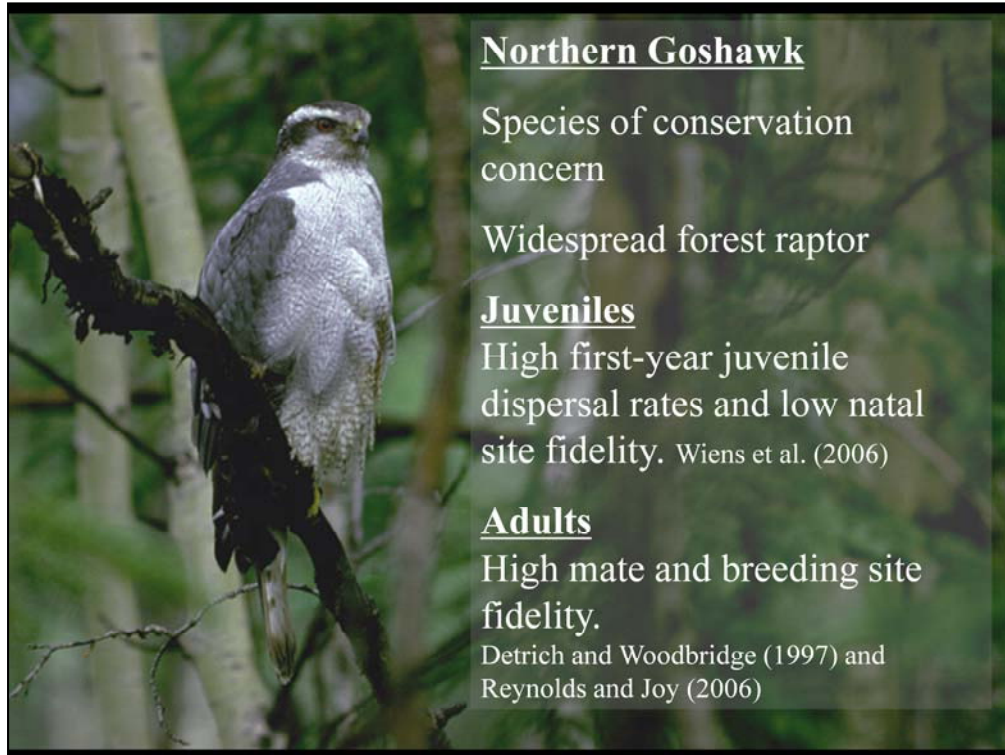


The next speaker will be myself.

Shelley Bayard de Volo

I will be presenting results from my doctoral research, that I just completed this Spring from Colorado State University

The title of my talk is:



(1) Our primary interest in studying phylogeography in the Northern Goshawk is that the species is one of conservation concern,

This stems from the fact that it is a forest dependent hawk, and often time uses mature forests for nesting and foraging.

(2) This species is also a very widespread species, occupying most of the forested regions of North America.

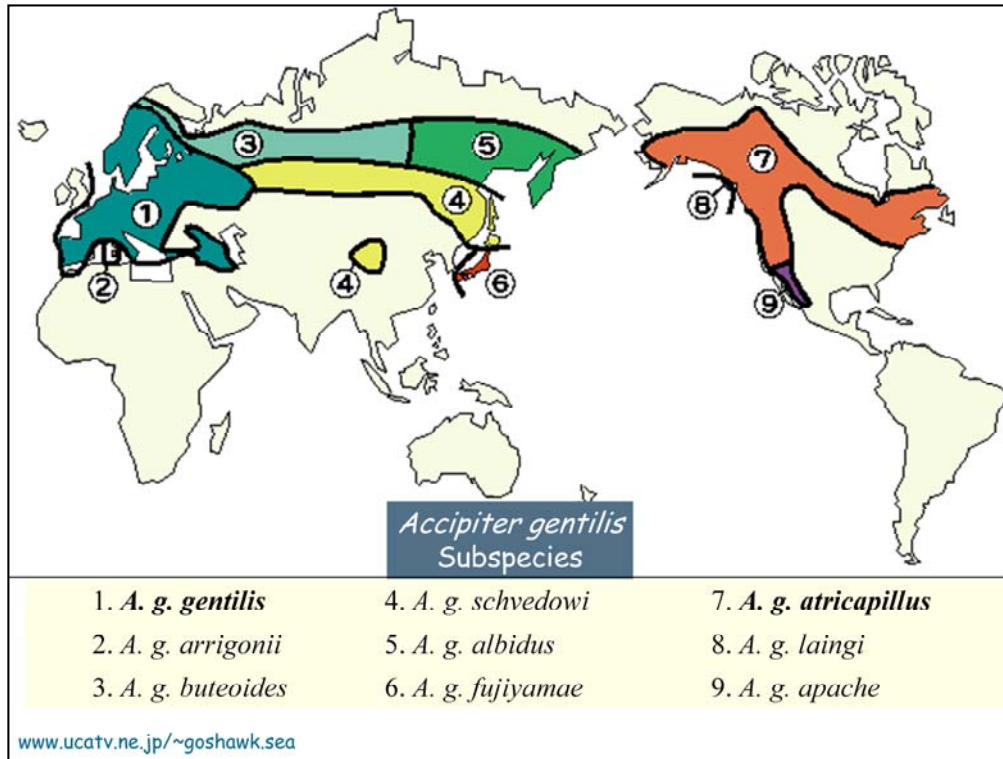
(I will show you a range map in the next slide).

(3) Goshawks also have a high capacity for dispersal.

