Geographic scales of population structure in boreal marine fishes and the influence of ice-age demography

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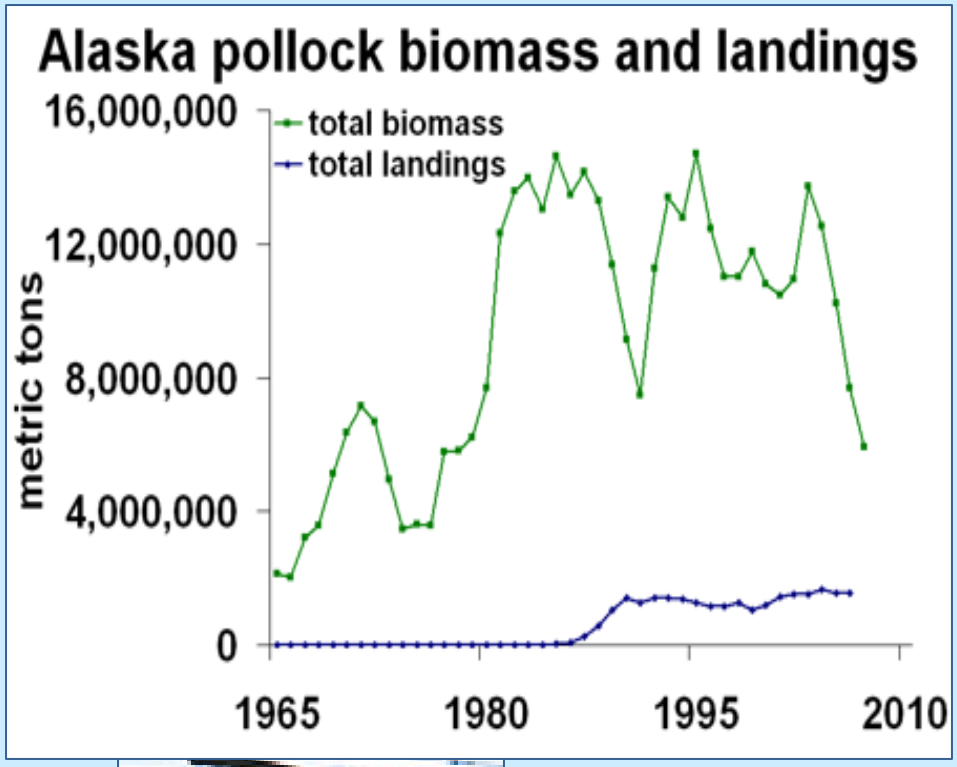
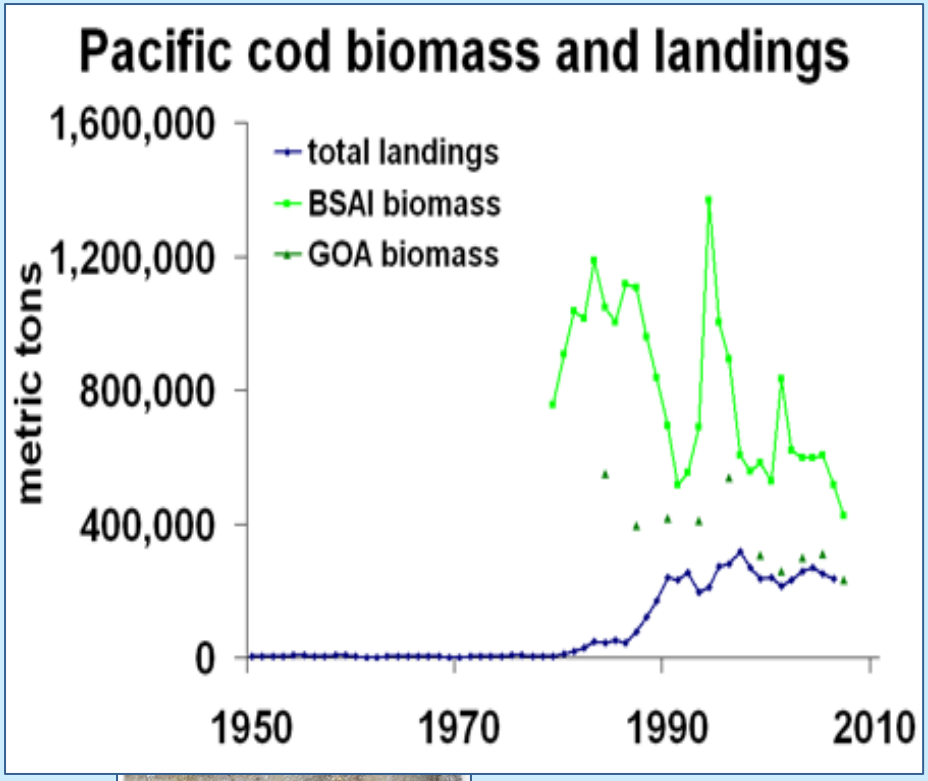
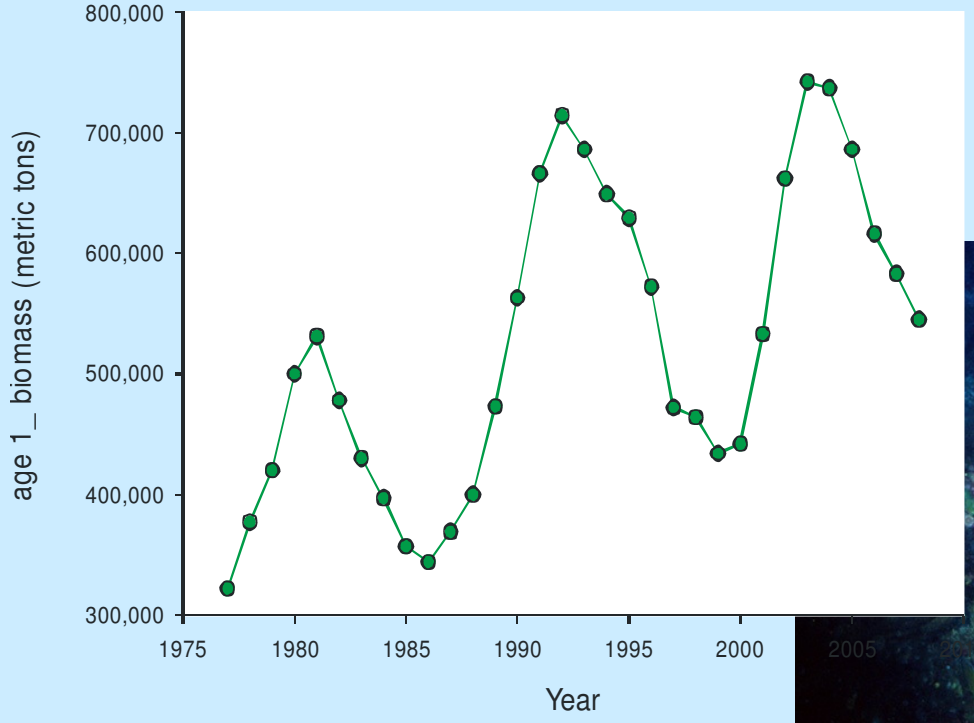
Decadal variability





(NOAA)

Atka mackerel



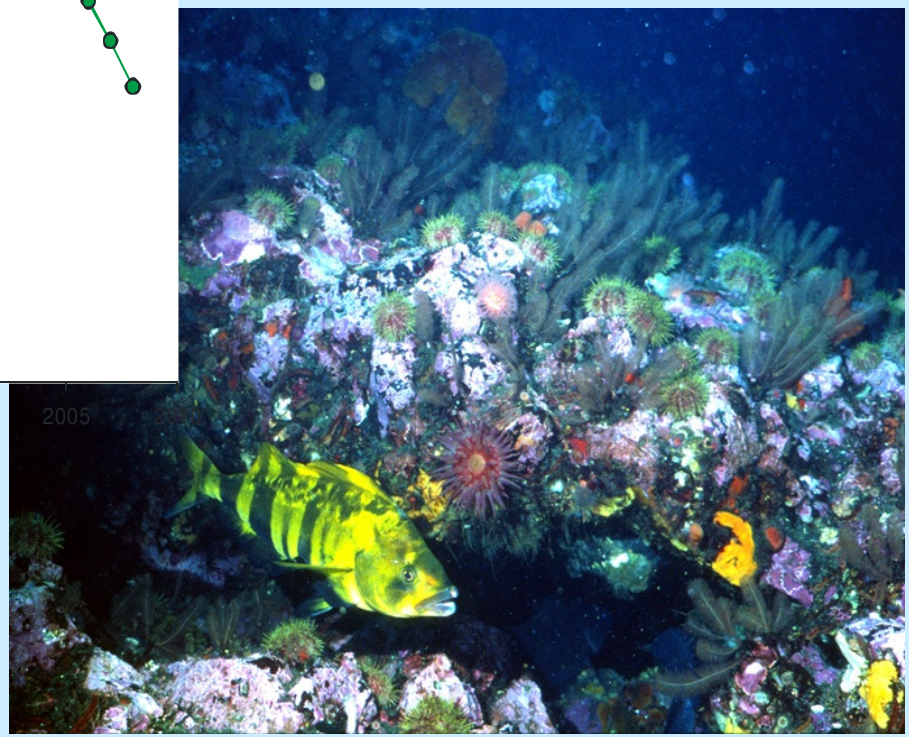
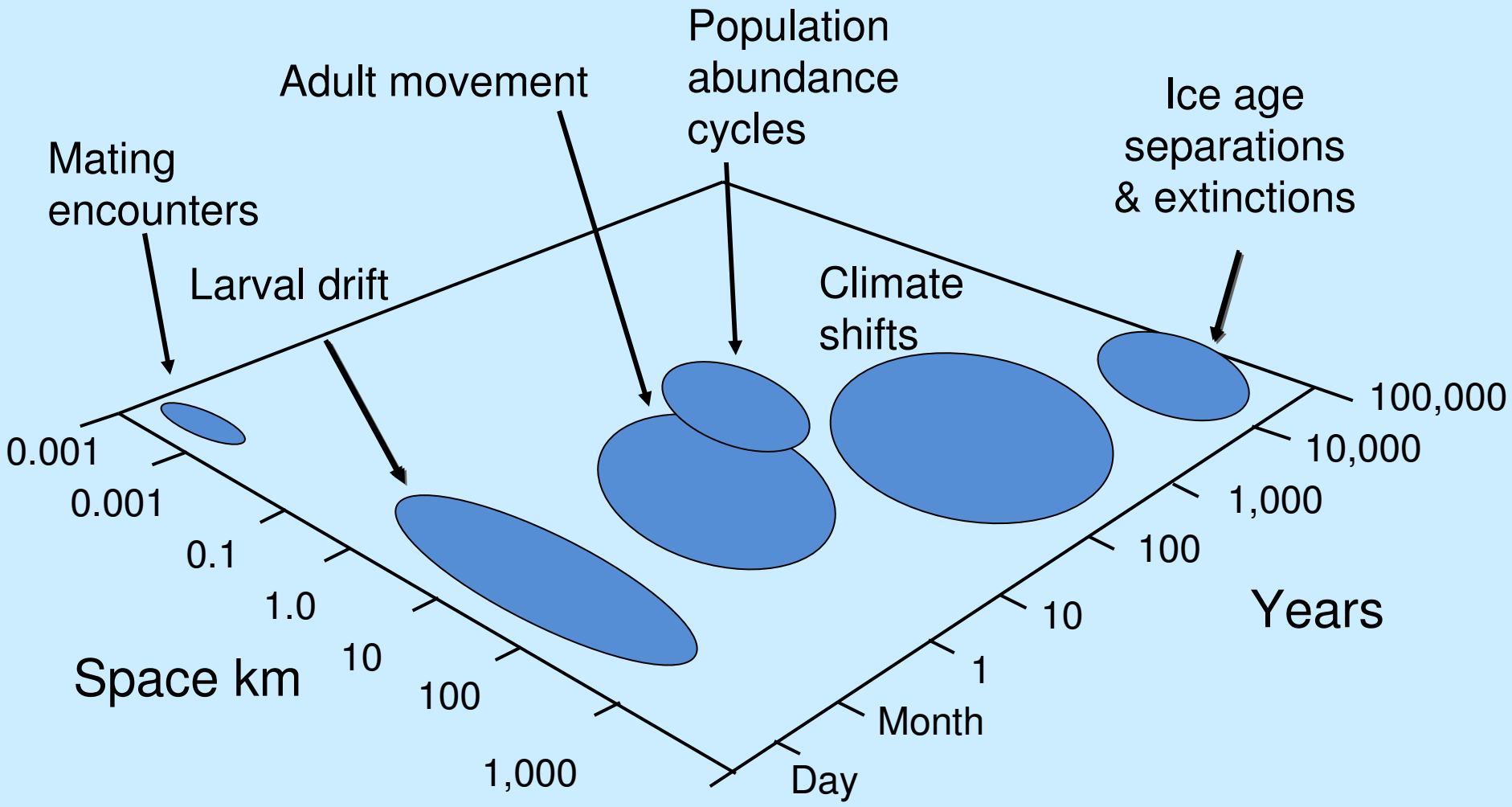


