

Lynx Genetic Considerations

Michael Schwartz

John Squires

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Big Topic, Turned to October Headlines for Focus



Lynx on the brink



Foul trouble dooms Lynx



Lynx lose to Fever

Genetics of Disease?
Avian Malaria? WNV?

Turns out, we don't need to worry.....



Minnesota Lynx on the brink of title after Maya Moore's winning shot



WNBA Finals: Foul trouble dooms Lynx as Fever force Game 5



Lynx lose to Fever, head home for Game 5

*By Candace Buckner
Special to the Pioneer Press*



DECIDING GAME 5

WNBA Finals | Wednesday, October 14 7:00 PM



Lynx Genetic Considerations

- 1) Mini review of lynx population genetic studies
- 2) Review of lynx hybridization studies
- 3) Needed genomic data

Population Genetics of Lynx

letters to nature

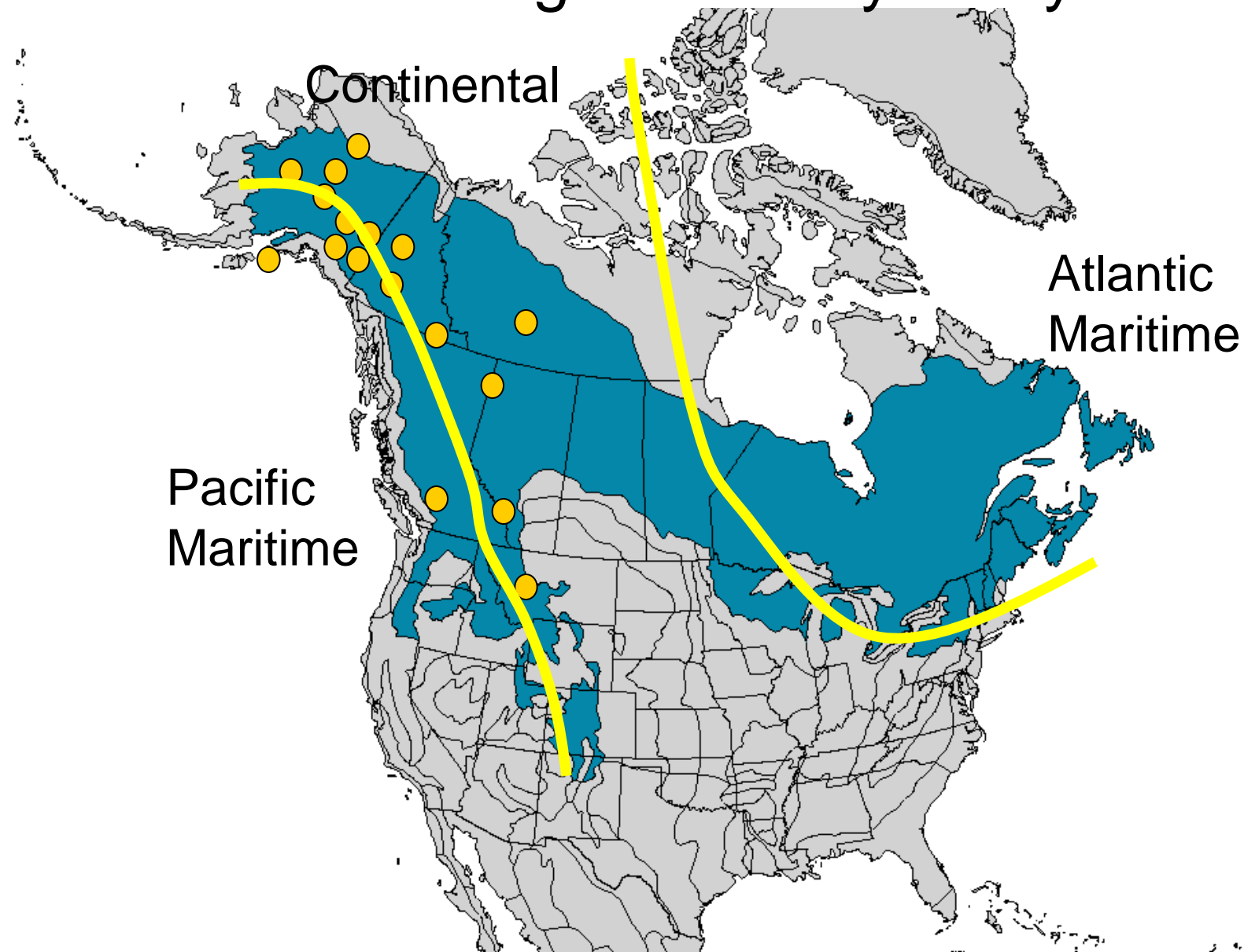
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DNA reveals high dispersal synchronizing the population dynamics of Canada lynx

**Michael K. Schwartz^{*†}, L. Scott Mills⁺, Kevin S. McKelvey[†],
Leonard F. Ruggiero[†] & Fred W. Allendorf[‡]**



Stenseth et al. (1999) Suggest Climate Causes Large Scale Cycle Synchrony



Lynx Isolated

“The conservation of lynx populations is of greatest concern in the western mountains of the conterminous United States at the southern periphery of the species range. Recruitment is low in this region and many lynx populations....are geographically **isolated.**”

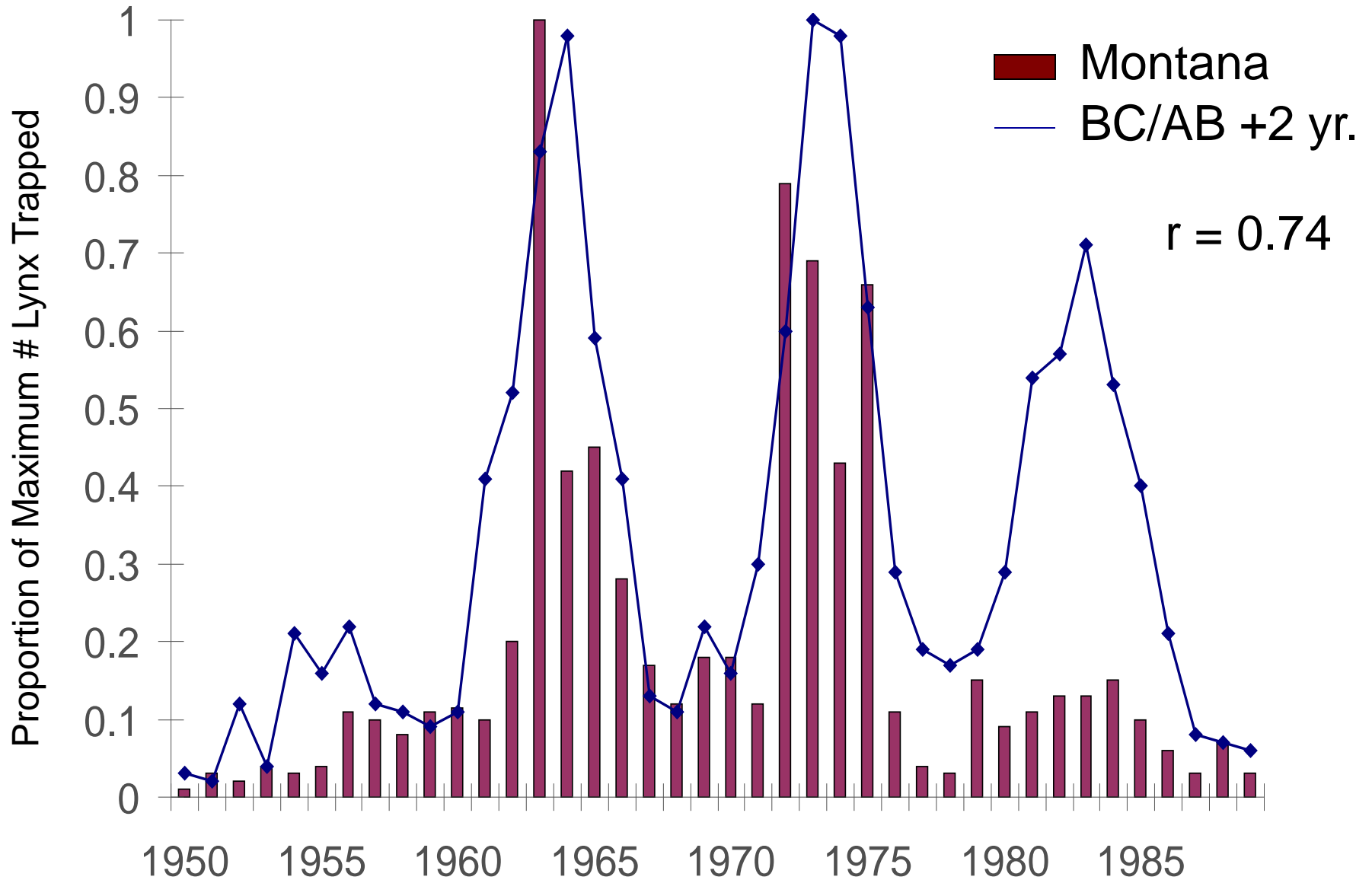
- Koehler and Aubry 1994

Lynx Connected: Large Scale Spatial Synchrony

We let dispersal between patches be distance-dependent in an exponential fashion and fixed the fraction of migrants leaving each patch each generation.

(p.1622 Ranta, *Science*)

Lynx Trapping Data Suggests Dispersal Common (McKelvey et al. 2000)



Population Structure and Migration

F_{st}

- Proportional reduction in heterozygosity due to population subdivision (0-1).
- High levels of gene flow drives F_{st} to 0.

F_{st} Results

Global Results (17 Populations):

$$F_{st} = 0.033 (+/- 0.002).$$

Pair-wise Results (Extremes):

F_{st} / Migrants

Fairbanks to Ladue Yukon: 0.001 \cong High

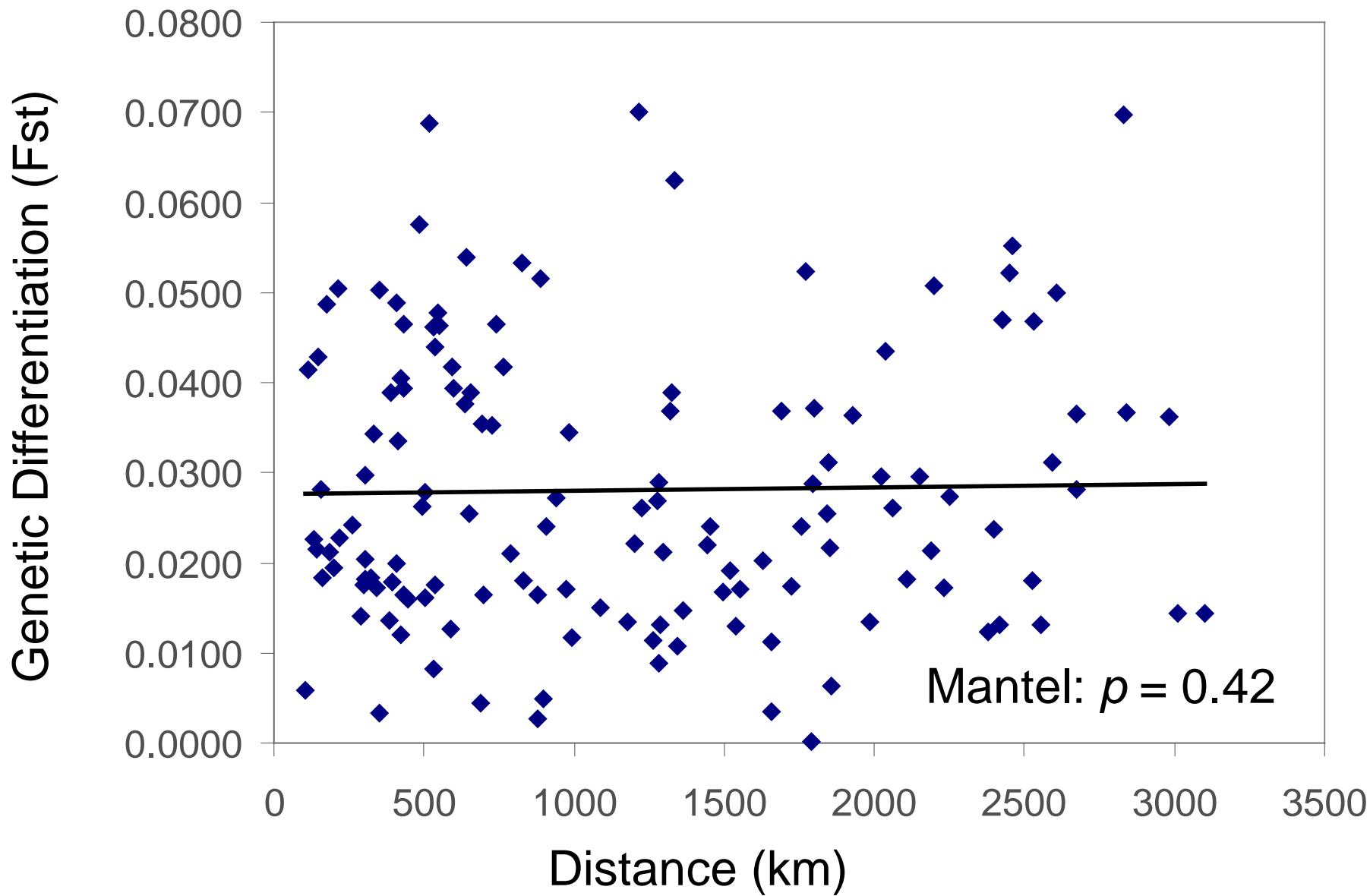
Kenai P. to Seeley Montana: 0.070 \cong 3.0

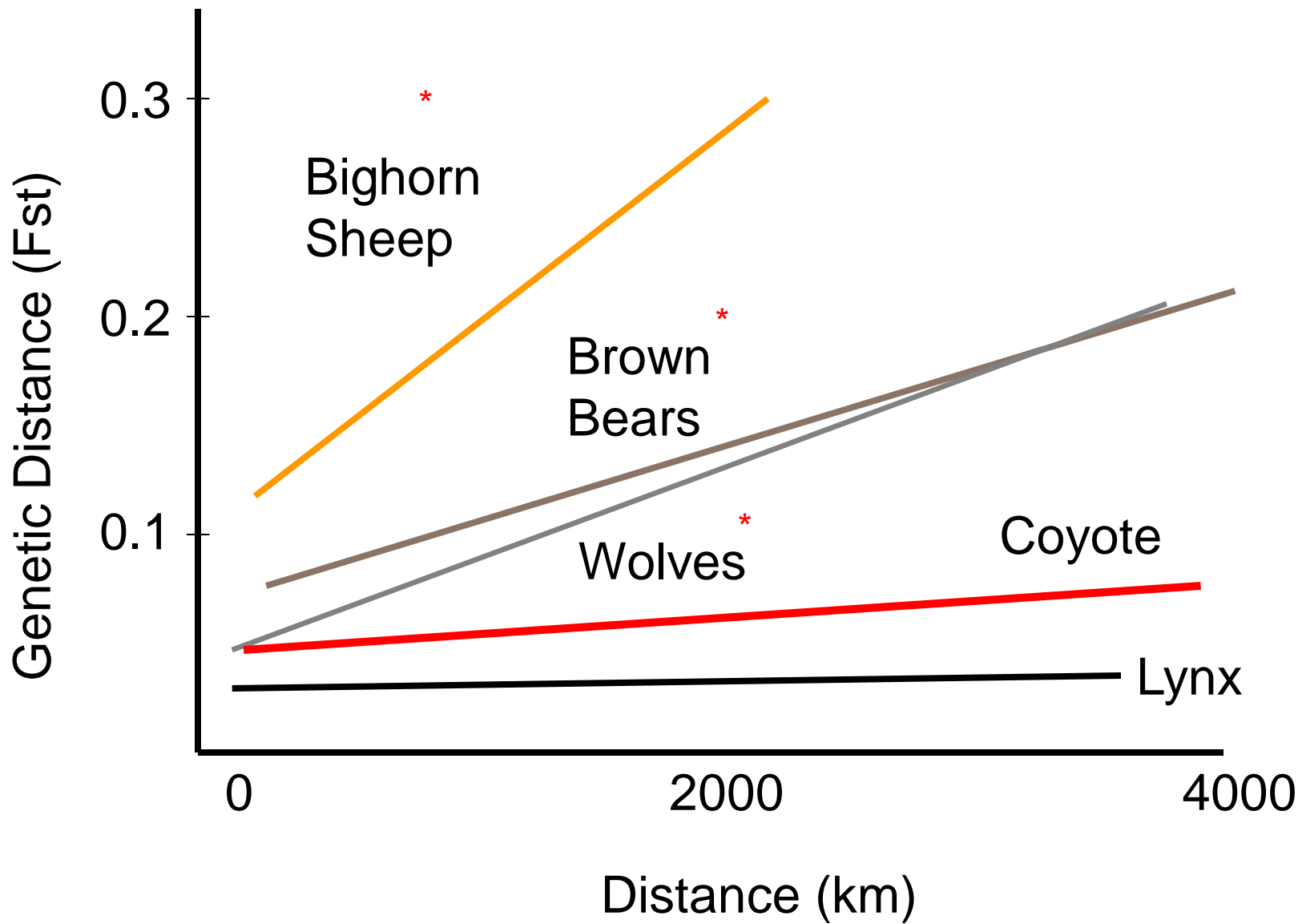


Kenai

Seeley
Lake

Distance Does Not Lead To Structuring





*significant p > 0.5

High gene flow across range

letters to nature

.....