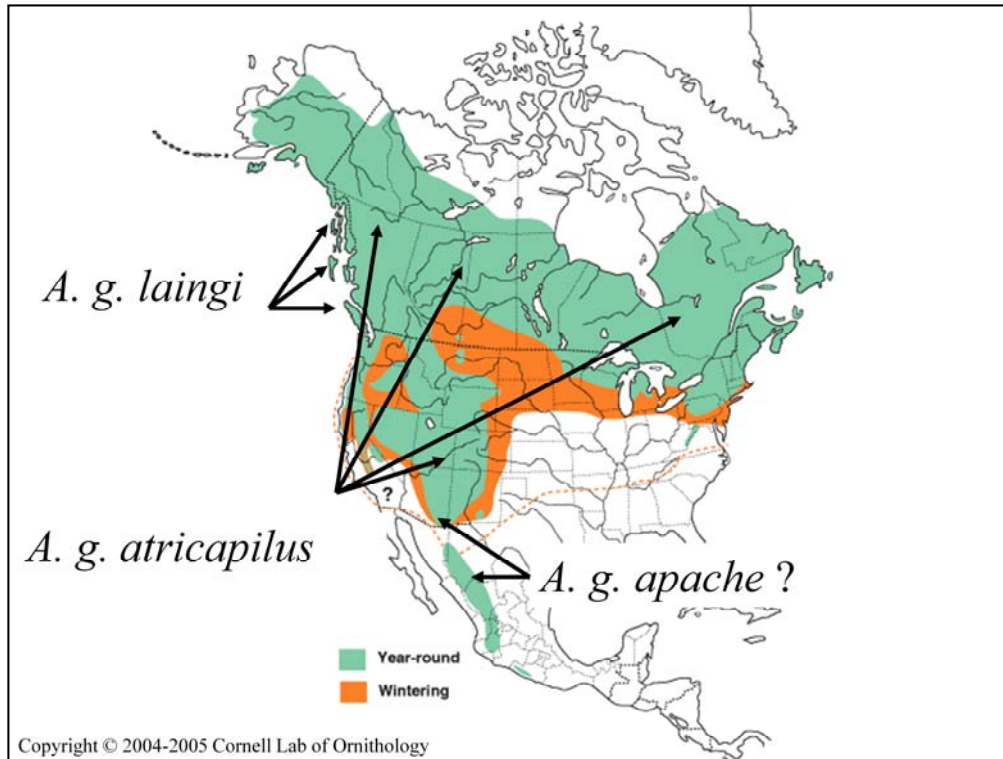
Juveniles exhibit very high dispersal rates their first year, and the species exhibits low natal-site fidelity.

(4) Once individuals find a territory and mate, they tend to stick with both for the remainder of their life.

These life history traits allow us to predict that goshawks may show some degree of genetic structure, but because of their capacity for natal dispersal it maybe at broad scales.



You can see here the species, is broadly distributed, having a Holarctic distribution



In North America **two subspecies** are currently recognized by the A.O.U. and USFWS

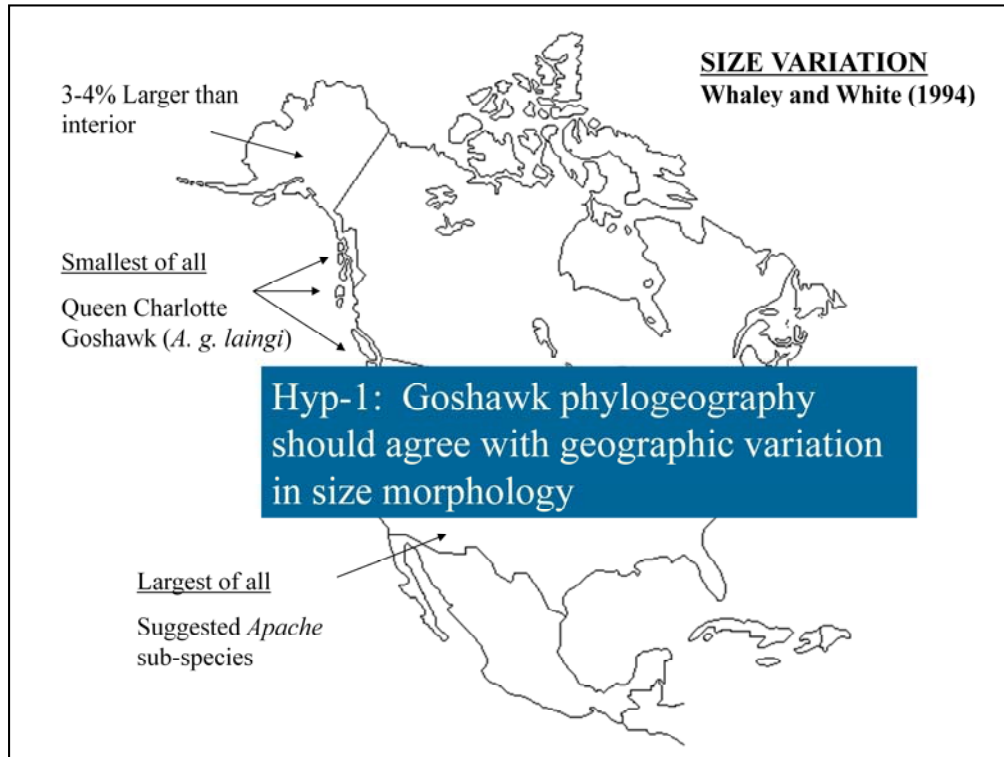
1. *A. g. atricapilus* occupies the bulk of the species' range in NA
2. **The Queen Charlotte goshawk** *A. g. laingi*, occupies the insular and coastal regions of British Columbia and SE Alaska.

It was recently (Nov 2007) listed as an endangered species in BC, but not in coastal AK

3. **A third subspecies** The **Apache goshawk** occupies SE Arizona and the Sierra Madre of Mexico.

