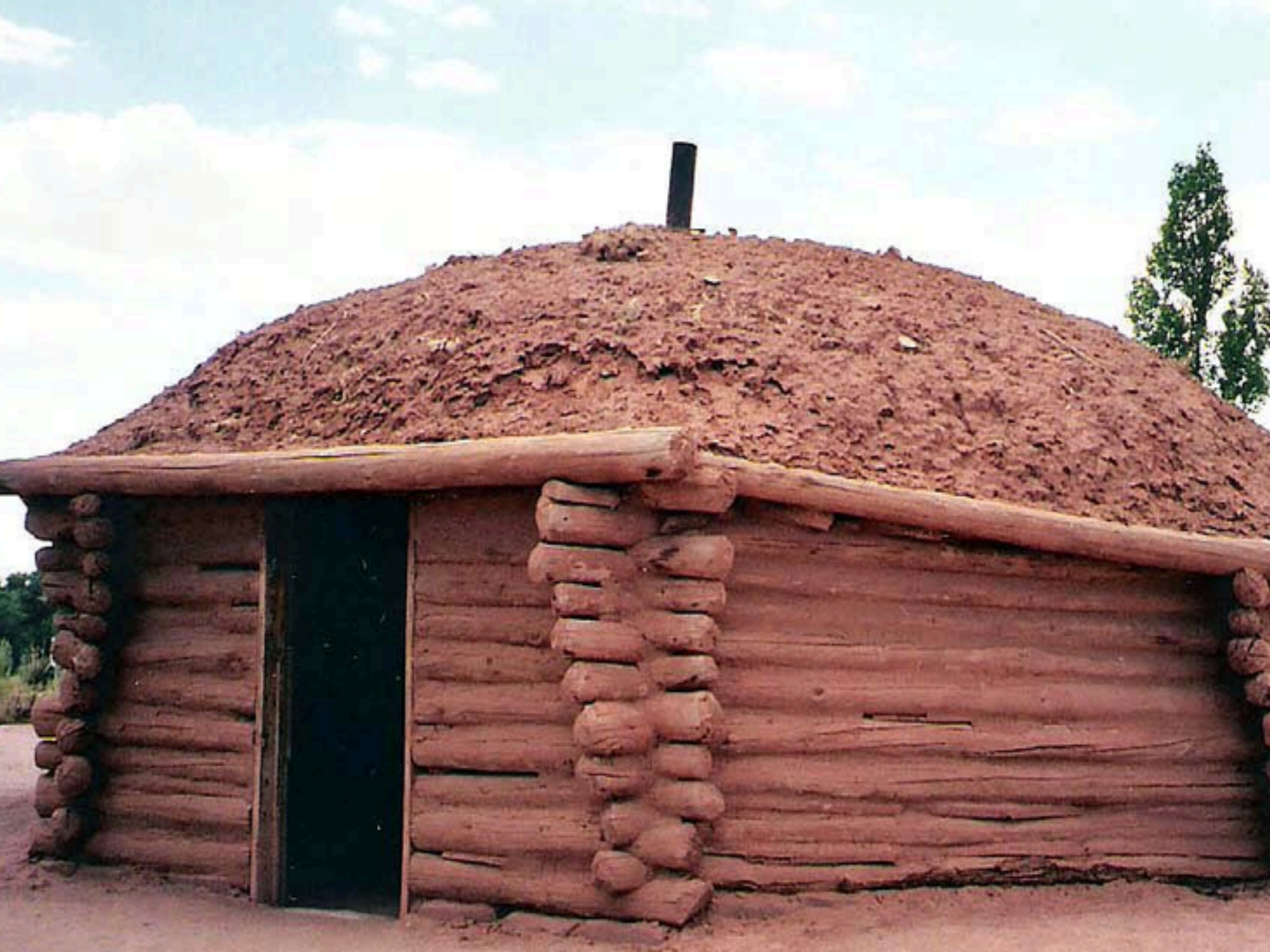
>20 deaths in 4 corners region



ATTENTION

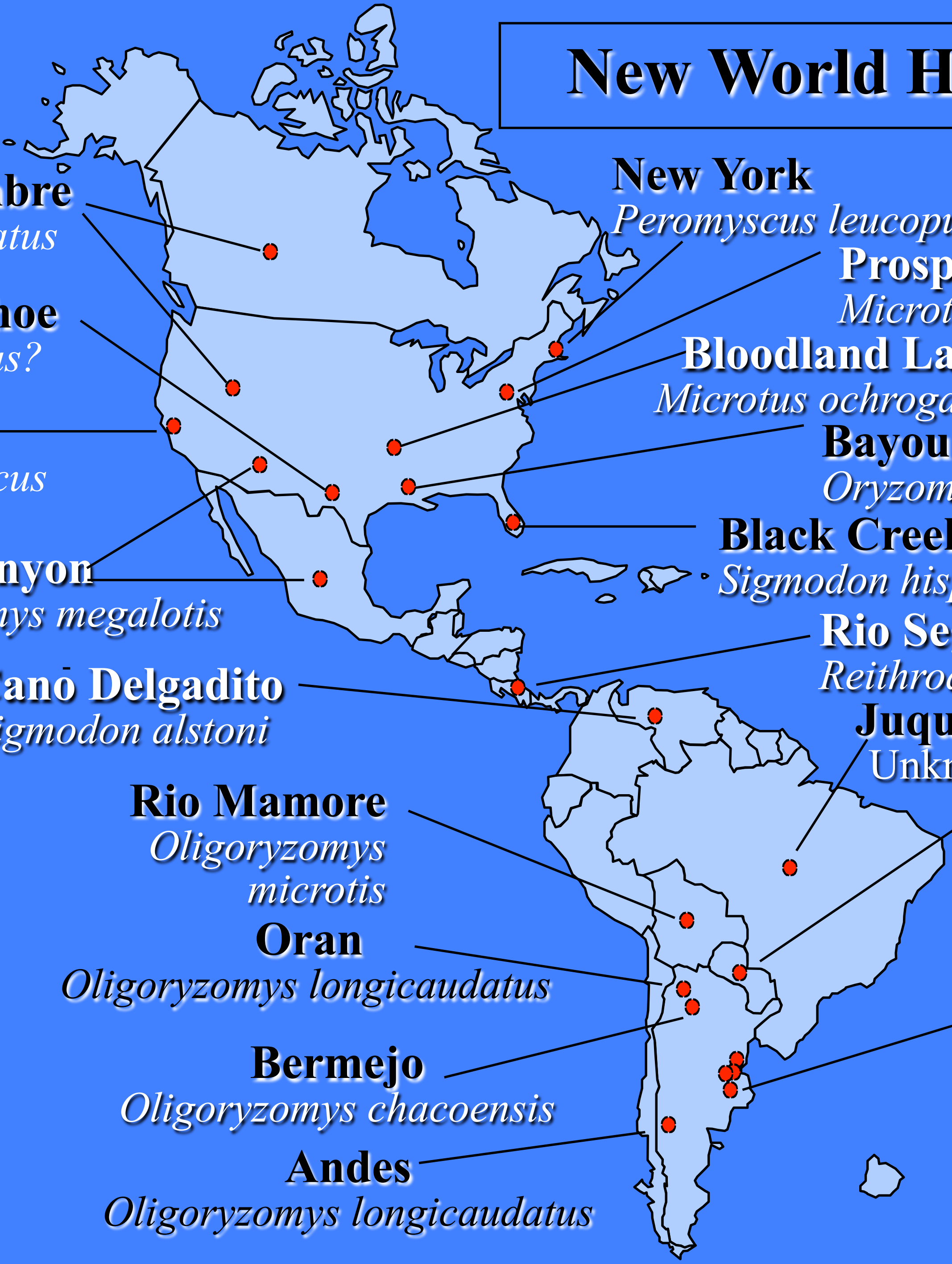
IF you have a
FEVER ALONG with
muscle aches AND
PAINS, PLEASE STAY
IN YOUR CAR AND
we will EXAMINE
you there.

Deer mouse is commensal with humans



MUSEUM OF SOUTHWESTERN BIOLOGY
UNIVERSITY OF NEW MEXICO

New World Hantaviruses



Sin Nombre
eromyscus maniculatus

Mule Shoe
Sigmodon hispidus?

Isla Vista
Microtus californicus

El Moro Canyon
Reithrodontomys megalotis

Caño Delgadito
Sigmodon alstoni

Rio Mamore
Oligoryzomys microtis

Oran
Oligoryzomys longicaudatus

Bermejo
Oligoryzomys chacoensis

Andes
Oligoryzomys longicaudatus

New York
Peromyscus leucopus

Prospect Hill
Microtus pennsylvanicus

Bloodland Lake
Microtus ochrogaster

Bayou
Oryzomys palustris

Black Creek Canal
Sigmodon hispidus

Rio Segundo
Reithrodontomys mexicanus

Juquitiba
Unknown

Laguna Negra
Calomys laucha

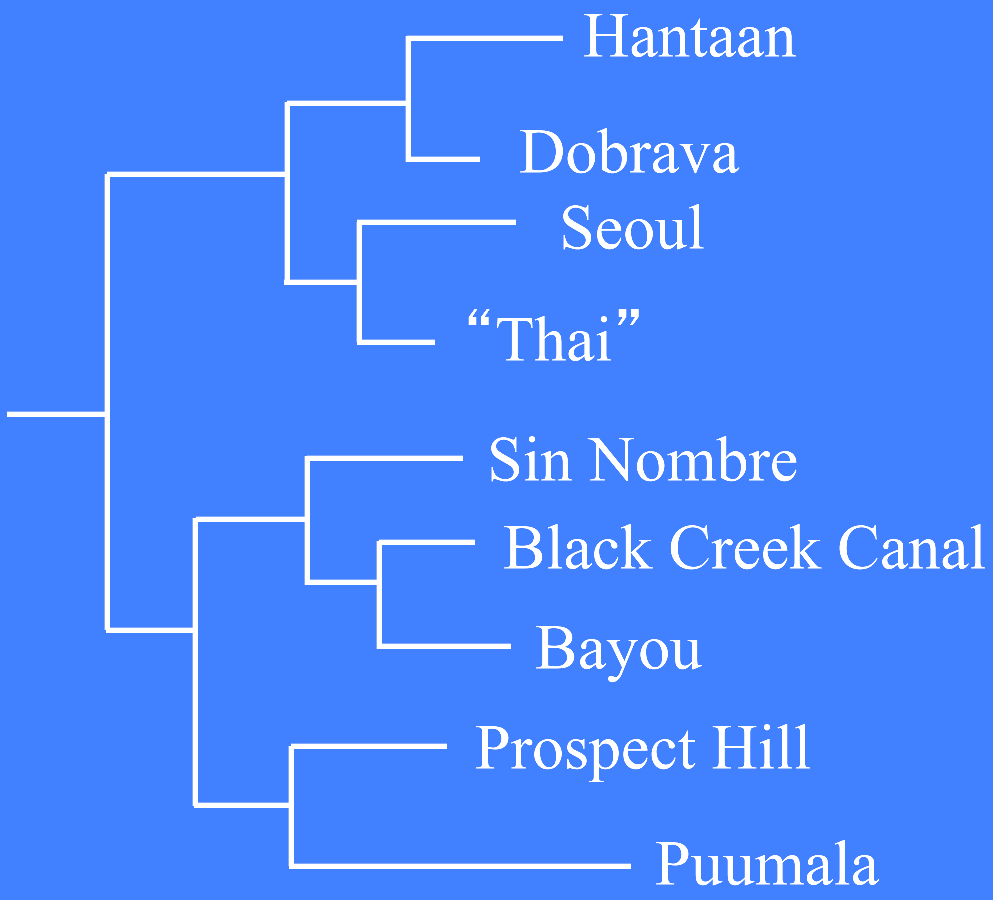
Maciel
Bolomys obscurus

HU39694
Unknown Host

Lechiguanas
Oligoryzomys flavescens

Pergamino
Akodon azarae

Phylogeny of Rodent Hantaviruses

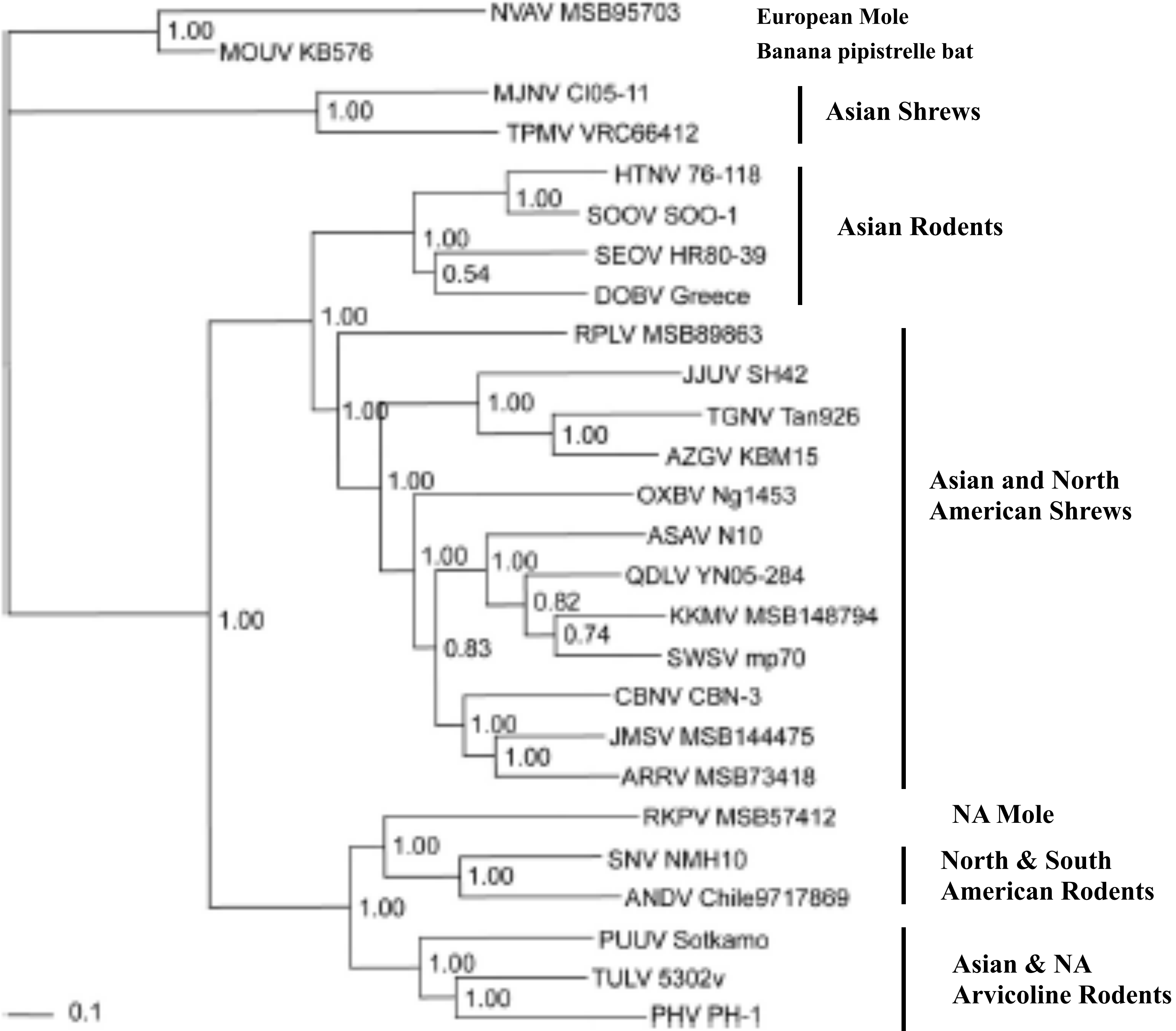


Virus Strain	Rodent Host
Hantaan	*Apodemus agrarius*
Dobrava	*Apodemus flavicollis*
Seoul	*Rattus norvegicus*
“Thai”	*Bandicota indicus*
Sin Nombre	*Peromyscus maniculatus*
Black Creek Canal	*Sigmodon hispidus*
Bayou	Unknown
Prospect Hill	*Microtus pennsylvanicus*
Puumala	*Clethrionomys glareolus*