DNA reveals high dispersal synchronizing the population dynamics of Canada lynx

**Michael K. Schwartz^{*,†}, L. Scott Mills^{*,} Kevin S. McKelvey[†],
Leonard F. Ruggiero[†] & Fred W. Allendorf[‡]**



Our Initial Conclusions

- Ample gene flow continent wide
- Limited structure possible at the edges (Kenai, Seeley)
- Tide Pool Model
- One Evolutionary Significant Unit



Ecological and genetic spatial structuring in the Canadian lynx

**Eli Knispel Rueness¹, Nils Chr. Stenseth¹, Mark O'Donoghue²,
Stan Boutin³, Hans Ellegren⁴ & Kjetill S. Jakobsen¹**

*¹Centre for Ecological and Evolutionary Synthesis, Department of Biology,
University of Oslo, P.O. Box 1031 Blindern, N-0315 Oslo, Norway*

- Rockies as barrier to gene flow in western Canada and “invisible barrier” south of Hudson coinciding with ecological Continental and Atlantic regions.

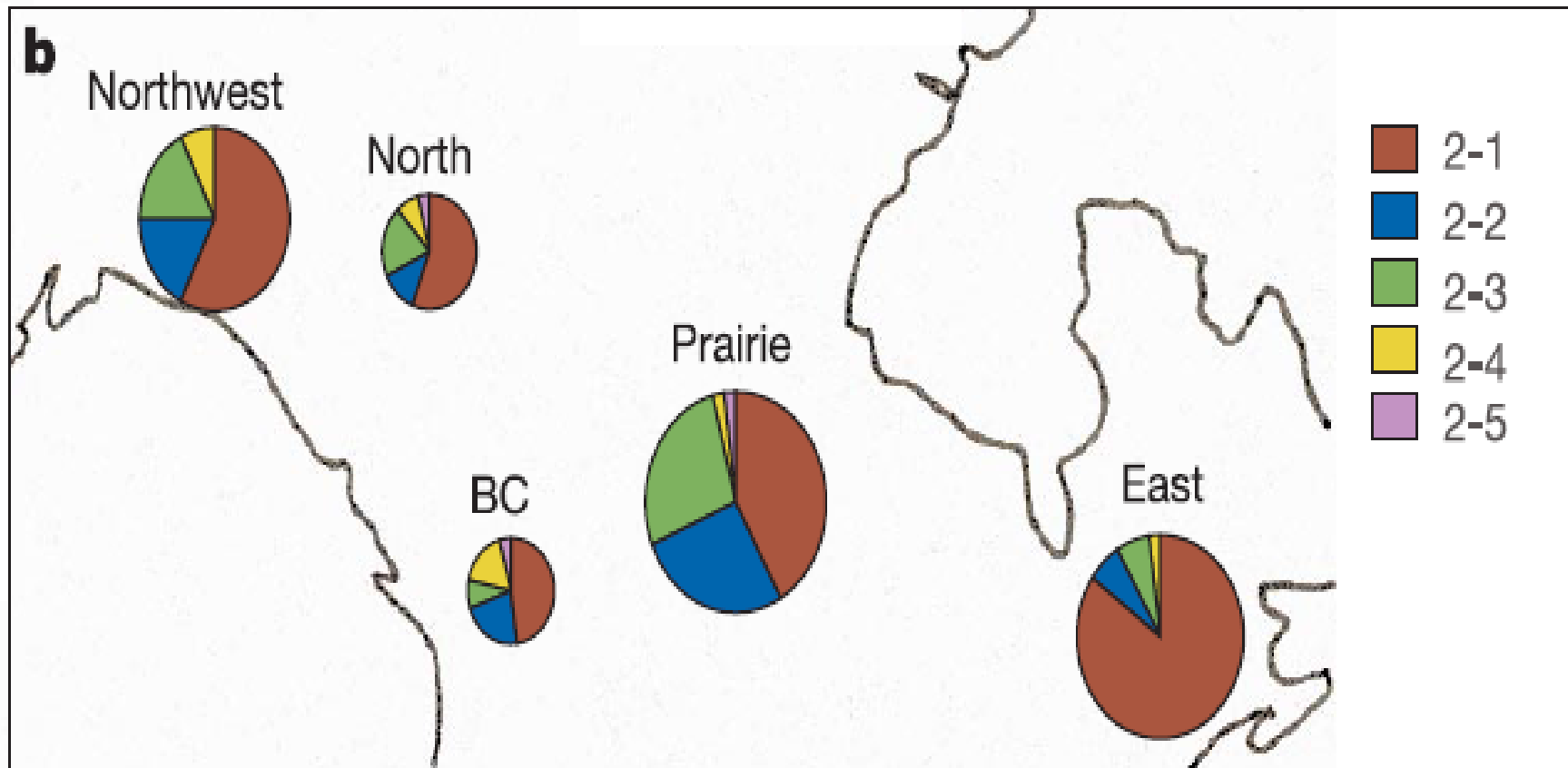
Very, very low F_{ST}

Table 1 Genetic differentiation between geographical regions

Microsatellites	Mitochondrial DNA				
	East	Prairie	North	Northwest	BC
East		0.0622**	0.0223*	0.0342*	0.0422*
Prairie	0.0062**		0.0301	-0.0074	0.0119
North	0.0091*	0.0017		0.0261	0.0027
Northwest	0.0156***	0.0095**	0.0027*		0.0073
BC	0.0136**	0.0097**	0.0172**	0.0244***	

Pair-wise F_{ST} estimates for microsatellites below diagonal and mtDNA above diagonal. Significant values indicated as * at the 0.05 level, ** at 0.01 level and *** at the 0.001 level.

Mitochondrial DNA

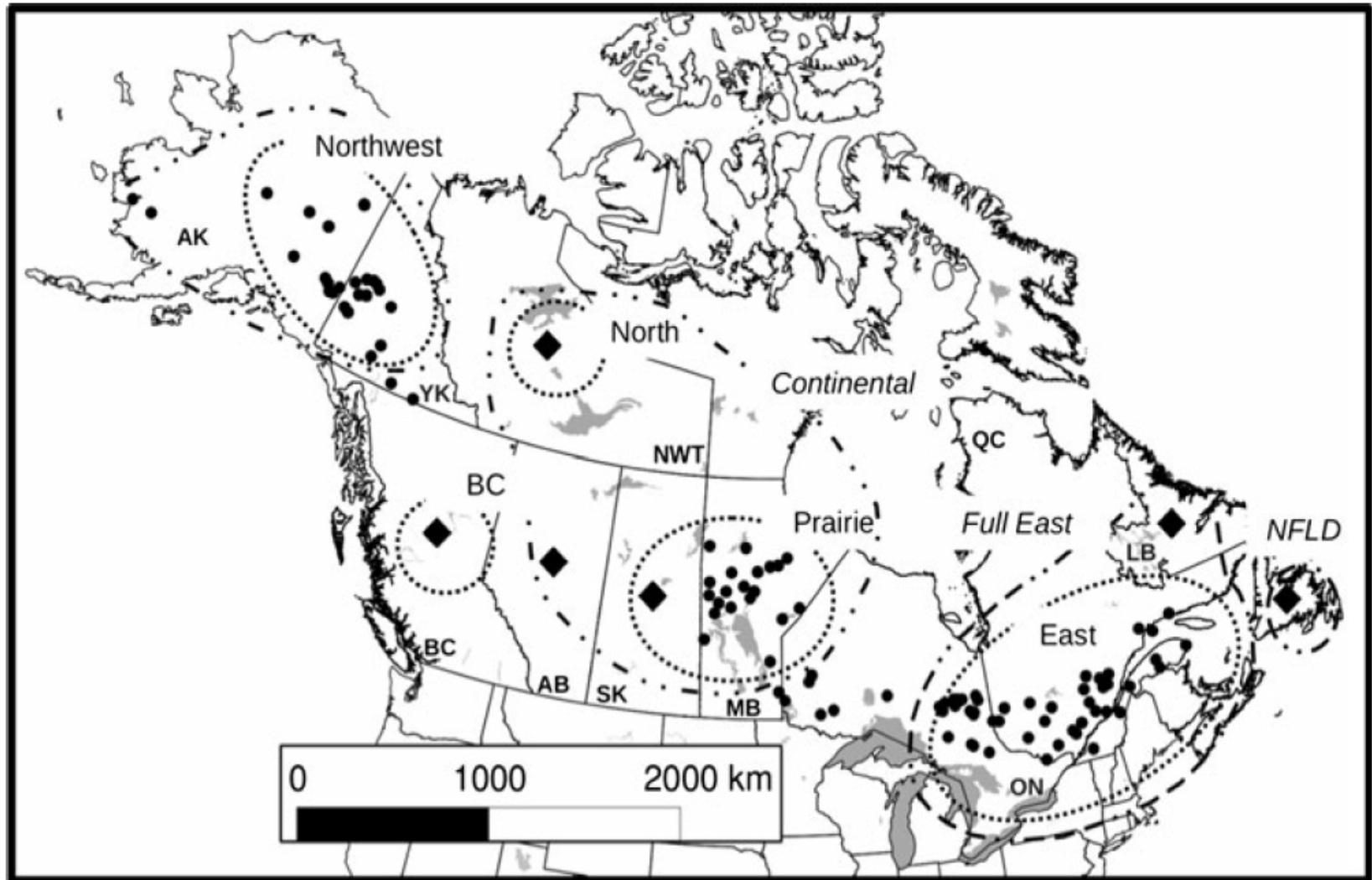


Dispersal promotes high gene flow among Canada lynx populations across mainland North America

J. R. Row · C. Gomez · E. L. Koen ·
J. Bowman · D. L. Murray · P. J. Wilson

- 17 microsatellites
- Large differentiation on Newfoundland vs. Mainland
 - F_{st} – 0.19 between NF and Mainland
- “subtle gene flow restriction between Ontario and Manitoba”
- Bayesian clustering - 2 clusters NF vs others.

Lynx Sample Distribution



Again, very low Fst

Table 2 Pairwise F_{ST} (lower)^a and R_{ST} (upper) between populations of Canada lynx across North America using data subset A

	East	Prairie	North	Northwest	BC
East		0.0069	0.0021	0.0004	0.0000
Prairie	0.0071***		0.0001	0.0030	0.0100
North	0.0080***	0.0018		0.00113	0.0002
Northwest	0.0069***	0.0061***	0.0035**		0.0034
BC	0.0077***	0.0034***	0.0008	0.0008	

The subtle role of climate change on population genetic structure in Canada lynx

JEFFREY R. ROW¹, PAUL J. WILSON², CELINE GOMEZ¹, ERIN L. KOEN², JEFF BOWMAN³, DANIEL THORNTON^{1,4} and DENNIS L. MURRAY¹

- Genetic variability correlated with winter climate gradient (snow depth and winter precipitation) – using spca (not with Bayesian clustering)
- Stronger relationship than IBD
- W-E genetic cline driven by PNO and NAO
- Individuals restrict dispersal across climate boundaries in absence of changes in habitat quality.
- Imprinting on snow conditions

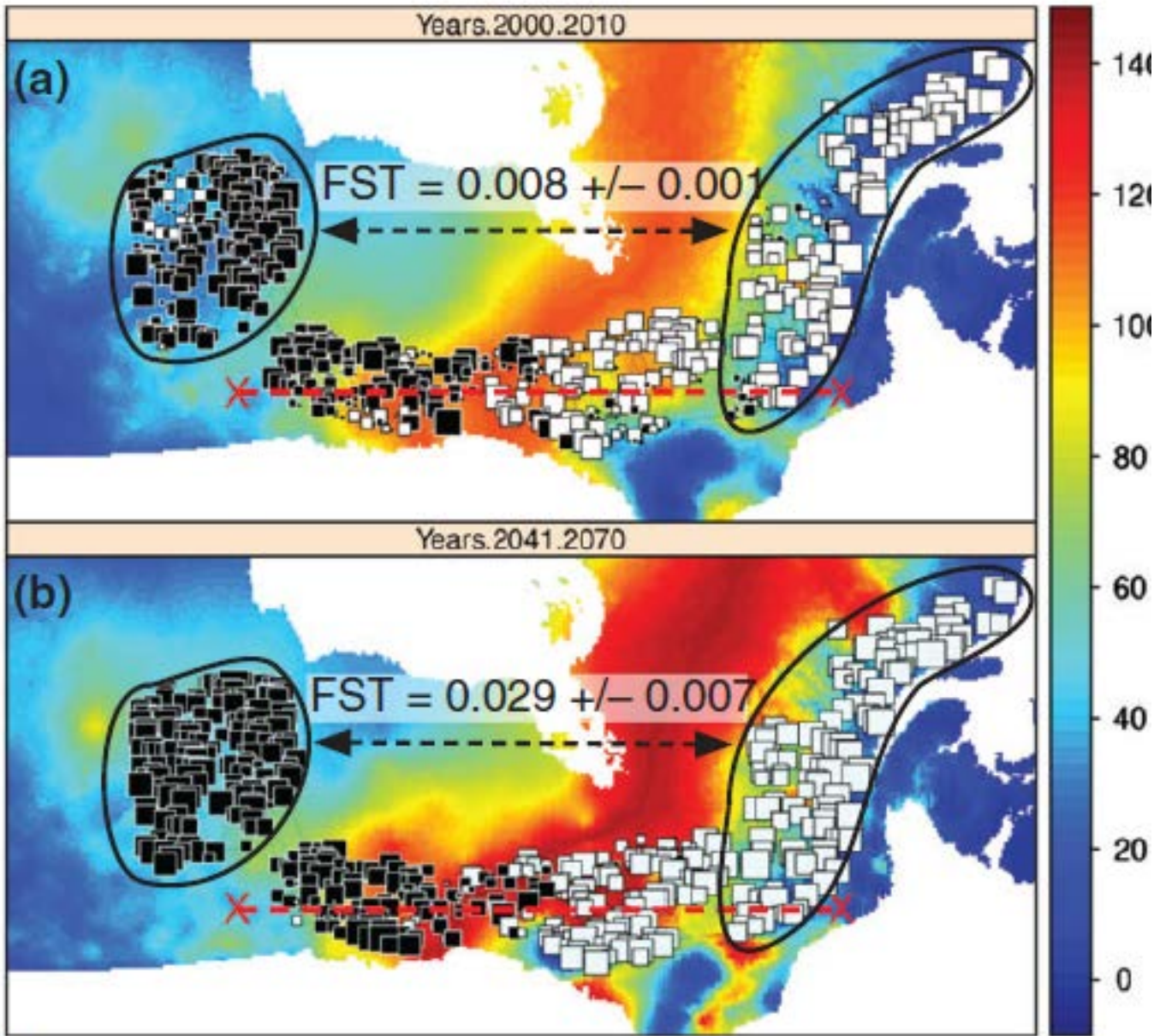


Climate Conditions: min and max temp, snow depth , precip, diff|max-min|



Ecological Conditions: open needle-leaved conifer, broad-leaved deciduous, close needle-leaved conifer, closed broad leaved decid.