It was first described by Taverner (1940), who reported the goshawks in this region were larger in size and darker in color.

His description, however was based on only three specimens, and thus the USFWS and AOU do not recognize it as a different spp, but rather consider goshawks in this part of the range the *atricapilus* spp.



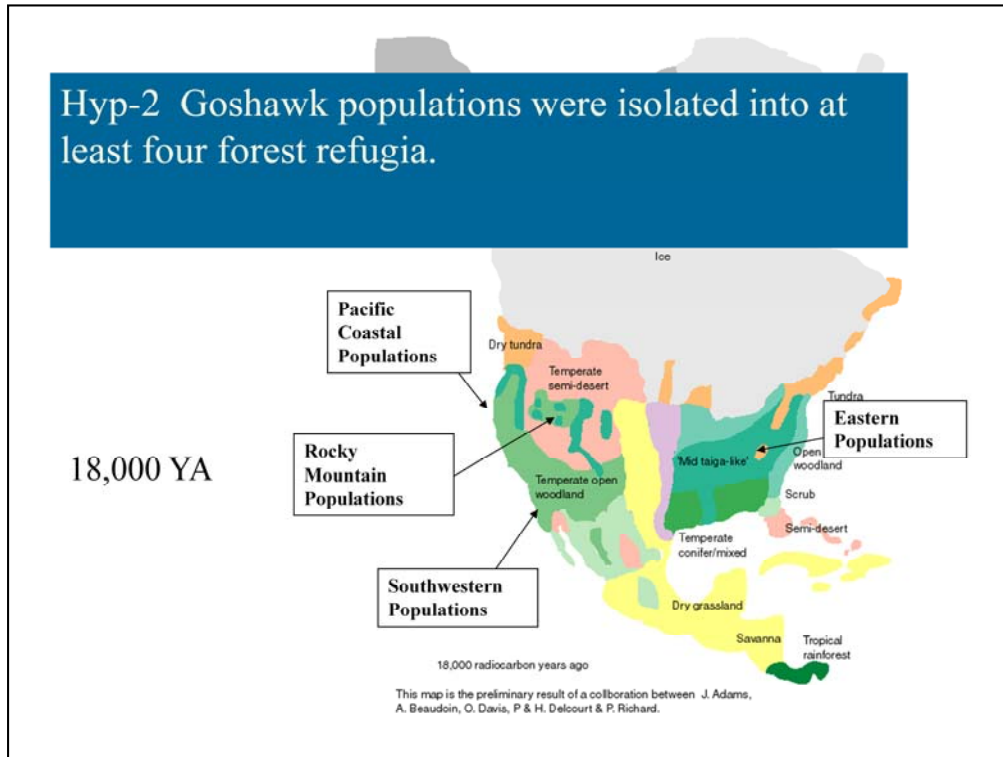
THERE IS FURTHER EVIDENCE OF SIZE VARIATION

Whaley and White looked at museum specimens and found

1. Goshawks in interior Alaska and Canada were 3-4% larger than the goshawks in the continental US, except for those in the SW, which were the largest of all
2. Goshawks in the East tended to be smaller than those in the West
3. Goshawks in the Pacific NW, namely the islands off the British Columbia Coast were the smallest of all in NA.

Hyp1 This led me to hypothesize that phylogeography in goshawks should correspond to this geographic variation in size morphology.

Their sample included 6 male and 16 female adult goshawks from SE AZ and Mexico individuals.



THE BASIS FOR THESE MORPHOLOGICAL DIFFERENCES

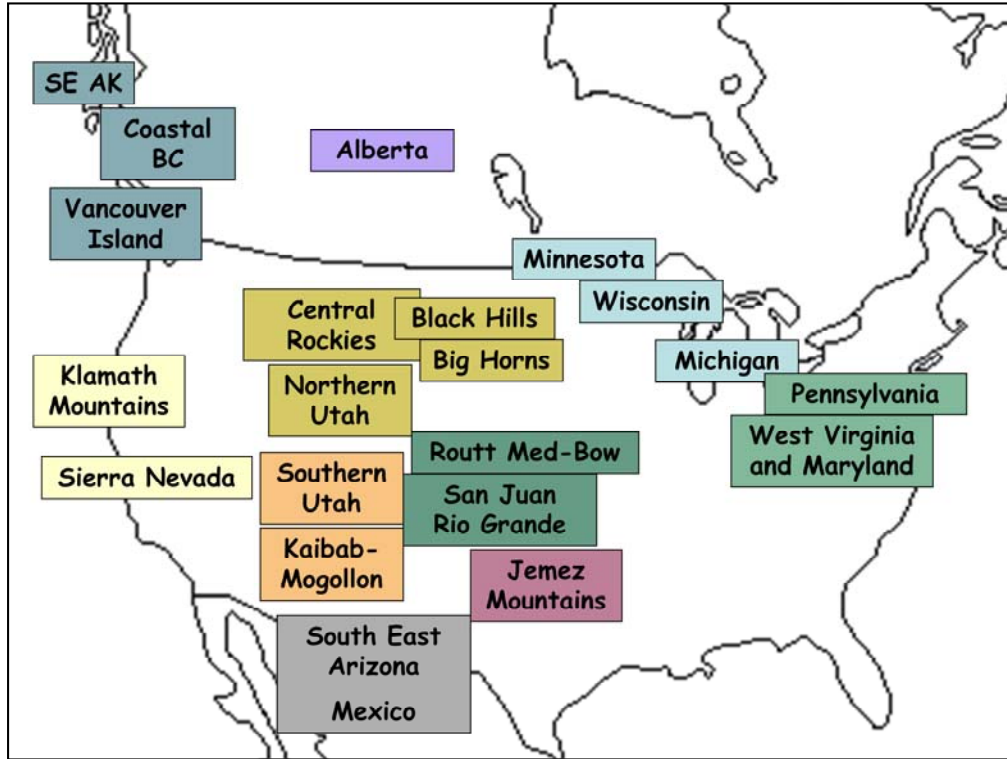
May, in part, be attributed to historical population isolation into separate geographic regions.