photo courtesy Bob Lauth

Sources of Genetic Population Structure



Ice-age Temperatures

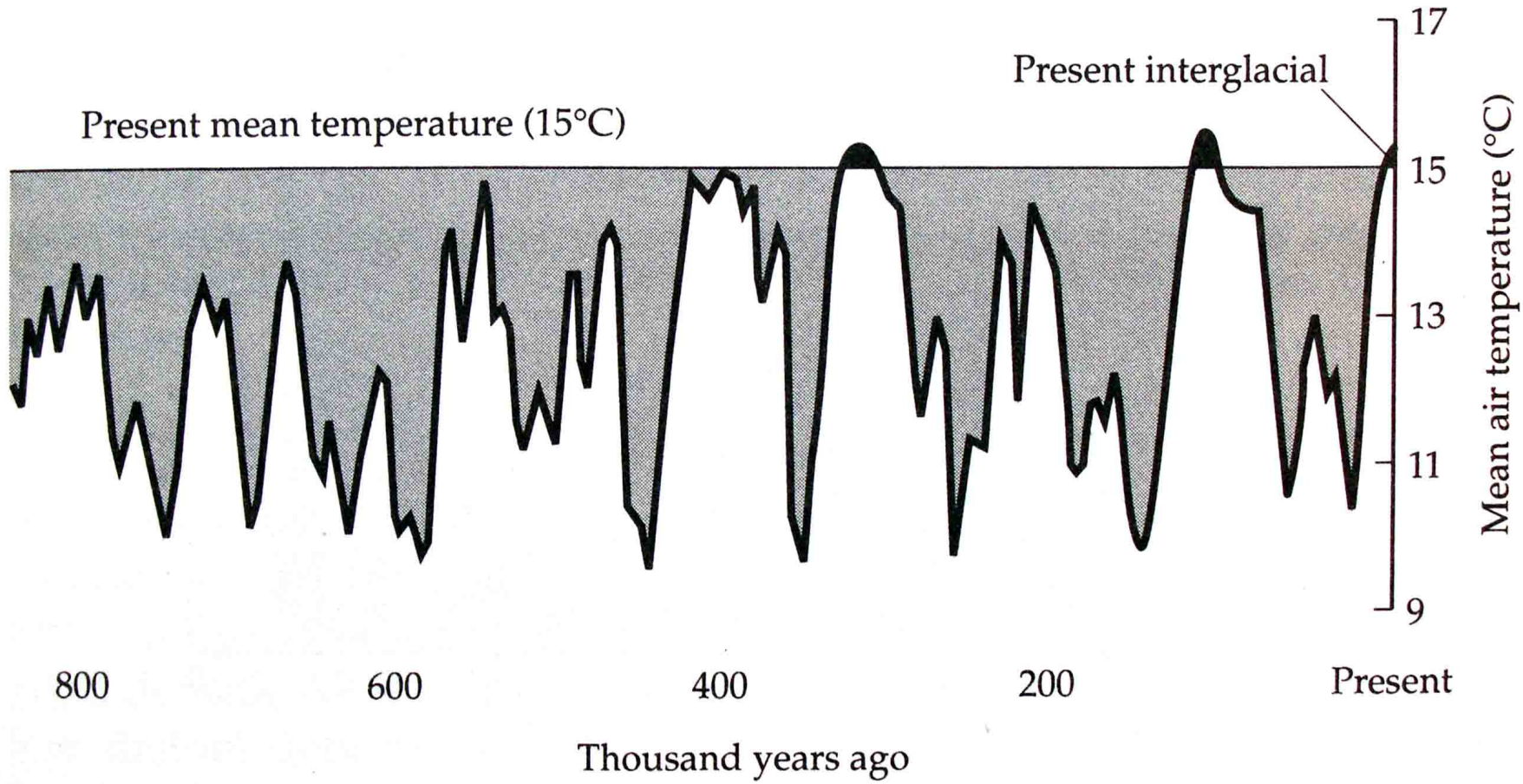
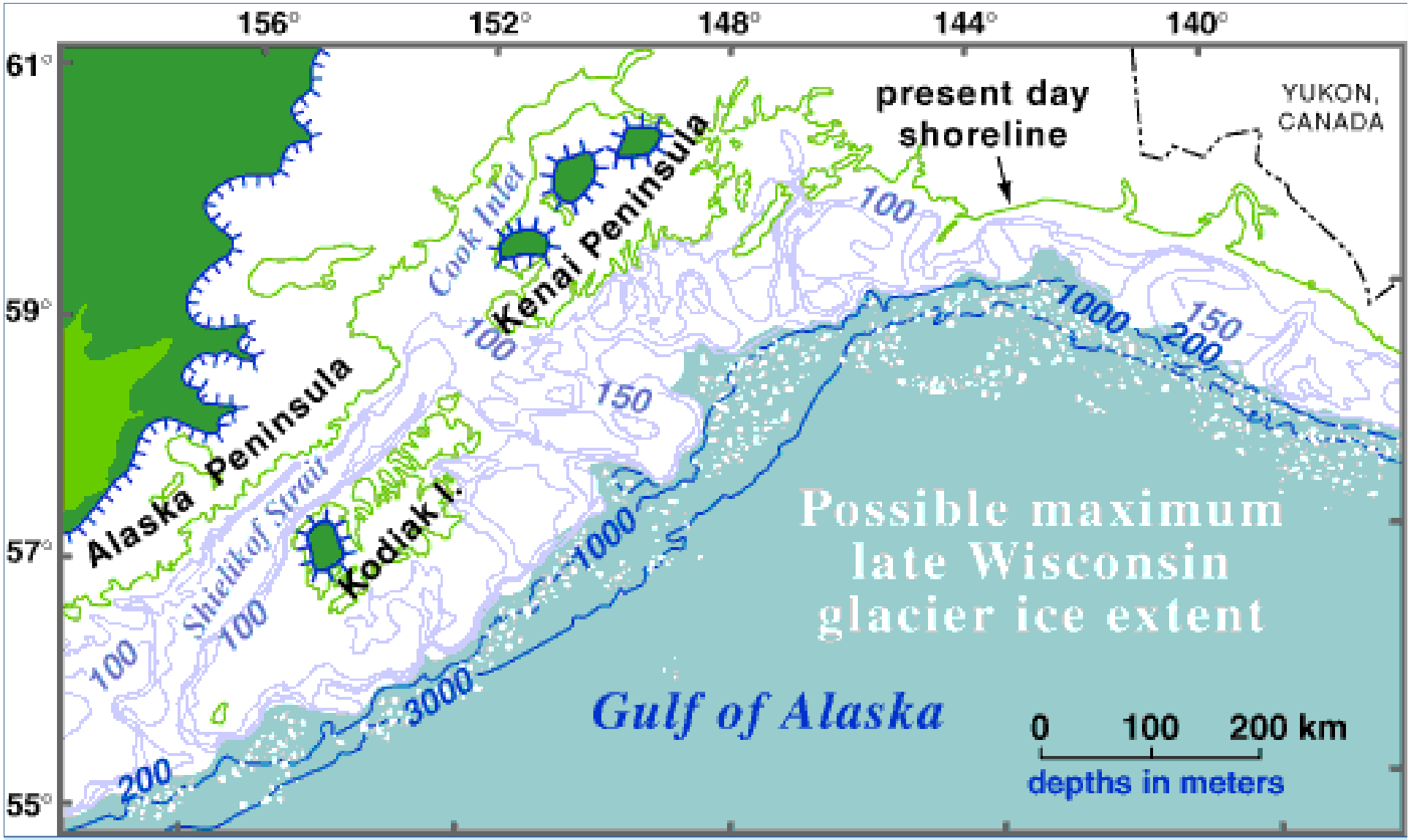


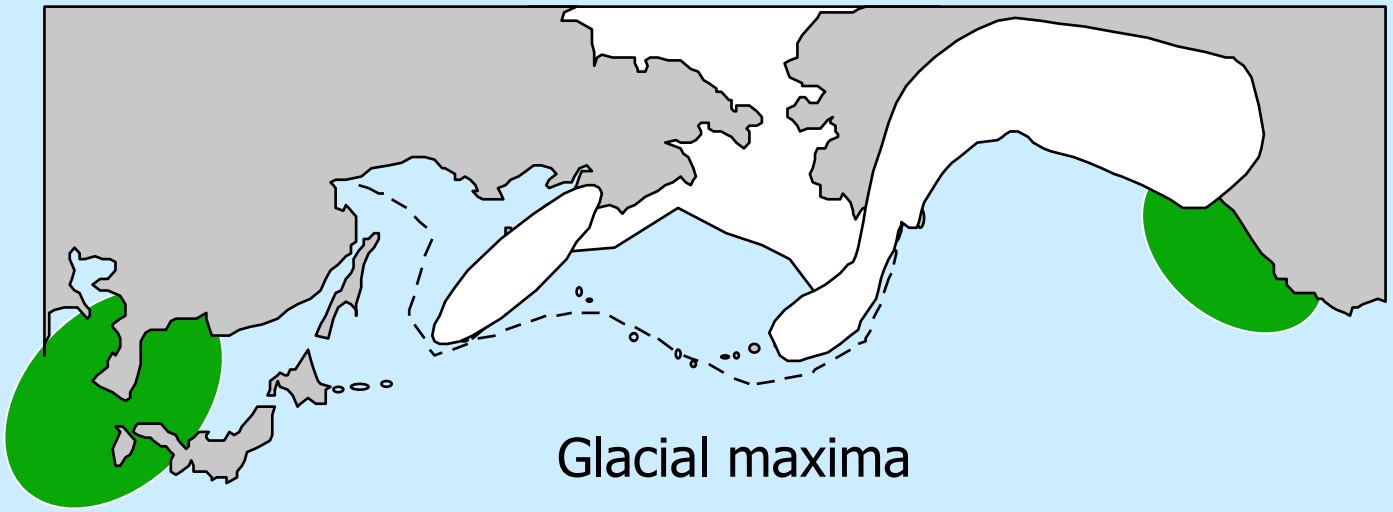
FIGURE 5 Temperature of the Earth for the last 850,000 years as inferred from ice volume derived by oxygen isotope measurements from ice cores.