PNA/NAO show the “invisible barrier” to gene flow



Fine-scale genetic structure and dispersal in Canada lynx (*Lynx canadensis*) within Alberta, Canada

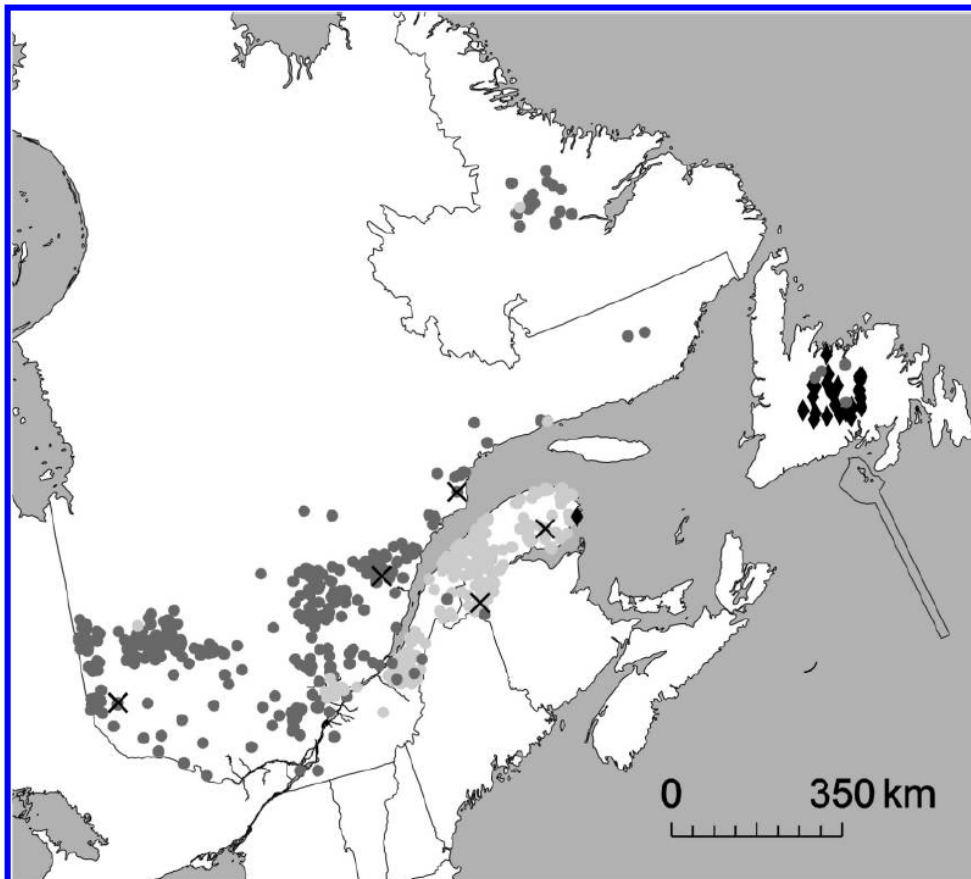
Véronique Campbell and Curtis Strobeck

Abstract: Although mammals are typically characterized by male-biased dispersal, field studies of lynx conflict as to whether dispersal is male-biased or lacks sex-bias. To resolve this issue we dissect fine-scale genetic structure and analyze dispersal in regard to gender using 19 microsatellite loci, teamed with extensive sampling ($n = 272$ adults) of Canada lynx (*Lynx canadensis* Kerr, 1792) throughout Alberta. The level of genetic variation was high (mean $H_e = 71.6\%$), as reported in previous genetic studies of lynx. **No significant barriers to gene flow were detected within Alberta's lynx population.** Despite several reports of long-distance movements in lynx, we observed a slight significant negative correlation between pairwise relatedness values and geographic distance ($r_M = -0.025$, $P = 0.048$), indicating a decrease in relatedness between individuals as their sampling distance increases. When the same analysis was performed separately on sexes, the slopes of the individual regressions did not differ significantly between males and females ($P = 0.708$). Our molecular results suggest a lack of sex-biased dispersal in Canada lynx, similar to reports on other lynx species.

Isolation of peripheral populations of Canada lynx (*Lynx canadensis*)

E.L. Koen, J. Bowman, and P.J. Wilson

- 14 microsatellites and 558 lynx to test “riverine barrier hypothesis”



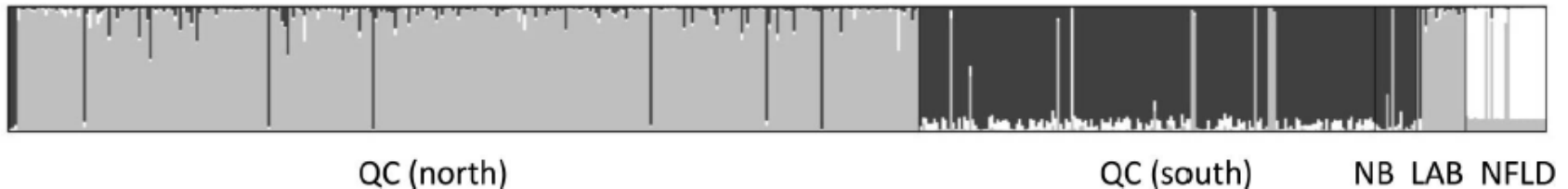
- St. Lawrence River is a barrier
- Not absolute – 24 indiv. crossing

Isolation of peripheral populations of Canada lynx (*Lynx canadensis*)

E.L. Koen, J. Bowman, and P.J. Wilson

- 14 microsatellites and 558 lynx to test “riverine barrier hypothesis”

Fig. 3. STRUCTURE plot (Pritchard et al. 2000), based on 10 replicates, representing the proportion of an individual’s genome assigned to one of three populations. Individual Canada lynx (*Lynx canadensis*) are grouped based on sample site (QC north, north of the St. Lawrence River in Quebec; QC south, south of the St. Lawrence River in Quebec; NB, New Brunswick; LAB, Labrador; NFLD, Newfoundland) and shading represents cluster assignment.



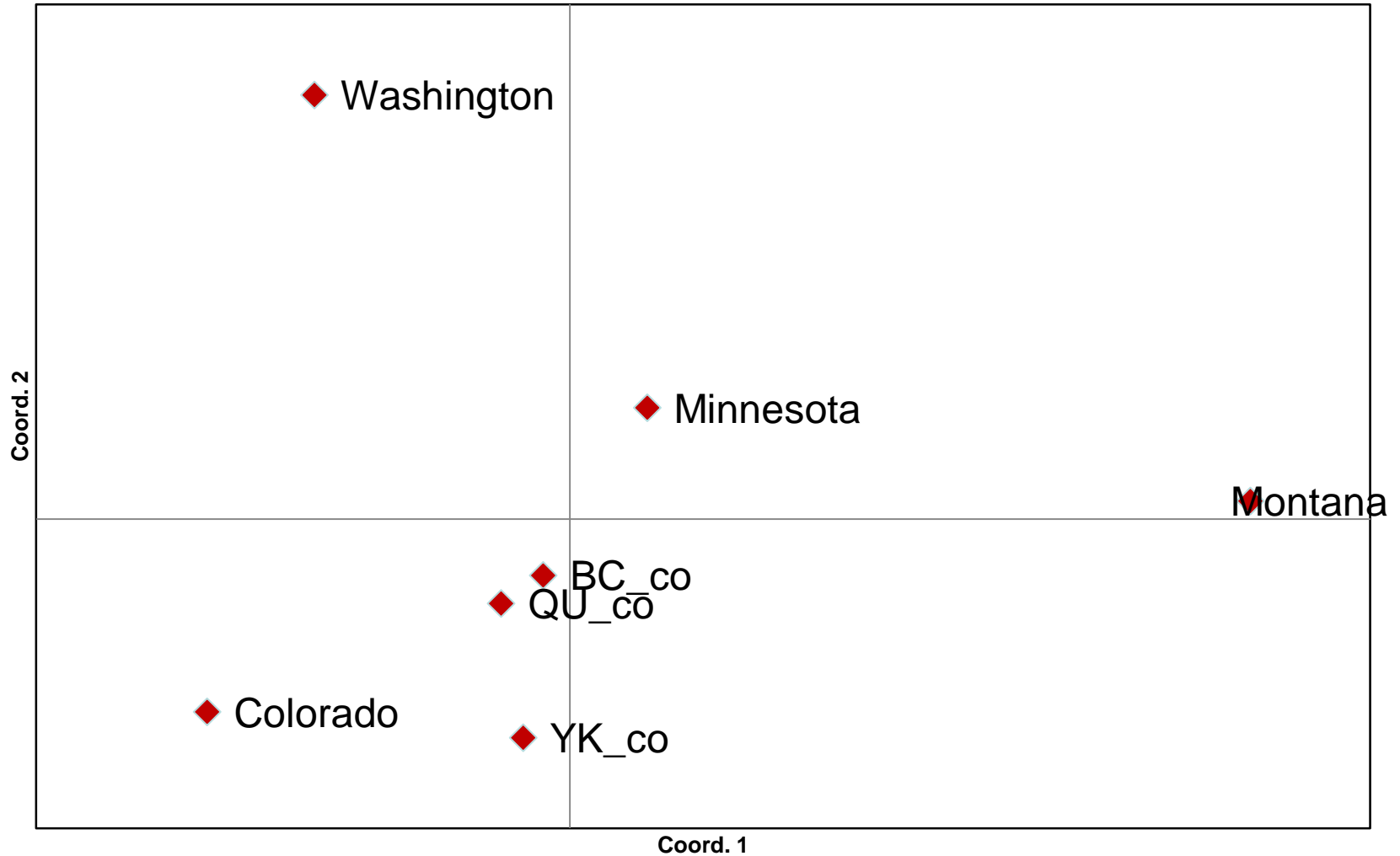
RMRS Genetic Data (2004-2006 only)

Principal Coordinates (PCoA)

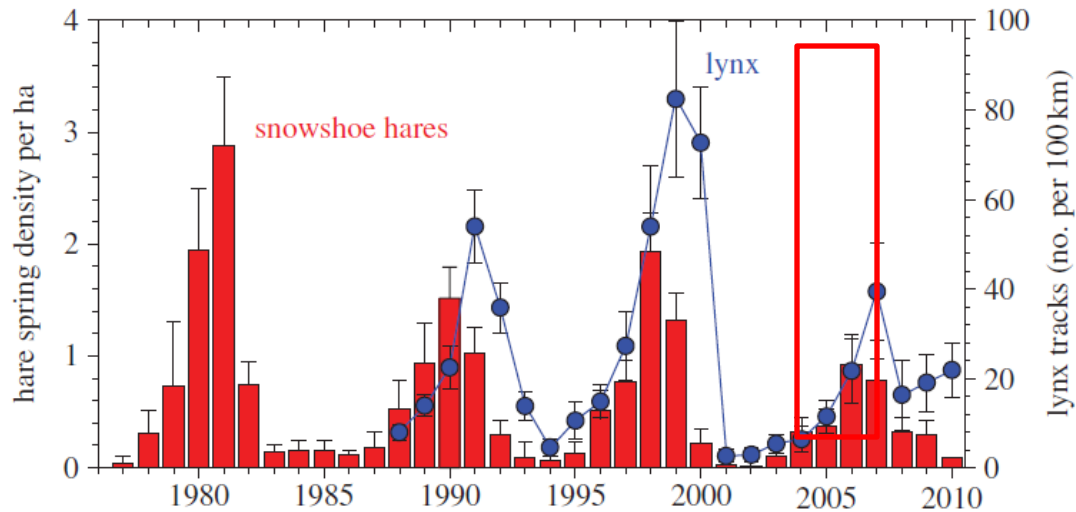
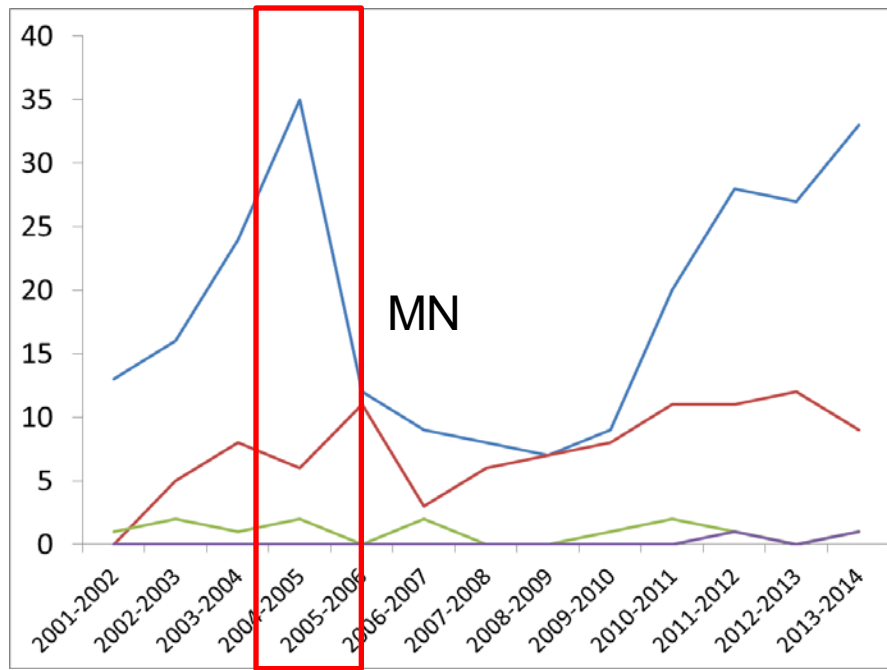


RMRS Genetic Data (2004-2006 only)

Principal Coordinates (PCoA)



Lynx Cycles

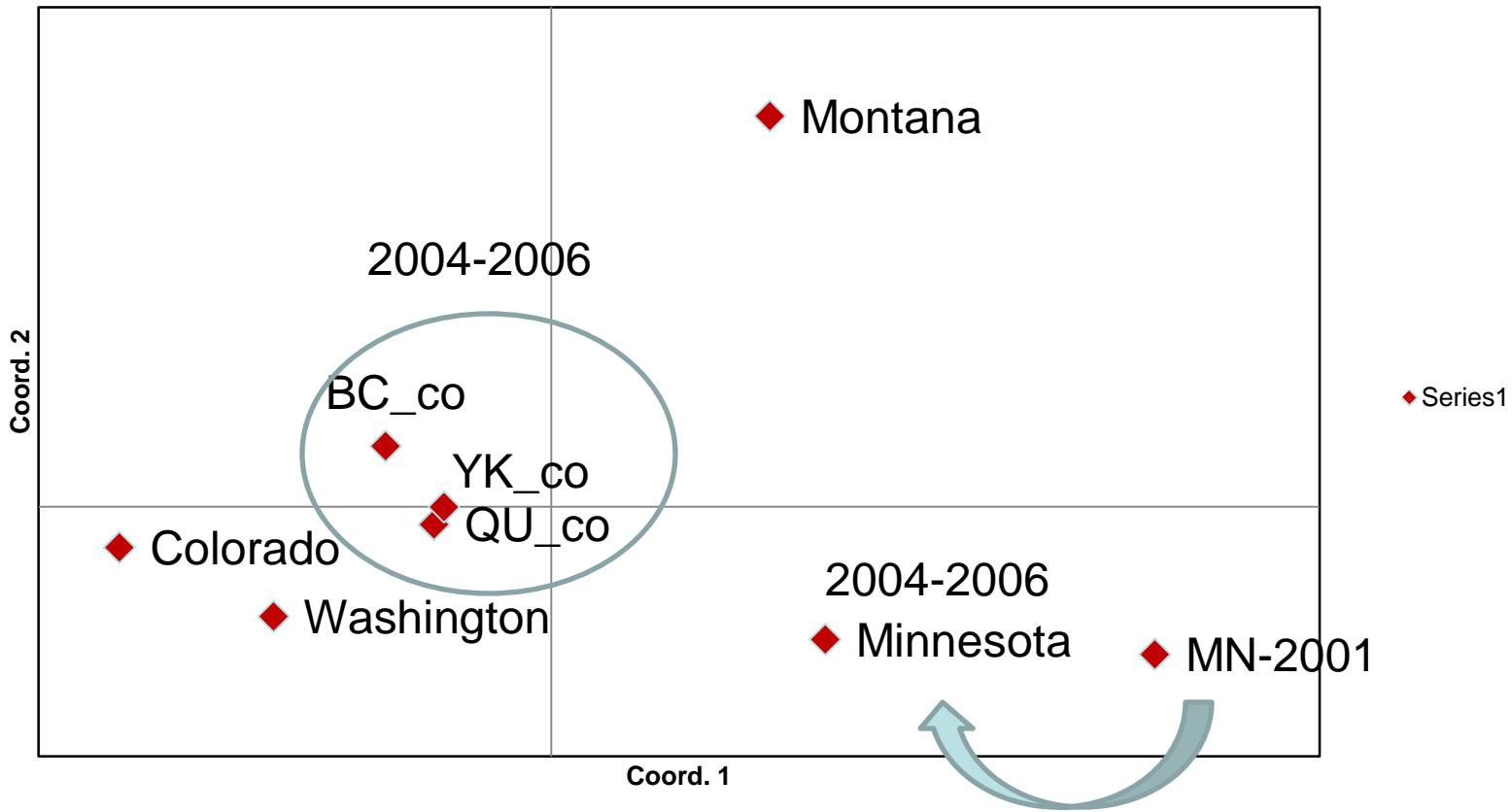


YU (Krebs et al. 2011)