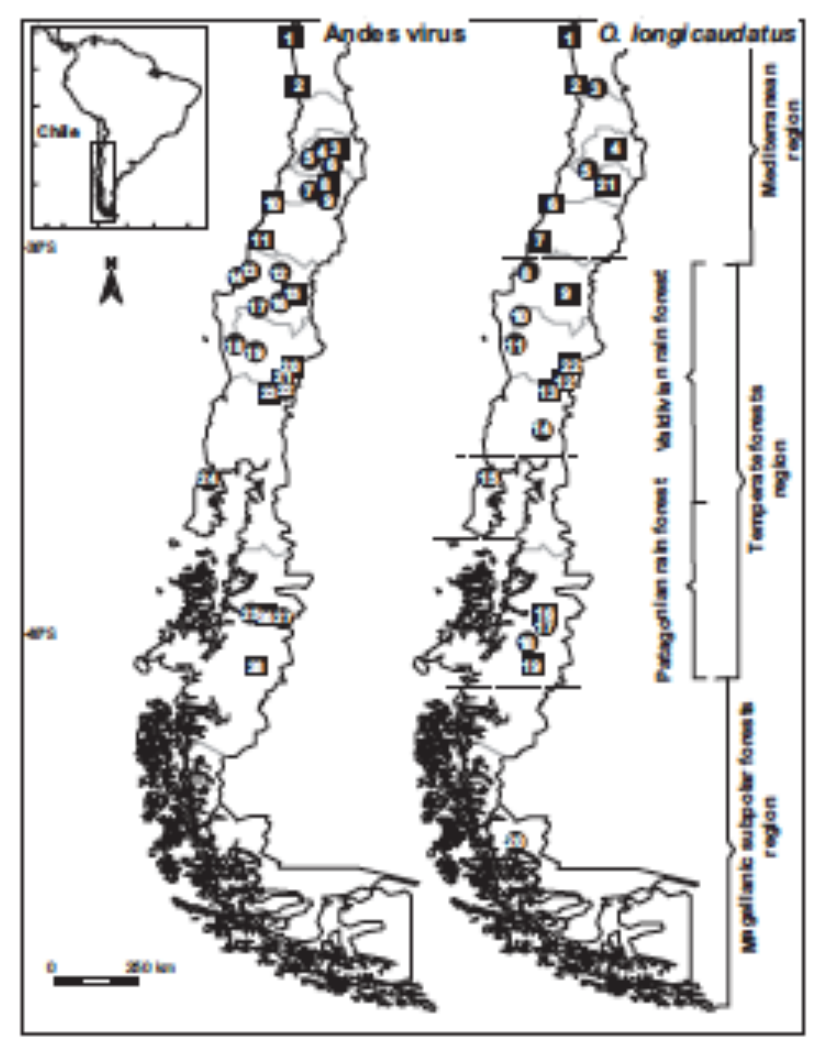
Arai S, Song J-W et al.
Hantavirus in northern short-tailed shrew, United States.
Emerging Infectious Diseases 2007

Many new hosts for new Hantaviruses

Rapid discovery with deep specimen archives


NVAV MSB95703
1.00
MOUV KB576
European Mole
Banana pipistrelle bat
MJNV CI05-11
1.00
TPMV VRC66412
Asian Shrews
HTNV 76-118
1.00
SOOV SOO-1
1.00
SEOV HR80-39
0.54
DOBV Greece
Asian Rodents
1.00
RPLV MSB89863
JJUV SH42
1.00
TGNV Tan926
1.00
AZGV KBM15
1.00
1.00
OXBV Ng1453
ASAV N10
1.00
1.00
QDLV YN05-284
0.82
KKMV MSB148794
0.74
SWSV mp70
0.83
CBNV CBN-3
1.00
JMSV MSB144475
1.00
ARRV MSB73418
Asian and North American Shrews
1.00
RKPV MSB57412
NA Mole
1.00
SNV NMH10
1.00
ANDV Chile9717869
North & South American Rodents
1.00
PUUV Sotkamo
1.00
TULV 5302v
1.00
PHV PH-1
Asian & NA Arvicoline Rodents
0.1

Beyond virus discovery to exploring population and expansion dynamics and responses to environmental change of host and pathogen



Torres-Perez et al 2011
Molecular Ecology

Chile:
Andes virus (ANDV)
and its host rodent,
Oligoryzomys longicaudatus

Despite major differences in evolutionary dynamics (e.g., substitution rates), geographic structure of host and virus converged across large spatial scales.

Environmental Interfaces of Parasites

Defines need for specimen-based biodiversity informatics

- Accelerating Climate Change
- Biodiversity Crisis
- Invasive Species
- Emerging Infectious Diseases
- Food Safety, Sustainability / Zoonoses
- Interface of Natural & Agricultural Systems

Threats to human population, natural systems, conservation, agriculture, global economy

Hoberg & Brooks/ Brooks & Hoberg, 2013 In: Balance of Nature & Human Impact, Cambridge.

Parasite Specimen Collections Allow Numerous Studies

- Phylogeny/ Phylogeography
- Geographic Distributions/ GIS/ SDM’s
- Host Association
- Patterns of Emergence
- Species Composition Over Time
- Faunal Structure & Assembly

Parasites = proxies for biocomplexity linking evolutionary & ecological time

Challenge of emerging infectious diseases stems from absence of comprehensive taxonomic inventories of world’s pathogens and parasites

> 40-50% of known species on the planet are parasites OR pathogens

70-75% of trophic linkages (ecological connectivity) involve parasites

> 60% of zoonoses are of wildlife origin

Climate Change Consequences

Climate change is eliminating ecological barriers & constraints on development & distribution for pathogen transmission.

Creates New Conditions.

Maps for distributions of hosts, pathogens & diseases are being redrawn.

Emergence of diseases & unanticipated "cascades" can drive perturbations in terrestrial, marine & aquatic ecosystems.

Parasites & Climate Change

- Latitudinal & altitudinal shifts
  - Modified geographic range/ Geographic mosaics
- Habitat alteration influences distribution
  - Change in permissive environments
- Ecological perturbation/ Novel environments
  - Breakdown in ecological isolation/ Invasion
- Windows for transmission
  - Extension of growth season; rapid development & reduced generation time
  - Resilience, thresholds, tipping points
- Cumulative and Ephemeral processes
- Host switching? Sympatry, Ecotone effects

Why Do We Need Integrated Archives?

- "The Past is the Key to the Present"
- Environments in rapid transition
  - Permanent change & loss
  - New ecological associations
- Permanent record of faunal structure
  - Hosts, Spatial & Temporal scale
- Documenting Stability & Change

Concept for Integrated Archives of Beringia

- Specimens accumulated across discrete points in time
- Geographically extensive, site intensive field sampling
  - Representative host assemblages in sympatry
- Standardized protocols as foundation for comparability
  - Integrated- morphological/ molecular pathways
- Inclusion of Parasitological Data within broader environmental context

- Voucher specimens of parasites are sporadically archived in survey, systematics, ecological, epidemiological studies……..

(No Morer Business as Usual)
Integrated Collections
Host/Parasite

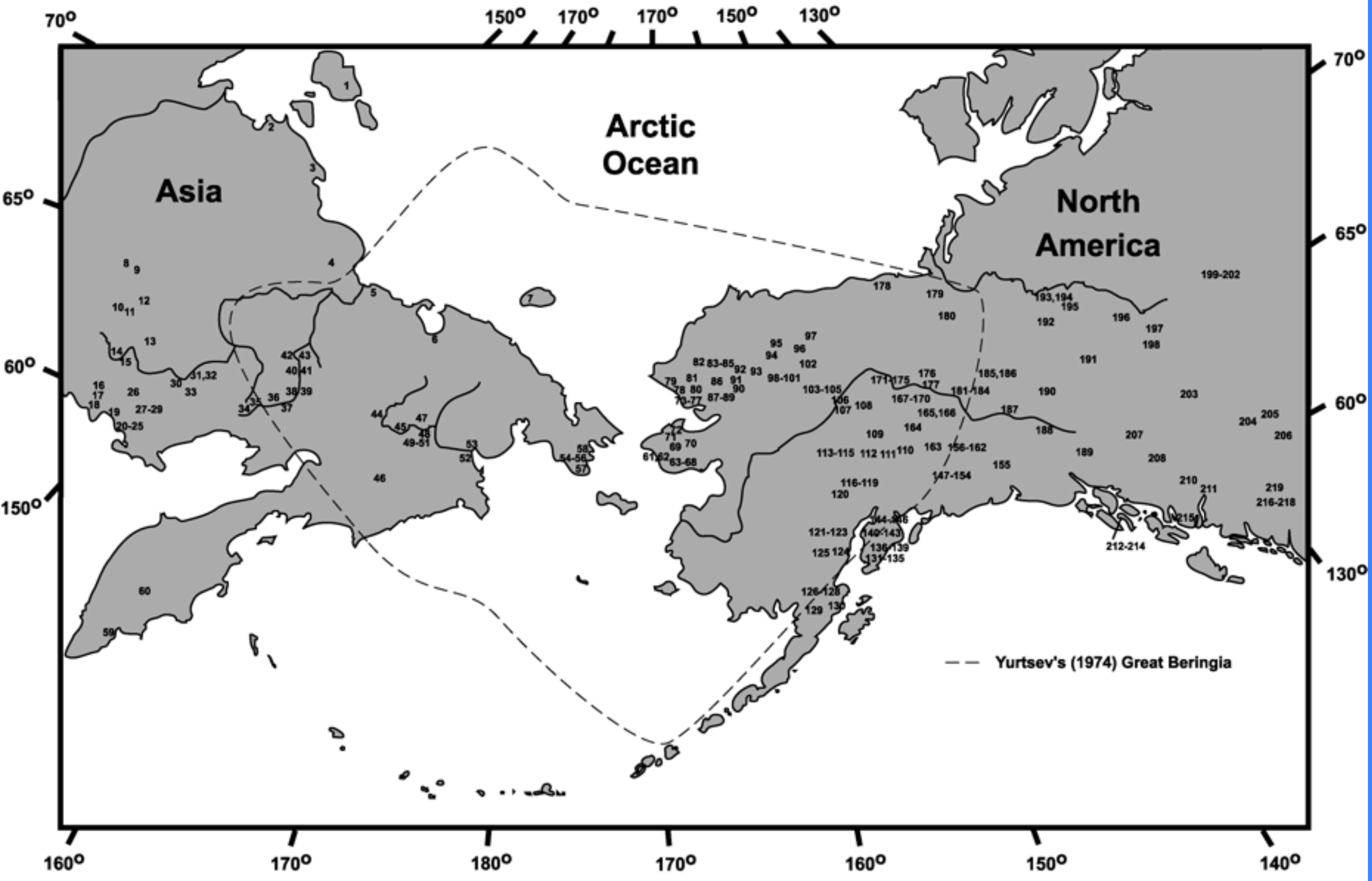
Mammalogy

V Fedorov, L Olson
University of Alaska
H. Henttonen
Vantaa, Finland
S Talbot
USGS-Alaska Science Center
N Dokuchaev
Magadan, Russia
Graduate Students
Chris Conroy
John Demboski
Karen Stone
Amy Runck
Kurt Galbreath
Byron Weckworth
Eric Tomasik
Michael Lucid
Aren Eddingsaas
Eric Waltari
Natalie Dawson
Andrew Hope

Parasitology

E Hoberg
US National Parasite Collection
R Eckerlin
N Virginia Community College
V Haukisalmi
Vantaa, Finland
K Galbreath
Northern Michigan University
S Kutz
University of Calgary
E Jenkins
University of Saskatchewan
S Telford III
Tufts University
Greg Ebel
University of New Mexico

Beringian Study Sites (1999-2012)



Biodiversity Lessons/ Baselines

- Archival specimen resources (informatics)
- Synoptic collections/ critical time frames
- Temporal/ Spatial networks- Holarctic
  - Mammalian Faunas- Rausch Helminthological Collections (1950’s)- Beringian Coevolution Project/ Integrated Inventories of Biomes of the Arctic (2000’s)-
  - Ungulate Faunas- Simmons (1970’s) & Nielsen, Neiland (1970’s) Parasitological Collections (1970’s)- Research Group for Arctic Parasitology (1990’s – 2000’s)
- Sliding baselines linking regions/ landscapes
  - Species, host association, geographic dist, prevalence, abundance
- Specimens as self correcting records of biodiversity (100 + years)

Hierarchies of Information

Temporal + Spatial Scale/ History and Biogeography

FAUNAL ASSEMBLAGES (historical)

↓

SPECIES (morphological/ molecular)

↓

CRYPTIC DIVERSITY (genetic partitions)

↓

POPULATIONS (genetic diversity/ geneflow)

- landscape epidemiology, local processes
- ephemeral patterns of emergence

Microparasites—
Viruses, Blood-borne Protozoans

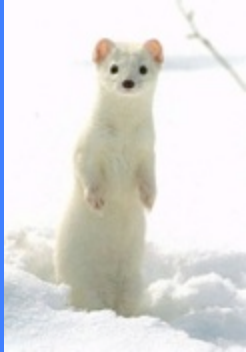
Endoparasites

- Nematode
  - Koehler---*Soboliphyme*
- Cestode
  - Galbreath/Hoberg--*Arostrilepis*
  - Wickstrom-*Paranoplocephala*

Ectoparasites

- Mites—ácaro
  - John Whitaker
- Ticks—garrapatas
  - Nixon Wilson
- Fleas-pulgas
  - Glenn Haas

Soboliphyme baturini



- Distribution centered on Beringia
- Stomach nematode parasite of Mustelids
- Adult Length: 2-4 cm
- Intensity: 3-5 per stomach, Up to 200
- Pathology not fully explored
  - Anemia
  - Ulcers
  - No known cases reported from humans

Paratenic & Definitive Hosts

- QUESTIONS:
    - 1) What are the **principal** definitive hosts of this nematode?
    - 2) Do shrews play a role in the lifecycle of this parasite?