Until 18,000 years ago much of the North America was covered by two large ice sheets which caused major climatic shifts resulting in distributional shifts of forests relative to where they are today.

This map shows a hypothesis of how forests were distributed 18,000 TYA

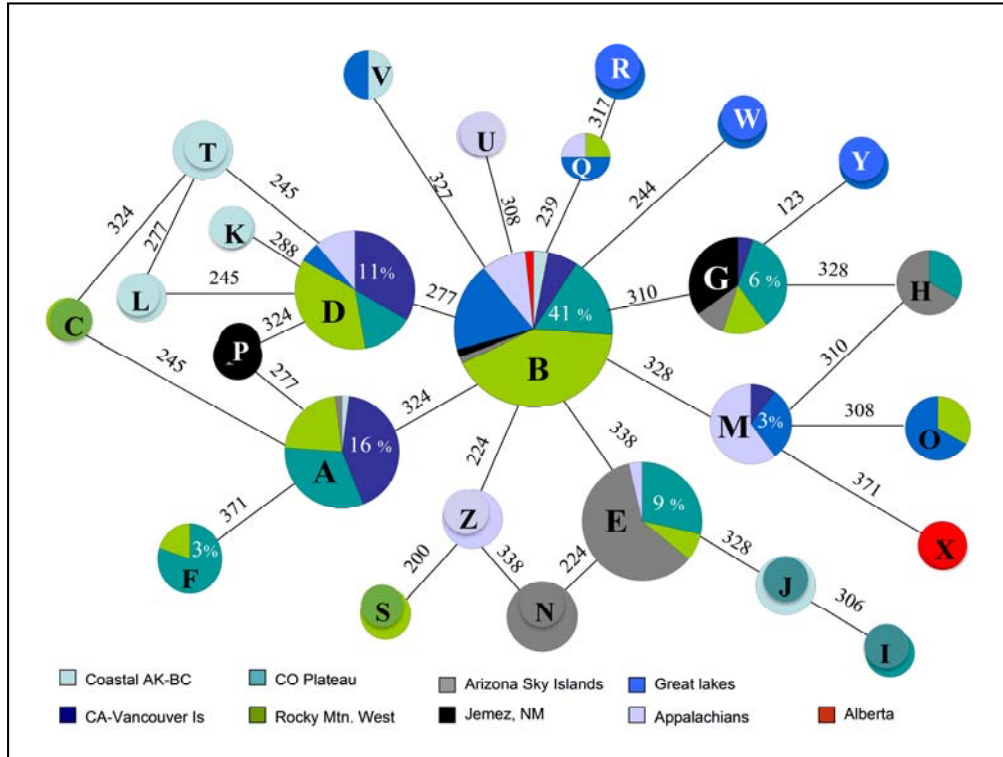
This led me to hypothesize that goshawk populations were isolated into different regions based of these historical forest refugia

John Adams and colleagues from the Oak Ridge national Laboratory



WE WERE ABLE TO SAMPLE A GOOD PART OF THE SPECIES RANGE IN THE US

And were able to also sample a little in SE AK, Coastal BC and Alberta.



RESULTS

This is a minimum spanning tree of haplotypes.

It is a hypothesis, based on parsimony, of the mutational relationships among haplotypes.

In all I found 26 haplotypes

1. Haplotype B was most abundant, and found in every population

41% of all samples had this haplotype

Because it was most abundant, and found in every population it is assumed to be **historical**, and all other haplotypes diverged from it.

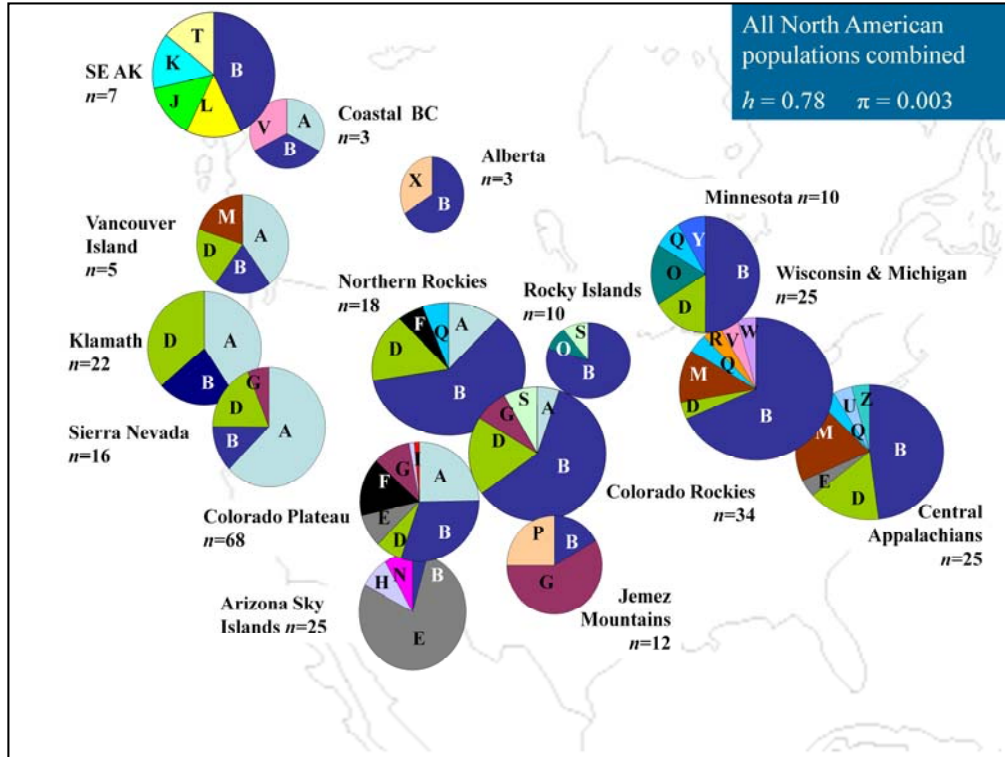
2. Haplotypes D, A and E and G were also relatively abundant – 42% of samples had these haplotypes.