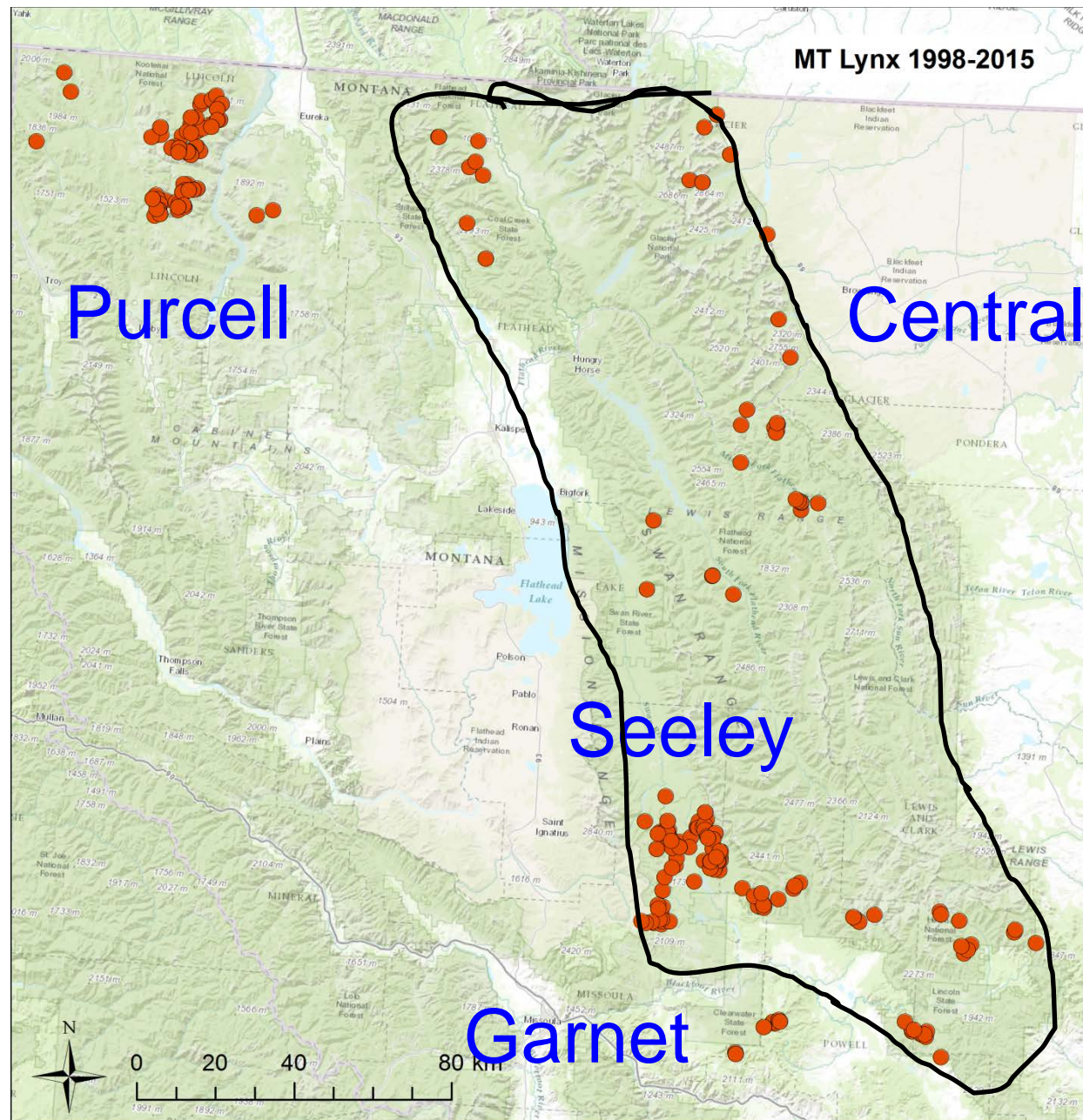
Figure 4. Snowshoe hare spring density at Kluane Lake, Yukon, 1977–2010, and an index of lynx numbers from winter snow tracking, 1988–2010. Lynx data from winters are plotted over the year ending each winter. Estimates with 95% confidence limits are given.

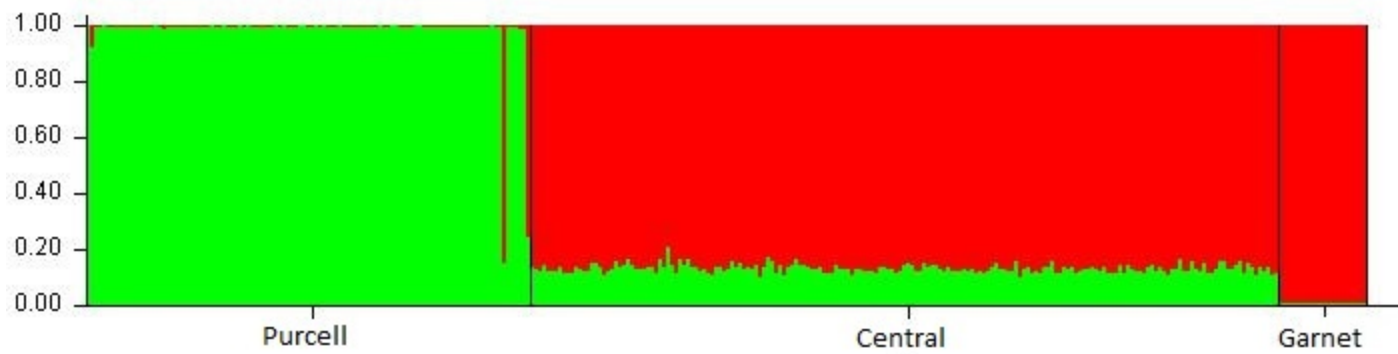
RMRS Genetic Data (2004-2006 only, MN 2001)

Principal Coordinates (PCoA)

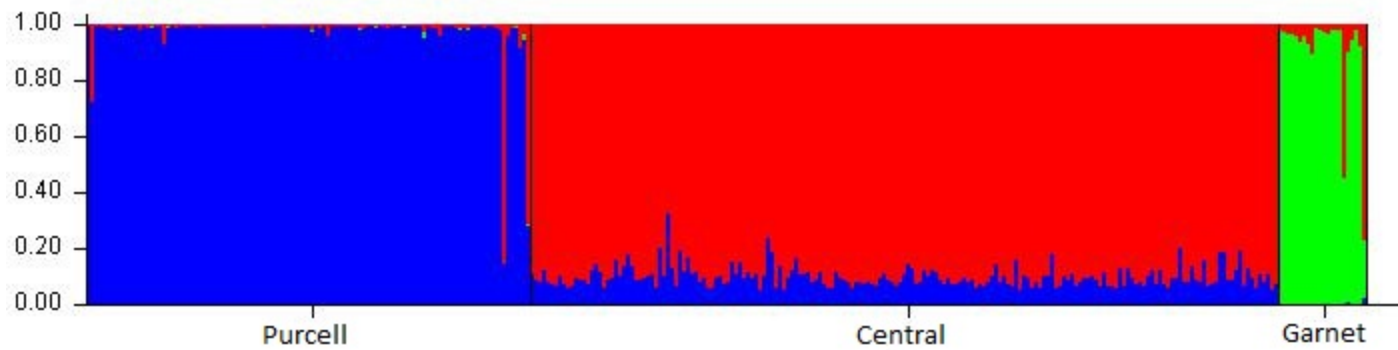


Squires 1998-2015 lynx genetic data

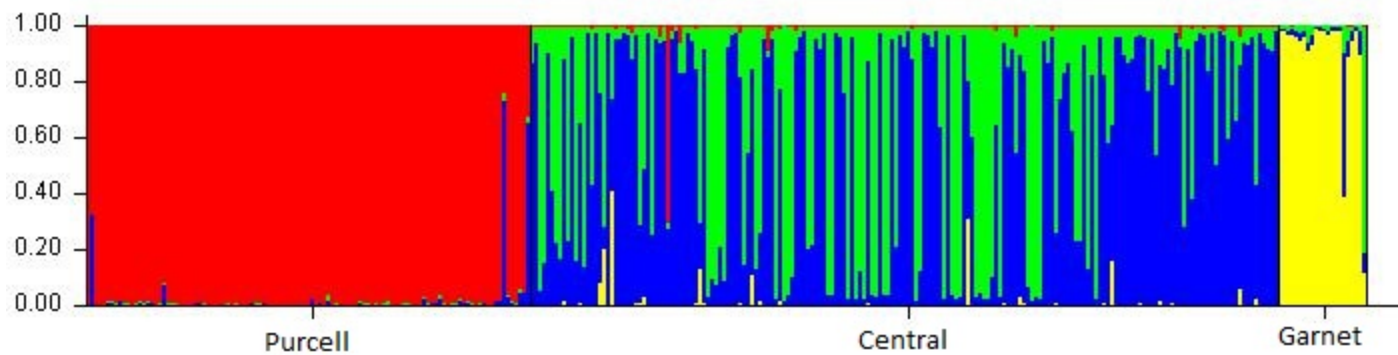




Structure k = 2

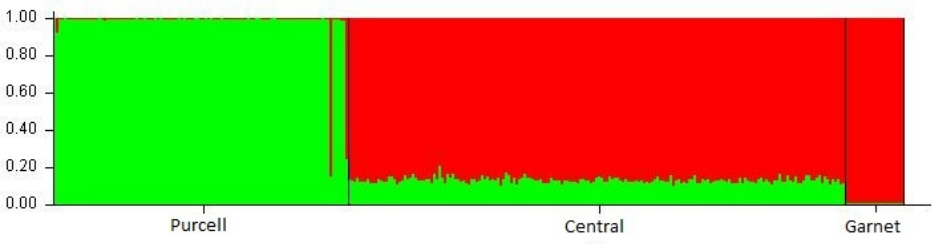
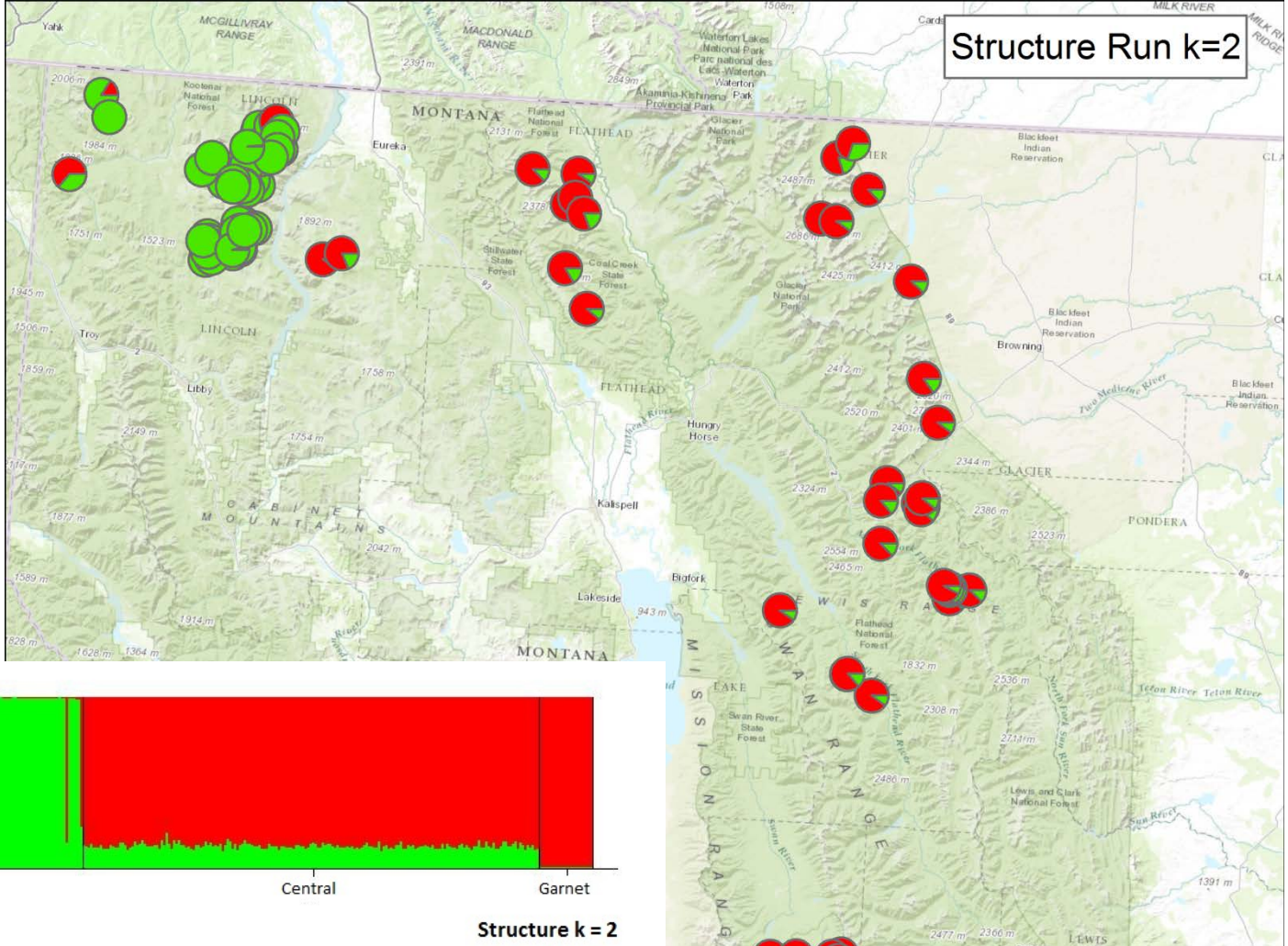


