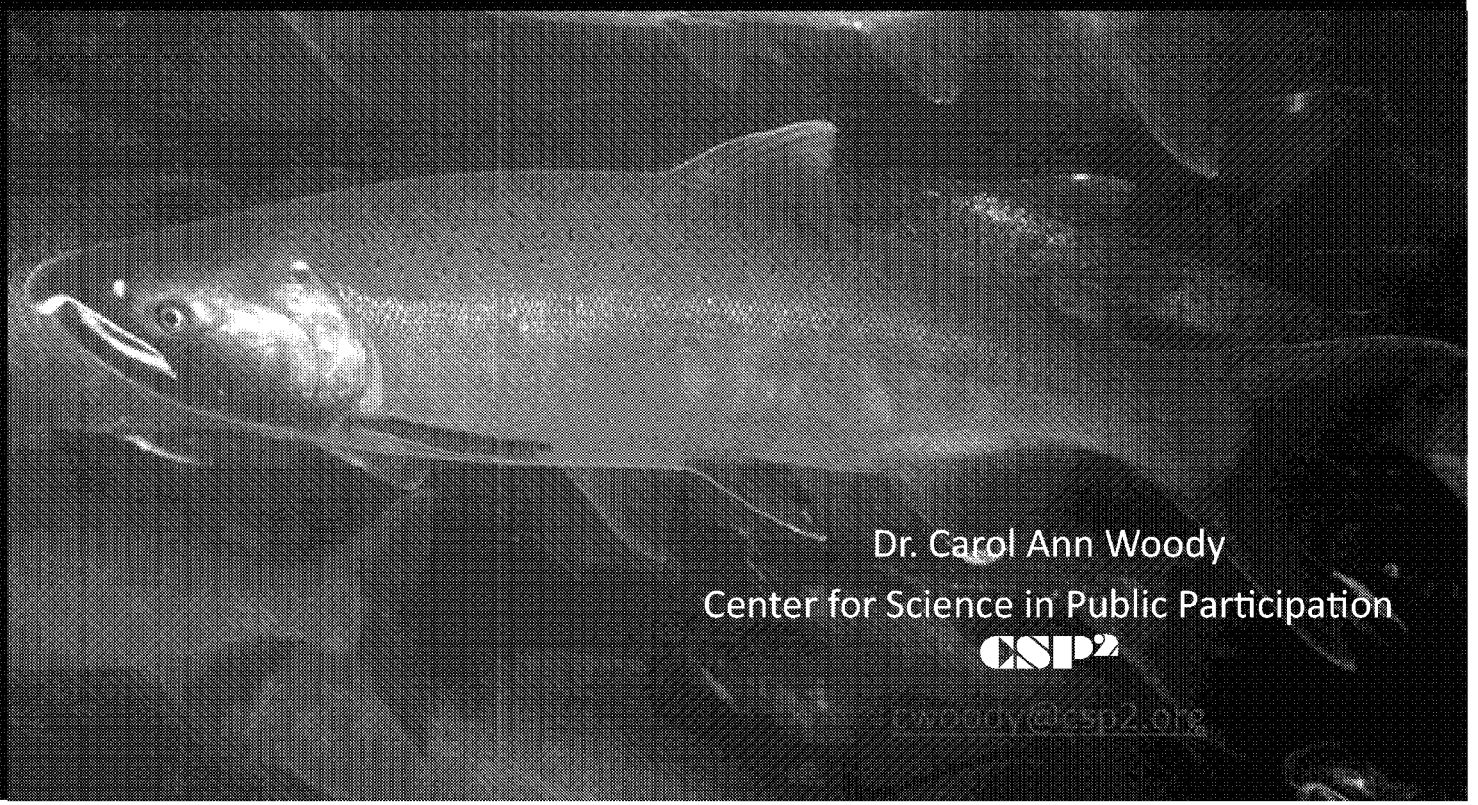
# Coho Salmon Spawning Distribution and Biodiversity in a Proposed Mining District, Bristol Bay, AK