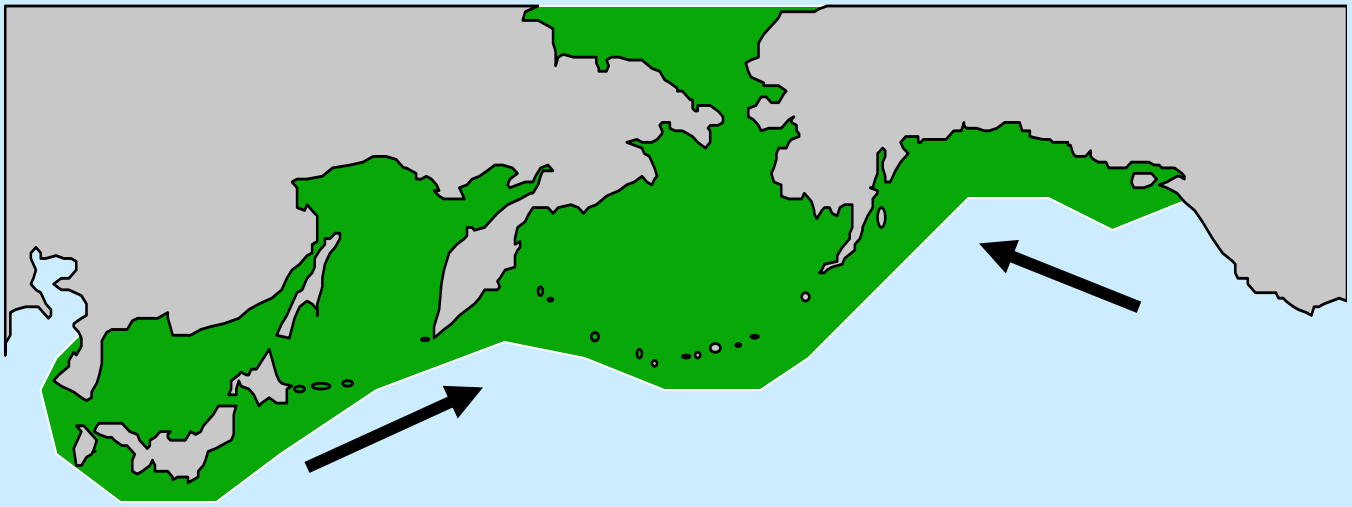
USGS

- Decrease in plankton productivity
- Elimination of near-shore nursery areas

Refuge-hybrid zone model



Glacial maxima



Pacific cod (*Gadus macrocephalus*)

Life history characteristics

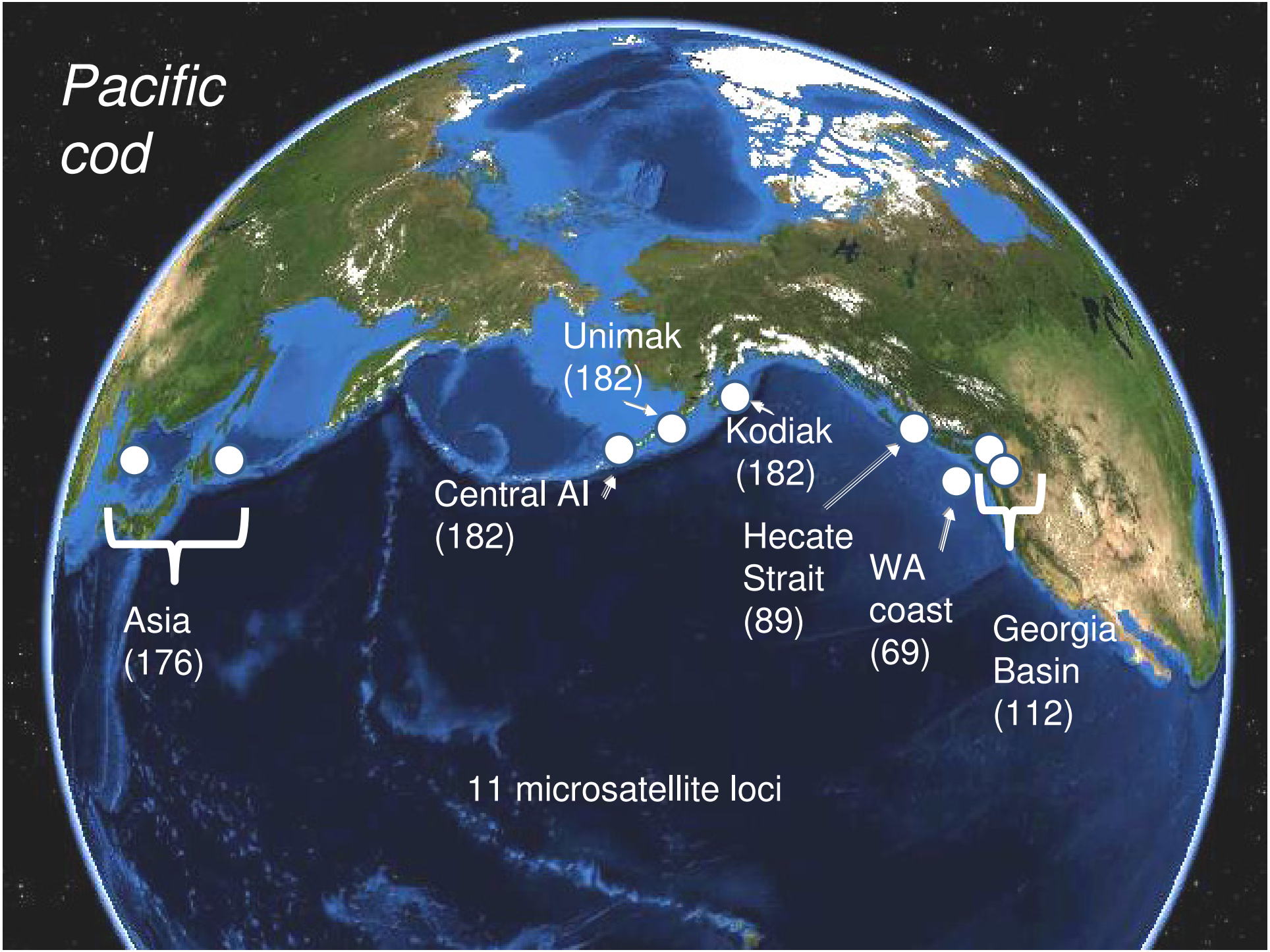
- Transoceanic
- Temperate/subpolar
- Demersal shelf/slope
- Lifespan ~ 18 y
- Age @ 50% maturity ~ 5y
- Highly fecund, demersal eggs, fast growing
- Seasonal migration

Genetic studies in North America

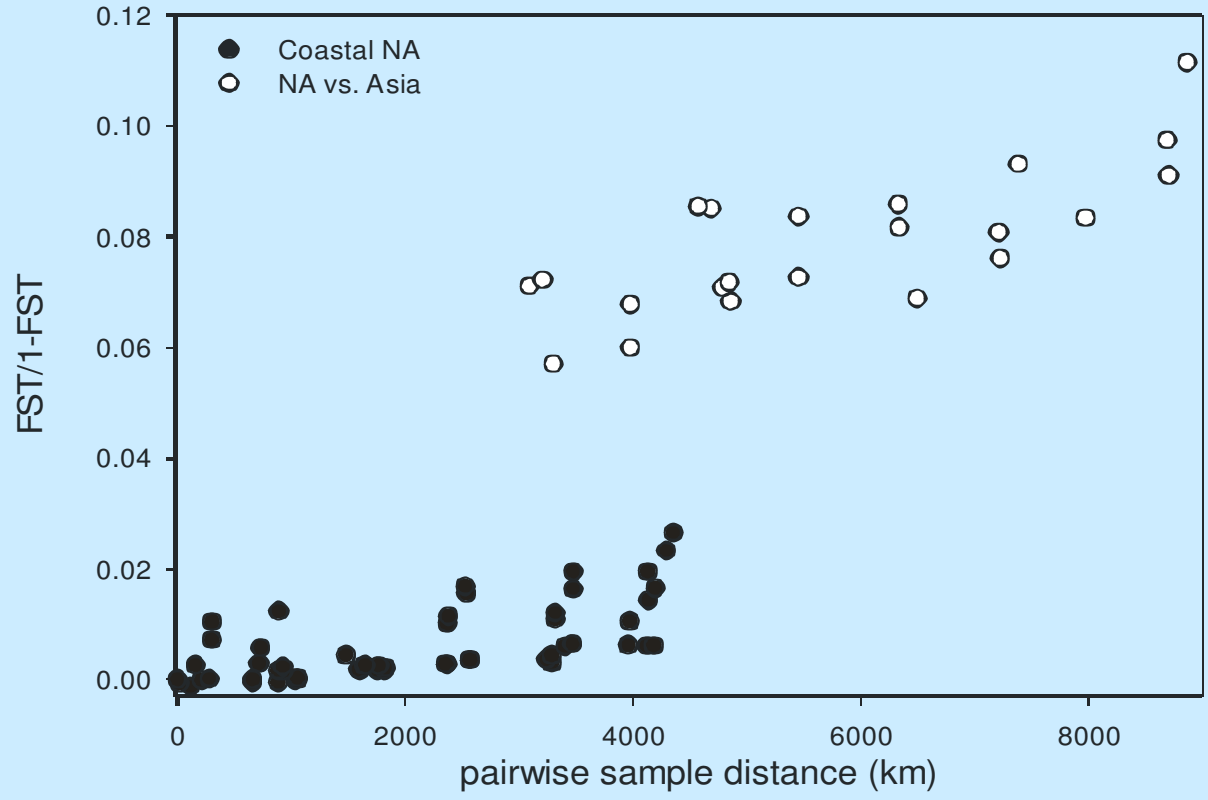
Grant et al. 1987 – allozymes

- Two stocks - NA and Asia

source:http://seattletimes.nwsource.com/art/pacificnw/2004/0502/taste01.jpg

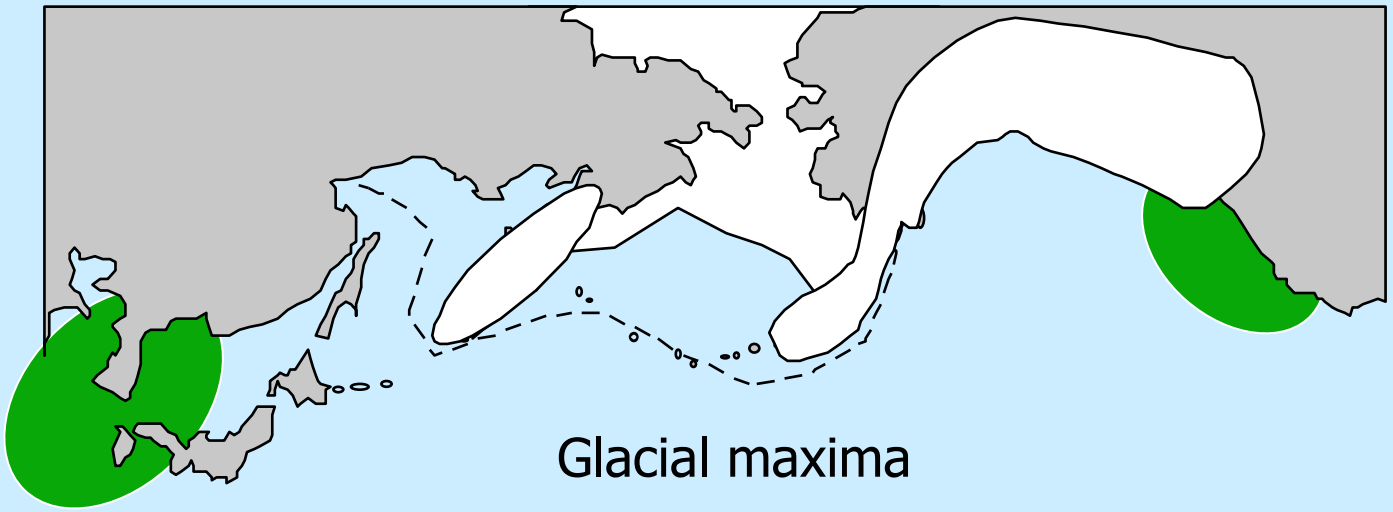

Pacific cod
Unimak (182)
Kodiak (182)
Central AI (182)
Hecate Strait (89)
WA coast (69)
Georgia Basin (112)
Asia (176)
11 microsatellite loci