3. Singletons -The remaining haplotypes were low frequency and even singletons, meaning they occurred in only one individual.

STAR-LIKE PATTERN –

haplotypes differ by very few mutational steps.

Indicates shallow and recent divergence

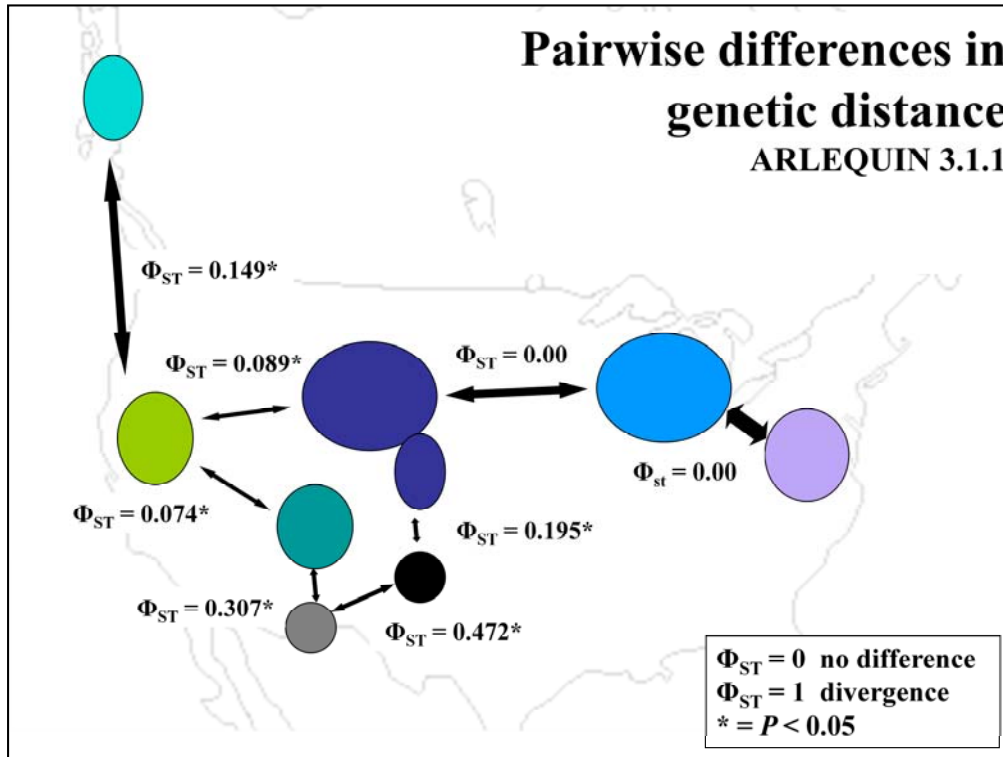


RESULTS

This is the geographic distribution of haplotypes and their relative frequencies.

There is a lot going on here, but **the main things I want you to pay attention to are.**

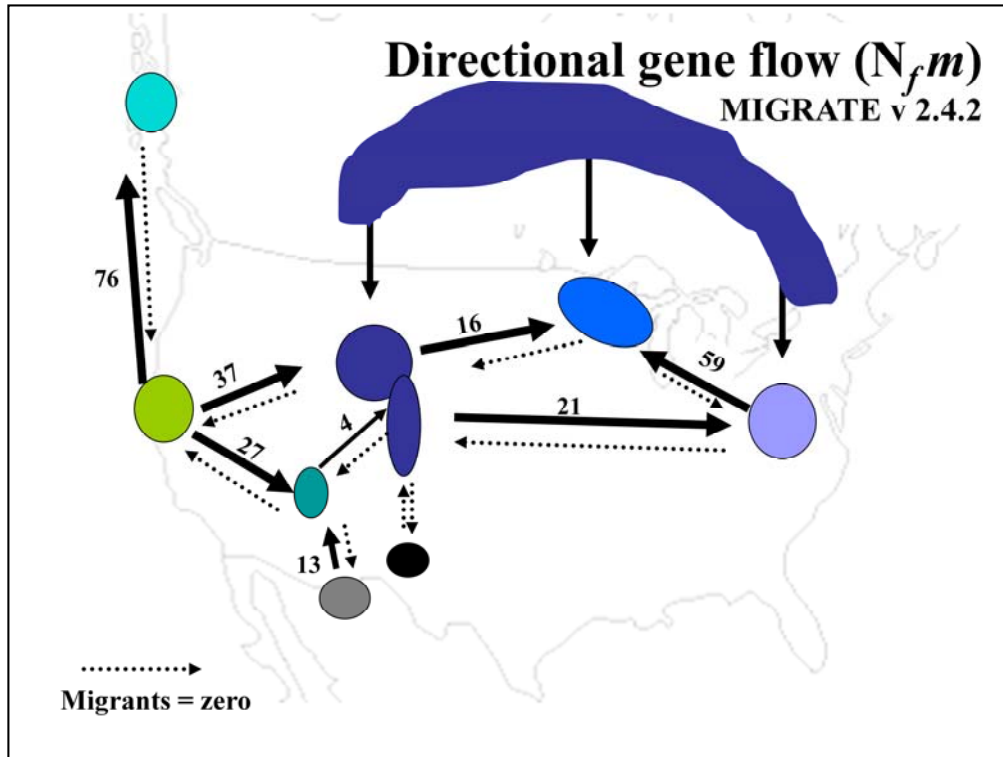
- (1) The distribution of the **B haplotype** – decreases east to west
- (2) The distribution of the **D haplotype** – decreases west to east
- (3) Of the seven samples from SE AK, four were unique to that region
- (4) A – haplotype decreases in the intermountain west
- (5) E-haplotype and G haplotypes – dominant in the southwest, and therefore likely arose in those populations