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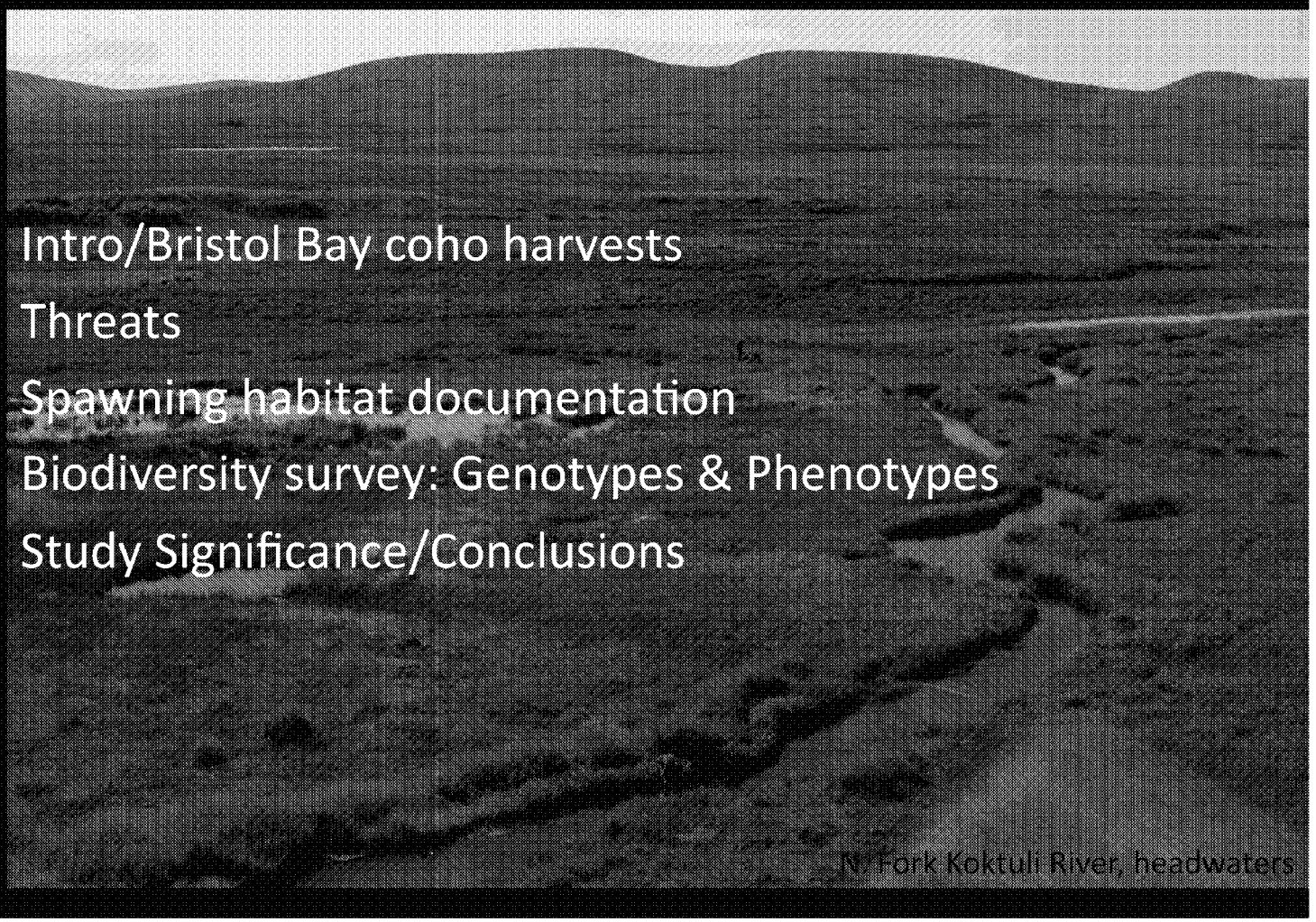
# Outline



- Intro/Bristol Bay coho harvests
- Threats
- Spawning habitat documentation
- Biodiversity survey: Genotypes & Phenotypes
- Study Significance/Conclusions