Pacific cod – global isolation by distance

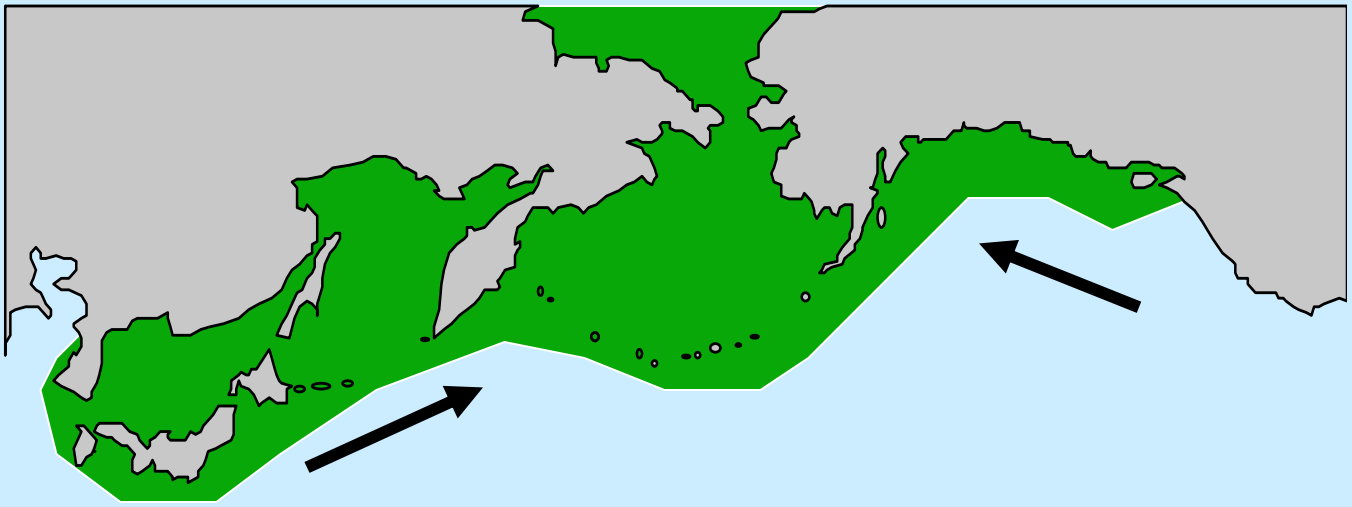


Canino et al. in prep

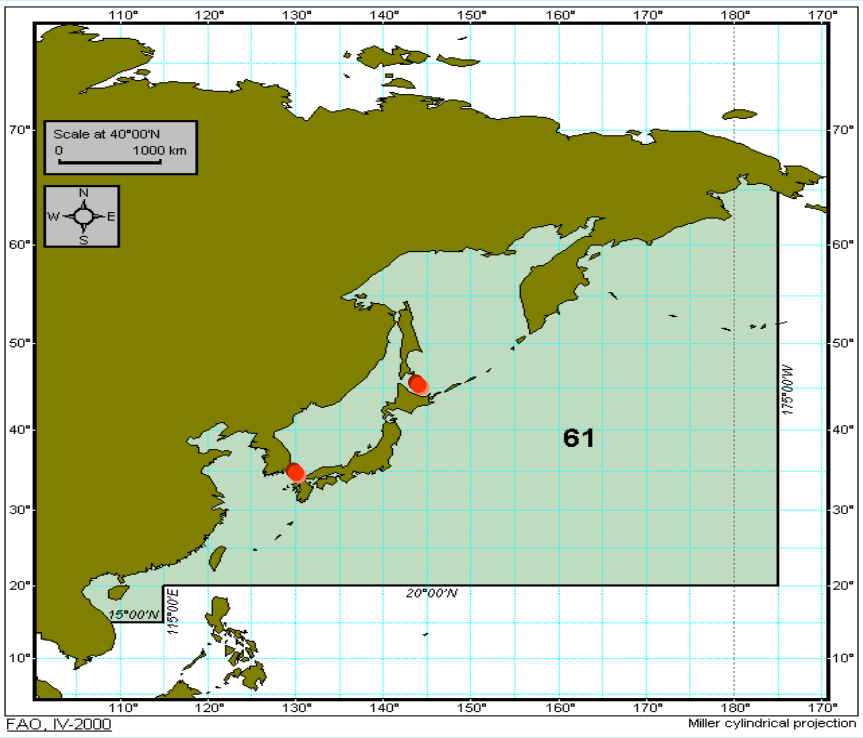
Refuge-hybrid zone model

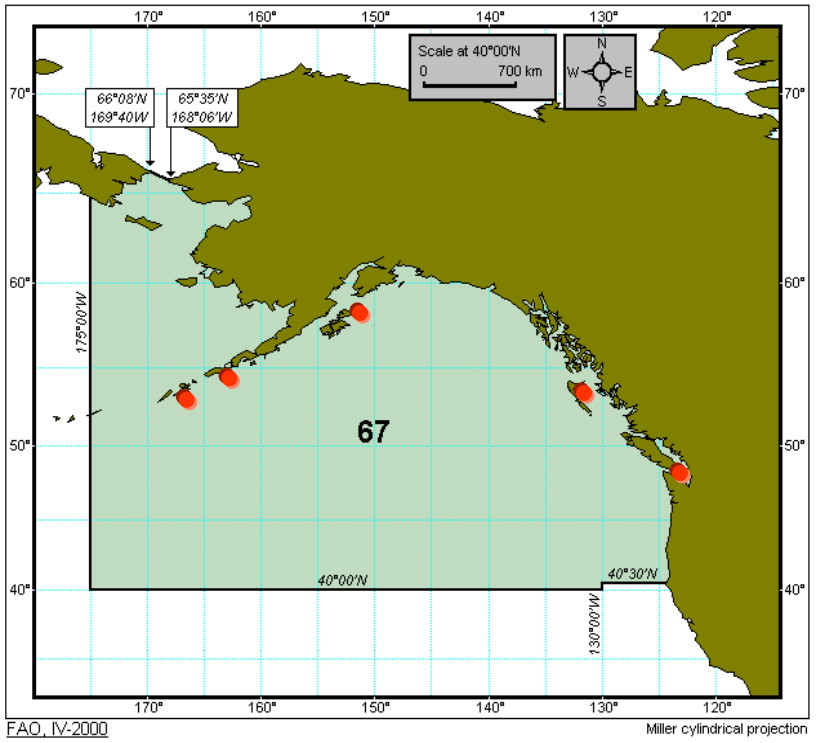


Glacial maxima



NAO Statistical Areas

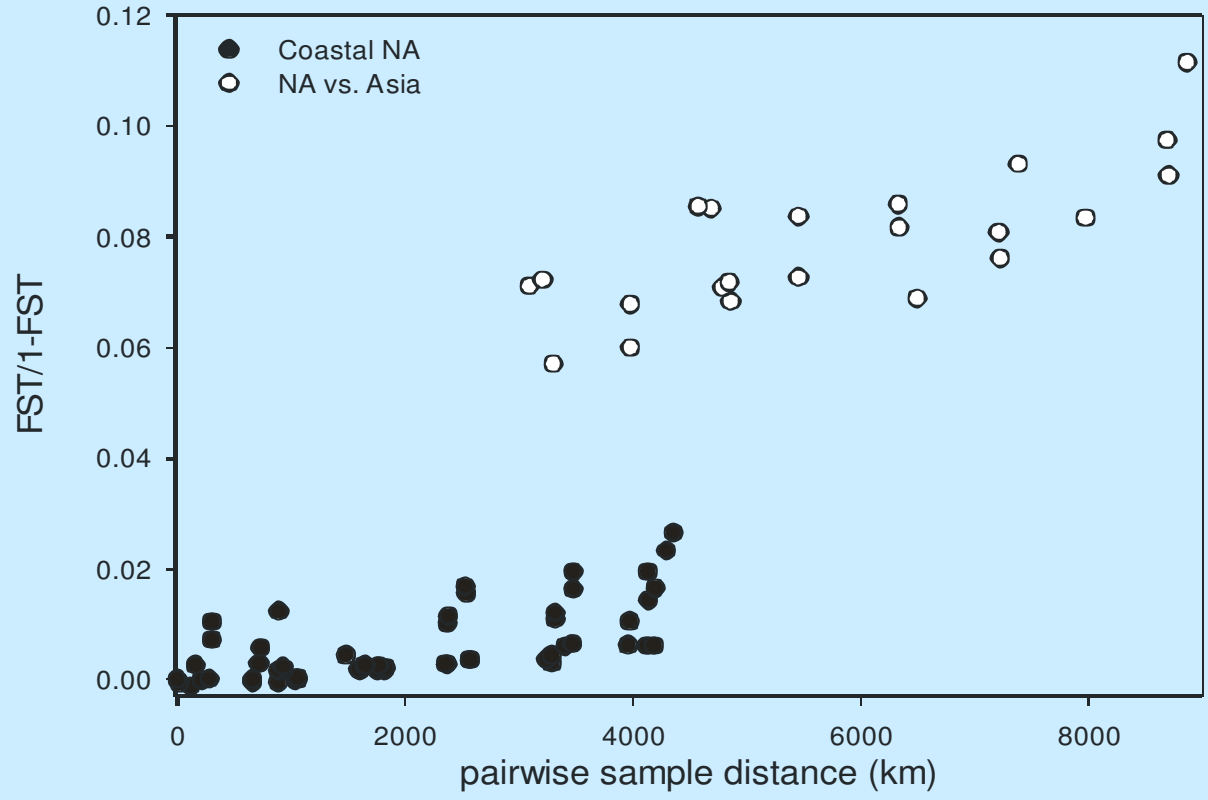




Assignment tests - microsatellites

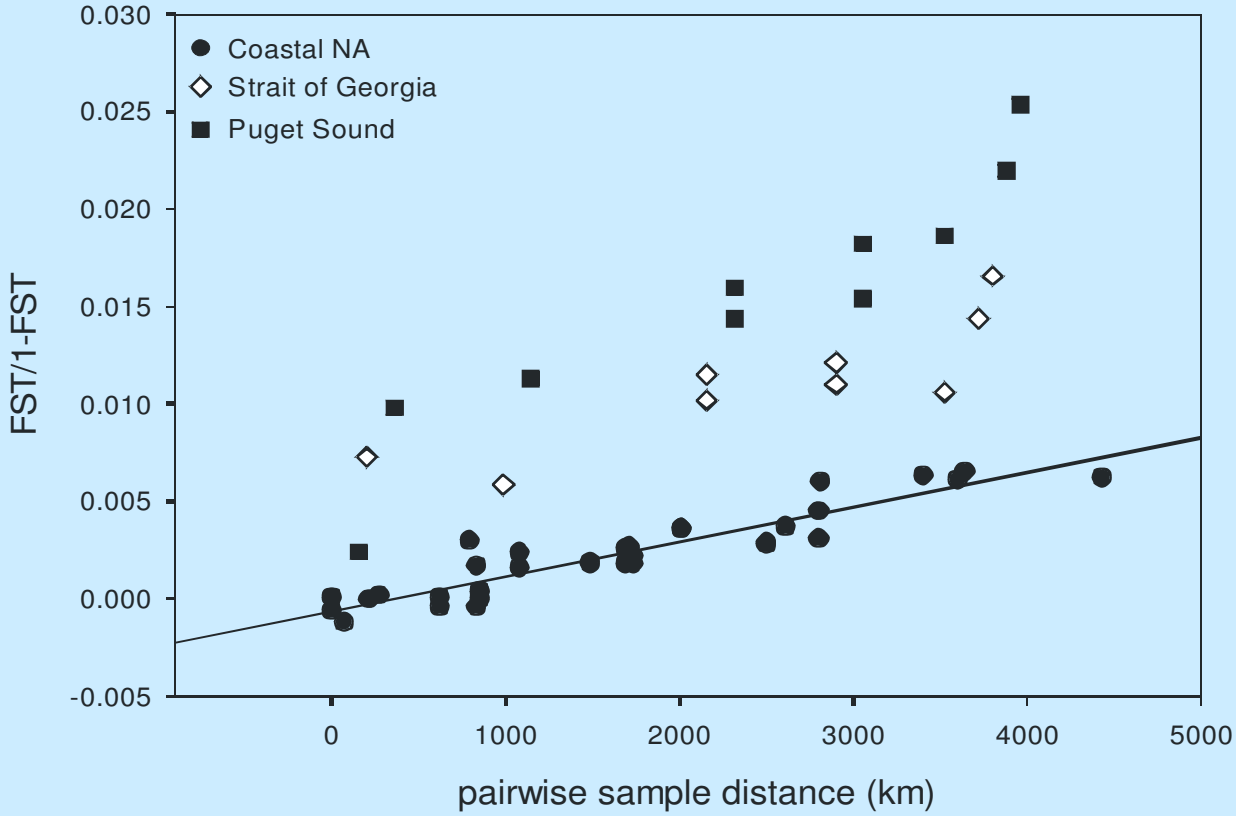
- Asian samples – 100% correct assignment to Asia, correct to KO or JPN ~ 97%
- North America – 99.3% correct self assignment