TO DETERMINE GENETIC STRUCTURE AMONG POPULATIONS

We used pairwise differences genetic distance

While there was a lot of genetic differentiation in the West, it was essentially non-existent in the east and among the East and the RM



WE USED MIGRATE TO ESTIMATE GENE FLOW OF FEMALES AMONG POPULATIONS.

What I want you to note here is that gene flow has been asymmetrical

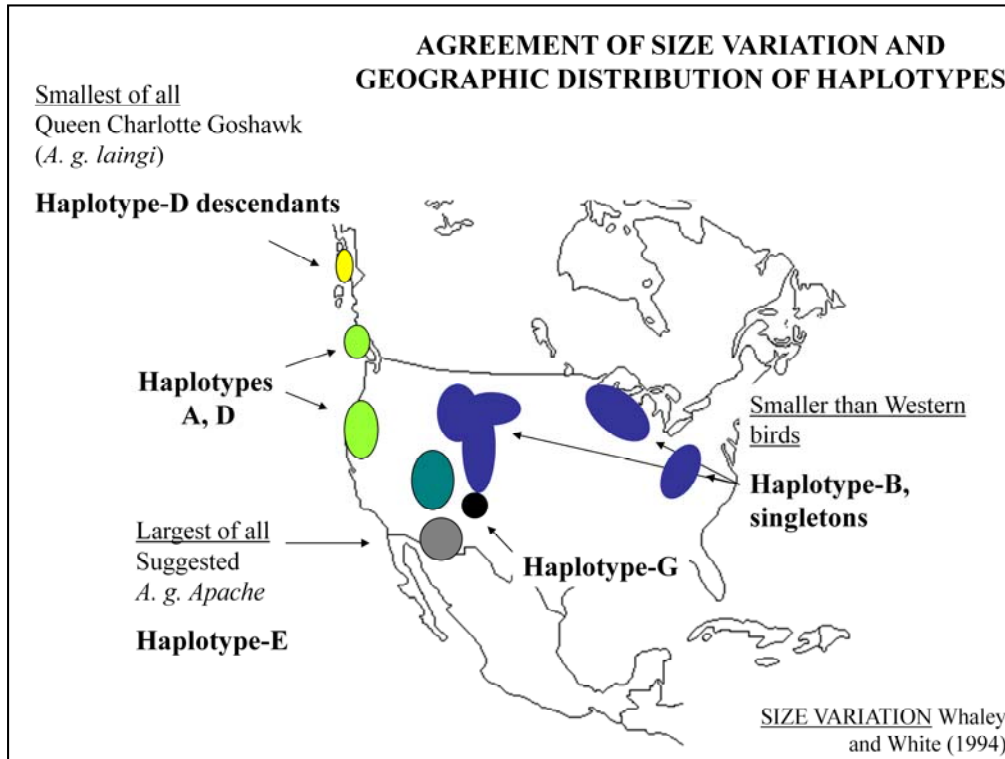
– Where the dotted arrows indicate zero migrants per generation.

What we see is a lot of gene flow from the **edge populations towards the Intermountain West**

And among the **Rocky Mountains and Eastern populations**

But its not likely that goshawks are migrating across the **Midwest from the RM.**

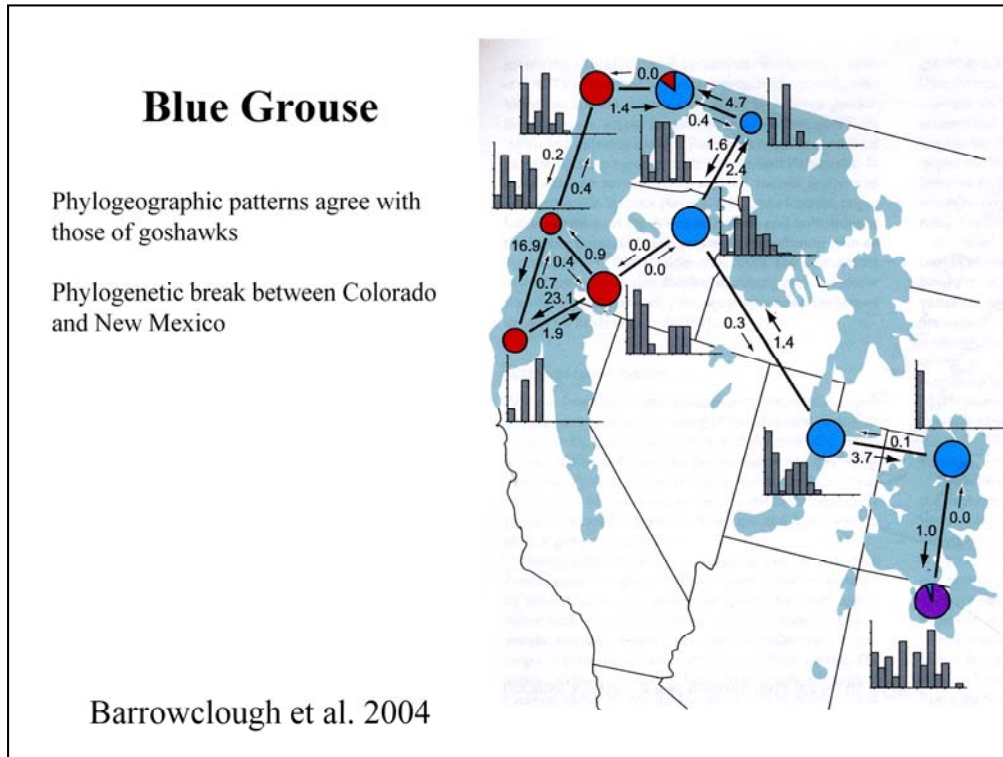
What's more likely occurring, is these populations are experiencing gene flow from a larger, more contiguous **Canadian population in the north.**