N. Fork Koktuli River, headwaters

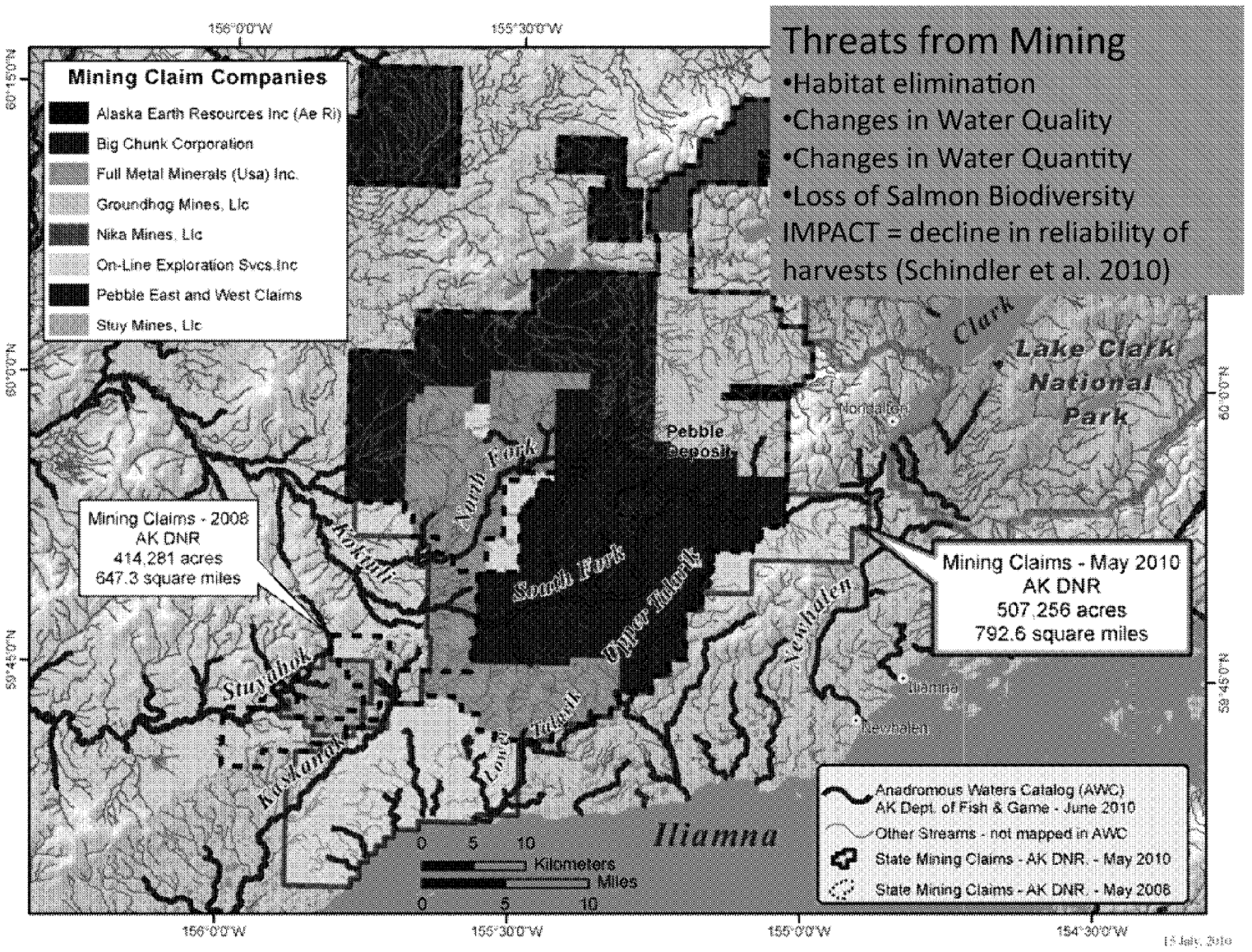
# Coho salmon

- Second least abundant Pacific salmon species in AK & US (Quinn 2005)
- Alaska represents 50% species range
- Occupy widest array of freshwater habitat ranging from large fourth order rivers to first order headwater streams. Rear 1-3 years in small streams.
- In Bristol Bay, spawn later than other salmon species, during more inclement weather which poses logistical challenges for studies (Price & Larson 1999, Dion & Hetrick 2006)
- Few Bristol Bay coho studies.

Tributary to S. Fork Koktuli

# Bristol Bay Coho Salmon Harvest

- Commercial (Jones et al. 2012)
  - AVG harvest = 84,335 (1991-2010)
  - 2011 harvest ~ 108,000
- Sport (ADFG Sport Fish 2011 data)
  - 20,706 anglers fished 98,522 day
  - top 3 species harvested were: **coho** (16,045), sockeye (15,232) & Chinook (10,897)
- Subsistence (ADFG Subsistence Div.)
  - ALL communities use coho salmon
  - Average harvest/household/all years = 108.3 lbs