Structure k = 3

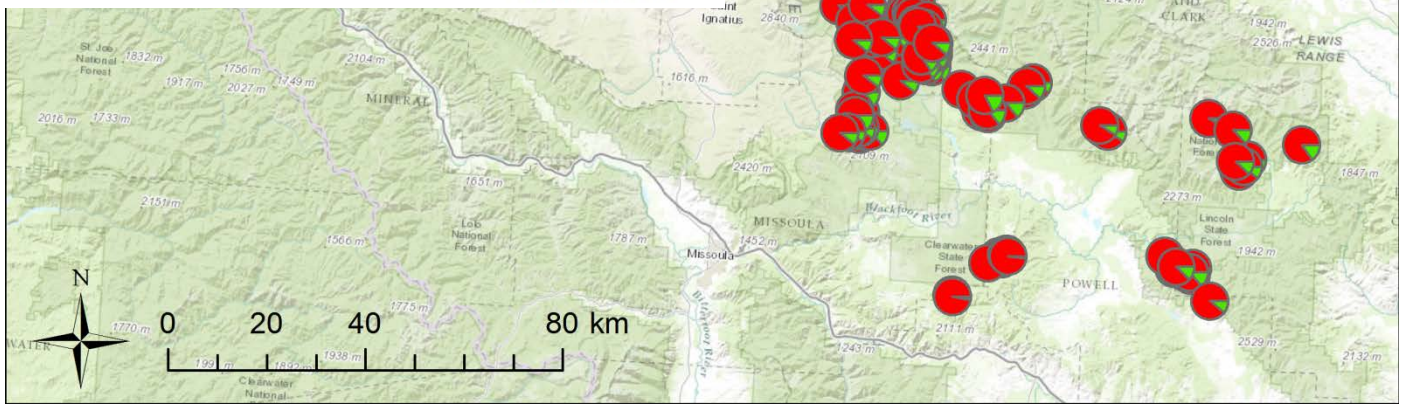


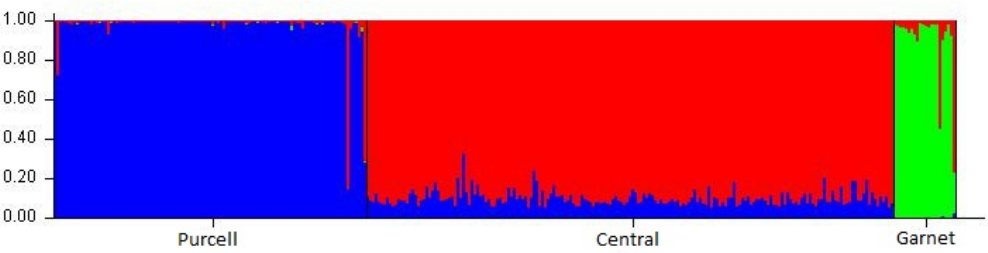
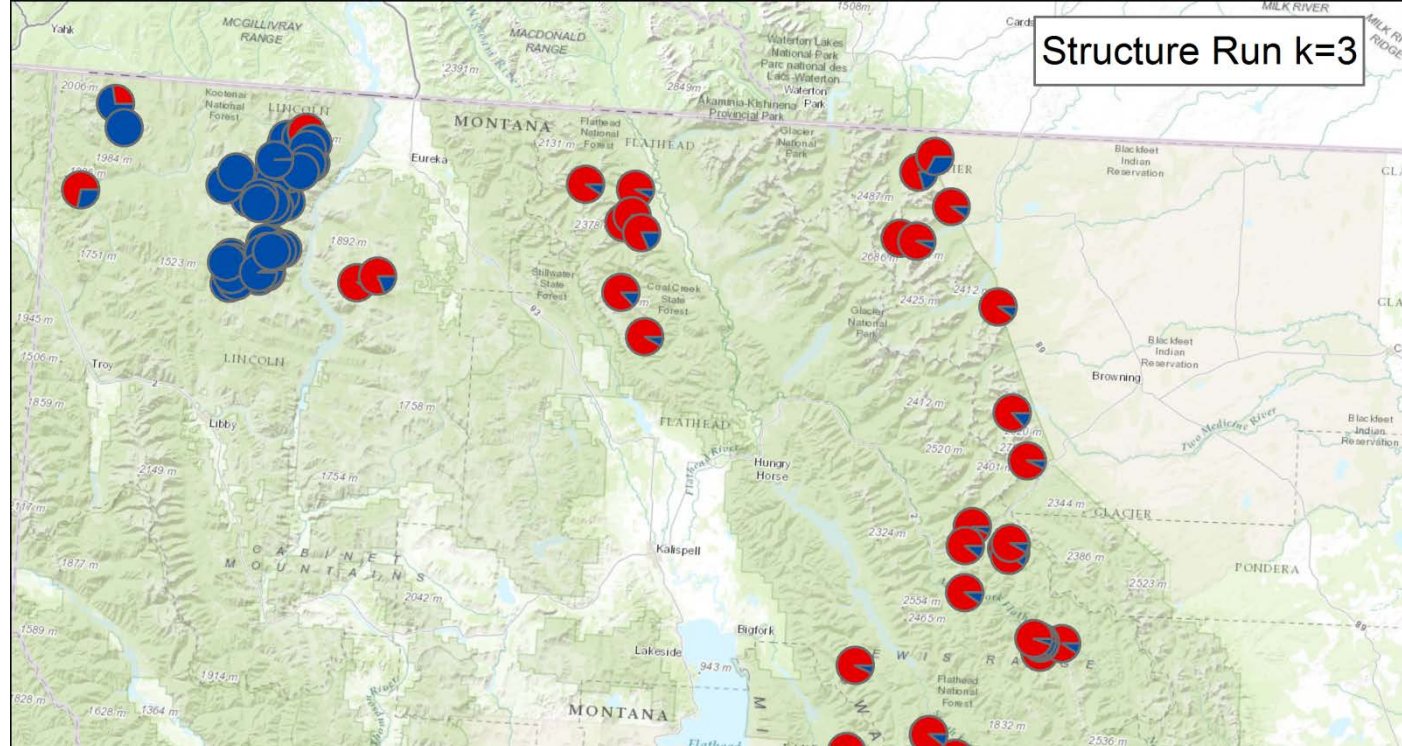
Structure k = 4

Structure Run k=2

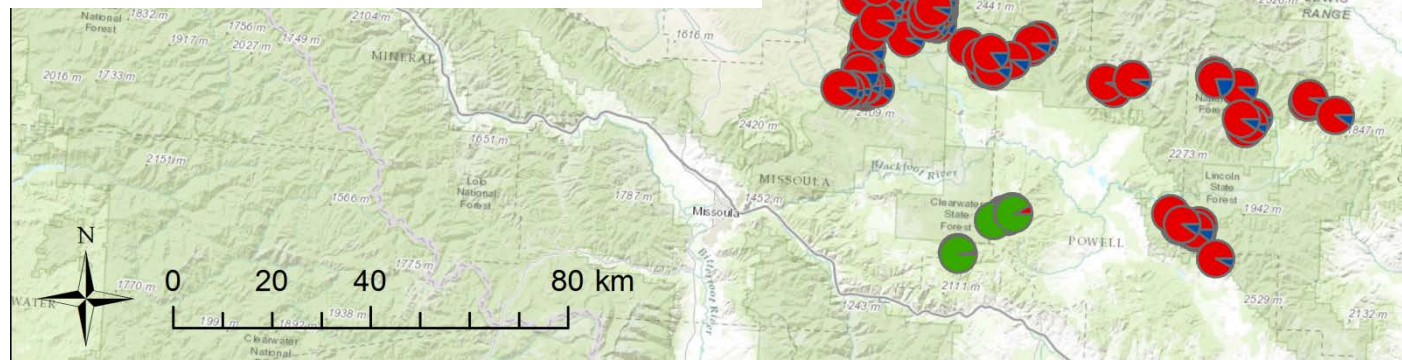


Structure k = 2

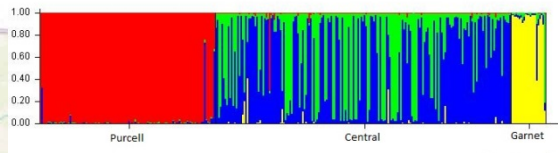
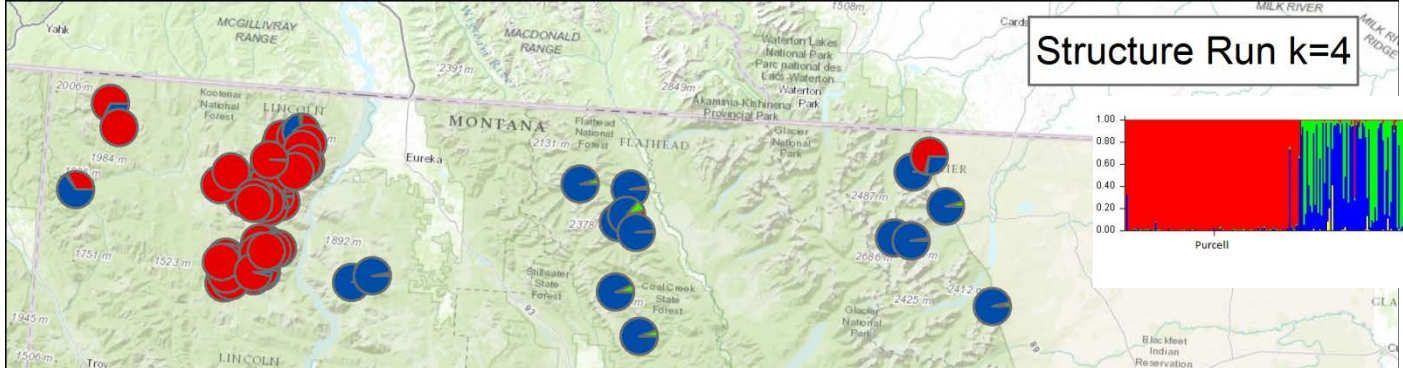




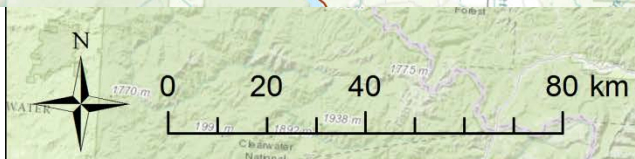
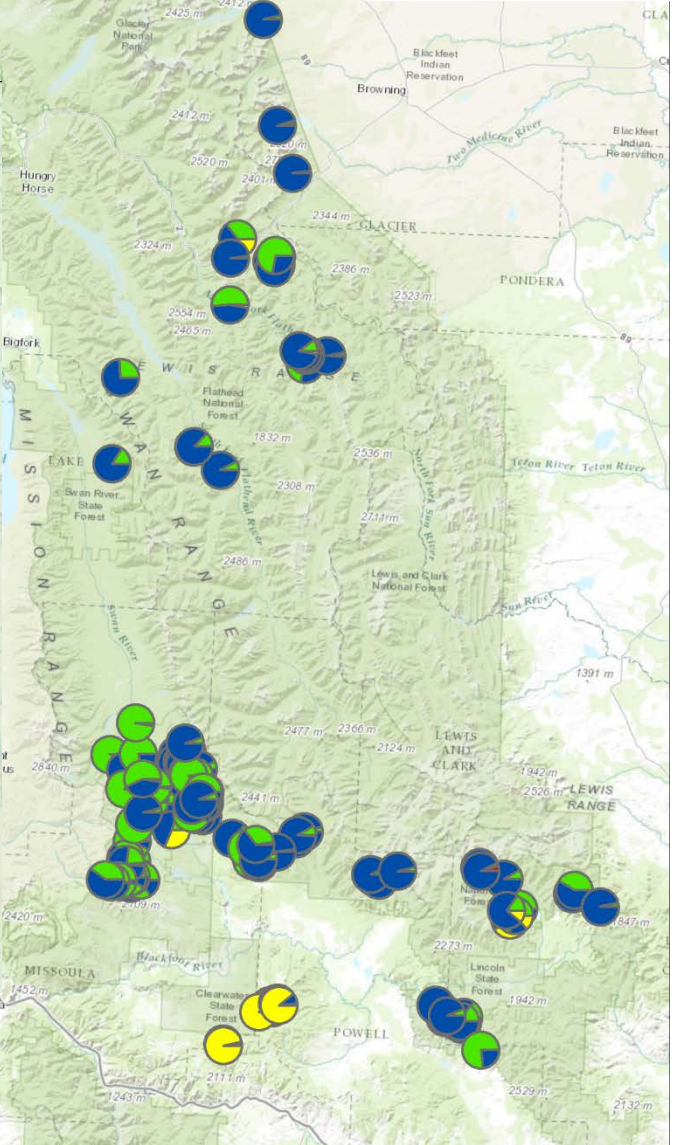
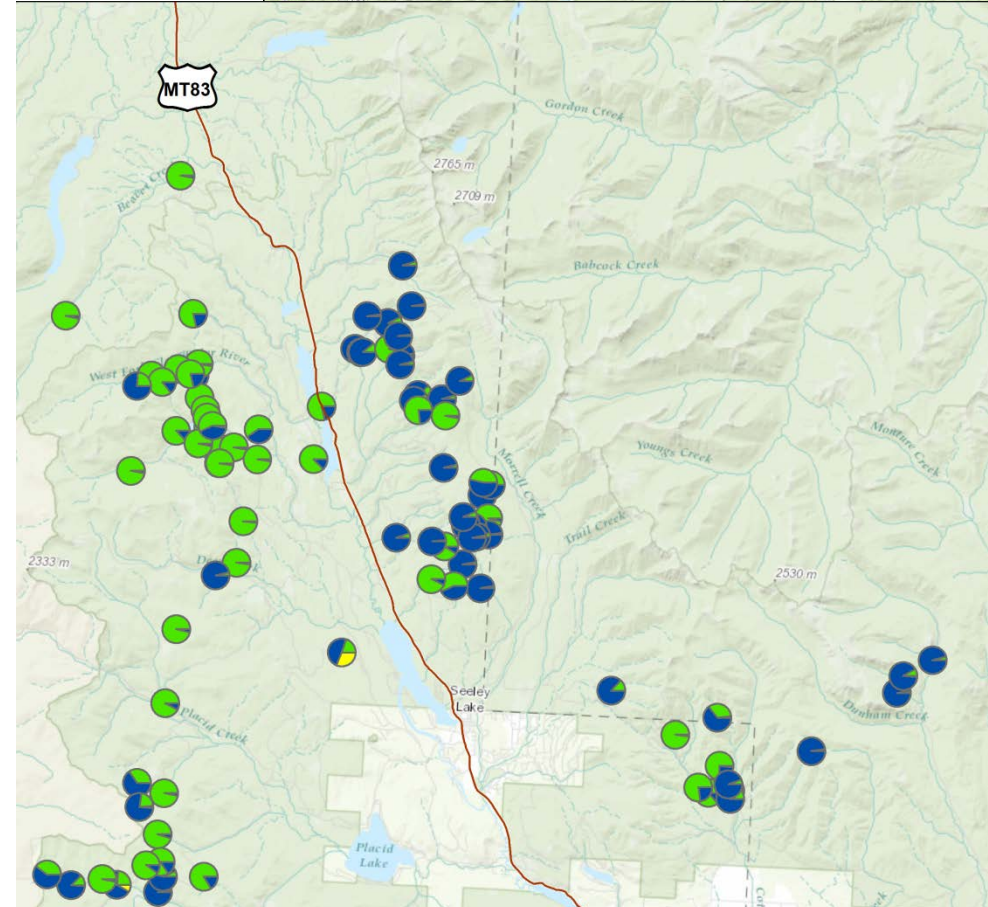
Structure k = 3