Summary of 749 necropsies

- Highest prevalence-marten
- Mink, ermine, fisher, wolverine had low infection rates
- Insectivores have larval form in diaphragm

Potential Hosts

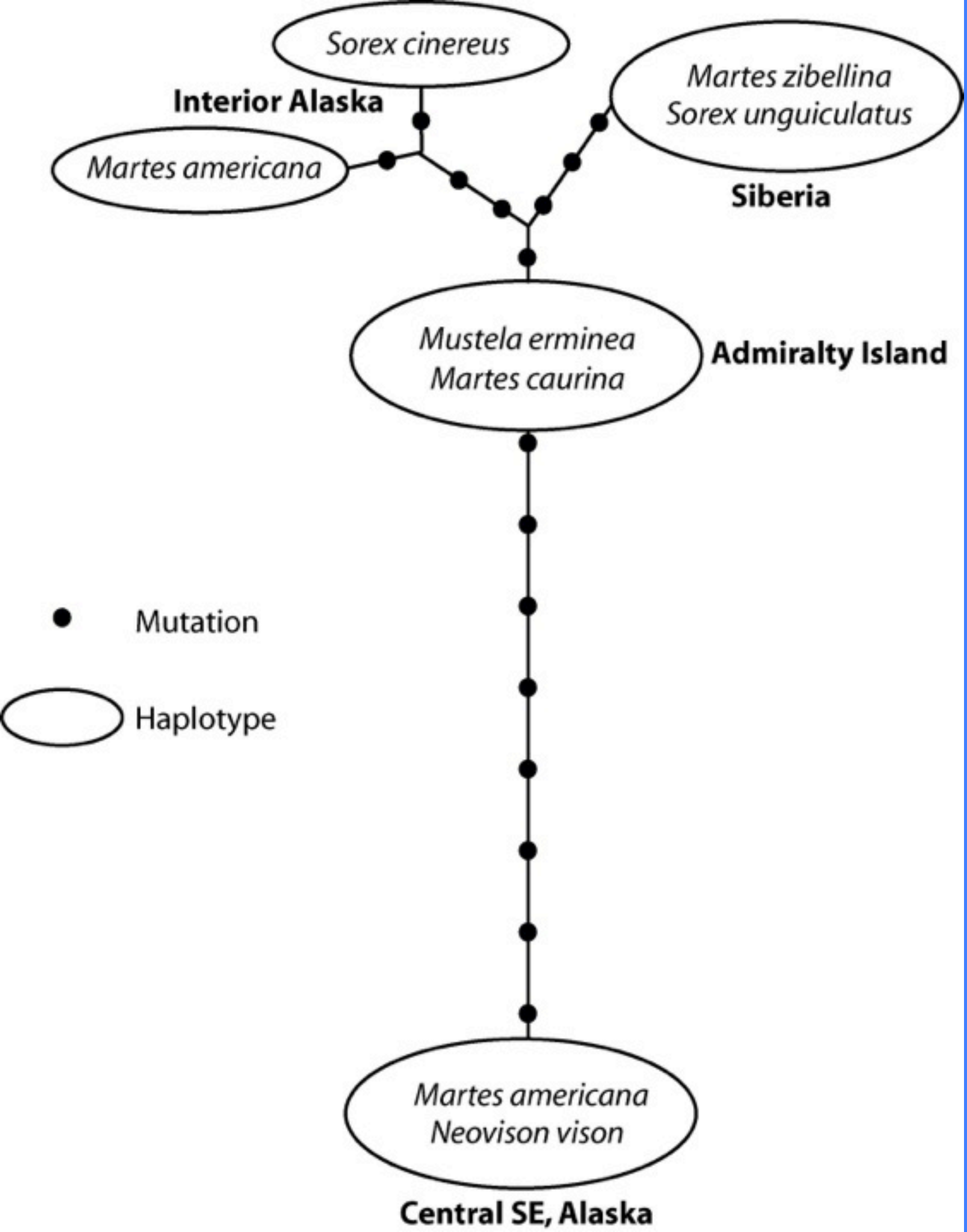
ND4 region of mtDNA

Shrew

Ermine

Mink

ND4 351bp *Soboliphyme baturini*



Koehler et al, 2007.
J Parasitology

Paratenic & Definitive Hosts
CONCLUSIONS

- Shrew *Soboliphyme* = Marten *Soboliphyme*
- Mink *Soboliphyme* = Ermine *Soboliphyme* = Marten *Soboliphyme*
- *Soboliphyme* are primarily found in marten (and introduced mink in Asia).
  - Juvenile form only found in Ermine.
  - Mink and ermine from heavily infected islands had few *Soboliphyme*.