Pacific cod – global isolation by distance

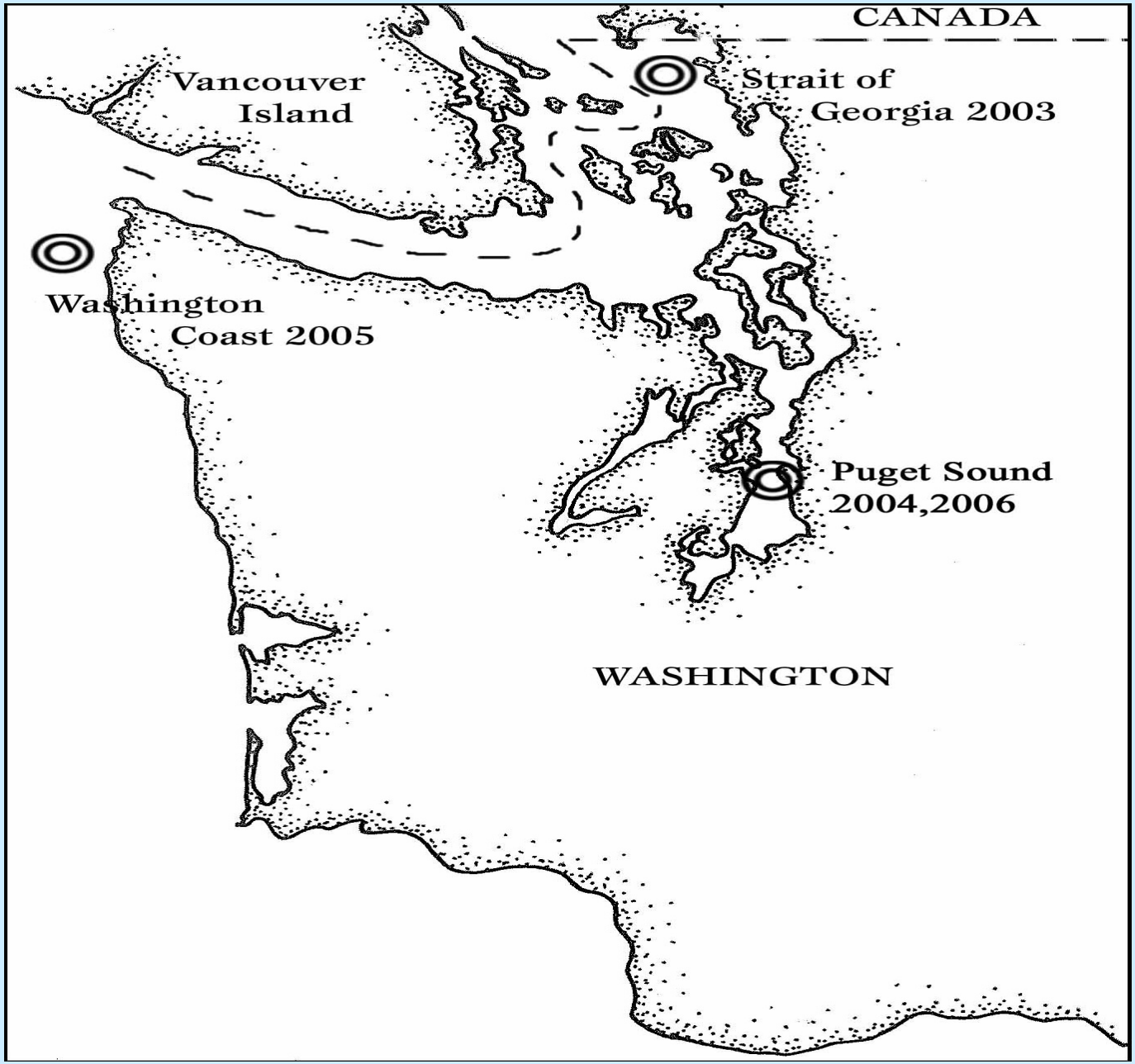


Canino et al. in prep

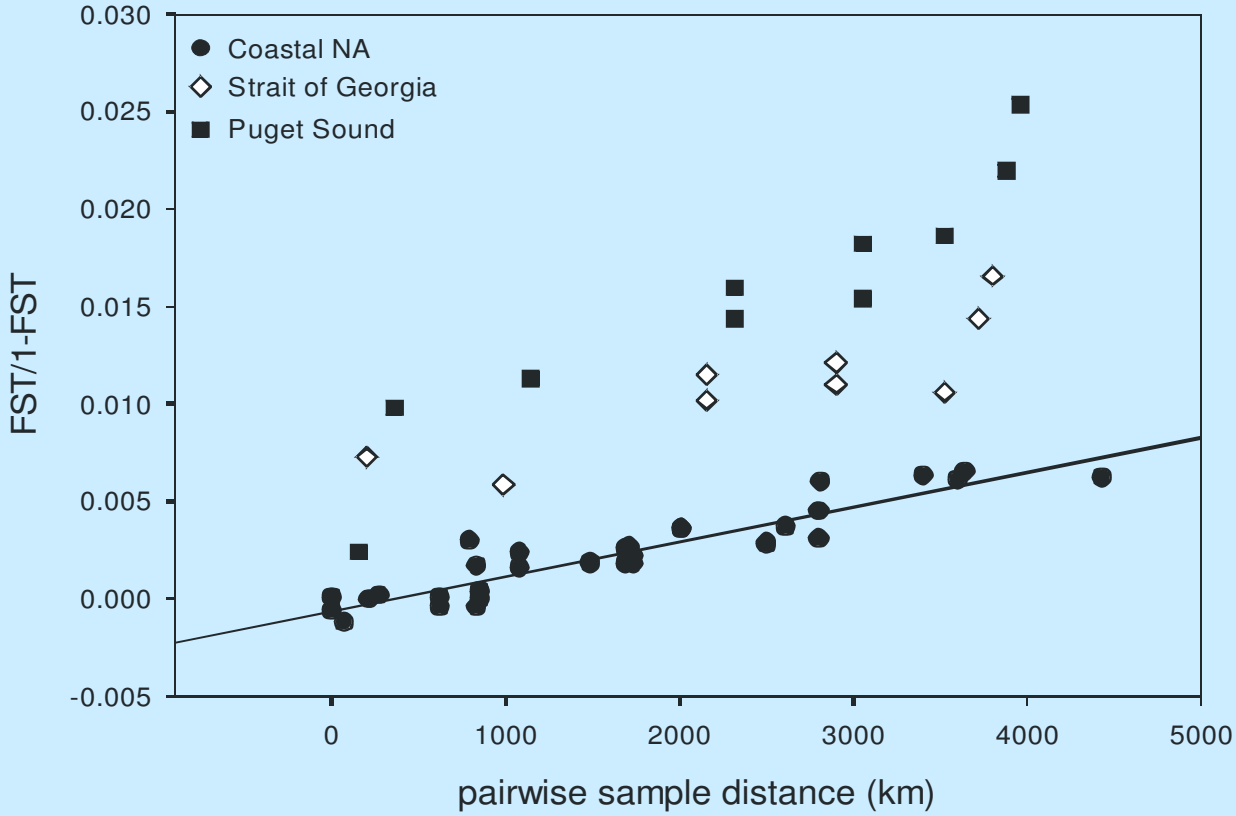
Pacific cod – isolation by distance in North America



Cunningham et al. 2009


CANADA
Vancouver
Island
Strait of
Georgia 2003
Washington
Coast 2005
Puget Sound
2004,2006
WASHINGTON

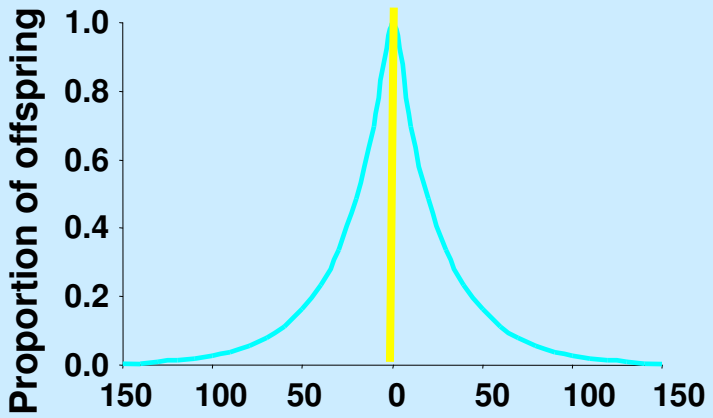
Pacific cod – isolation by distance in North America



Cunningham et al. 2009

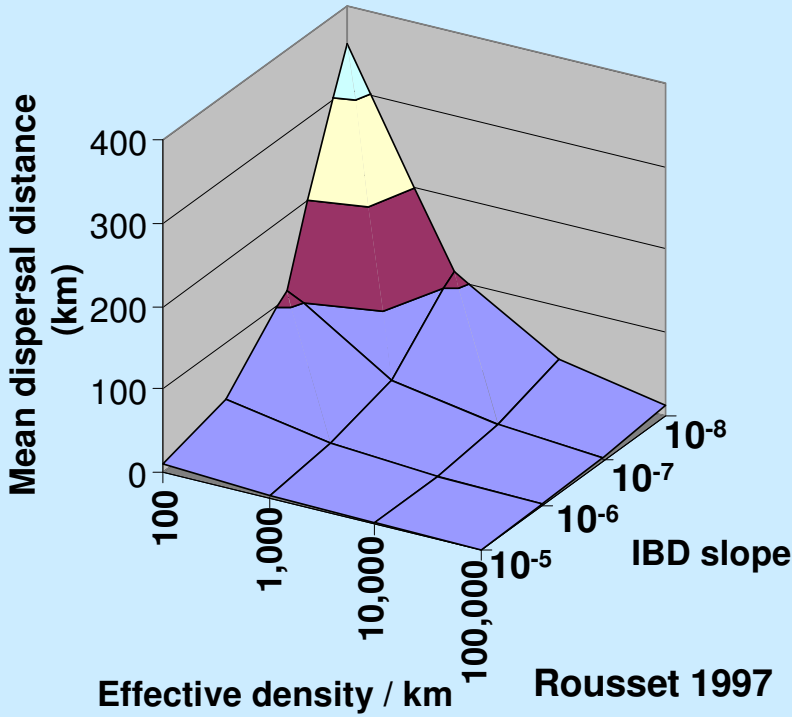
Estimation of mean dispersal distances

- Assumptions
  - Exponential dispersal curve
  - Genetic equilibrium
  - All locations have same dispersal
- Depends on population density



- Pacific cod
  - Effective density
    - Stock assessment
    - $N_e/N=10^{-3}$
    - N_e range 10 – 10^5 individuals / km

- mean dispersal distance – 26 km



Cunningham et al. 2009

Pacific cod – microsatellites

North America

- evidence for discrete fjord stocks
- monotonic isolation-by-distance pattern along contiguous shoreline indicates limited effective dispersal

Ocean basin scales

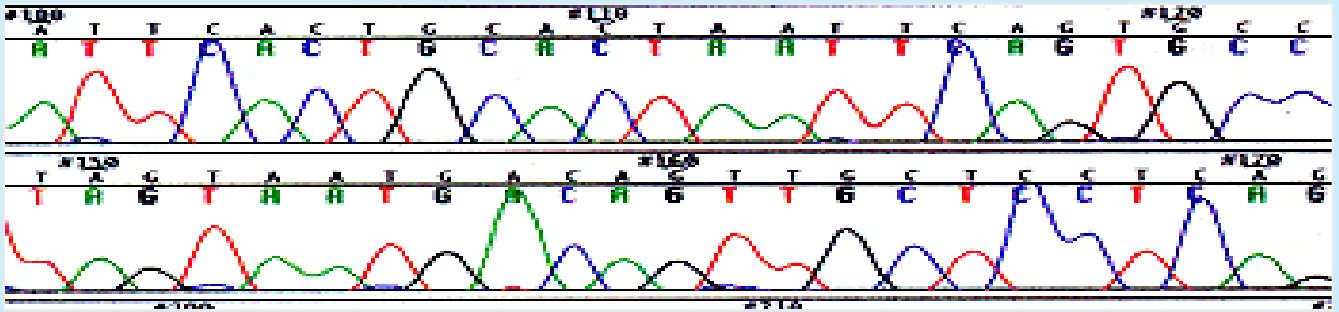
- large genetic divergence between Asian and N American populations resulting from isolation during ice-age glaciation and lack of effective trans-Pacific gene flow following secondary contact