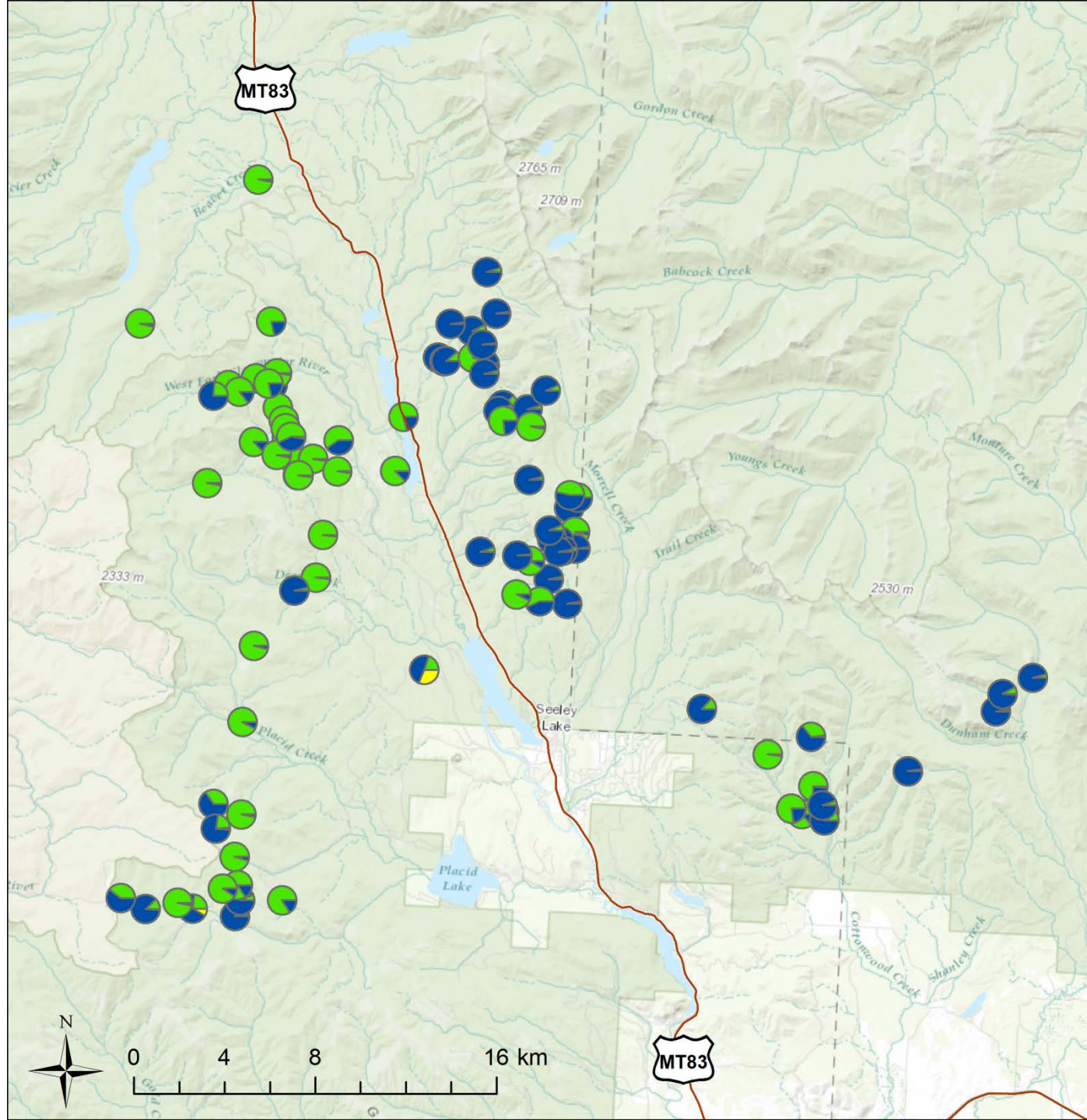


Structure Run k=4



Structure k = 4

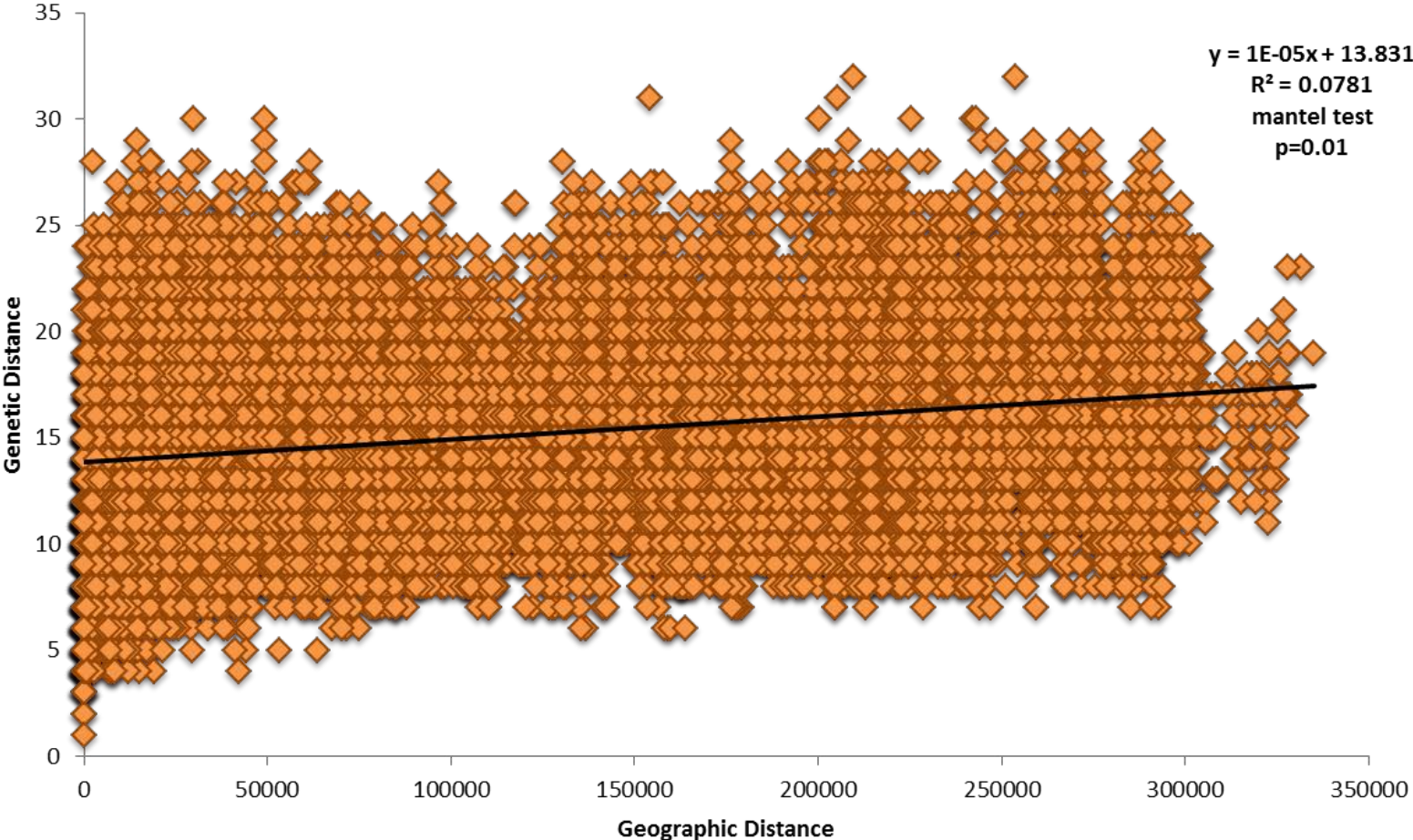






Isolation by Distance

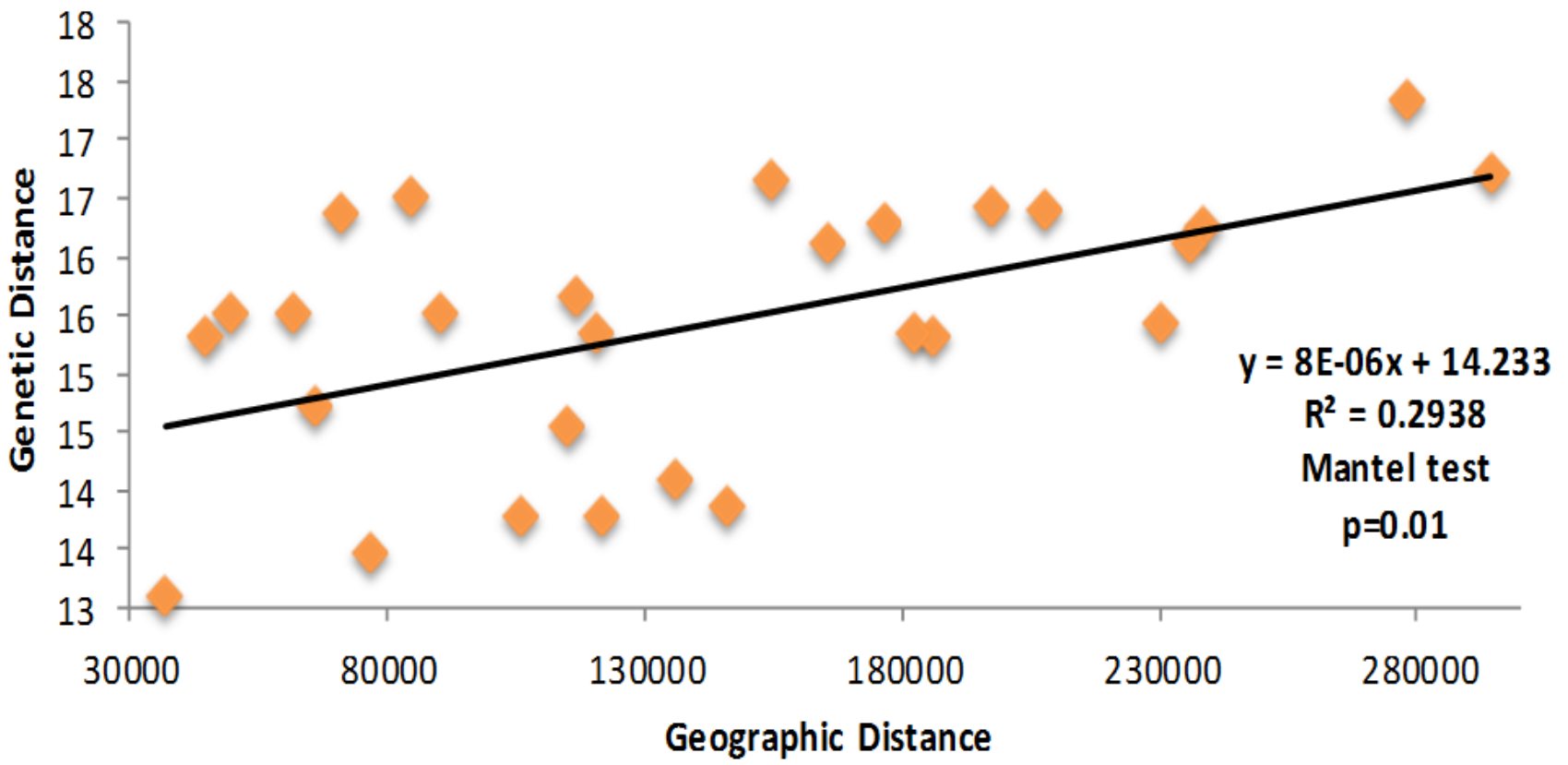
All individual lynx





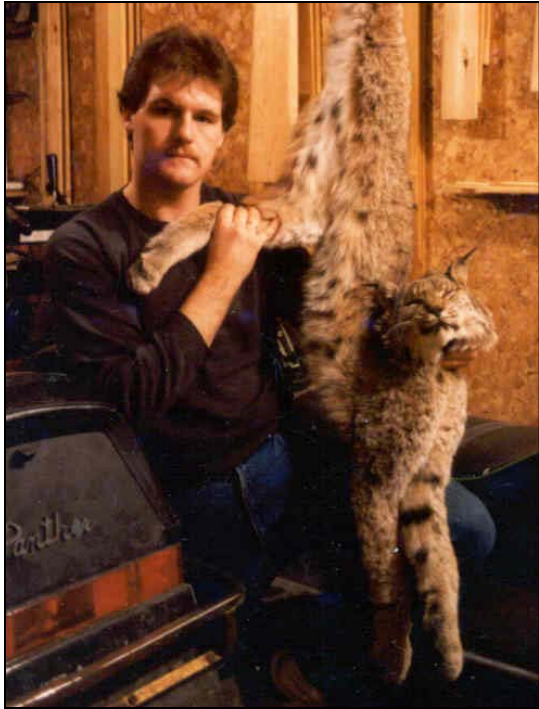
Isolation by Distance

All lynx in 8 sampled populations



Lynx Genetic Considerations

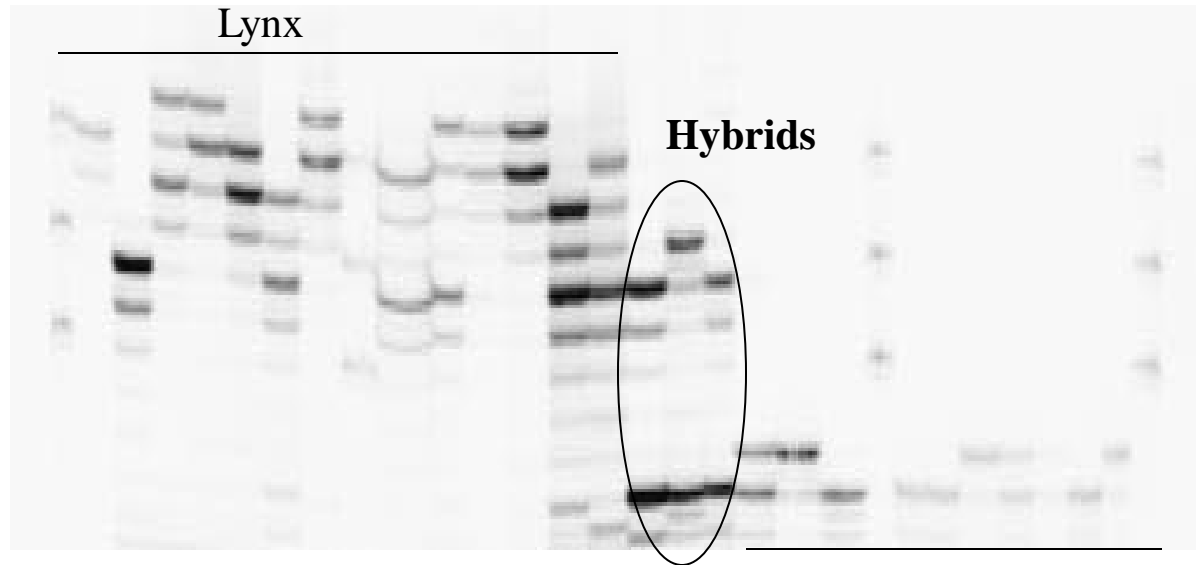
- 1) Mini review of lynx population genetic studies
- 2) Review of lynx hybridization studies
- 3) Needed genomic data