Results also agree with the geographic variation in size morphology found by Whaley and White.

AND

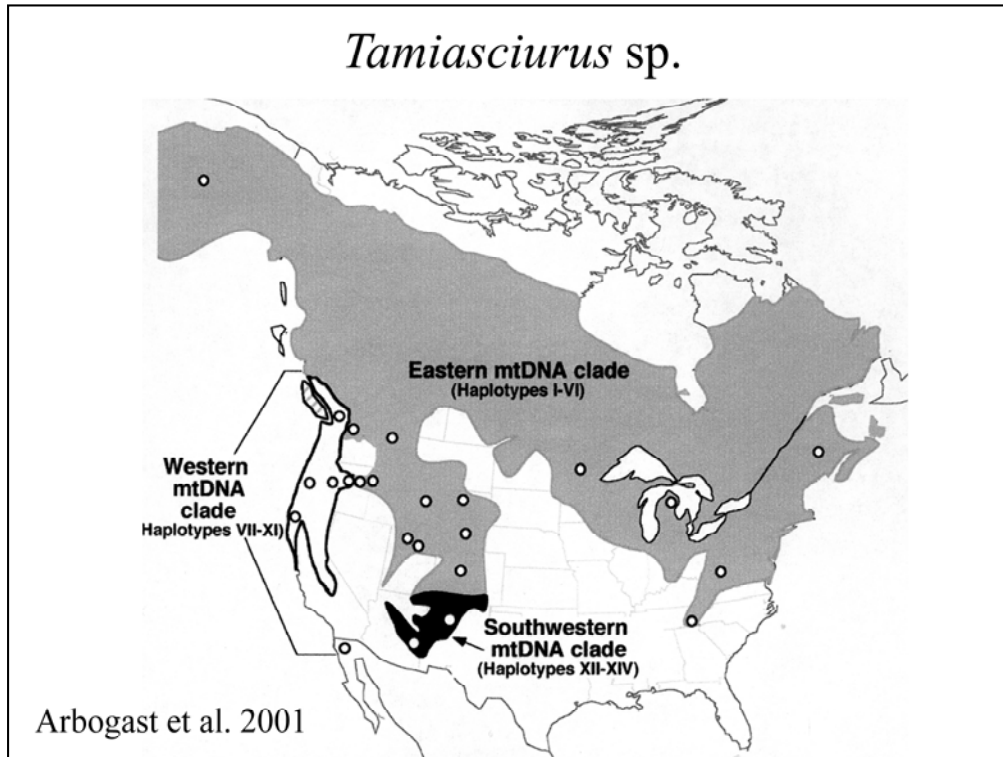
Interestingly, three of the unique haplotypes found in SE AK were descendent of the D-haplotype, pointing to postglacial gene flow into that area from Pacific Coast populations.



THE PHYLOGEOGRAPHIC PATTERNS FOUND IN THIS STUDY agree with several other studies.

Barrowclough et al. found similar patterns in the West for Blue Grouse and interestingly, they found a significant phylogenetic break between Colorado and New Mexico.

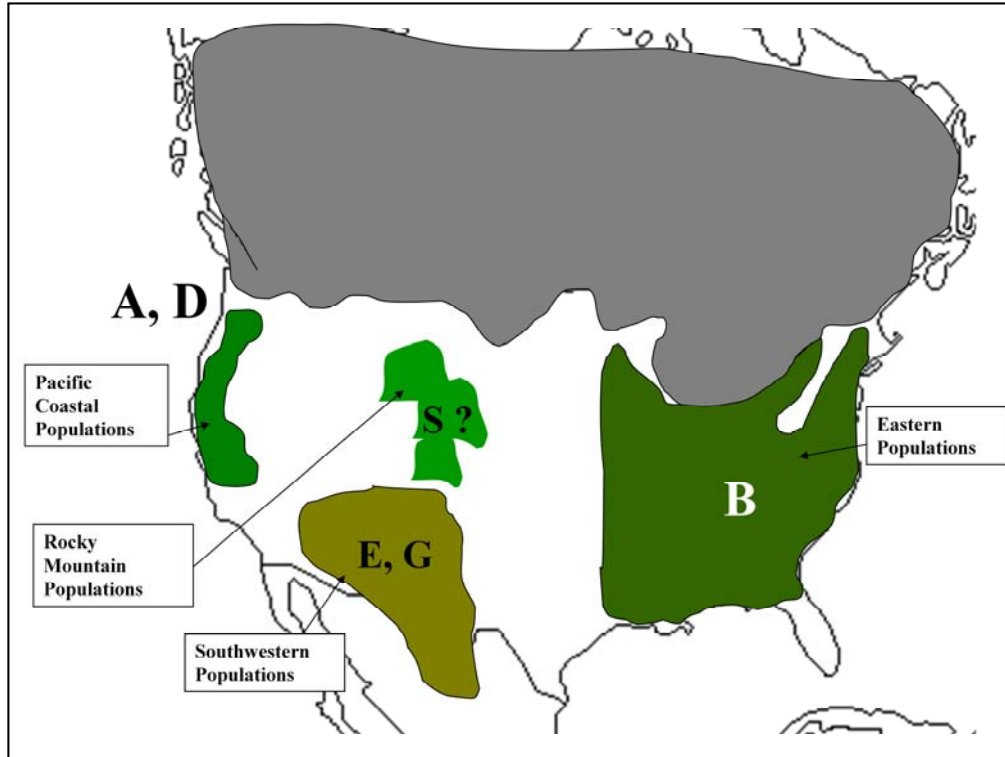
They also found a phylogenetic break among Pacific Coastal populations and Rocky Mountain populations