Soboliphyme Phylogeography

Hypotheses

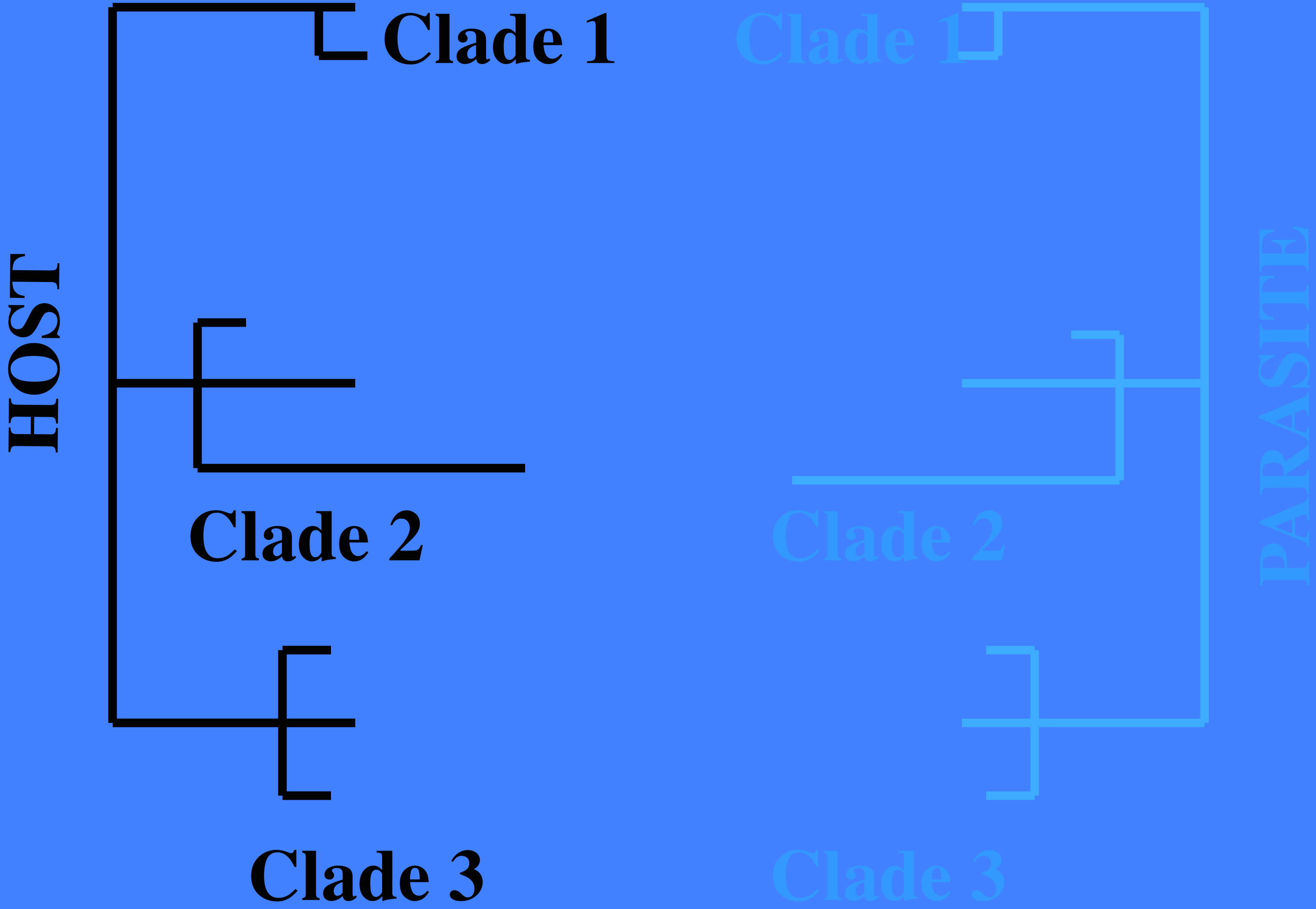
1. **Codiversification**

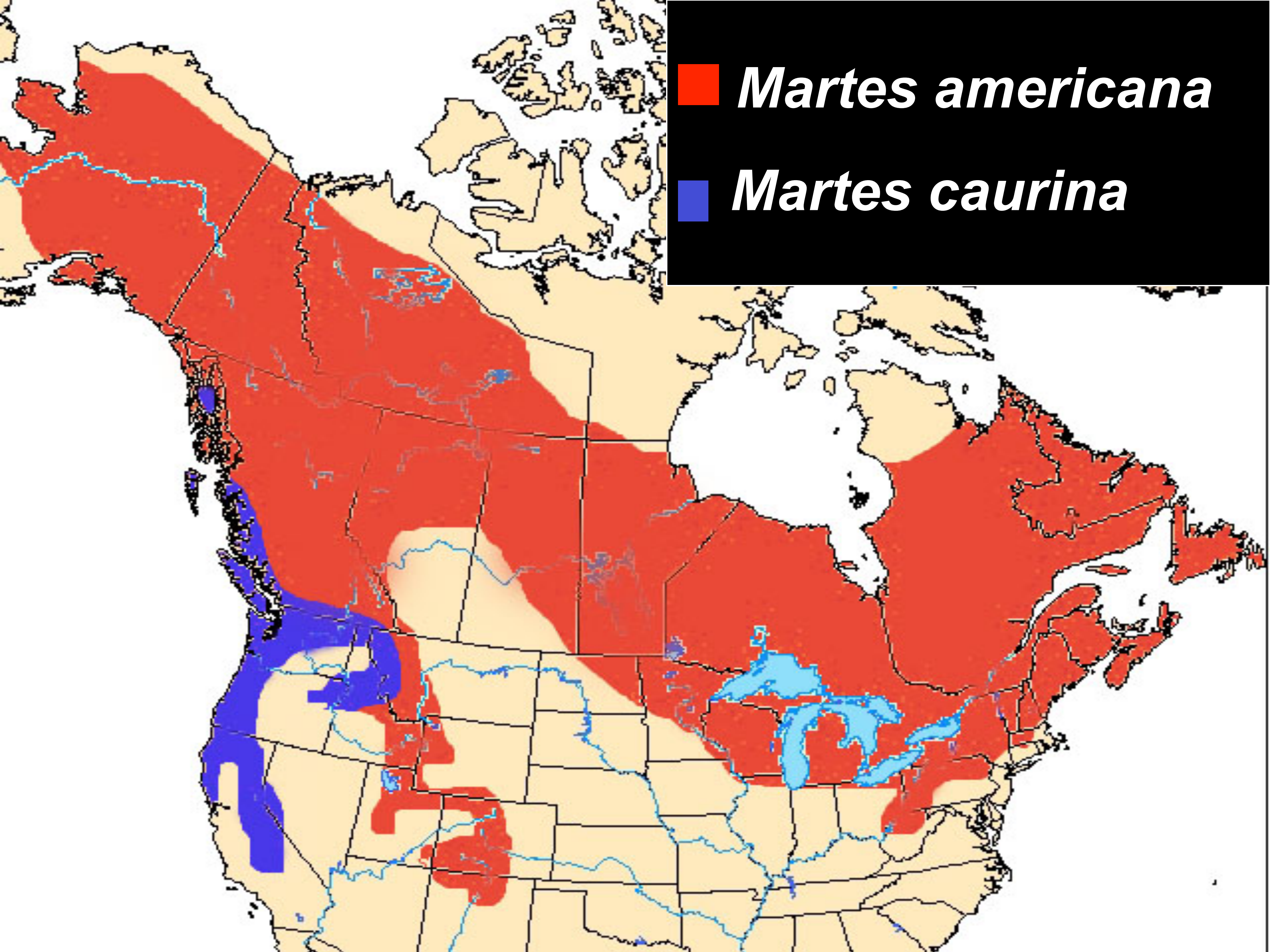
   Parasite tree tracks host tree

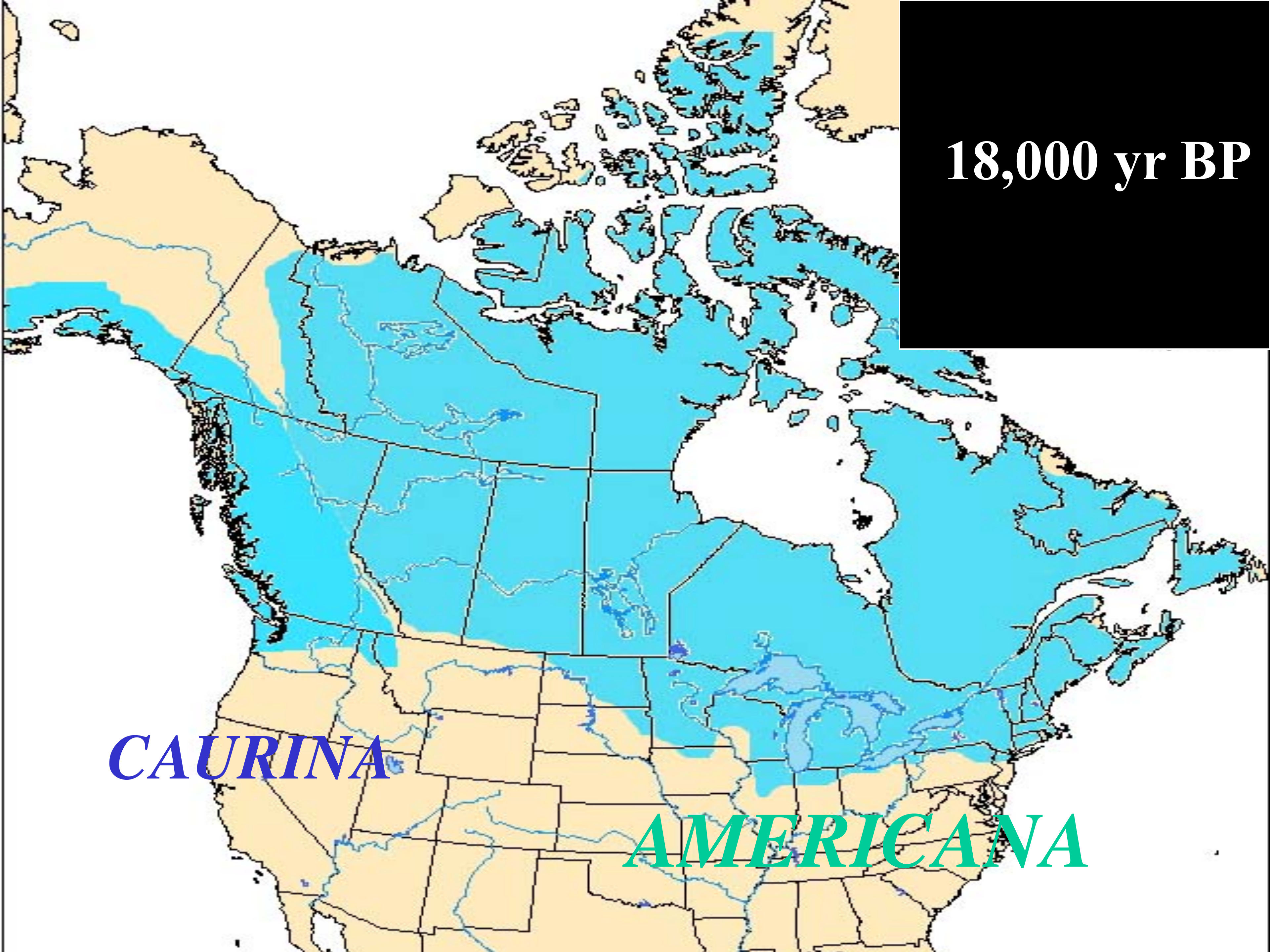
2. **Geographical diversification**

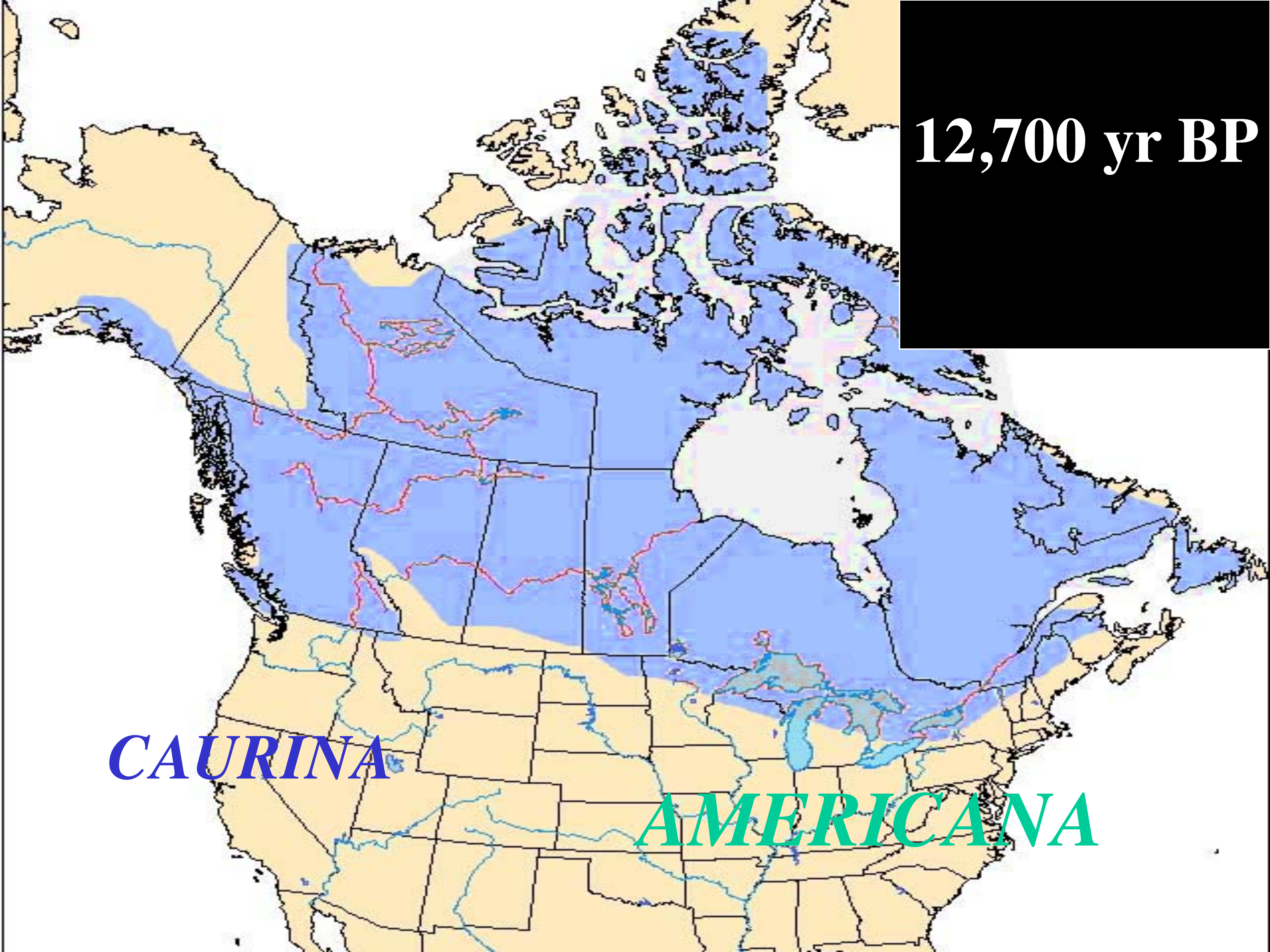
   Parasite tree reflects (climate-related) vicariant events