Lc 106

Lynx

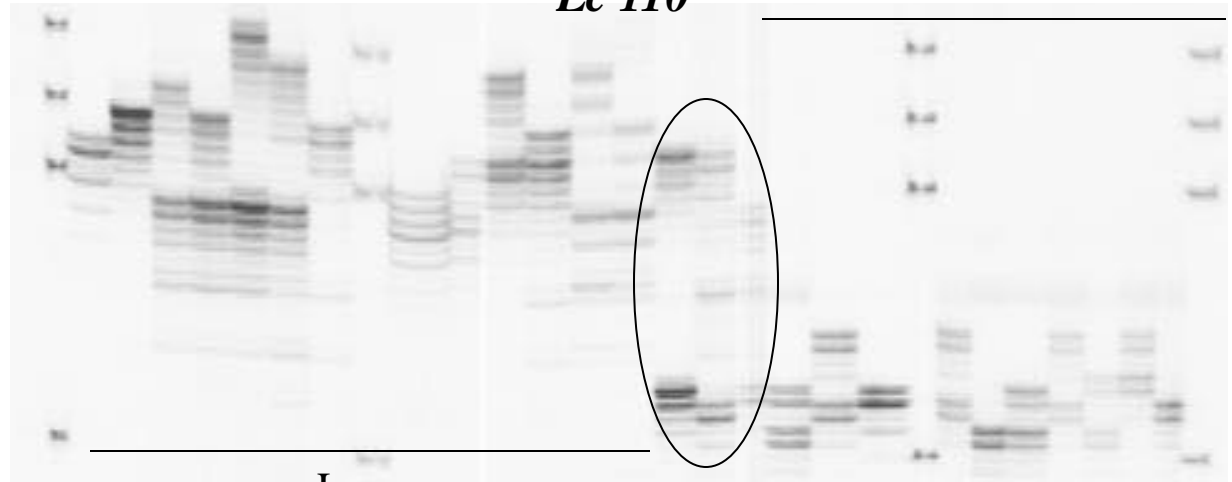
Hybrids



Bobcats

Lc 110

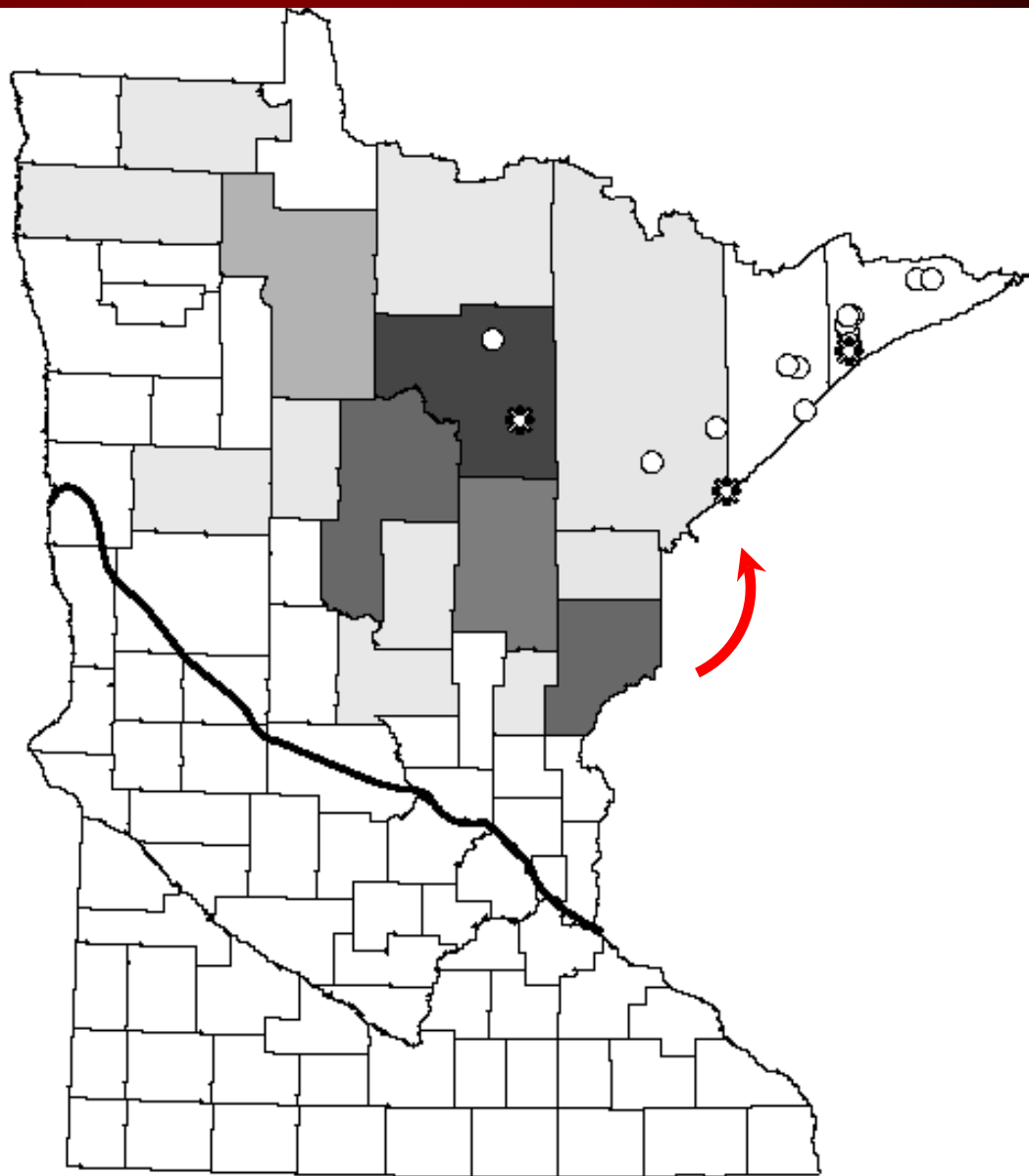
Bobcats



Lynx

**Number of bobcats trapped
by county (1989 - 2002)**

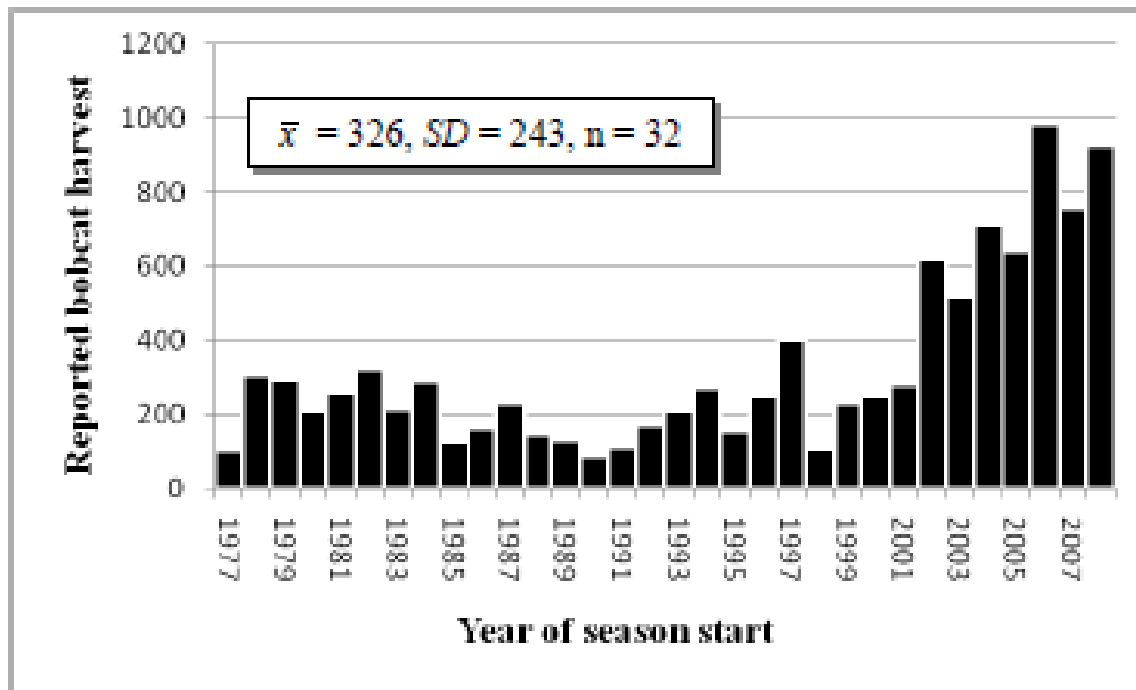
- 0 - 50
- 51 - 100
- 101 - 150
- 151 - 200
- 201 - 250
- 251 - 300
- 301 - 350
- 351 - 400



0 100 200 400 Kilometers

Bobcat Numbers on the Increase

Figure 1.2. Reported harvest of bobcats in Minnesota from 1977-1978 through 2008-2009 seasons.



Genetic Monitoring of Lynx in Minnesota

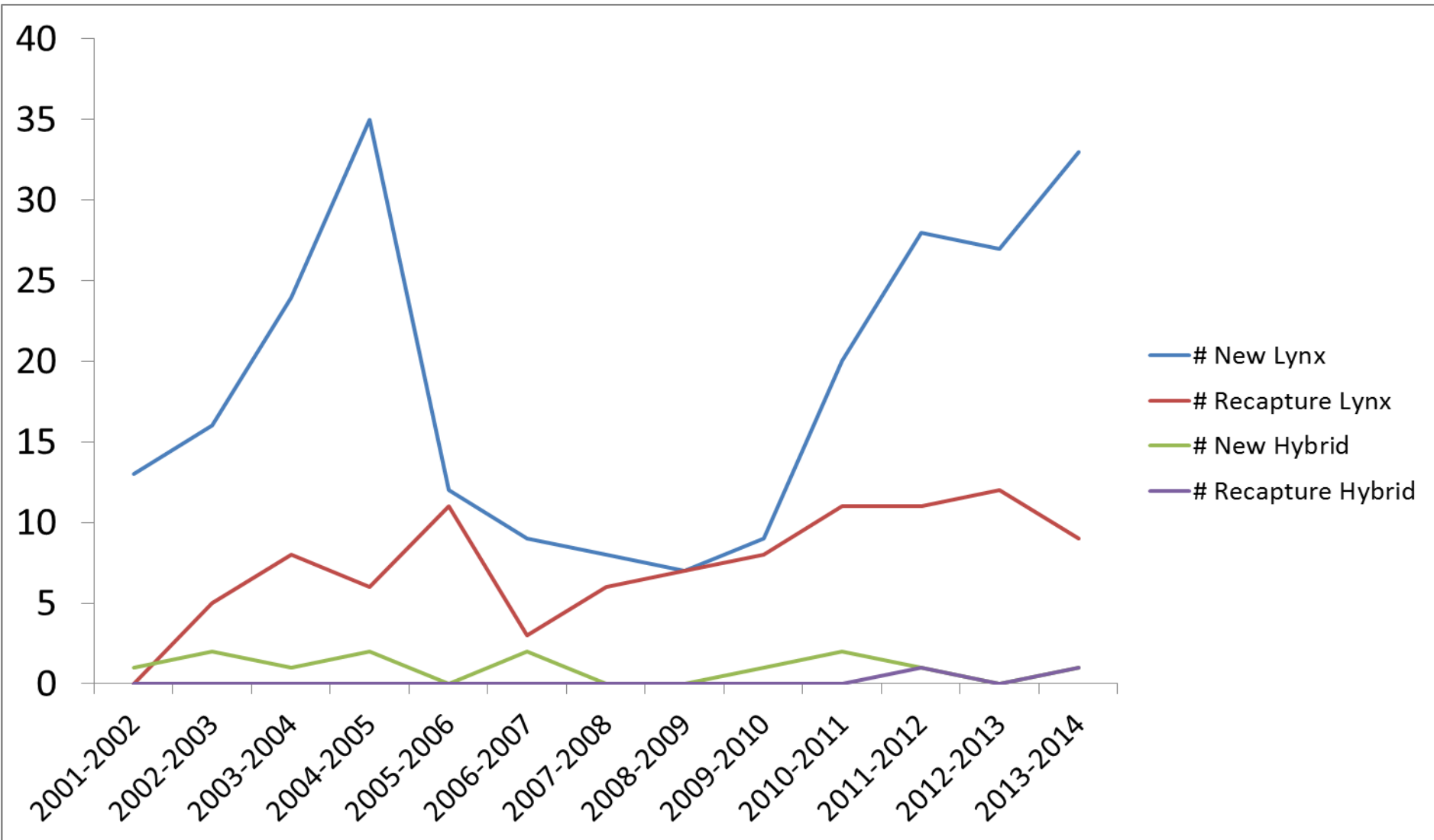


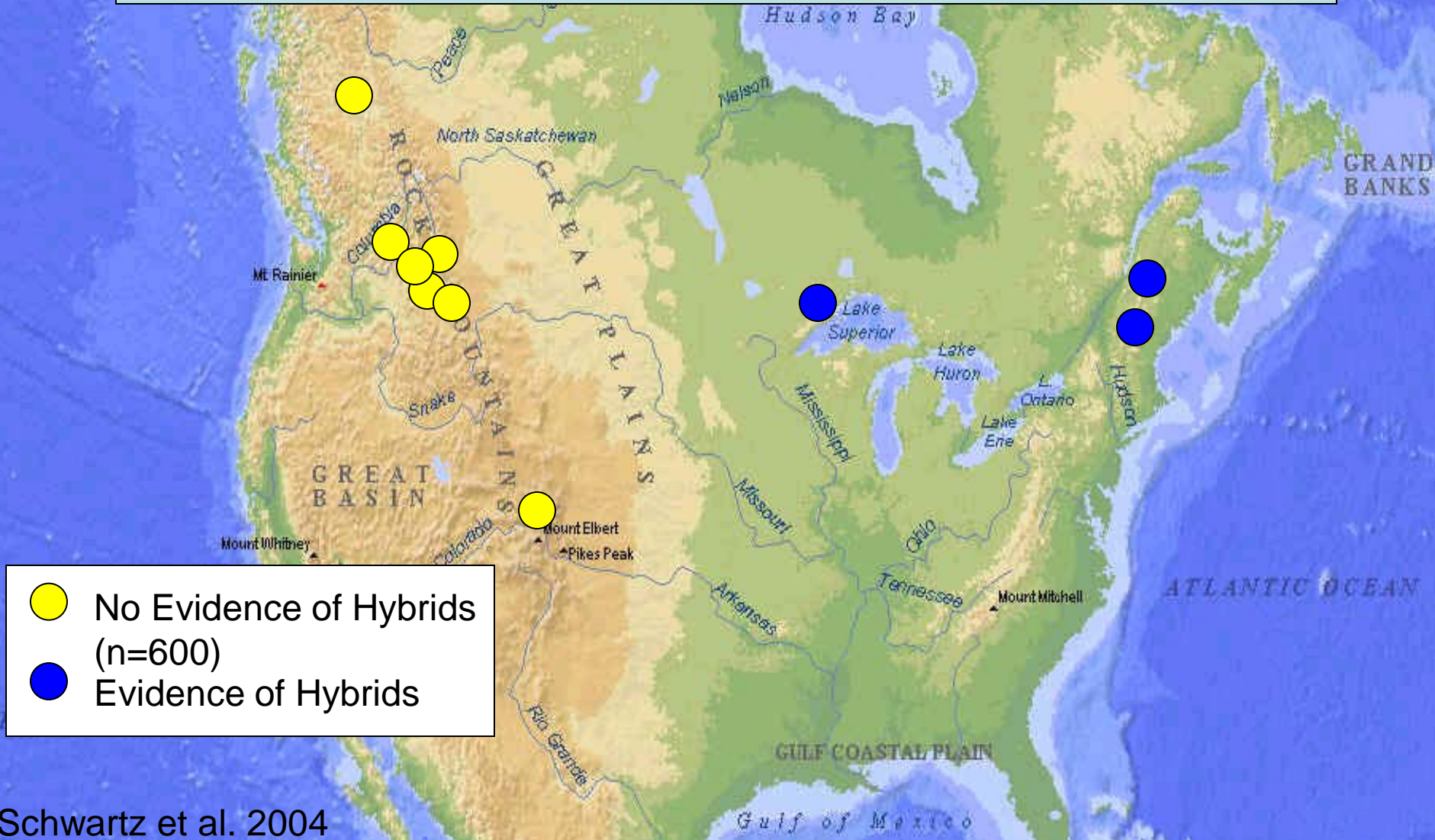
TABLE 1.—Physical characteristics of five Canada lynx (*Lynx canadensis*) – bobcat (*L. rufus*) hybrids collected from 1986–2003 in Maine and Minnesota, USA and New Brunswick, Canada compared to published estimates for diagnostic characters of parent species

Diagnostic characters ^a				
	Ear tuft length	Tail coloration	Hind feet	Pelage
Bobcats	<2.5 cm long	White hairs on ventral surface	Smaller, less fur males = 17.0 cm, females = 15.5 cm	Distinct spots, reddish
Canada lynx	>2.5 cm long	Tip completely black	Heavily furred in winter, 20.3–25.0 cm long	Gray, few spots
1998 Maine hybrid ^b	4.0/3.5 cm	A few white hairs interspersed	17.5 cm long	Reddish brown, few spots on ventral surface
2002 Maine hybrid ^b	3.8/3.8 cm	A few white hairs interspersed	20.0 cm long	Reddish brown, some spotting present
All Hybrids (n = 5)	5 lynx-like	5 intermediate in character	5 intermediate in character	At least 3 with bobcat-like spots

^a Ear tuft lengths, tail coloration and pelage reported by Anderson and Lovallo (2003). Hind foot lengths reported for bobcats by Larivière and Walton (1997) and for lynx by Tumilson (1987)

^b Individual measurements provided for those hybrids with most complete morphology