Arbogast et al 2001 looked at phylogeographic patterns in tree squirrels of the genus *Tamiasciurus*

They patterns they found are nearly identical to those found in my study.
 Interestingly goshawks really like to eat tree squirrels.

1. They also found the phylogeographic break between Rocky Mountain and New Mexico
2. among Pacific Coastal populations and Rocky Mountain populations
3. And a lack of genetic difference among Eastern and Rocky Mountain populations

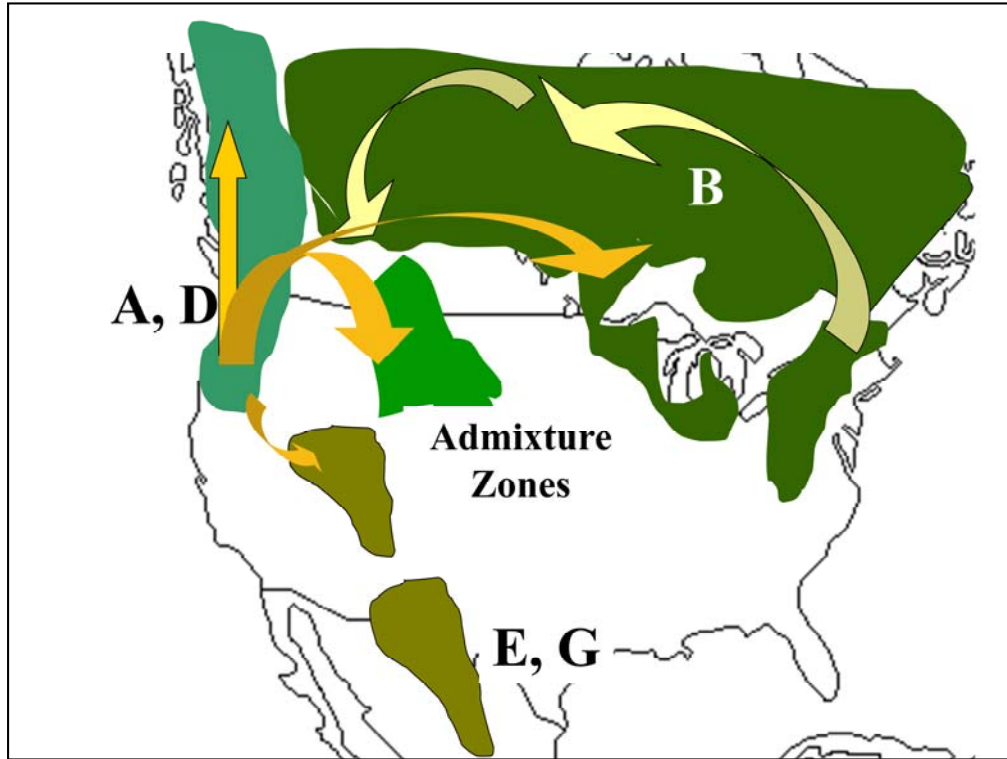


TO PUT THESE PATTERNS IN CONTEXT WITH HISTORY

We found evidence to support three historical populations, based on these major haplogroups

But we did not find strong evidence for a Rocky Mountain population.

Its possible that any signal of one was lost with post-glacial gene flow and admixture into the Intermountain West.



Following the retreat of the ice sheets, goshawk populations likely expanded in a manner such as this as they followed expanding forests into the north.

Final Thoughts

What about the Apache Goshawk?

mtDNA data support a unique population segment, which isolated from other populations.

But....more data are needed!

1. Assessment using nuclear markers, from across the geographic range.
2. Sample populations in:
 - Canada
 - Mexico
 - Oregon, Washington, New Mexico,
 - North East US (New England)

We found evidence that populations in the range of the Apache goshawks comprised a unique population segment, and are probably pretty isolated from other populations.

BUT Making subspecific designations is difficult , and in this case it requires more data!

1. **Data are needed from the nuclear genome, and I have submitted a funding proposal to complete that work over the next year**
2. **Other data needed include:**
 1. **Sampling more from the Pacific Northwest**
 2. **Sampling from the Canadian North**
 3. **Sampling from Mexico**
 4. **And the Northeast**

SAMPLES

D. Brinker
C. Ferland
J. Keane
P. Kennedy
J. Kirkley
M. Miller
S. Patla
R. Ramey
R. Reynolds
H. Snyder
R. Skorkowsky
A. Smith
C. Stabb
K. Titus
J. Warder
B. Woodbridge
J. Woodford

Graduate Committee

Mike F. Antolin, Biology, CSU Kenneth P. Burnham, FWCB, CSU
Richard T. Reynolds, RMRS USDA-FS Marlis R. Douglas, FWCB, CSU

Antolin Lab

Technical Assistance
Dan Tripp, Lisa Savage, Reesa
Conrey, Elizabeth Harp, Amariah
Anderson, Heather Franklin

Undergraduate lab assistants

Alison Campbell
John Michael Drewy

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Reynolds Lab

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Thanks !!!!

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