Codiversification



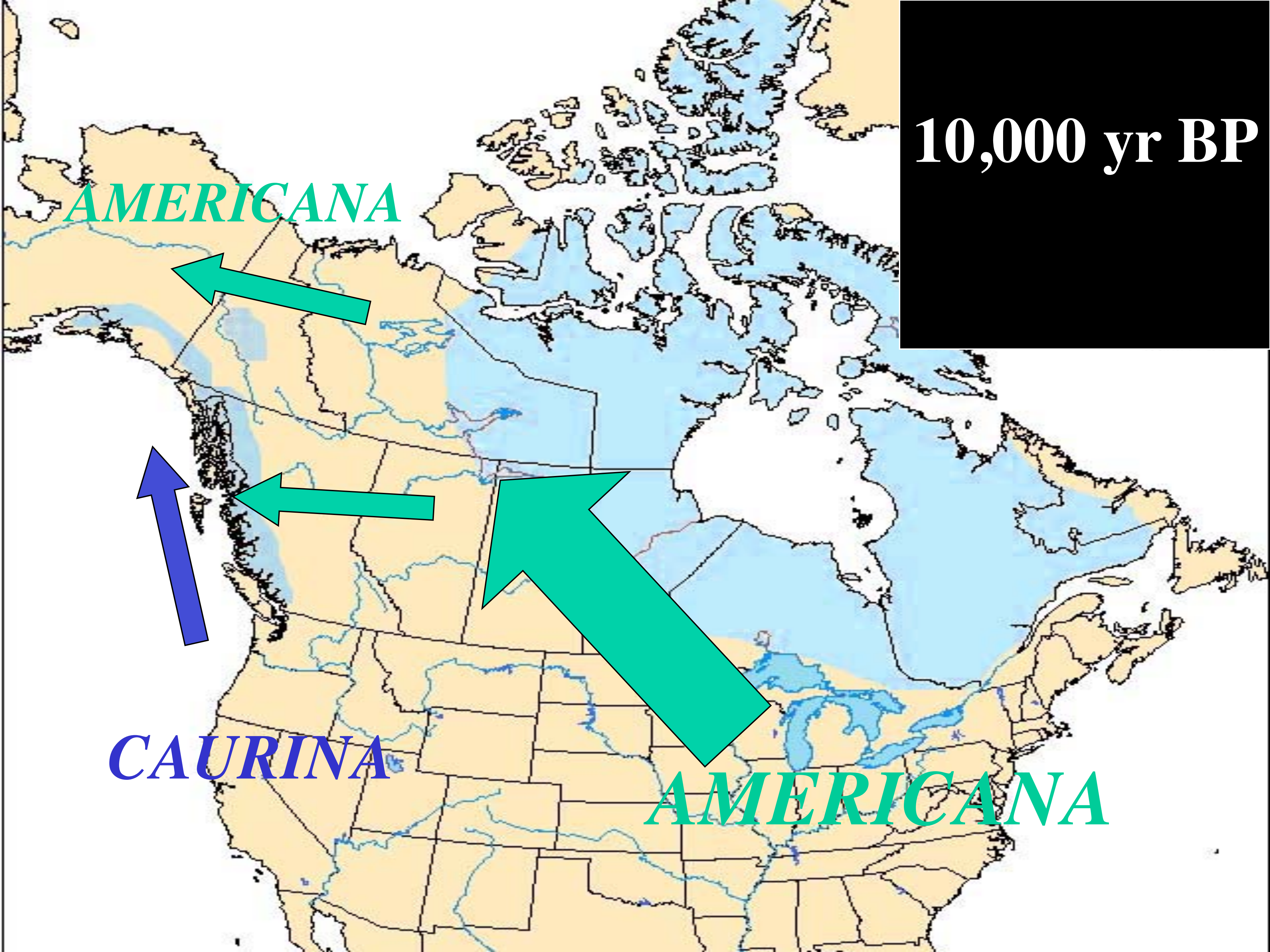

🟥 *Martes americana*
🟦 *Martes caurina*


18,000 yr BP
CAURINA
AMERICANA

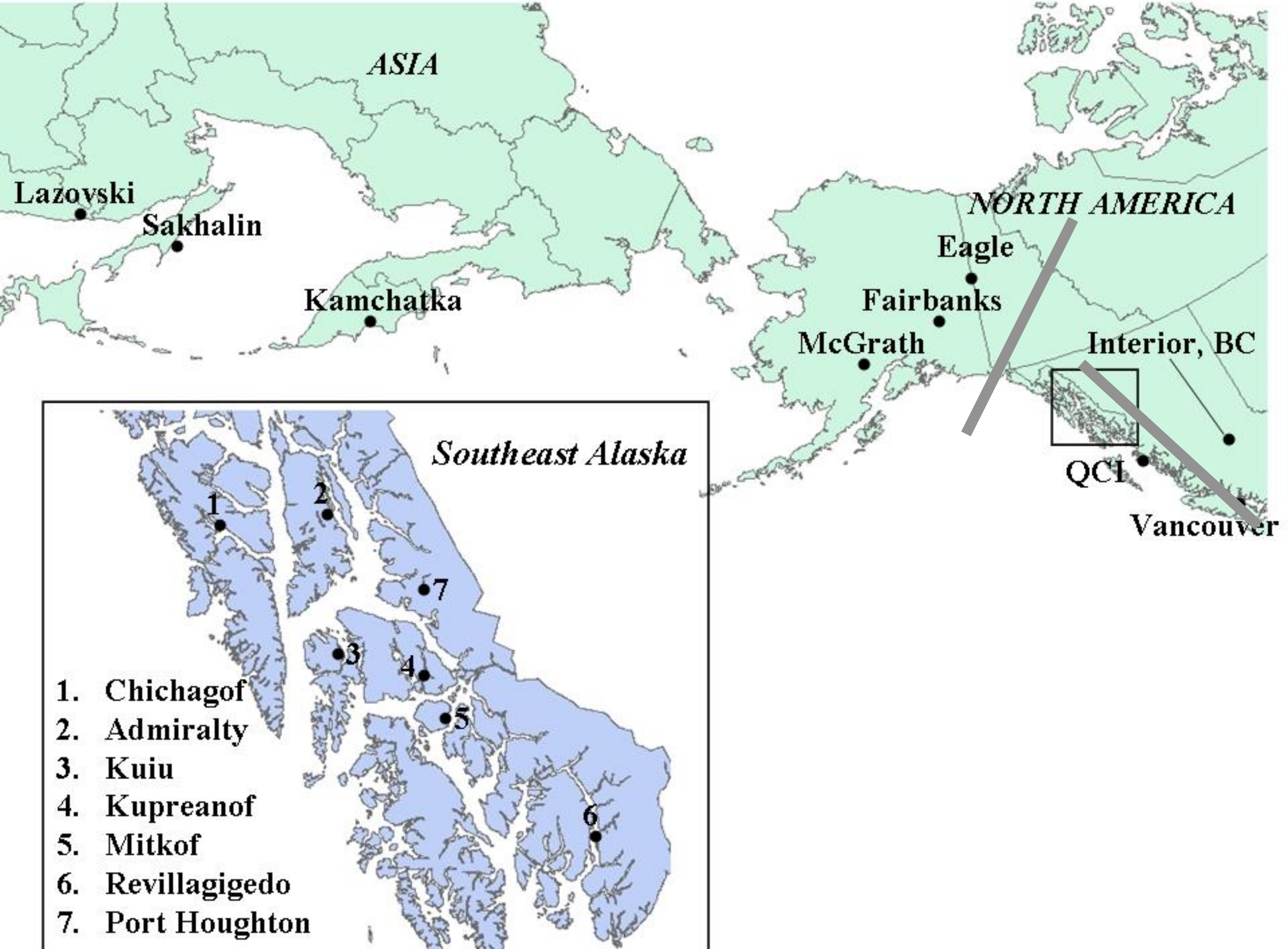


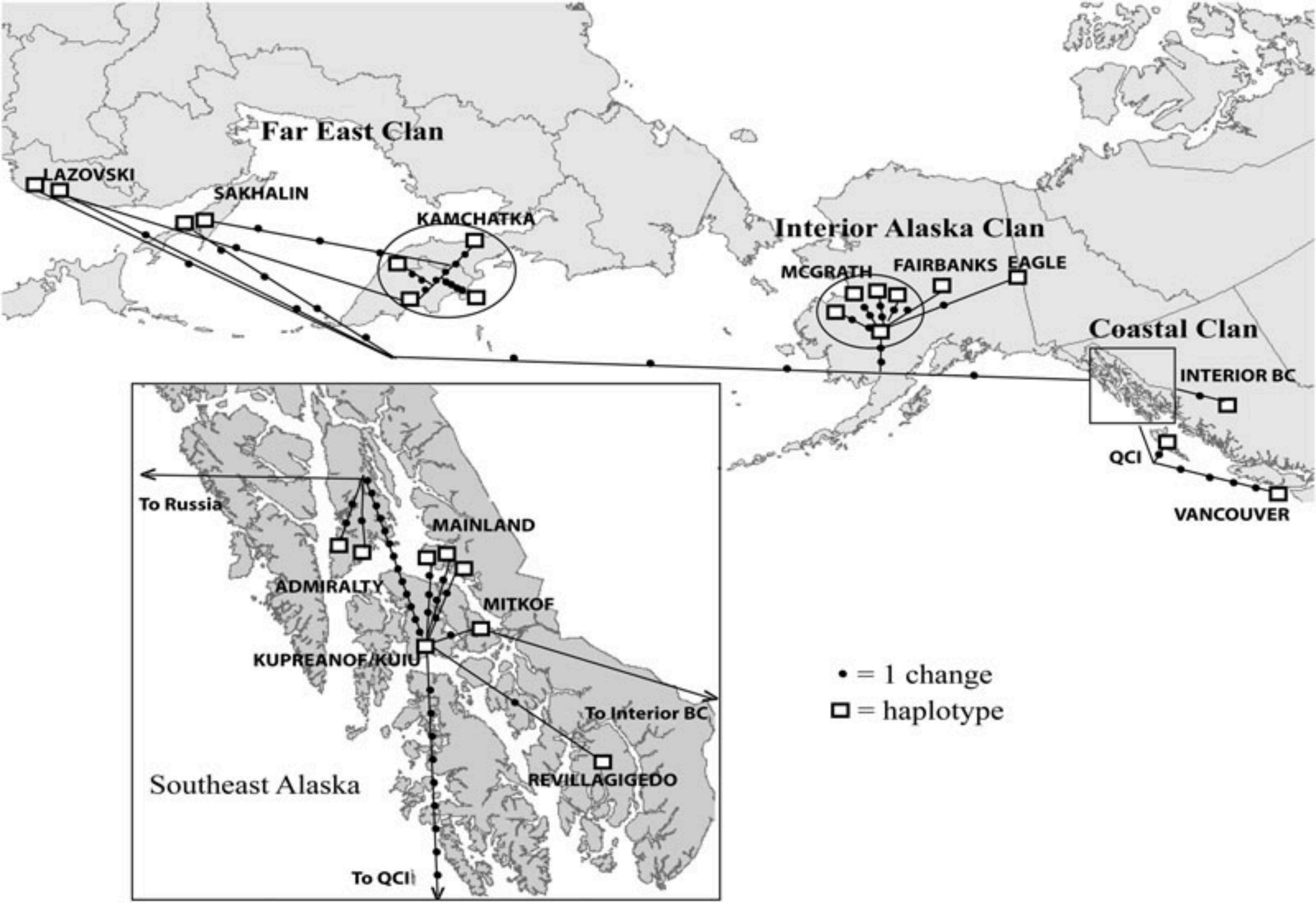
12,700 yr BP

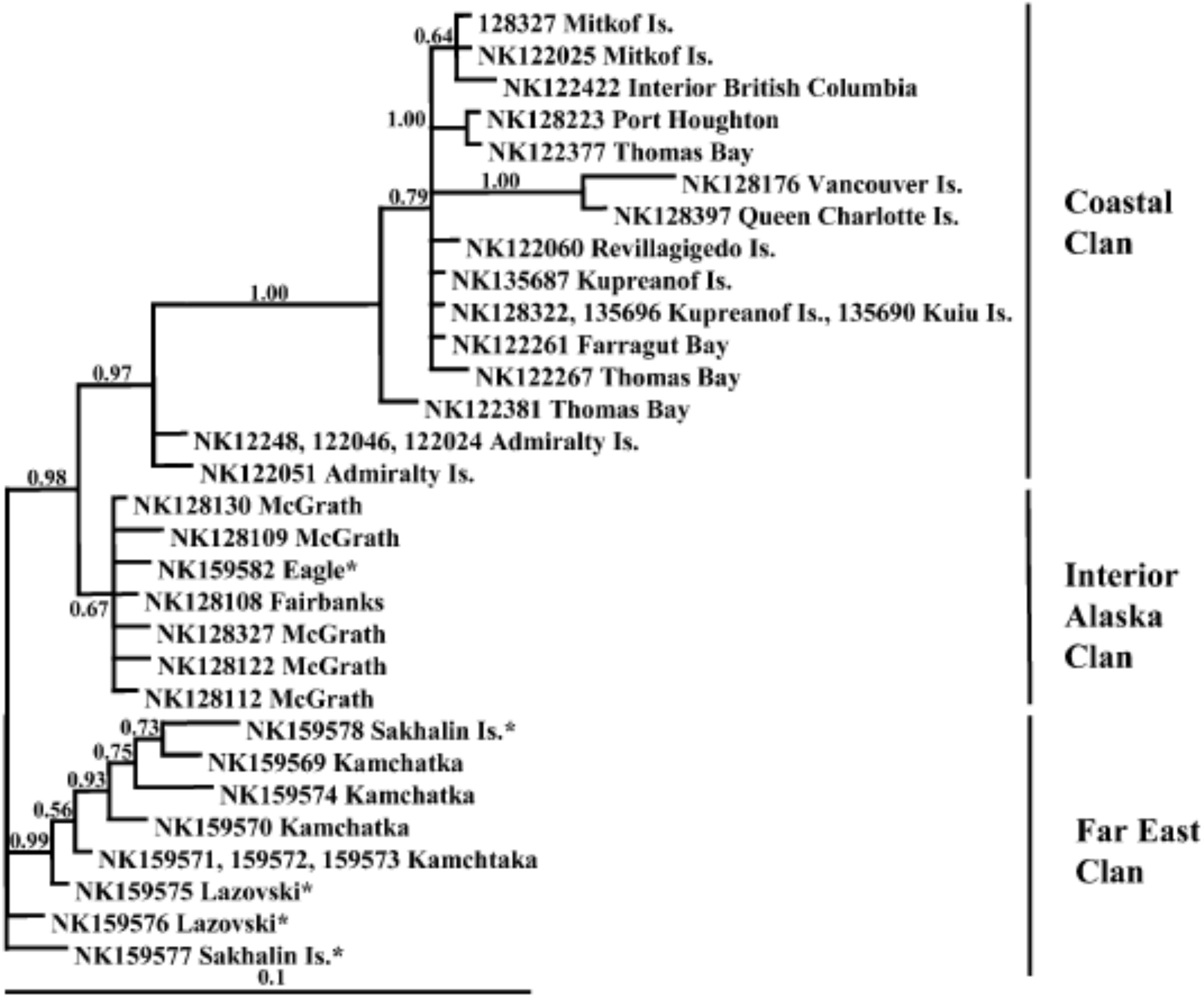
10,000 yr BP

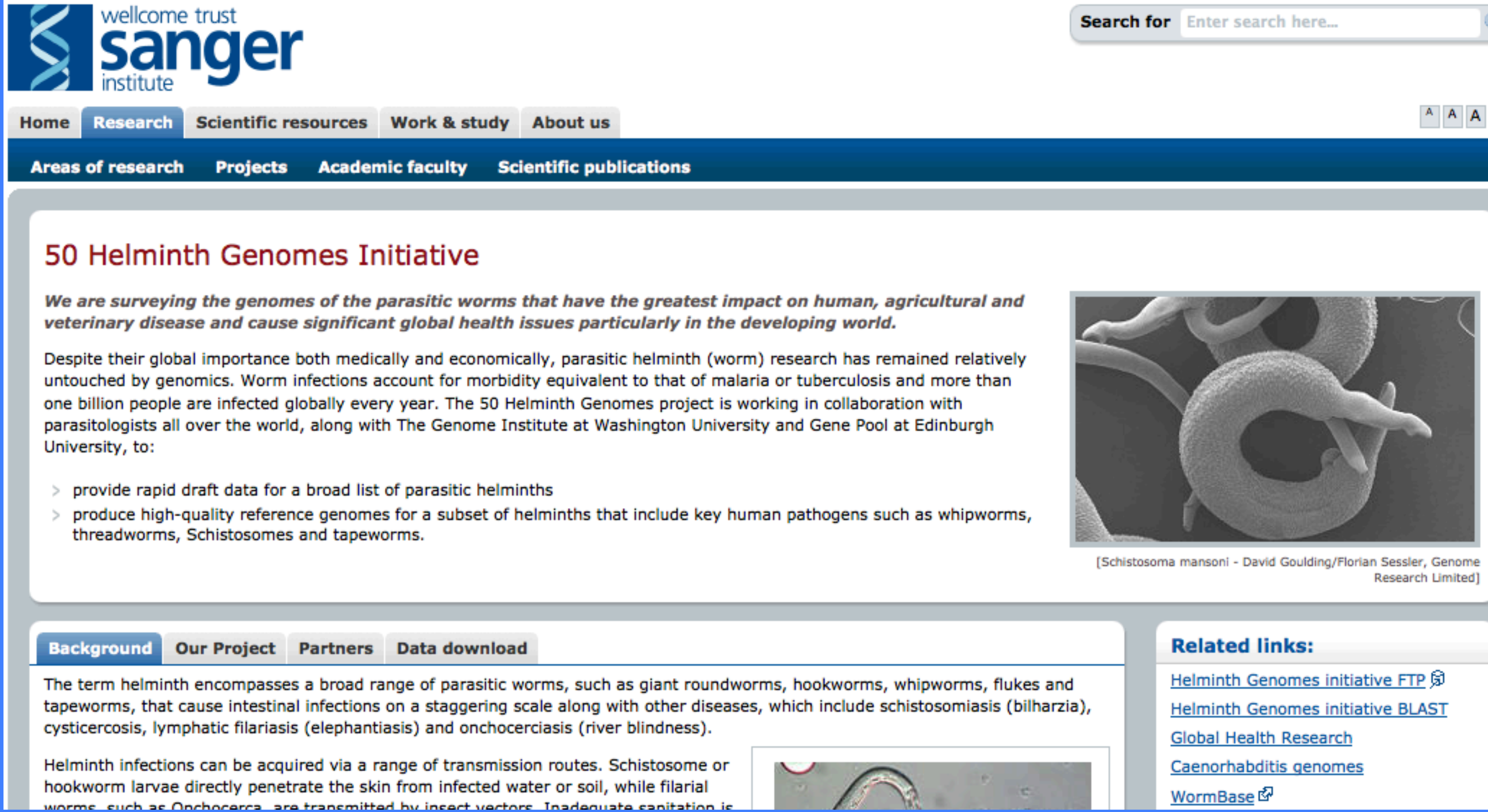


Vicariant Events


ASIA
NORTH AMERICA
Lazovski
Sakhalin
Kamchatka
Eagle
Fairbanks
McGrath
Interior, BC
QCI
Vancouver
Southeast Alaska
1
2
3
4
5
6
7
1. Chichagof
2. Admiralty
3. Kuiu
4. Kupreanof
5. Mitkof
6. Revillagigedo
7. Port Houghton


Far East Clan
LAZOVSKI
SAKHALIN
KAMCHATKA
Interior Alaska Clan
MCGRATH
FAIRBANKS
EAGLE
Coastal Clan
INTERIOR BC
QCI
VANCOUVER
To Russia
MAINLAND
ADMIRALTY
MITKOF
KUPREANOF/KUIU
To Interior BC
REVILLAGIGEDO
Southeast Alaska
To QCI
• = 1 change
□ = haplotype


0.64
128327 Mitkof Is.
NK122025 Mitkof Is.
NK122422 Interior British Columbia
1.00
NK128223 Port Houghton
NK122377 Thomas Bay
1.00
0.79
NK128176 Vancouver Is.
NK128397 Queen Charlotte Is.
NK122060 Revillagigedo Is.
NK135687 Kupreanof Is.
NK128322, 135696 Kupreanof Is., 135690 Kuiu Is.
NK122261 Farragut Bay
NK122267 Thomas Bay
1.00
NK122381 Thomas Bay
0.97
NK12248, 122046, 122024 Admiralty Is.
NK122051 Admiralty Is.
0.98
NK128130 McGrath
NK128109 McGrath
NK159582 Eagle*
0.67
NK128108 Fairbanks
NK128327 McGrath
NK128122 McGrath
NK128112 McGrath
0.73
NK159578 Sakhalin Is.*
0.75
NK159569 Kamchatka
0.93
NK159574 Kamchatka
0.56
NK159570 Kamchatka
0.99
NK159571, 159572, 159573 Kamchtaka
NK159575 Lazovski*
NK159576 Lazovski*
NK159577 Sakhalin Is.*
0.1
Coastal Clan
Interior Alaska Clan
Far East Clan



50 Helminth Genomes Initiative

We are surveying the genomes of the parasitic worms that have the greatest impact on human, agricultural and veterinary disease and cause significant global health issues particularly in the developing world.

Despite their global importance both medically and economically, parasitic helminth (worm) research has remained relatively untouched by genomics. Worm infections account for morbidity equivalent to that of malaria or tuberculosis and more than one billion people are infected globally every year. The 50 Helminth Genomes project is working in collaboration with parasitologists all over the world, along with The Genome Institute at Washington University and Gene Pool at Edinburgh University, to:

- provide rapid draft data for a broad list of parasitic helminths
- produce high-quality reference genomes for a subset of helminths that include key human pathogens such as whipworms, threadworms, Schistosomes and tapeworms.

[Schistosoma mansoni - David Goulding/Florian Sessler, Genome Research Limited]

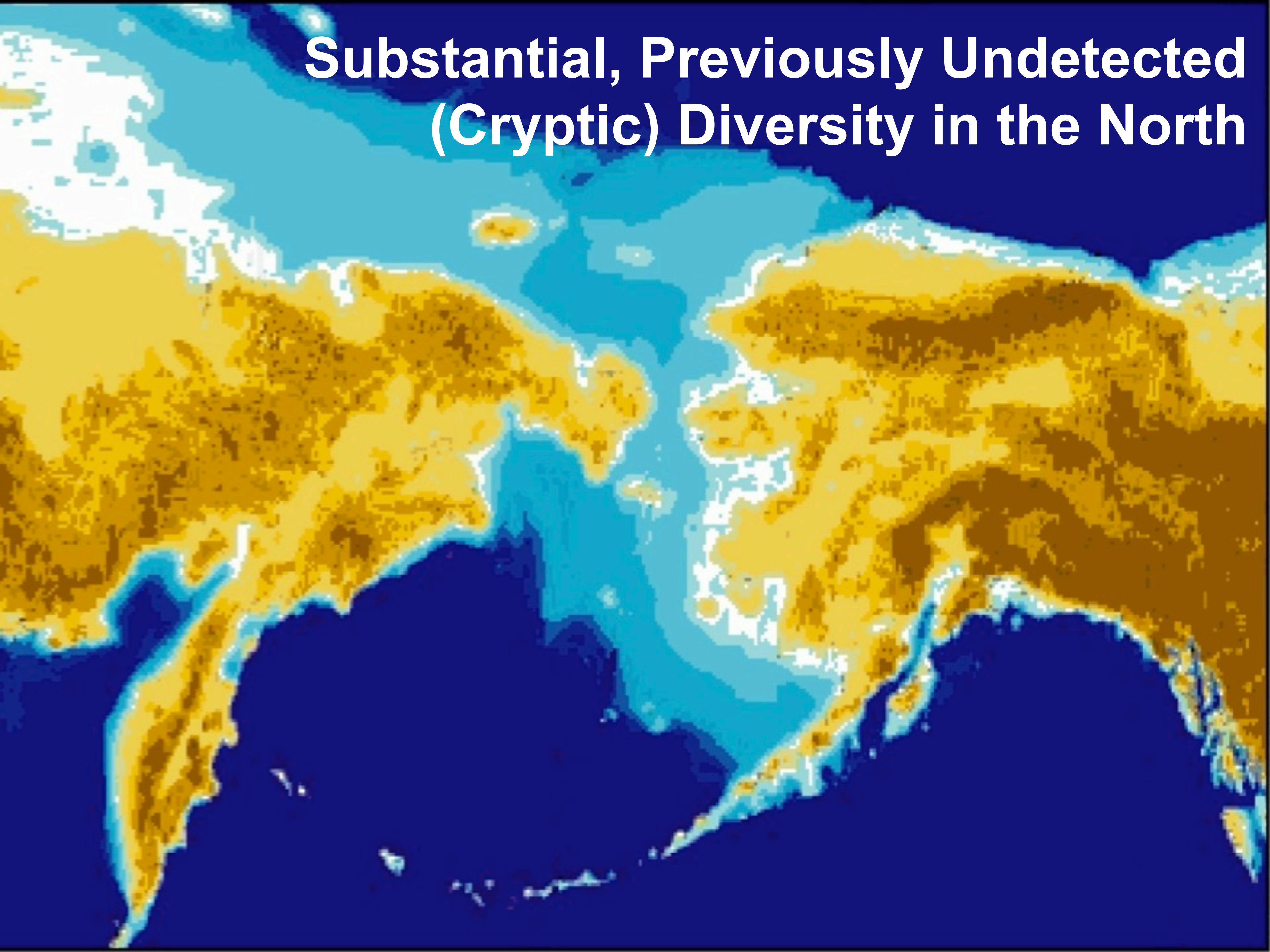
The term helminth encompasses a broad range of parasitic worms, such as giant roundworms, hookworms, whipworms, flukes and tapeworms, that cause intestinal infections on a staggering scale along with other diseases, which include schistosomiasis (bilharzia), cysticercosis, lymphatic filariasis (elephantiasis) and onchocerciasis (river blindness).