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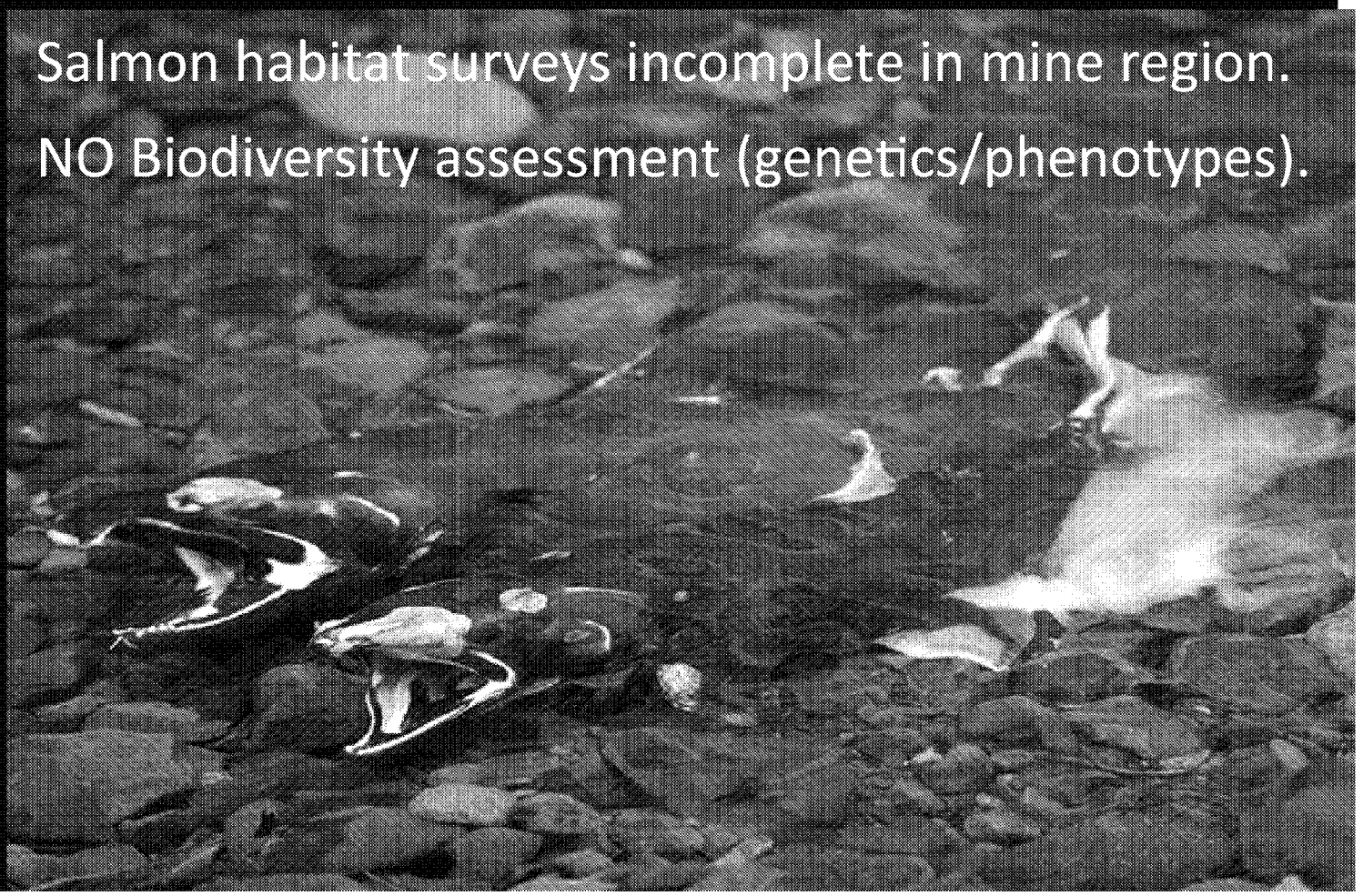
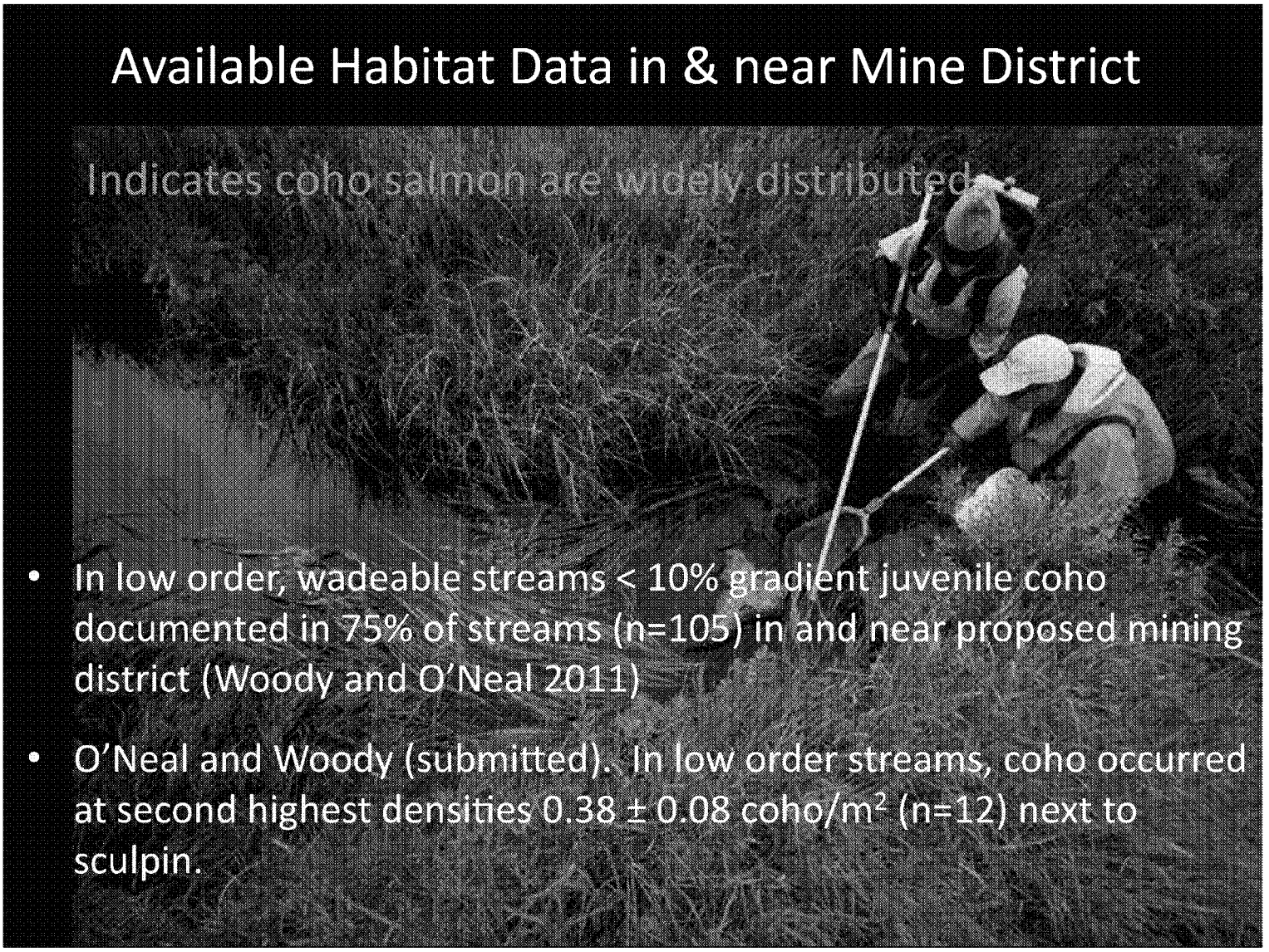
# Lack of Data on Coho in Proposed Mine Region

- Salmon habitat surveys incomplete in mine region.
- NO Biodiversity assessment (genetics/phenotypes).



# Available Habitat Data in & near Mine District



Indicates coho salmon are widely distributed

- In low order, wadeable streams < 10% gradient juvenile coho documented in 75% of streams (n=105) in and near proposed mining district (Woody and O'Neal 2011)
- O'Neal and Woody (submitted). In low order streams, coho occurred at second highest densities 0.38 ± 0.08 coho/$m^2$ (n=12) next to sculpin.

# Available coho salmon biodiversity: Genotypes

**NO studies in or near mine district.**

BUT 3 Important Alaska Studies:

- **Olsen et al. 2003**. Conservation genetics. 4:557-569.
- **Olsen et al. 2004**. TAFS. 133:476-483.
- **Olsen et al. 2011**. Conservation Genetics. 12:223-241.

**These studies indicate Alaskan coho spawning populations tend to be small & genetically distinct, more so than other salmon species. As such coho are at relatively higher risk of genetic diversity loss and extirpation due to habitat loss than chum and Chinook salmon.**

# Available Coho Salmon Biodiversity: Phenotypes

- Life history traits (e.g., age and size at maturity) are heritable and influenced by natural selection. Significant differences among populations of the same species in such traits indicates adaptive biodiversity related to fitness.
  - No phenotypic data for coho populations in mine region.