Other species with signatures of ice-age vicariance

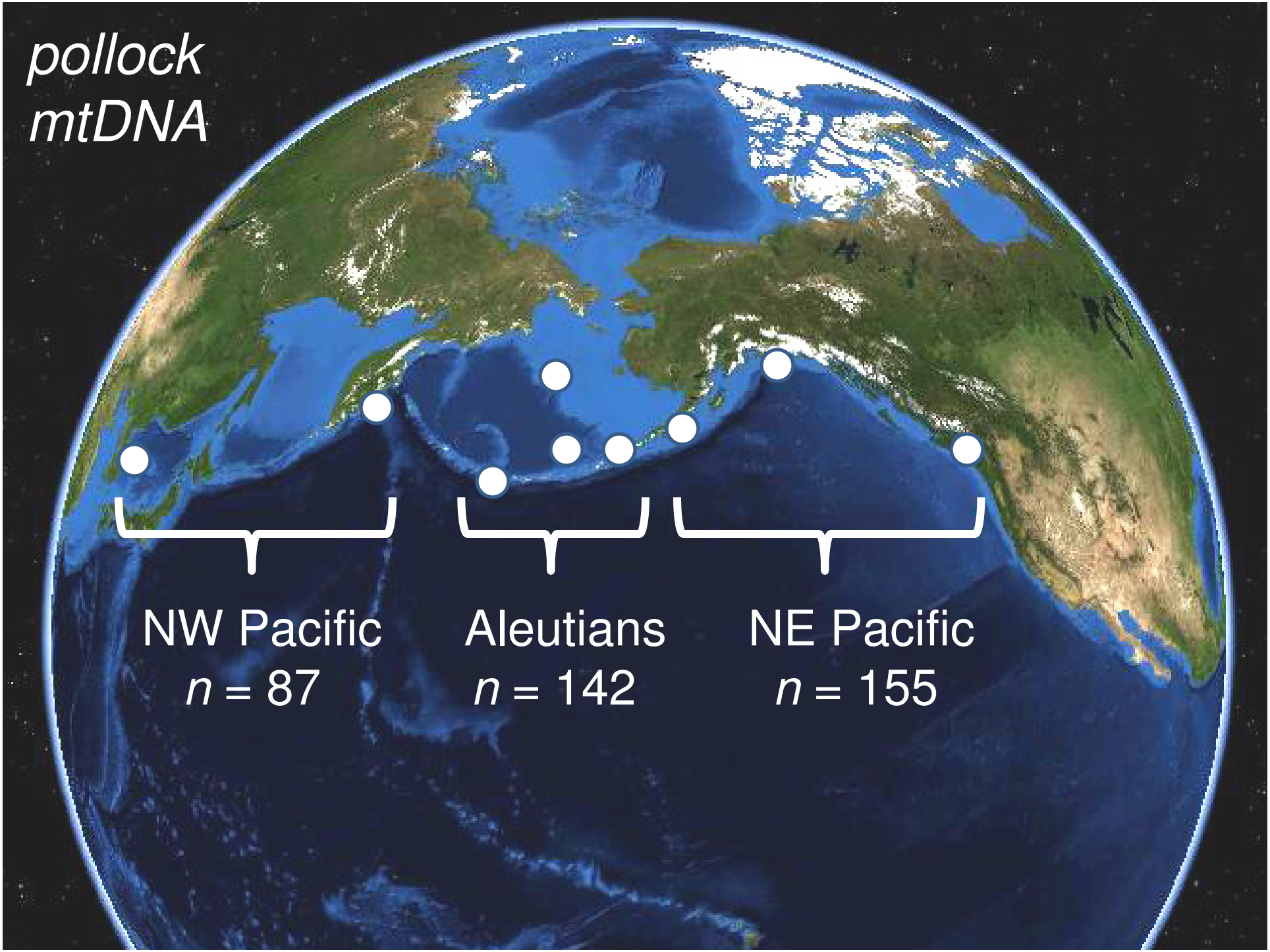
- yellowfin sole - Grant et al. 1983
- Pacific herring - Grant & Utter 1984
- walleye pollock – Grant et al. 2006