Helminth infections can be acquired via a range of transmission routes. Schistosome or hookworm larvae directly penetrate the skin from infected water or soil, while filarial worms, such as Onchocerca, are transmitted by insect vectors. Inadequate sanitation is

Related links:

- Helminth Genomes initiative FTP
- Helminth Genomes initiative BLAST
- Global Health Research
- Caenorhabditis genomes
- WormBase

"..now building these data into a web-based resource called WormBase-ParaSite. Second, are identifying the major gene families both across the nematodes and platyhelminths."

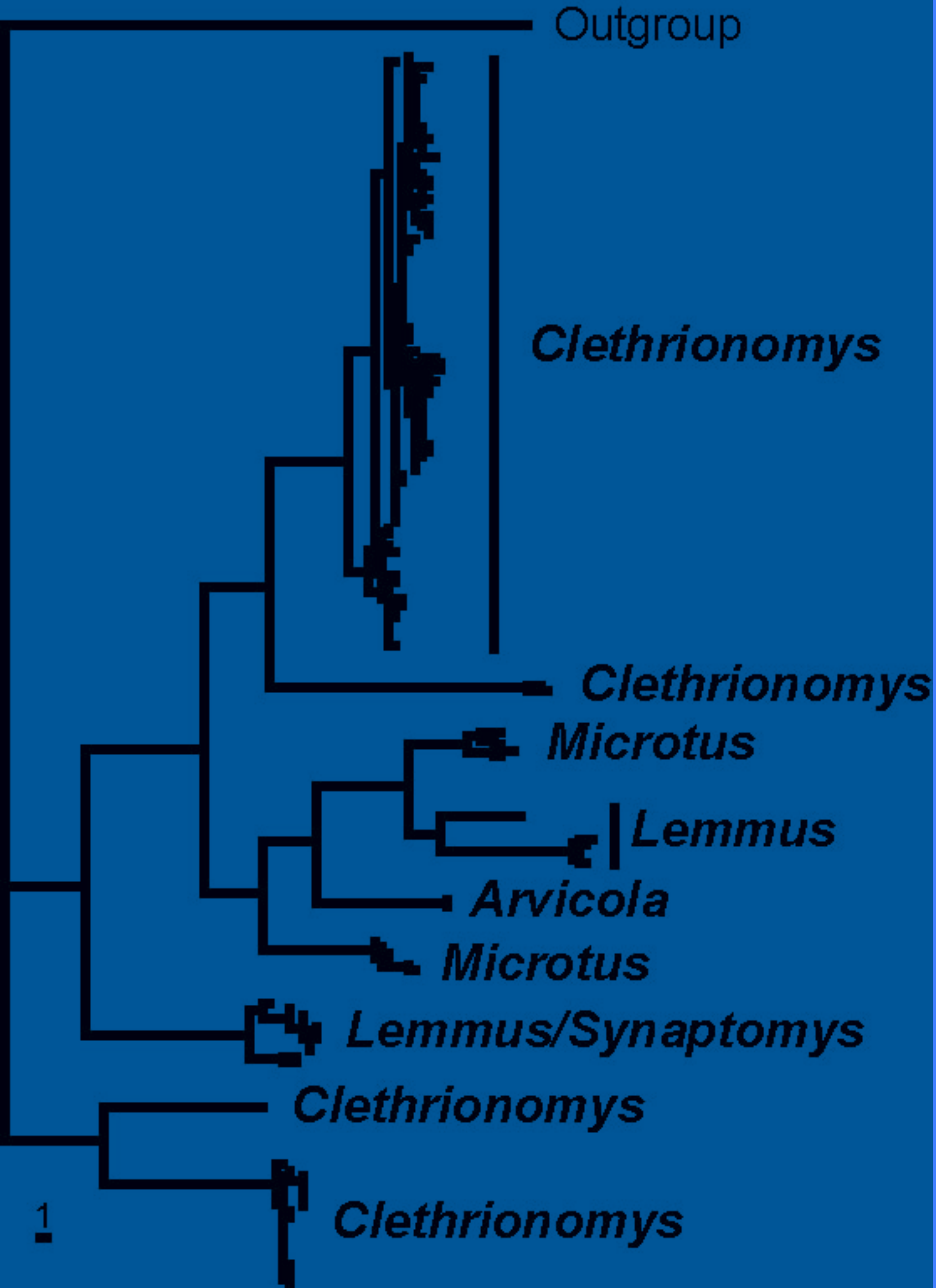


Substantial, Previously Undetected (Cryptic) Diversity in the North

Cestode (tapeworm):

Arostrilepis horrida

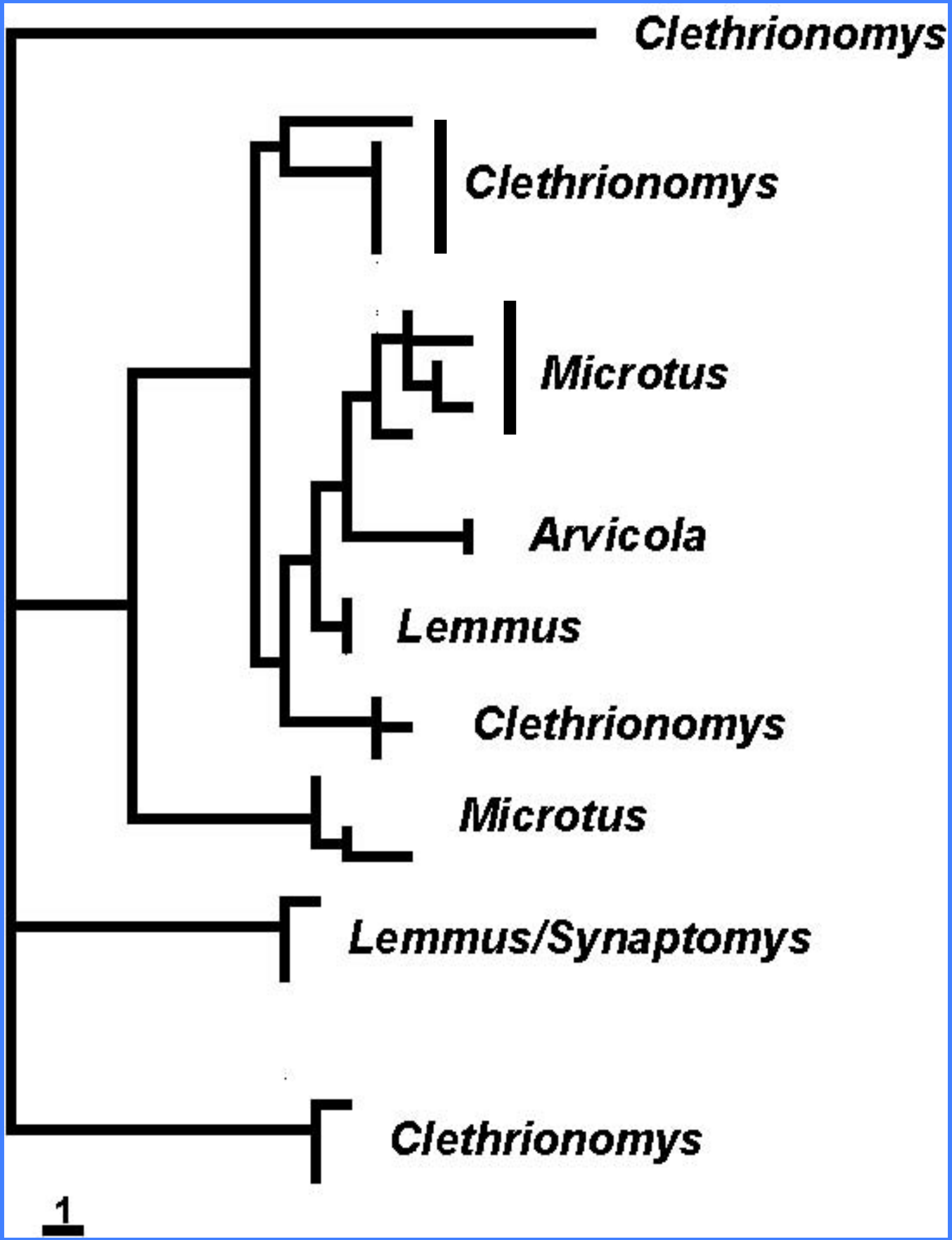
- Parasite of voles and lemmings
- Holarctic distribution (Europe to Canada)
- Substantial morphological variation
- Recent descriptions of new *Arostrilepis* species suggest hidden diversity



Cryptic diversity?

1. Mitochondrial DNA (cytb, 570 bp) - Nine divergent lineages
2. host (genus) specific

- Red-backed voles (*Clethrionomys*)
- *Microtus* voles
- Lemmings (*Lemmus* and *Synaptomys*)
- *Arvicola*

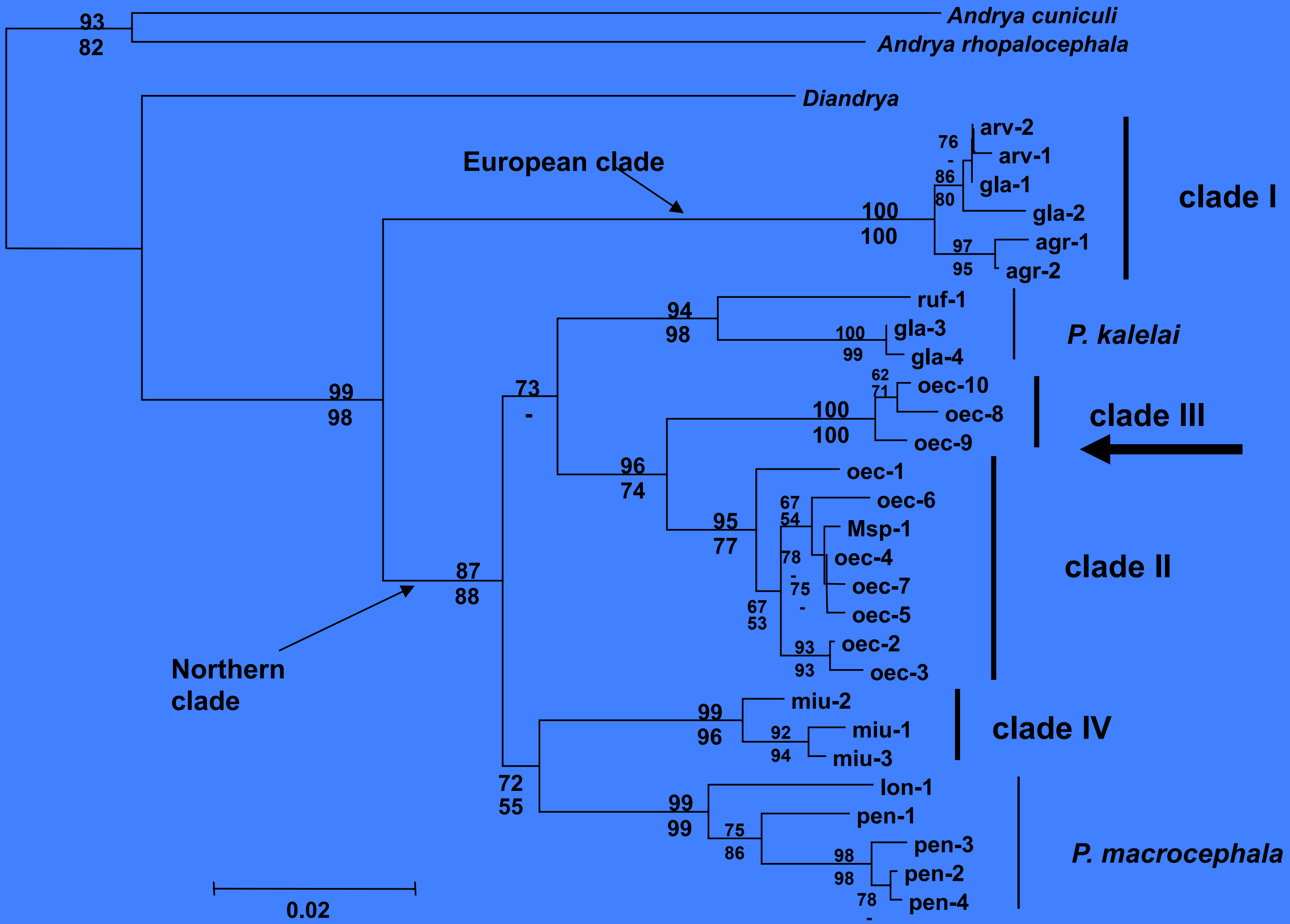


Nuclear DNA (ITS2, 534 bp) corroborates mtDNA diversity

Questions

- **Cryptic diversity within *Arostrilepis horrida*?**
  - **Yes-->10 cryptic lineages**

- **Process of diversification?**
  - **Early, possibly rapid, diversification parallels microtine hosts and related to climate shifts**