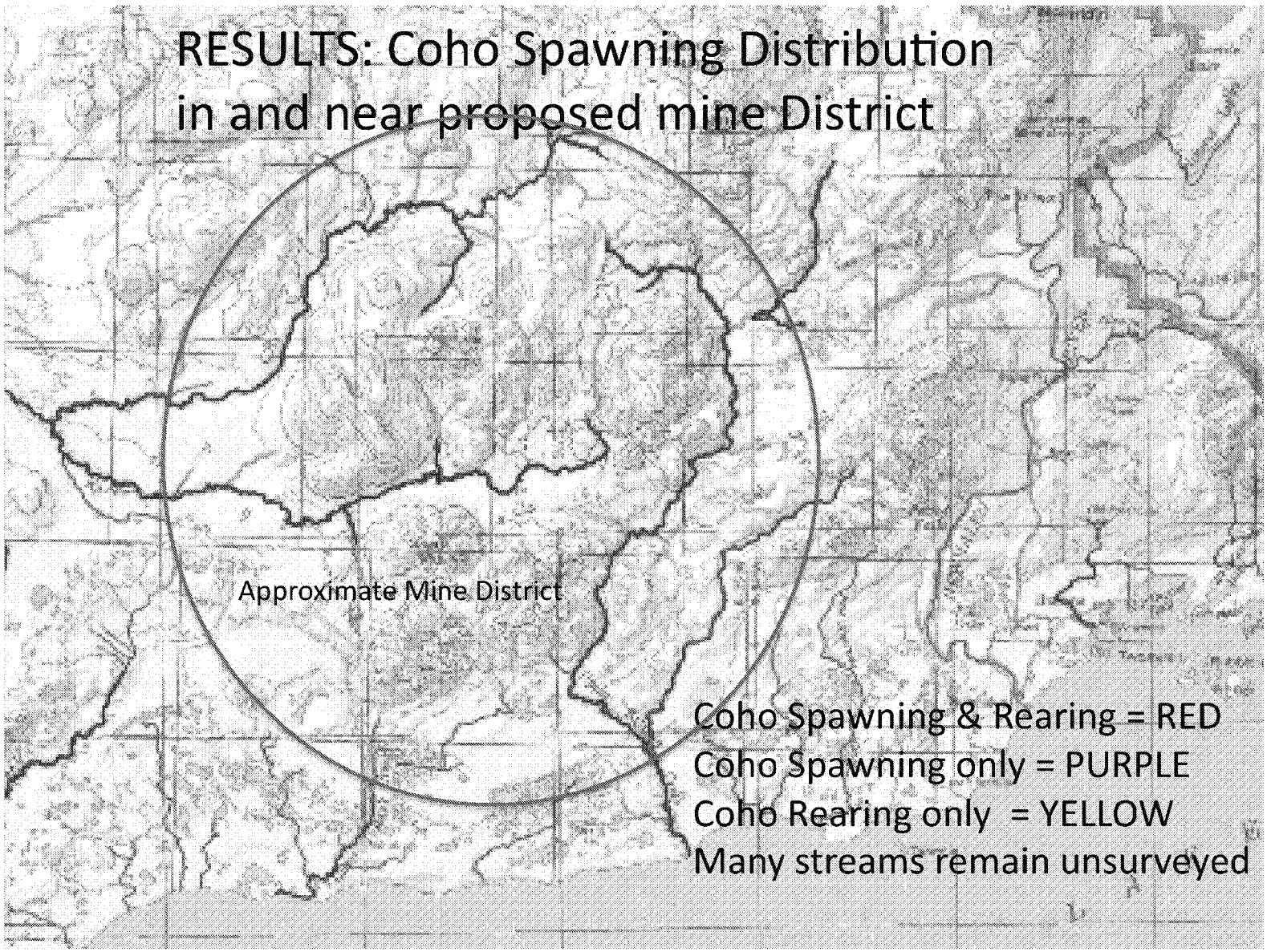
# Methods:

- Coho spawning habitat documentation
  - Conducted low level (50-150 m) helicopter surveys for spawning/migrating coho during 2009, 2011
  - Georeferenced (GPS) spawning & migrating coho
  - Nominated spawning habitat to ADFG Anadromous Waters Catalog (AWC).
  - Mapped using AWC ARCINFO database (ADFG 2013).