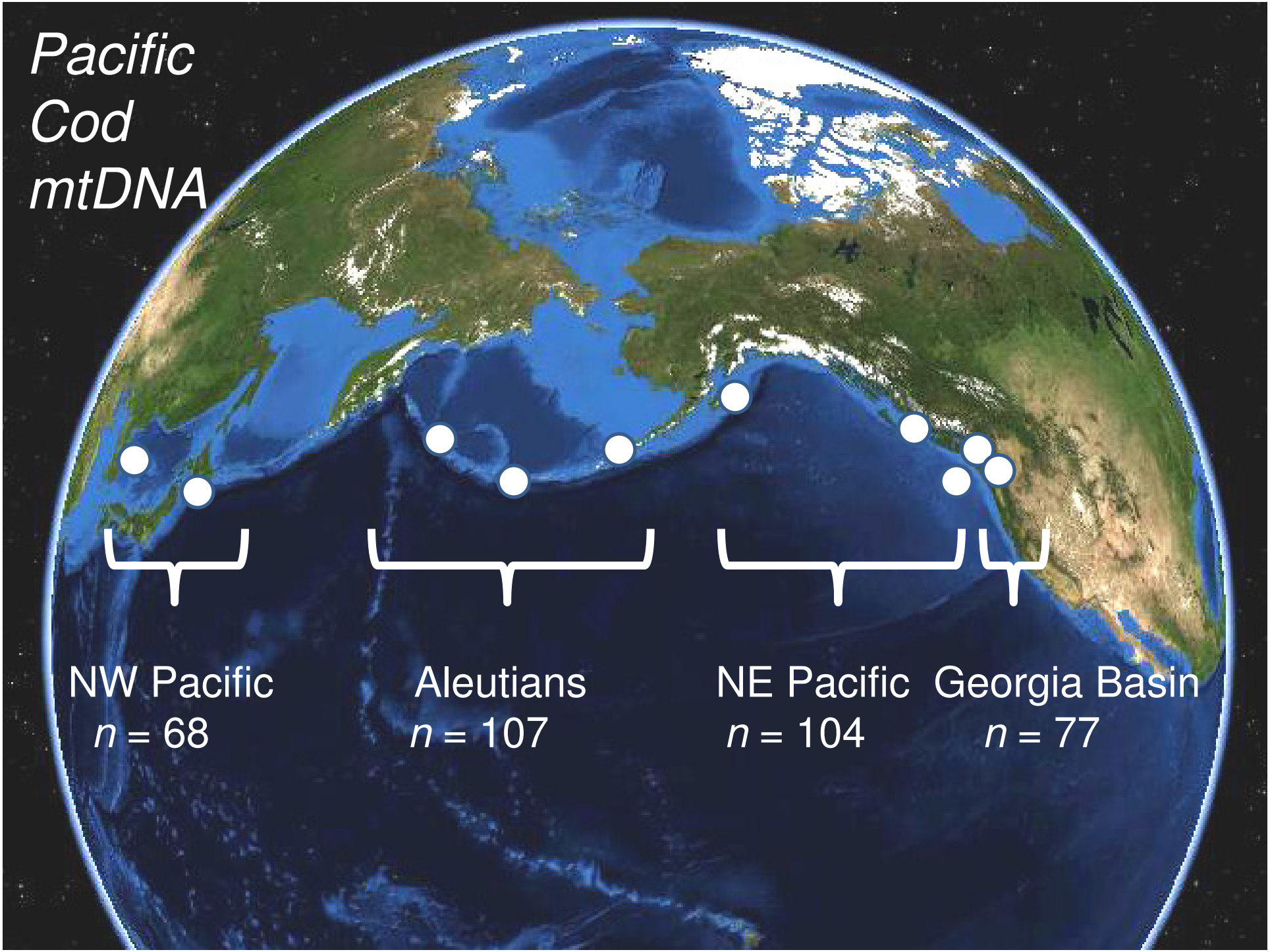
Another climatic effect - expansion

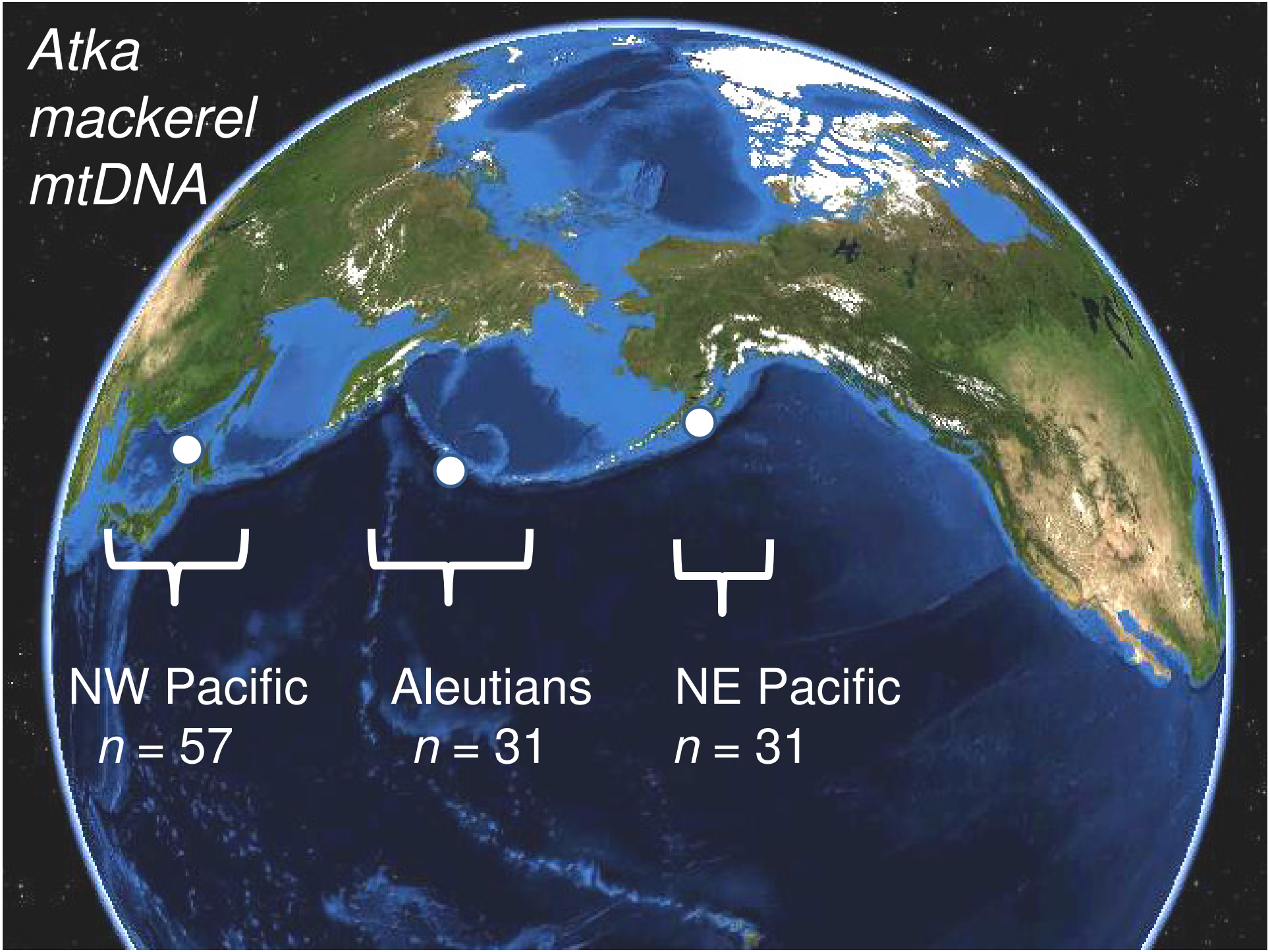
mitochondrial DNA sequences

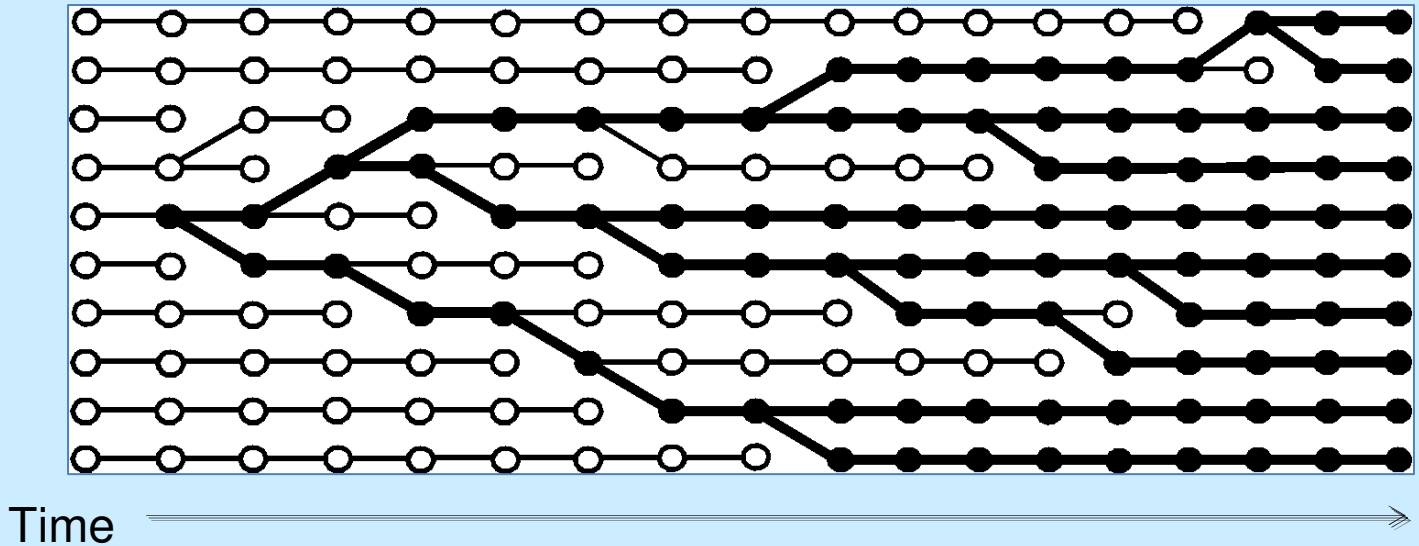


- pollock – cytochrome oxidase I - 630 bp
- Pacific cod - ND2+Cytb - 1510 bp
- Atka mackerel - Dloop - 648 bp

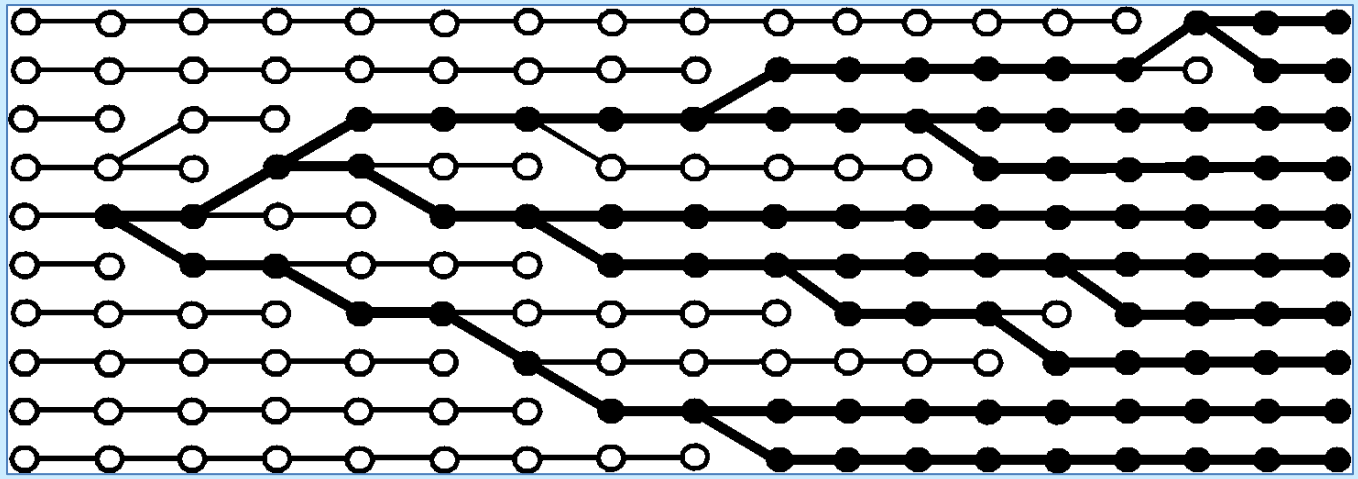

pollock
mtDNA
NW Pacific
n = 87
Aleutians
n = 142
NE Pacific
n = 155


Pacific
Cod
mtDNA
NW Pacific
n = 68
Aleutians
n = 107
NE Pacific
n = 104
Georgia Basin
n = 77