Canada Lynx – Bobcat Hybridization in North America



Schwartz et al. 2004
Pilgrim et al. 1998

Continental-scale assessment of the hybrid zone between bobcat and Canada lynx

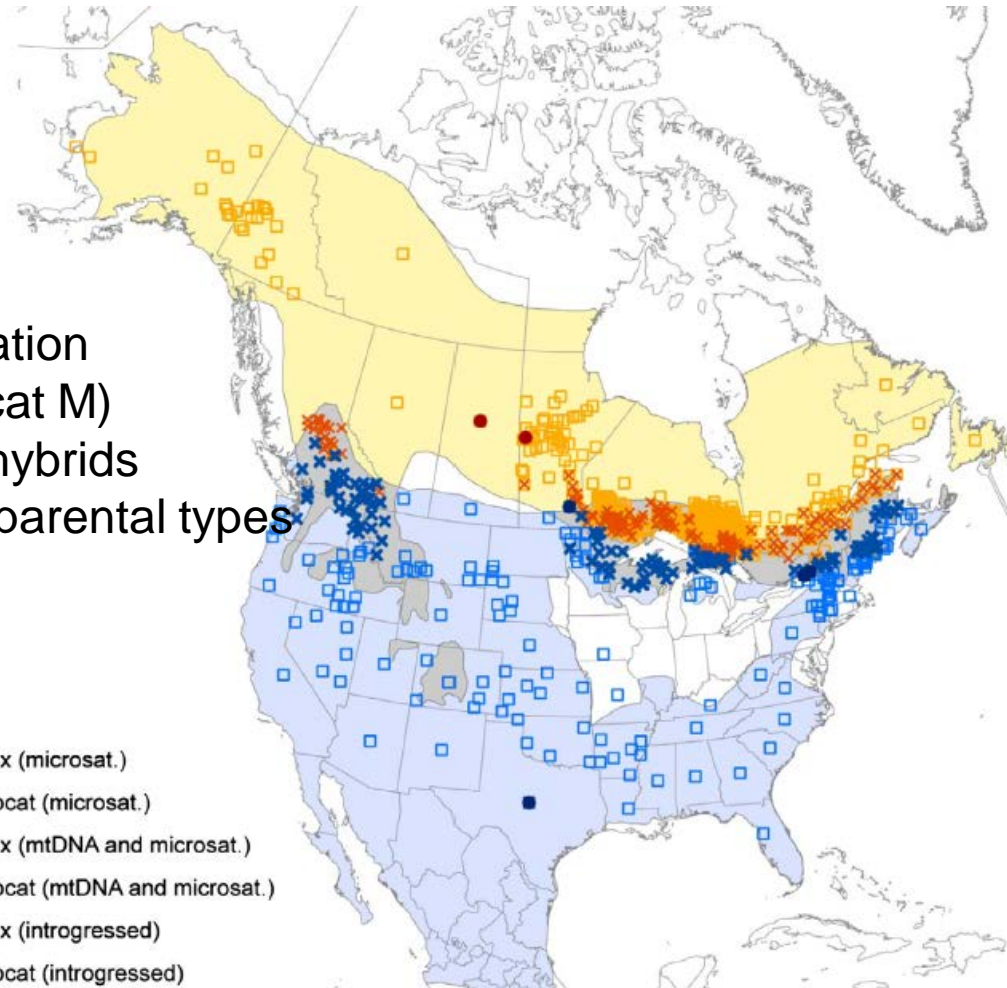


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^c Environmental and Life Sciences, Trent University, 2140 East Bank Drive, Peterborough, Ontario K9J 7B8, Canada



- bi-directional hybridization (mostly lynx F x bobcat M)
- 7 of 2851 individuals hybrids
- Backcrossing to both parental types

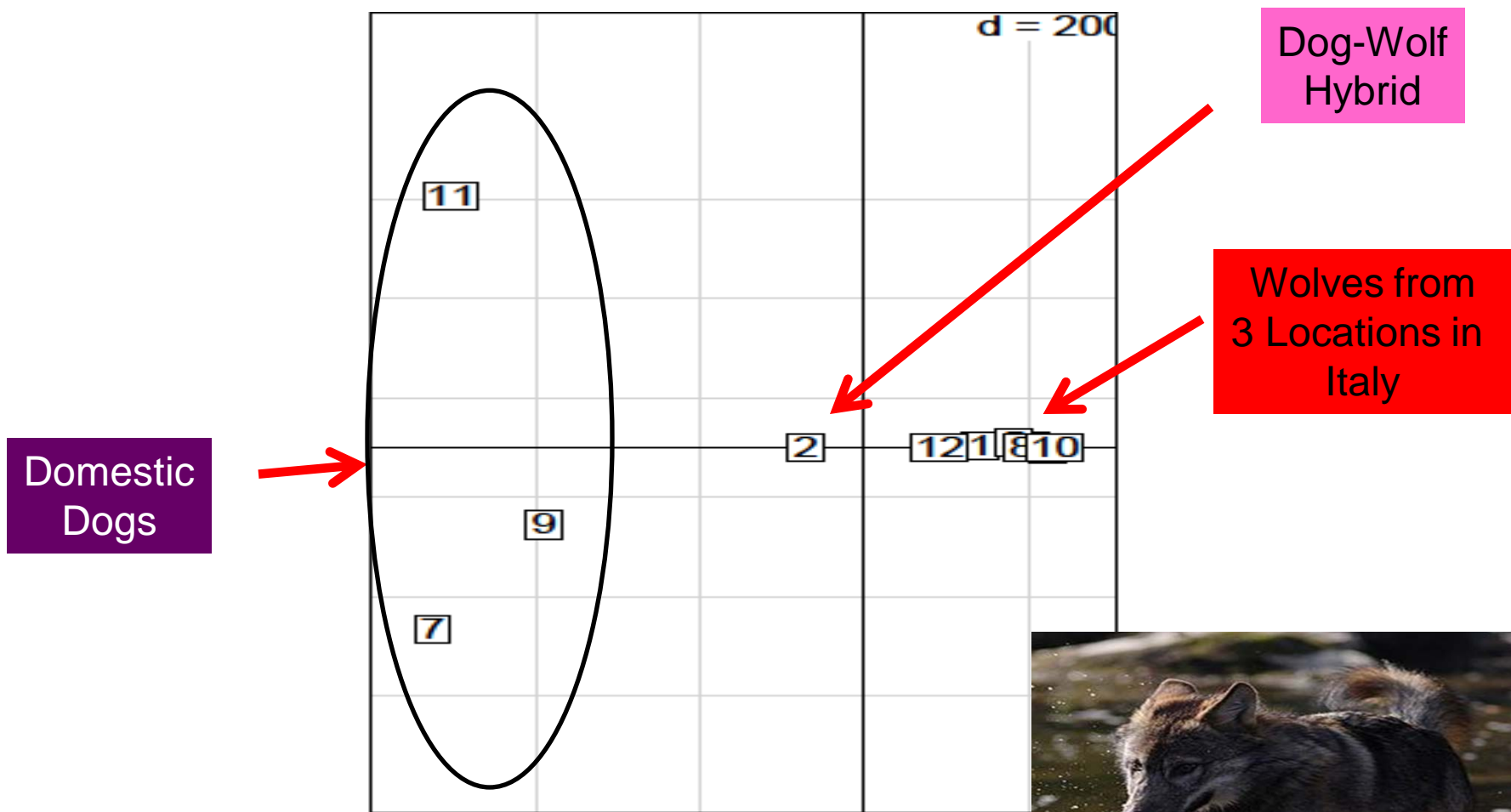
Lynx Genetic Considerations

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What is Genomics?

Genomic data: genetic information (e.g. DNA sequences) at **thousands to millions of loci** across the genome of a sample of organisms. Often focuses on **mapping** of these sequences and understanding their **interactions**

#1: Increase Power and Precision



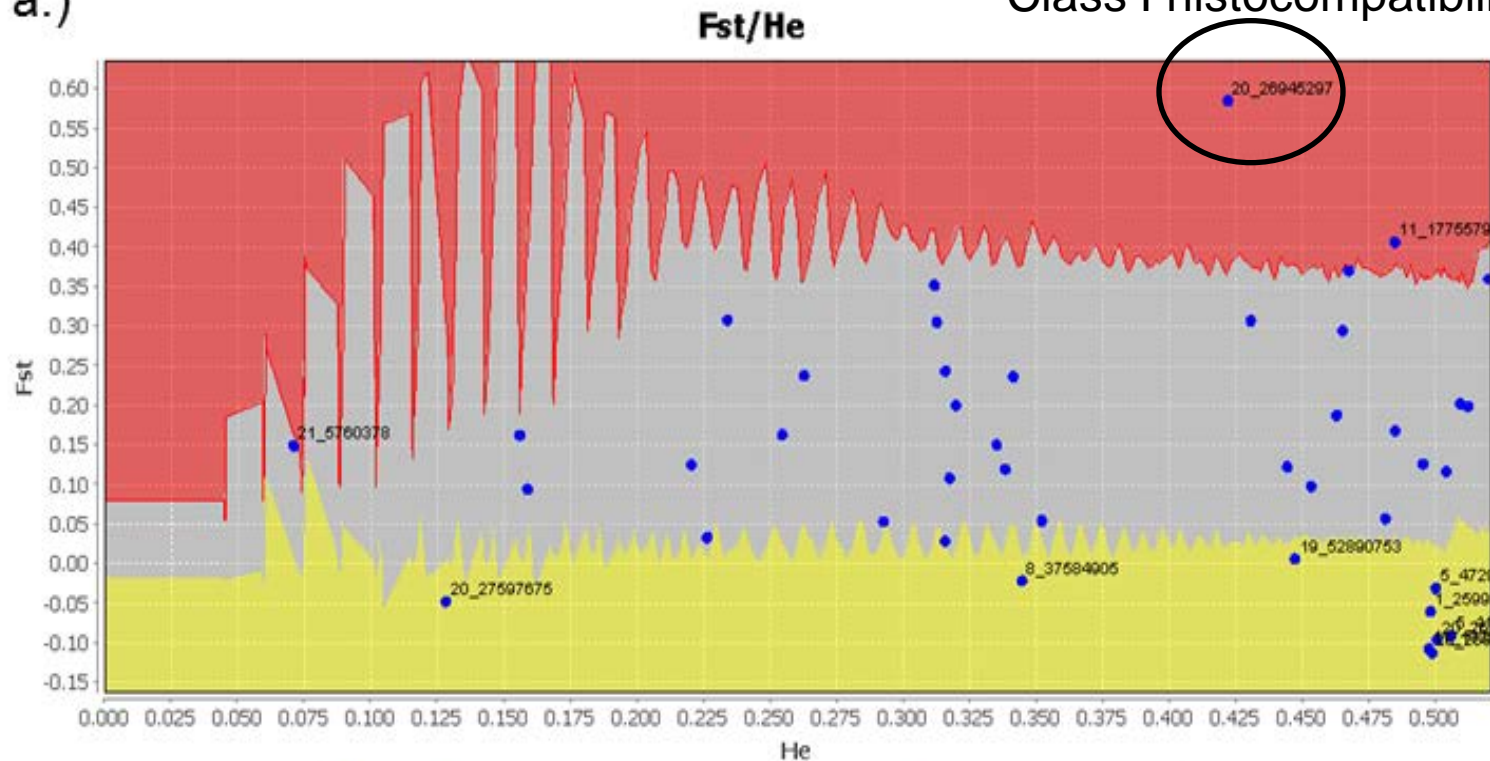
166,000 Molecular Markers



#2 Separate: Neutral vs. Adaptive Genes

8,188 exons from >5,000 genes targeted; Roffler et al. (in prep)

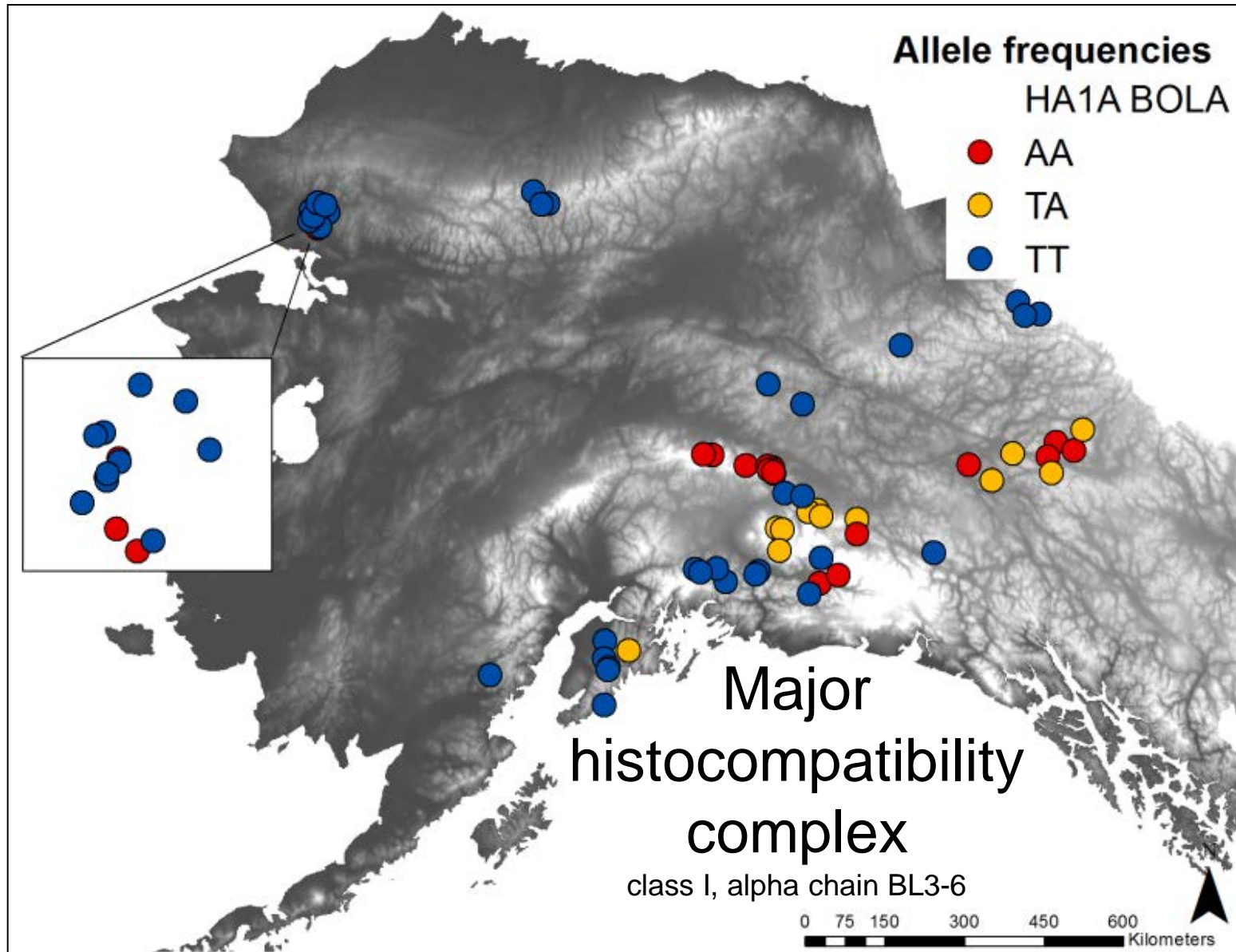
a.)



● Markers — Candidate balancing selection — Candidate neutral — Candidate positive selection



Spatial Distribution of Alleles at Locus Putatively Under Selection



Can we find genes under selection with lynx?



Leading Edge of the Range – Drift Wins, Unless Selection is Very Strong or Ne Large

Effective population size influences whether a local population can respond to selection = local adaptation

$$(4N_e * s \gg 1)$$

selection overpowers drift



Drift Wins

First Principles of Population Genetics: Effective Population Size

Effective population size influences whether a local population can respond to selection = local adaptation



$(4N_e * s \gg 1)$
selection overpowers drift

Summary Points

- Boreal forest is almost no barrier for lynx
- Intriguing results about climate in East
- Periphery and some features = limited barrier
- Tide pool model
- When tide is out – substructure develops
- Genomics can address climate and periphery questions while also looking for genes under selection



Where do we go from here?

- Sampling (during multiple phases of cycle)
- Genomic studies to increase power
- Look for genes under selection at range margin, with focus on the NAO



What else should we do?

- 1) Conserve genetic diversity at the broad scale!!!!!!
- 2) Recognize that adaptive variation may = reduced gv at leading and trailing edge due to selection or drift.
- 3) Conserve gradients, and recognize the importance of peripheral populations (where selection occurs)

