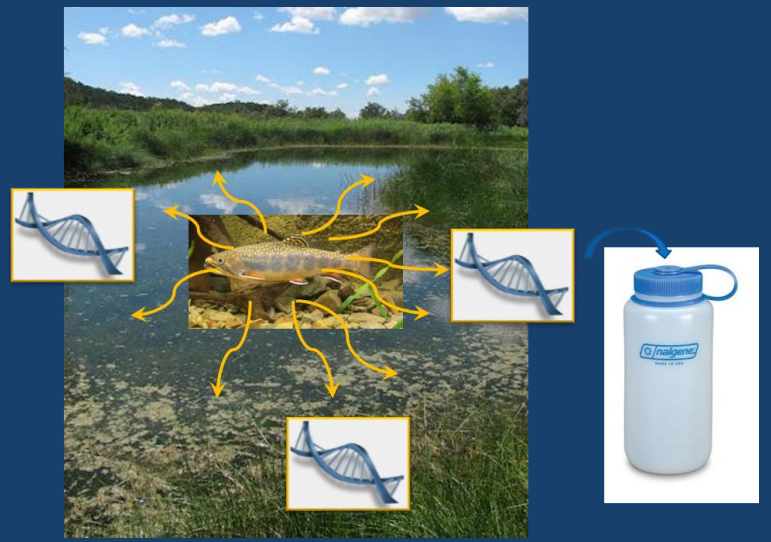
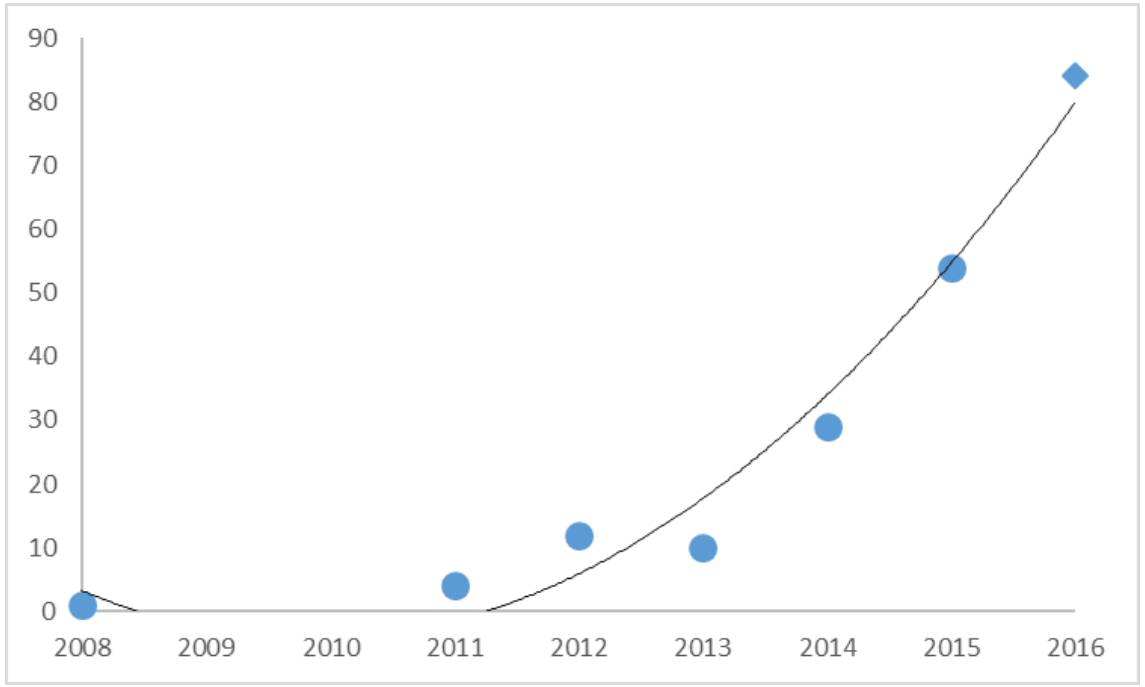
Environmental DNA detection of salmonids