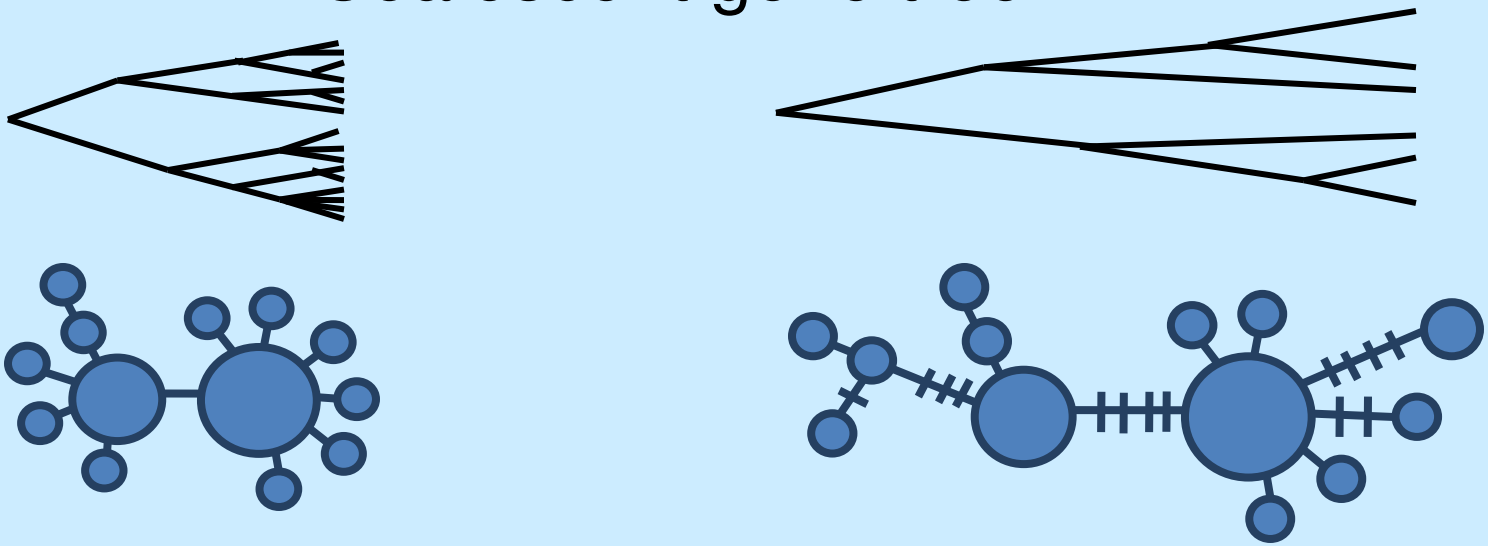

Atka mackerel mtDNA
NW Pacific
n = 57
Aleutians
n = 31
NE Pacific
n = 31



Coalescent gene tree

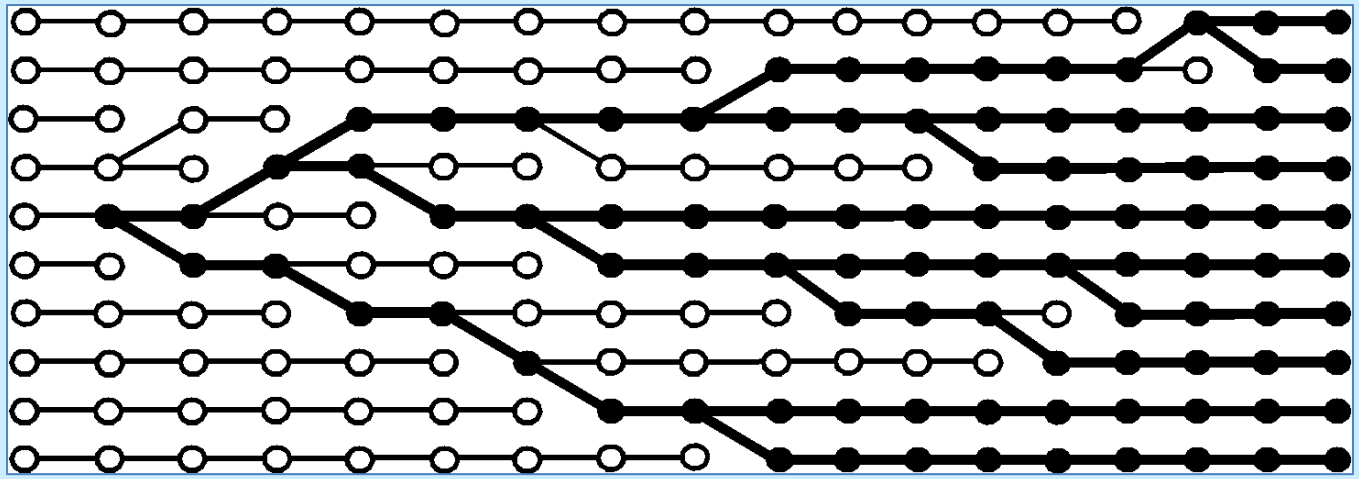


Coalescent gene tree

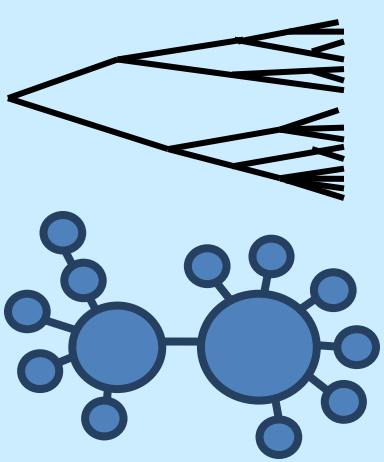


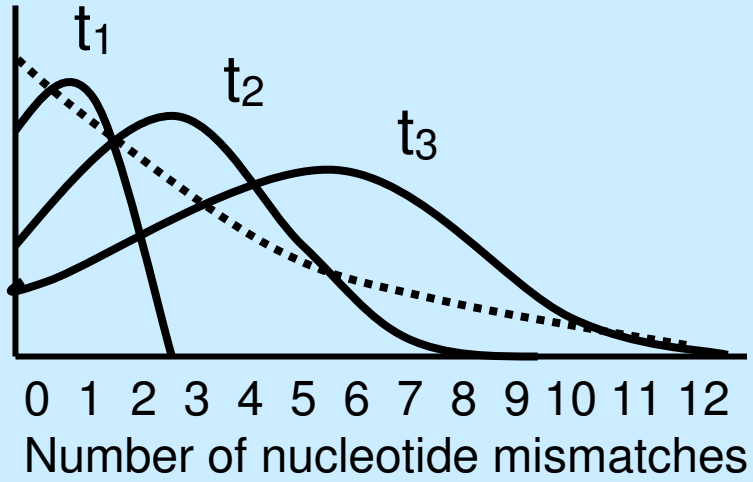
Expanding N_e

Constant N_e



Time

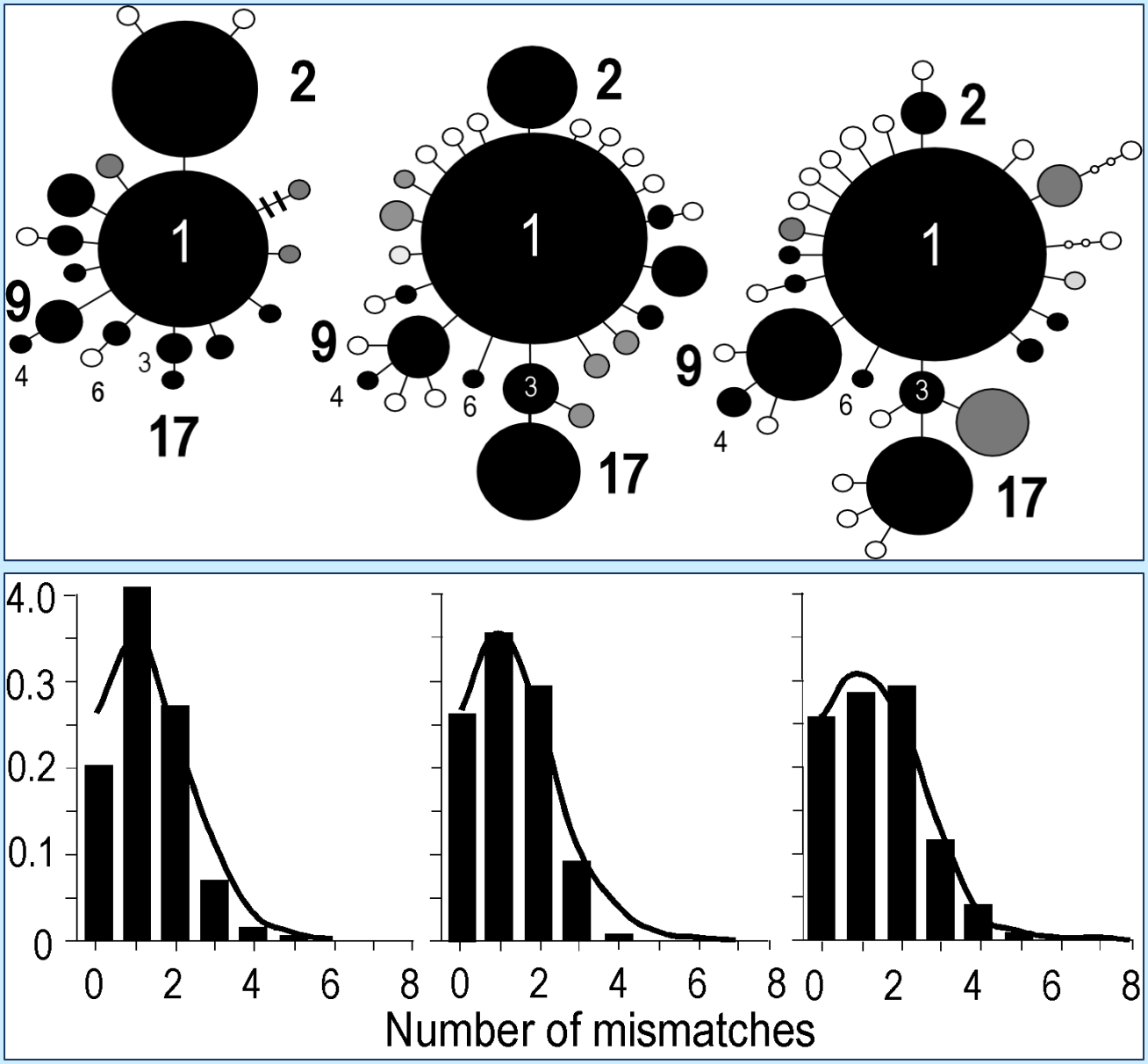




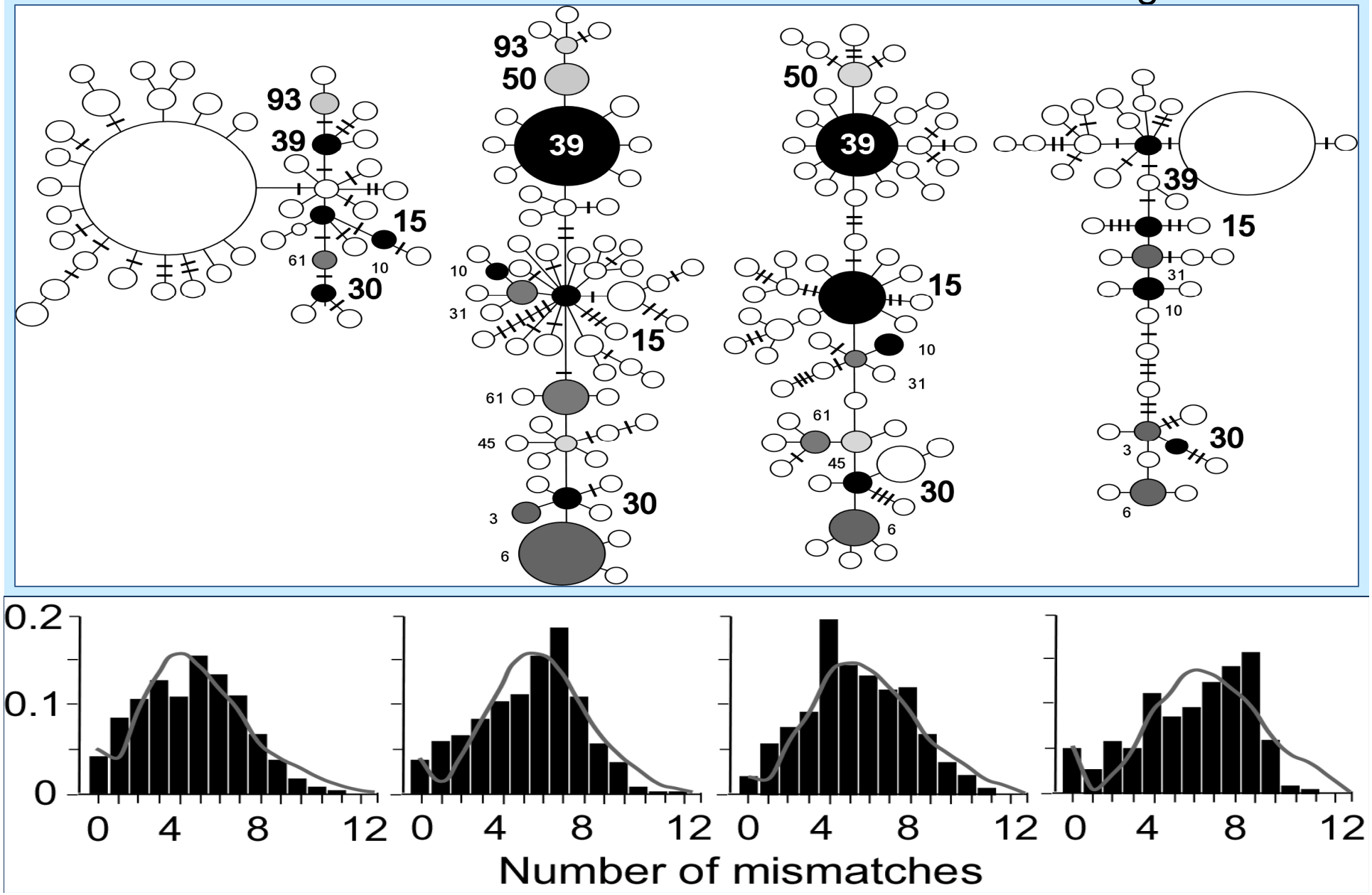
Expanding populations create waves in the mismatch distribution

Pollock

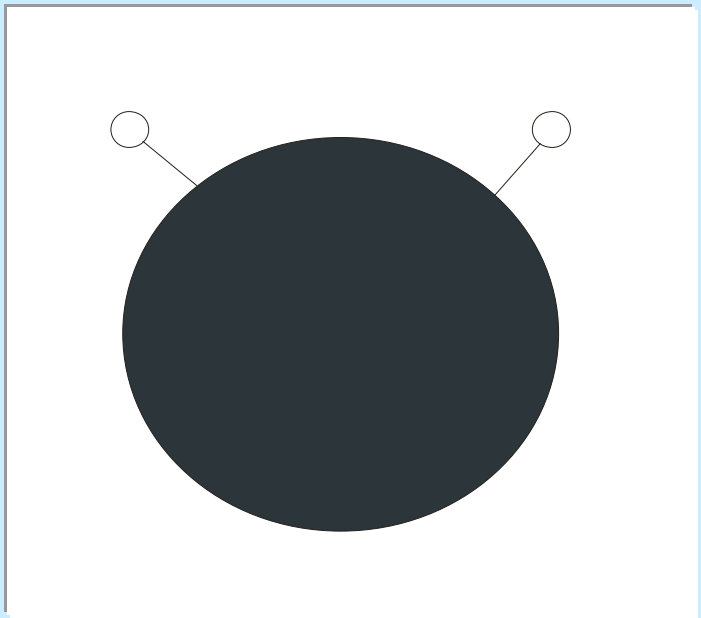
NW Pacific Bering Sea-Aleutians NE Pacific

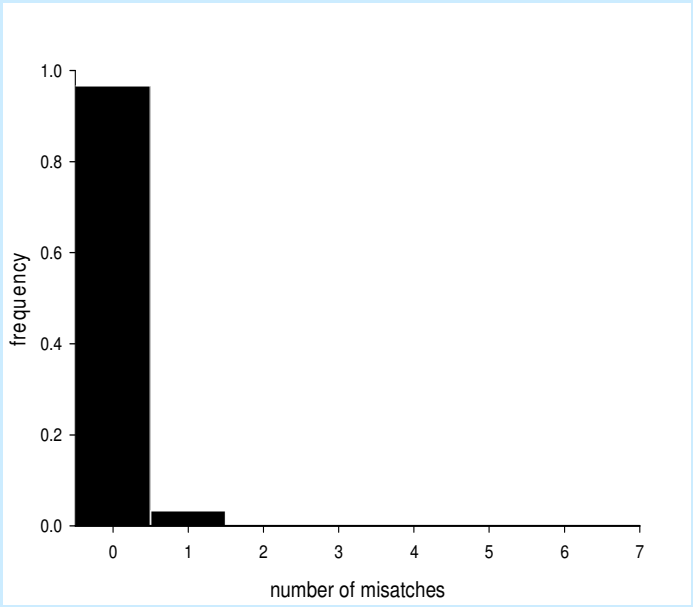


Pacific Cod


NW Pacific
Aleutians
NE Pacific
Georgia Basin
93
39
15
61
10
30
93
50
39
10
31
15
61
45
30
3
6
50
39
15
10
31
61
45
30
6
39
15
31
10
3
30
6
0.2
0.1
0
0 4 8 12
0 4 8 12
0 4 8 12
0 4 8 12
Number of mismatches

Atka mackerel





- extremely shallow genealogy
- mismatch distribution on origin
- extremely low mtDNA diversity likely indicates strong and very recent bottleneck

Species	haplotype diversity (h)	nucleotide diversity (π)
Atka mackerel	**0.0333**	**0.00007**
walleye pollock	0.8160	0.0024
Pacific cod	0.9810	0.0039
Atlantic cod	0.3044	0.0013

History matters

Pacific cod – ice-age signals of isolation and expansion persist to contemporary time

Atka mackerel – recent bottleneck stripped nearly all variation from mtDNA

- Not severe enough to cause significant loss of diversity in nuclear microsatellites or allozymes – loss by drift 4x slower

  - H_e 37allozyme loci = 0.137 (Lowe et al. 1998). Global F_{ST} = 0.004
  - H_e 9 microsatellites = 0.797 (Canino et al. unpubl). Global F_{ST} = 0.002

- Recent bottleneck/expansion event likely precludes accumulation of significant differentiation in highly dispersive species – genetic approach uninformative

Integrating genetics and stock assessment?

Eventually, but will require:

- More informative genetic markers
- More sophisticated models
  - seascape genetics models (e.g. Galindo et al. 2006)
  - simulation-based models w/in Bayesian framework
  - assessment models evaluating adult/larval source/sink relationships (Stenseth et al. 2006)
- Multidisciplinary approaches
  - oceanography, acquired tags, behavior

Acknowledgements

- Fisheries Interaction Team, NMFS
  - Sandy Neidecther
  - Libby Loggerwell
  - Peter Munro
  - Liz Connors
- AFSC, NMFS
  - Steve Barbeaux
- NWFSC, NMFS
  - Mike Rust
- University of Alaska
  - Olav Olmseth
- WDFW
  - Sue Hoffman
  - Greg Bargmann
  - Wayne Palsson
- Kodiak Laboratory, NMFS
  - Kally Spalinger
  - Dan Urban
- DFO, Canada
  - Sandy McFarlane
- Hokkaido Fisheries Research Institute
  - Takashi Yanagimoto
  - Akira Nishimura
- University of South Korea
  - Qtae Jao

Photo courtesy Sandi Neidetcher