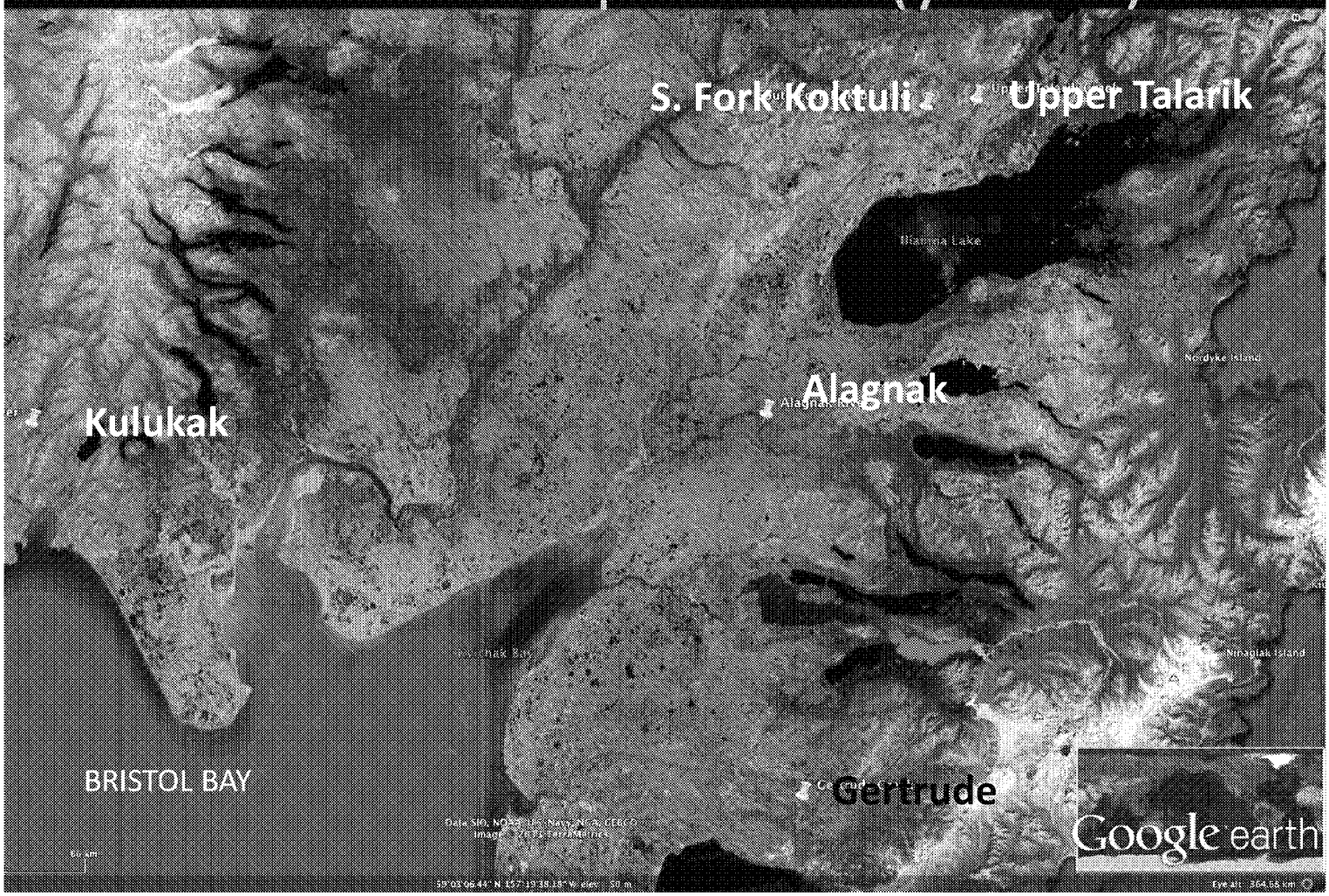
# Methods

Biodiversity

- Genotypic – 8 micro-satellite loci from S. Fork Koktuli (Nushagak) & Upper Talarik Creek (Kvichak)
- Phenotypic – Age & size at maturity, collected & analyzed scales for age, surveyed for length (MEH) & depth.


RESULTS: Coho Spawning Distribution
in and near proposed mine District
Approximate Mine District
Coho Spawning & Rearing = RED
Coho Spawning only = PURPLE
Coho Rearing only = YELLOW
Many streams remain unsurveyed

# Genetic Sample Sites (yellow)



Genotypic comparison of 8 microsatellite loci among 5 Bristol Bay coho populations. Data from US Fish and Wildlife Service Conservation Genetics Lab, Anchorage, AK.

| System | Tributary | Code | Year | n |
|---|---|---|---|---|
| Alagnak River | Alagnak River | ALAG | 1997 | 89 |
| King Salmon River | Gertrude Creek | GERT | 1997 | 96 |
| Nushagak River | South Fork Koktuli River | HSKA | 2011 | 78 |
| Kvichak River | Upper Talarik Creek | HUTA | 2011 | 73 |
| Kulukak River | Kulukak River | KULU | 1997 | 91 |