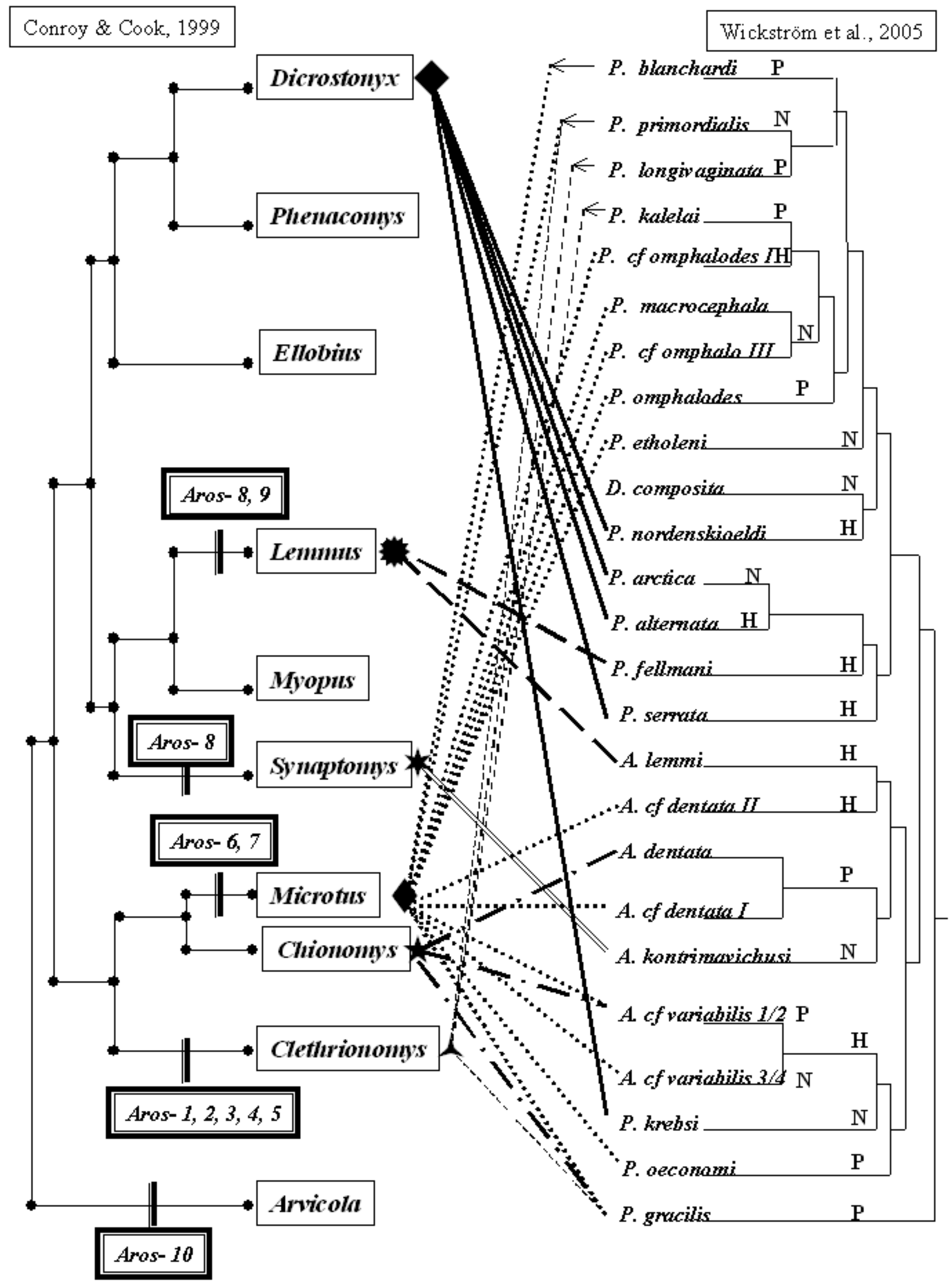
Paranoplocephala omphalodes Wickstrom et al 2005

Earlier view: single generalist holarctic species

Arostrolepis horrida

Cryptic Diversity

Host specific --genera



Paranoplocephala omphalodes

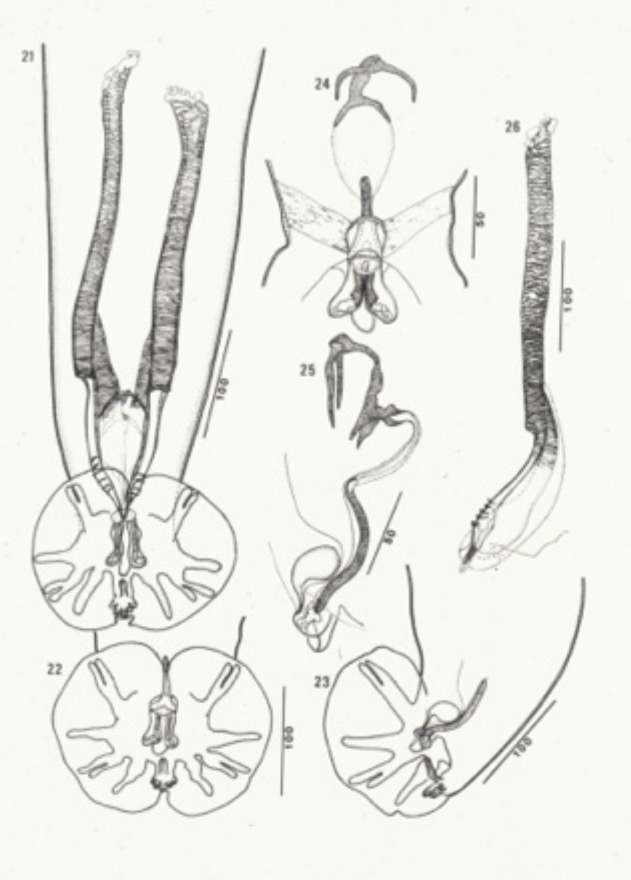
Cryptic Diversity

Host switching

Preliminary Summary of Investigations of Beringian Specimens

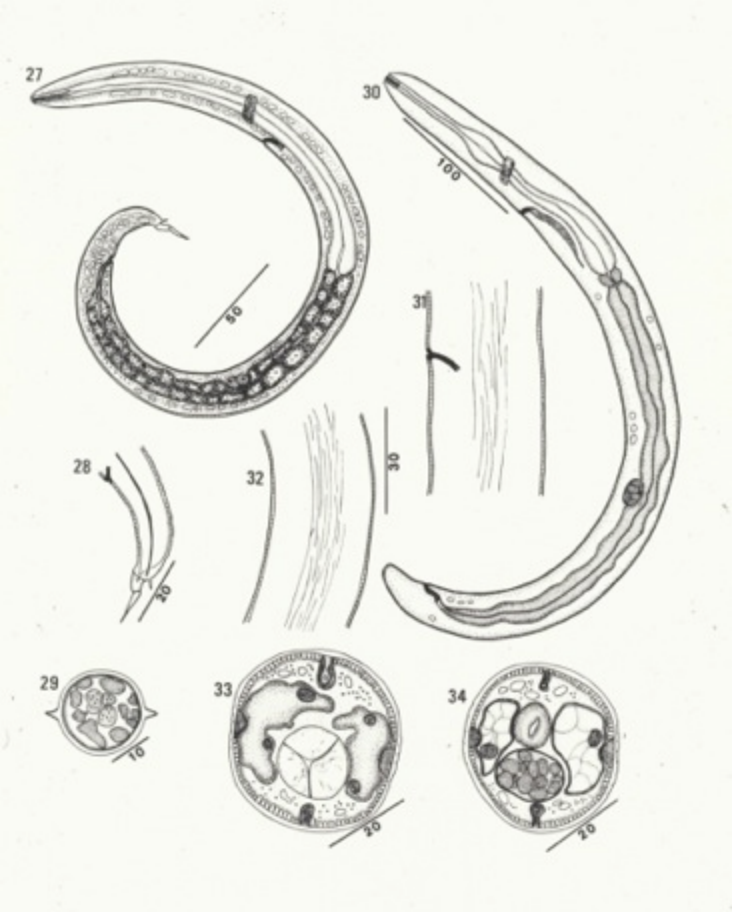
- Significant Phylogeographic Structure in the Arctic
- Ice Ages and Climate Fluctuation-
  - Fragmented Populations and Promoted Diversification
- Spatially Concordant Clades and Contact Zones
  - Suggest Common Biogeographic History
- Bering Land Bridge-
  - **Deep, Few Trans-Beringian Sister Relationships**
  - **Shallow, Close Genetic Relationships**
- Beringia-

  Center of Endemism for Hosts and Parasites
- Cryptic Cestode Diversity--Host Switching common
- Clean Slate Hypothesis-Genetic Signature of Expansion



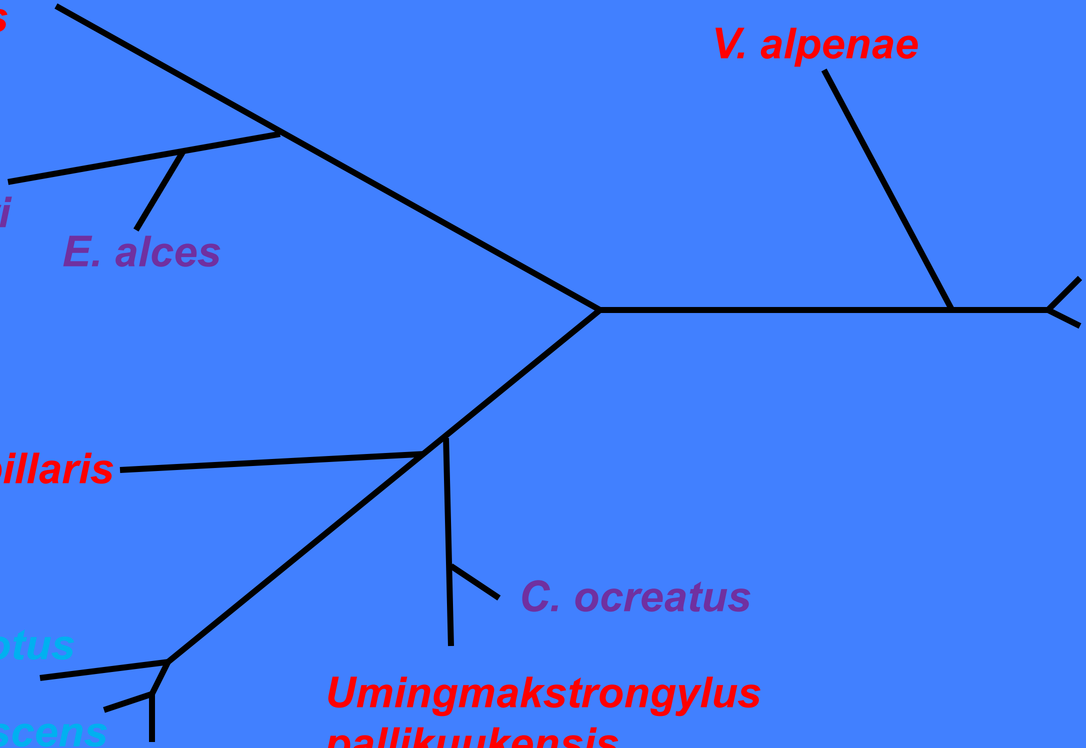
Umingmakstrongylus
Lung Parenchyma
Muskoxen

Umingmakstrongylus **L3**
Foot Muscle
Deroceras



Hoberg et al. Can. J. Zool. 1995

Protostrongylid First Stage Larvae/ Unrooted NJ Tree/ ITS-2



P. andersoni
P. odocoilei
P. tenuis

V. alpenae

E. rangiferi

E. alces

Varestrongylus n. sp.

