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
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

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
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)

Proportion of Maximum # Lynx Trapped

Montana
BC/AB +2 yr.

$r = 0.74$
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):

<table>
<thead>
<tr>
<th></th>
<th>F$_{st}$</th>
<th>Migrants</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fairbanks to Ladue Yukon:</td>
<td>0.001</td>
<td>≈ High</td>
</tr>
<tr>
<td>Kenai P. to Seeley Montana:</td>
<td>0.070</td>
<td>≈ 3.0</td>
</tr>
</tbody>
</table>
Kenai
Seeley Lake
Distance Does Not Lead To Structuring

Mantel: $p = 0.42$
Adapted from Forbes and Hogg (1999)
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
• 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 Fst

<table>
<thead>
<tr>
<th>Microsatellites</th>
<th>Mitochondrial DNA</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>East</td>
</tr>
<tr>
<td>East</td>
<td>0.0622**</td>
</tr>
<tr>
<td>Prairie</td>
<td>0.0062**</td>
</tr>
<tr>
<td>North</td>
<td>0.0091*</td>
</tr>
<tr>
<td>Northwest</td>
<td>0.0156***</td>
</tr>
<tr>
<td>BC</td>
<td>0.0136**</td>
</tr>
</tbody>
</table>

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.

Reuness et al. 2003
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
  - Fst – 0.19 between NF and Mainland
- “subtle gene flow restriction between Ontario and Manitoba”
- Bayesian clustering - 2 clusters NF vs others.
Again, very low Fst

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

<table>
<thead>
<tr>
<th></th>
<th>East</th>
<th>Prairie</th>
<th>North</th>
<th>Northwest</th>
<th>BC</th>
</tr>
</thead>
<tbody>
<tr>
<td>East</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.0000</td>
</tr>
<tr>
<td>Prairie</td>
<td>0.0071***</td>
<td></td>
<td>0.0001</td>
<td>0.0030</td>
<td>0.0100</td>
</tr>
<tr>
<td>North</td>
<td>0.0080***</td>
<td>0.0018</td>
<td></td>
<td>0.00113</td>
<td>0.0002</td>
</tr>
<tr>
<td>Northwest</td>
<td>0.0069***</td>
<td>0.0061***</td>
<td>0.0035**</td>
<td></td>
<td>0.0034</td>
</tr>
<tr>
<td>BC</td>
<td>0.0077***</td>
<td>0.0034***</td>
<td>0.0008</td>
<td>0.0008</td>
<td></td>
</tr>
</tbody>
</table>

Row et al. 2012
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 THORNTON¹,⁴ 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 snow the “invisible barrier” to gene flow

(a) FST = 0.008 +/- 0.001

(b) FST = 0.029 +/- 0.007
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, teemed with extensive sampling (*n* = 272 adults) of Canada lynx (*Lynx canadensis* Kerr, 1792) throughout Alberta. The level of genetic variation was high (mean *H*<sub>e</sub> = 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*<sub>M</sub> = −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.
• 14 microsatellites and 558 lynx to test “riverine barrier hypothesis”

• St. Lawrence River is a barrier
• Not absolute – 24 individ. 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)

- Montana
- Minnesota
- QU_co
- YK_co
- BC_co
- Washington
- Colorado
- NE_Lynx
RMRS Genetic Data (2004-2006 only)

Principal Coordinates (PCoA)

- Washington
- Minnesota
- Colorado
- BC_co
- QU_co
- YK_co
- Montana

Coord. 1

Coord. 2
Lynx Cycles

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)

- Montana
- BC_co
- YK_co
- QU_co
- Colorado
- Washington
- Minnesota
- MN-2001

2004-2006
Squires 1998-2015 lynx genetic data
Isolation by Distance

All individual lynx

$y = 1E-05x + 13.831$

$R^2 = 0.0781$

mantel test

$p=0.01$
Isolation by Distance
All lynx in 8 sampled populations

\[ y = 8 \times 10^{-6}x + 14.233 \]

\[ R^2 = 0.2938 \]

Mantel test
\[ p = 0.01 \]
Lynx Genetic Considerations

1) Mini review of lynx population genetic studies

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Schwartz et al. 2004
Bobcat Numbers on the Increase

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

\[ \bar{X} = 326, \text{SD} = 243, n = 32 \]
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.

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

<sup>a</sup> 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 Tumlison (1987).

<sup>b</sup> 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
- 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)

Class I histocompatibility antigen
Spatial Distribution of Alleles at Locus Putatively Under Selection

Roffler et al. in prep.
Can we find genes under selection with lynx?
Effective population size influences whether a local population can respond to selection = local adaptation

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

$(4N_e s \gg 1)$ 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

\[ (4Ne^*s >> 1) \]

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)