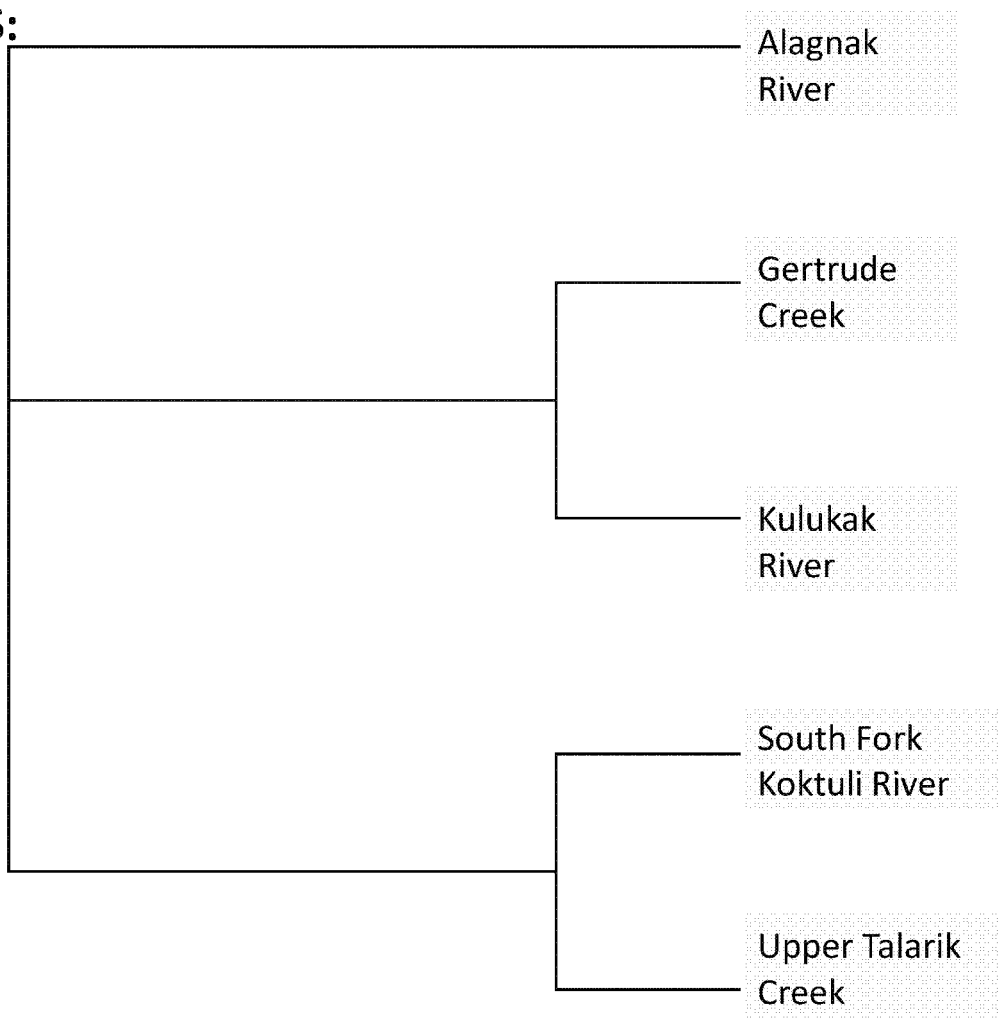
microsatellite loci analyzed = Oke2, Oke3, Oke4, Oki1, Oki 3, Oki11, Oneu3, Ots105
No significant departures observed from HW equilibrium, therefore populations were compared using GENEPOP & Fstat

## BIODIVERSITY RESULTS:
## Genotypic

All spawning populations differed significantly from each other (Fst p = 0.026; 99% CI = 0.014- 0.044)

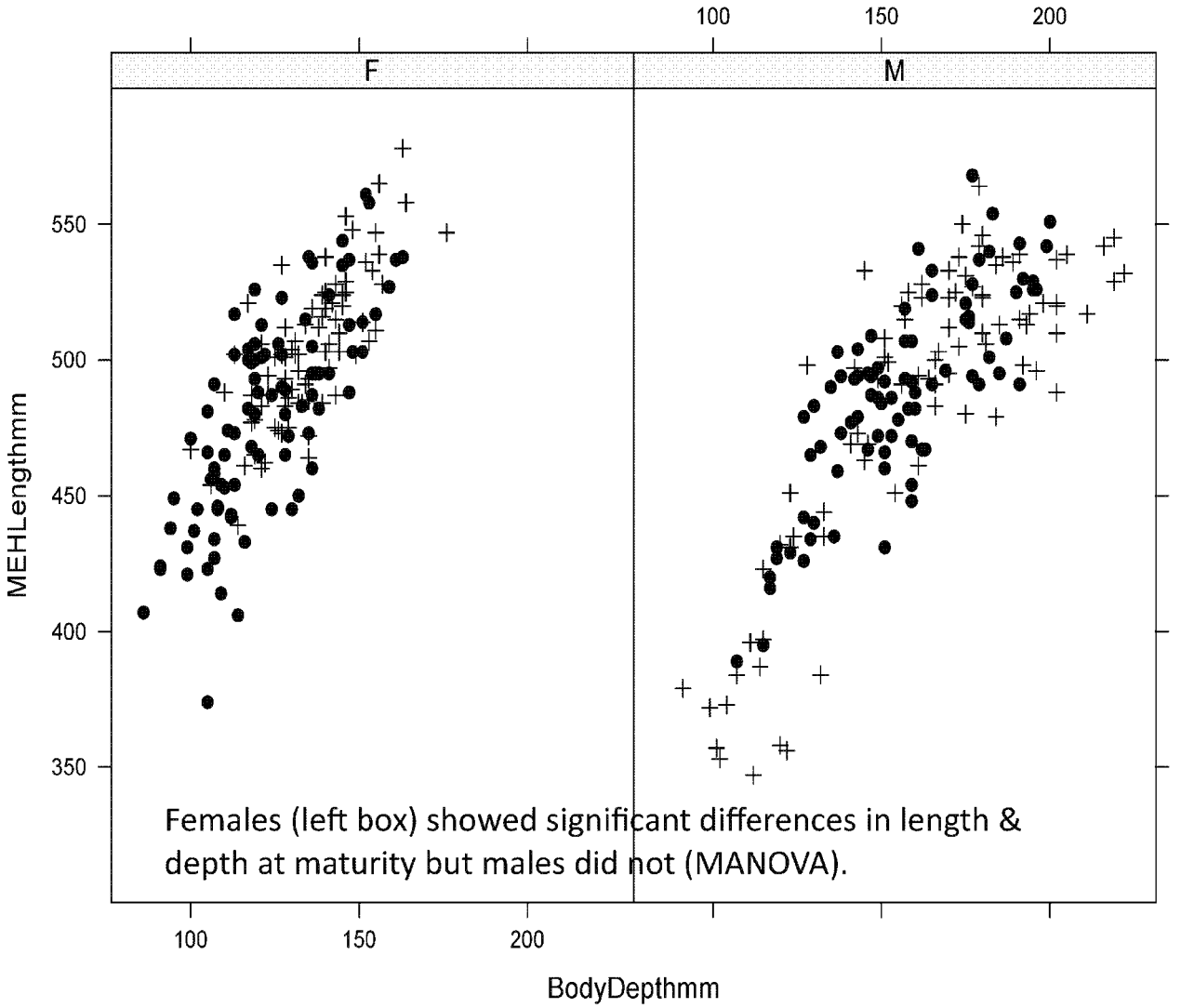
This phenogram (PHYLIP) shows grouping based on genetic analysis.