M. capillaris

C. ocreatus

O. macrotus

P. rufescens

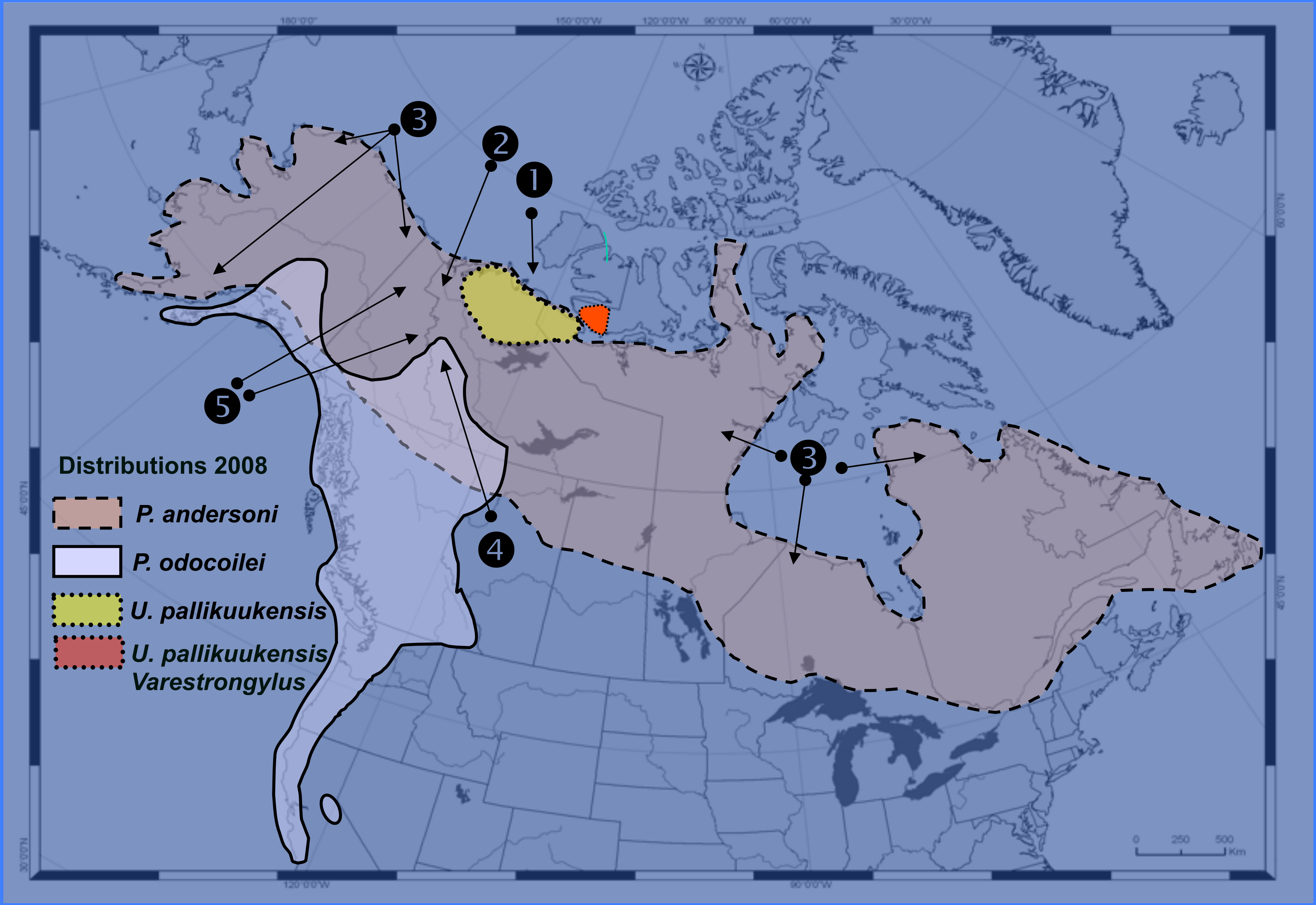
P. stilesi

Umingmakstrongylus pallikuukensis

🟥 DSL, North American
🟪 DSL, Eurasian
🟦 ST, North American

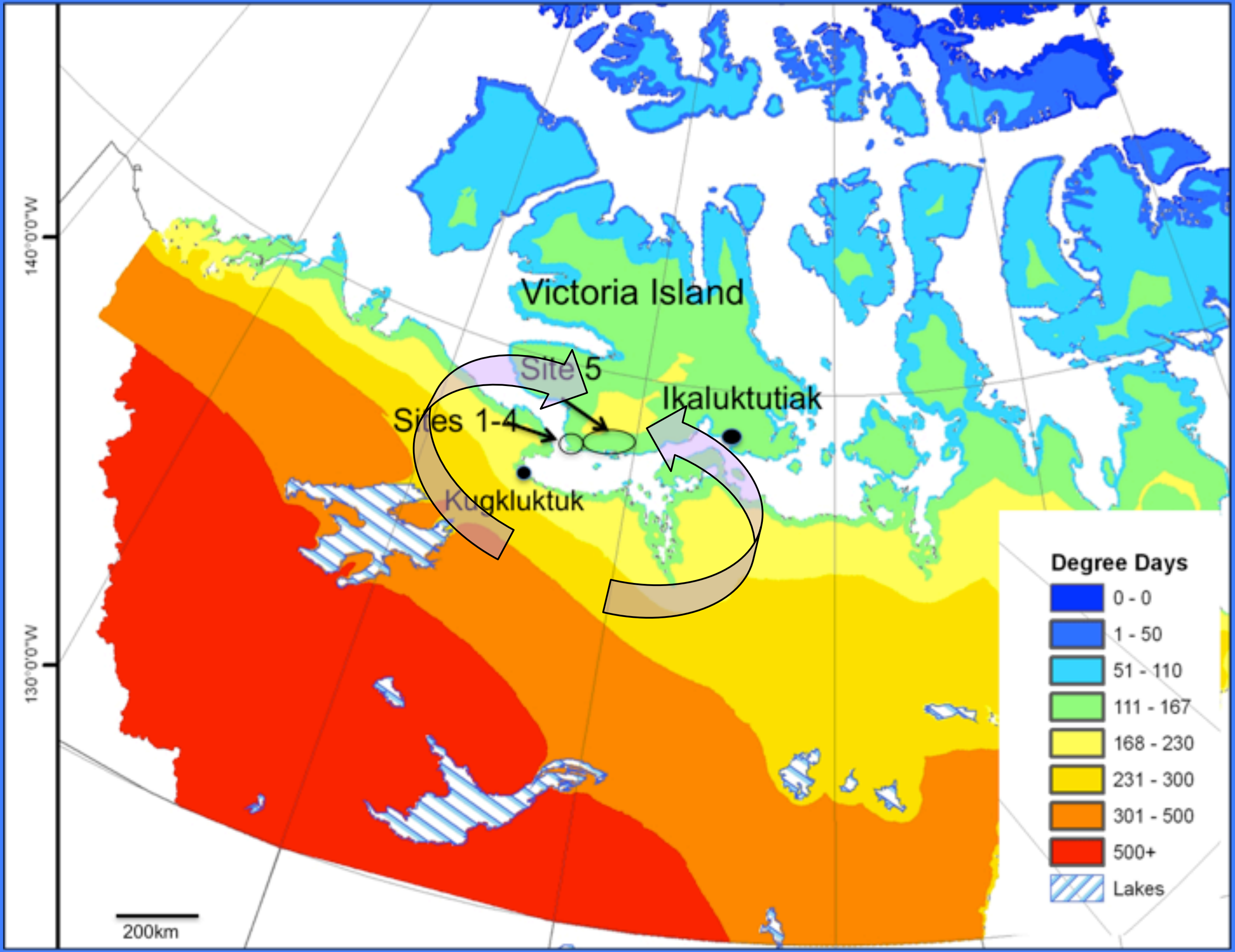
Kutz, Asmundsson, Hoberg et al. (2007)

Climate Change and Protostrongylids- Emergent Patterns in North America

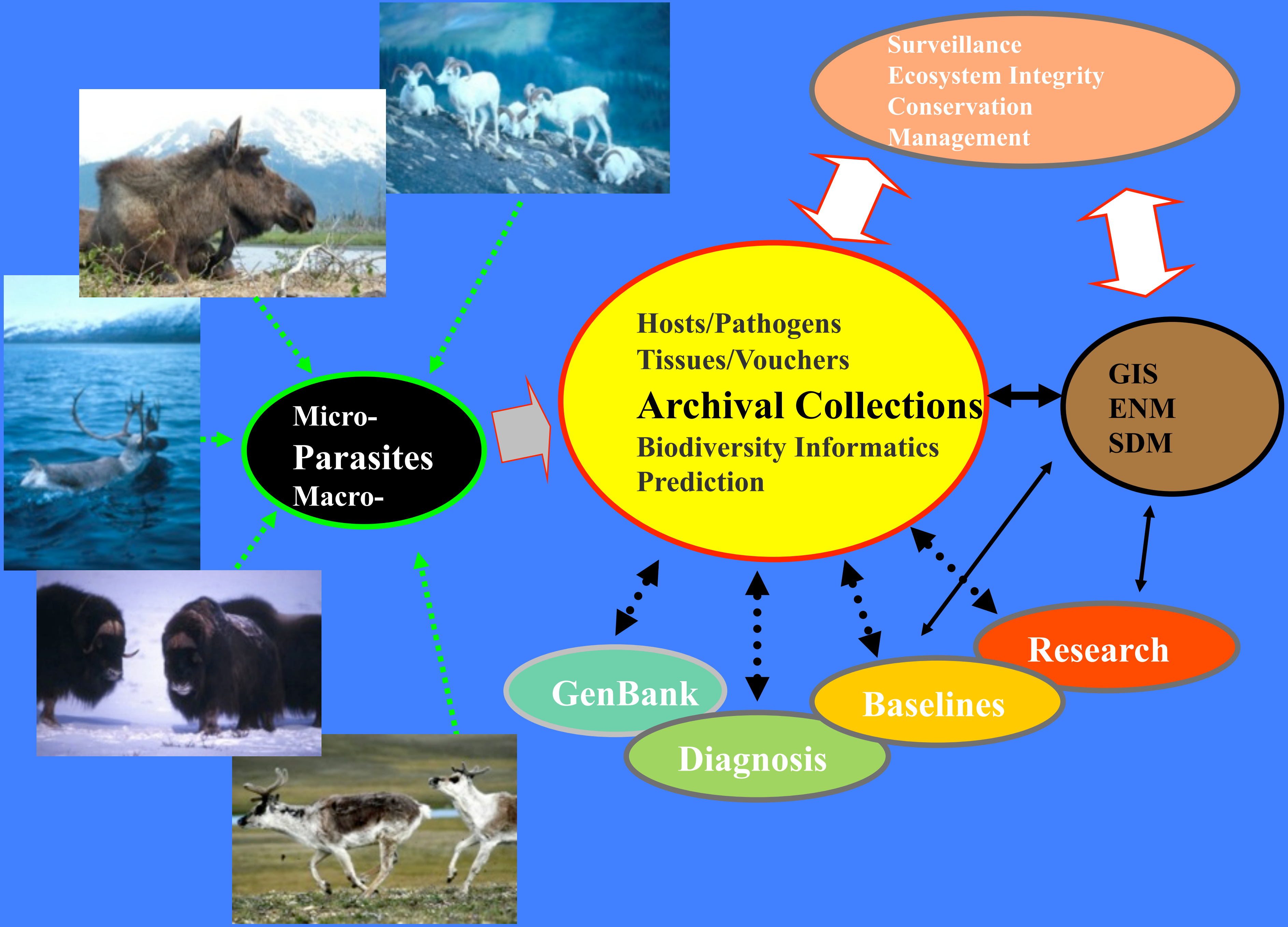


Hoberg et al. (2008) Rev. sci tech. Off. Int. Epiz. 27: 511-528.

Geographic colonization- *Umingmakstrongylus* and *Varestrongylus* to Victoria Island



2 C temperature increase 2000-2006/ shift in permissive environments
Geo Expansion revealed by archival specimens/ field collections



Micro-
Parasites
Macro-

Hosts/Pathogens
Tissues/Vouchers
Archival Collections
Biodiversity Informatics
Prediction

Surveillance
Ecosystem Integrity
Conservation
Management

GIS
ENM
SDM

GenBank

Diagnosis

Baselines

Research

Biodiversity Toolkit -specimens

Archival Collections/ Informatics

Comparative baselines tracking transitions

Historical Analogues

Rapid Diagnostics

Population Genetics

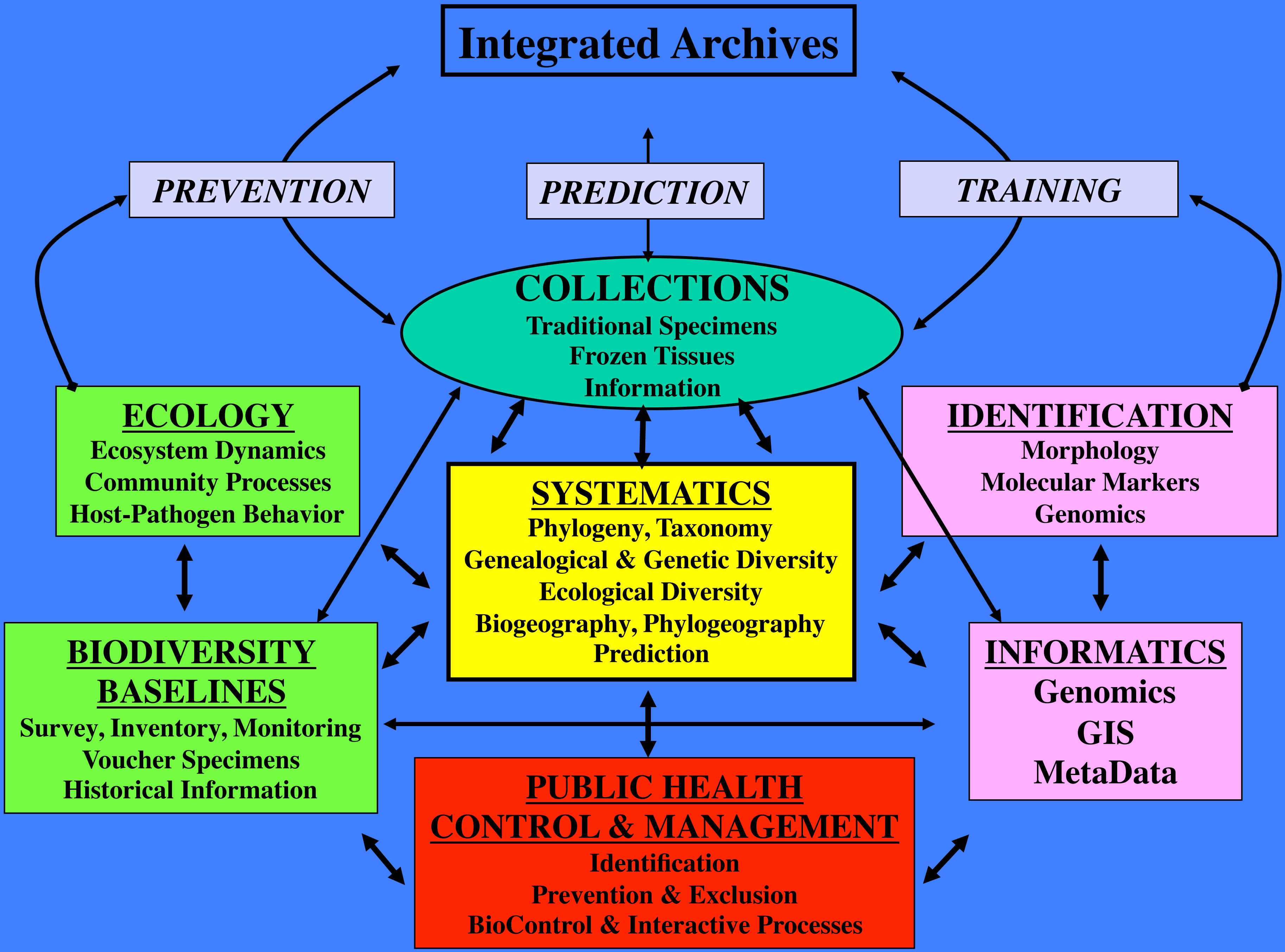
Molecular Epidemiology

Evolutionary & Ecological Models

Capacity for Integrative Collaboration

Creating culture that values collections

Ultimate authoritative source of biodiversity information



Integrated Archives

PREVENTION

PREDICTION

TRAINING

COLLECTIONS
Traditional Specimens
Frozen Tissues
Information

ECOLOGY
Ecosystem Dynamics
Community Processes
Host-Pathogen Behavior

SYSTEMATICS
Phylogeny, Taxonomy
Genealogical & Genetic Diversity
Ecological Diversity
Biogeography, Phylogeography
Prediction

IDENTIFICATION
Morphology
Molecular Markers
Genomics

BIODIVERSITY BASELINES
Survey, Inventory, Monitoring
Voucher Specimens
Historical Information

INFORMATICS
Genomics
GIS
MetaData

PUBLIC HEALTH CONTROL & MANAGEMENT
Identification
Prevention & Exclusion
BioControl & Interactive Processes

Ejercicio para Lunes:

1) Leer **Pyke and Ehrlich. 2010 Biological Reviews 85:** 247-266.

2) Explorar **Arctos Y Vertnet o MapofLife o ADW**

Trata saber (o recoger en archivo de Excel) algunos datos: Cuantos musetras existen de 5 especies de 3 grupos por un region (e.g. Uruguay, Santa Cruz Depto (Bolivia):

De donde estan (cuales sitios)? Y donde estan ahora (qual museo)? Devcuando? Por quien? Haga una mapa del distribucion.

Global biodiversity crisis is not solely extinction....

Global ecological disruption is concurrently a crisis of emerging infectious diseases

Climate change is emerging as a primary driver of ecological perturbation on local, regional and global scales—but how do we assess it?