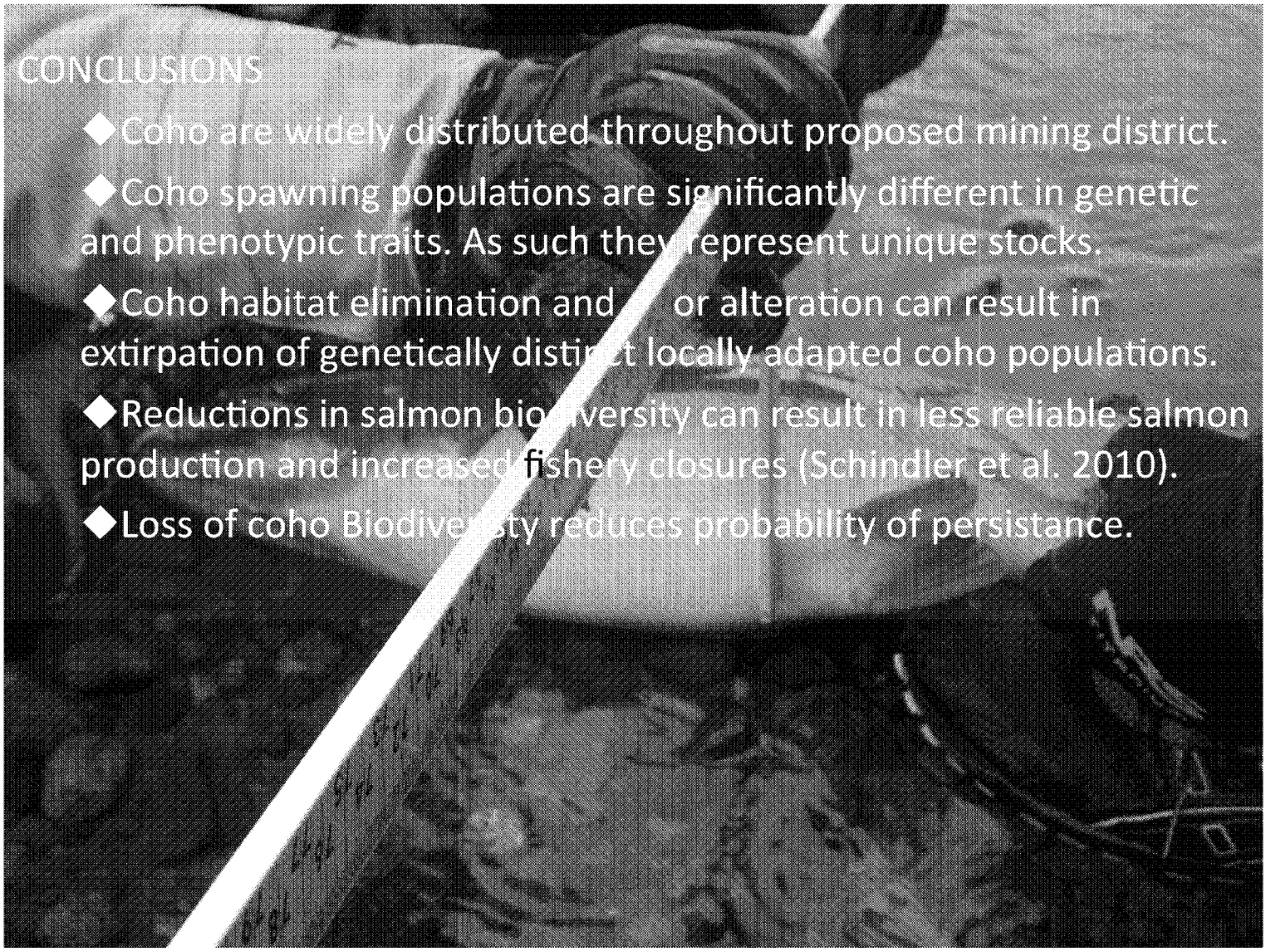
**BOTTOM LINE:**
**ALL surveyed coho populations in Bristol Bay are genetically unique. Habitat elimination would result in elimination of unique genetic diversity.**



# BIODIVERSITY RESULTS: Phenotypic

- Significant differences between male age distribution (Pearsons Chi Square test; $p = 0.007$); more 1. observed in S. Fork Koktuli than expected and more 2. observed in Upper Talarik than expected.
- Females showed no significant differences in age distribution among sites BUT…
- Females showed significant differences in length and depth at maturity, males did not (MANOVA w/ Pillai-Bartlett statistic (Krzanowski 1988).


F
M
MEHLengthmm
BodyDepthmm
350
400
450
500
550
100
150
200
Females (left box) showed significant differences in length & depth at maturity but males did not (MANOVA).


CONCLUSIONS
◆Coho are widely distributed throughout proposed mining district.
◆Coho spawning populations are significantly different in genetic and phenotypic traits. As such they represent unique stocks.
◆Coho habitat elimination and/or alteration can result in extirpation of genetically distinct locally adapted coho populations.
◆Reductions in salmon biodiversity can result in less reliable salmon production and increased fishery closures (Schindler et al. 2010).
◆Loss of coho Biodiversity reduces probability of persistance.