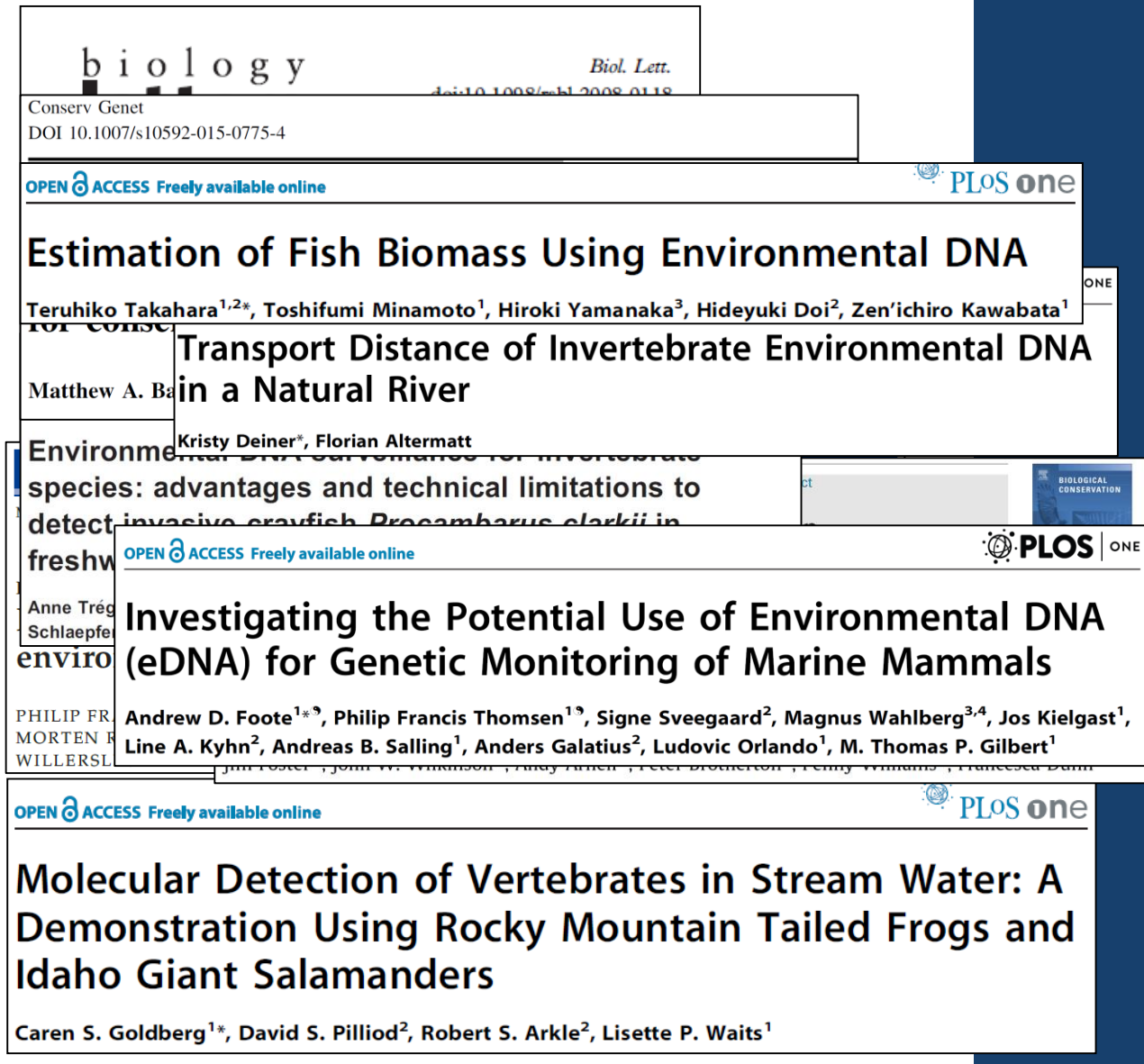
Katherine Strickler
Caren Goldberg
Alexander Fremier



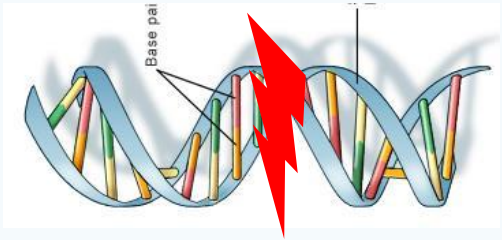
Washington State University

eDNA detection papers





Processes affecting eDNA detection

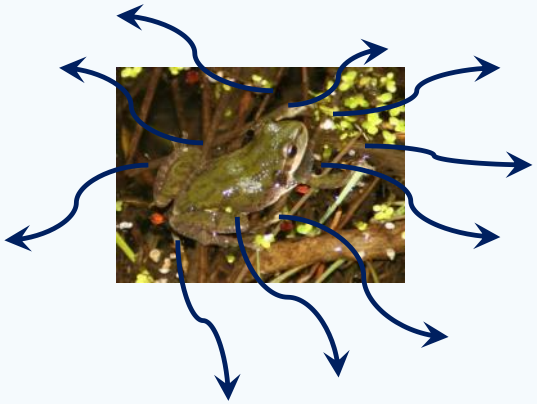


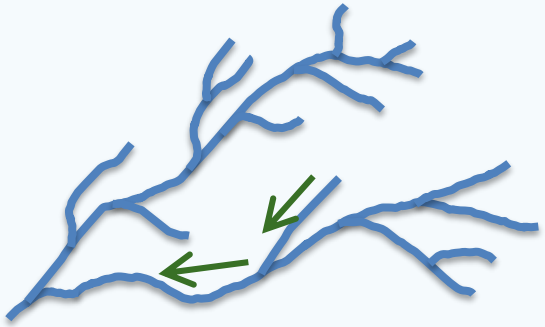
Degradation

Production

Detection at a location within a site

Diffusion/Transport





Our focus: understanding processes

- Degradation rates related to pH, UV, and temperature
- eDNA transport in streams

- Cross-sectional distribution of eDNA
- Longitudinal distribution of eDNA

- Detection of nuclear vs. mitochondrial DNA

Salmonid assays

- Bull trout - ITS1 (repeated nuclear gene)
- Brook trout - cyt b (mitochondrial)
  - Wilcox et al. (2013) assay
- Chinook – COI (mitochondrial)
  - Laramie et al. (2015) assay

Yakima Training Center

- 8 sites on Lmumma and Alkali Creeks (2012-2013)
- Ran assays for brook trout, bull trout, and Chinook

Yakima Training Center

- Brook trout detected at 1 site in Alkali Creek
- No other species detected

Brook Trout

- 64 surveys over 3 years (2013-2015) in Yakima and Idaho
- Ran brook trout assay for all samples

- Detections:
  - Upper Alkali Creek (YTC)
  - Lower Yakima River
  - American River
  - Union Creek
  - SF of the Tieton River (slightly positive in 1 samples at 1 site)

Bull Trout

- 62 surveys over 3 years (2013-2015) in Yakima and Idaho
- Detected eDNA at every site with redd counts
- Detected eDNA at 1 site that field crews didn't find redds
  - Lake Pend Oreille tributary
  - above a recent barrier

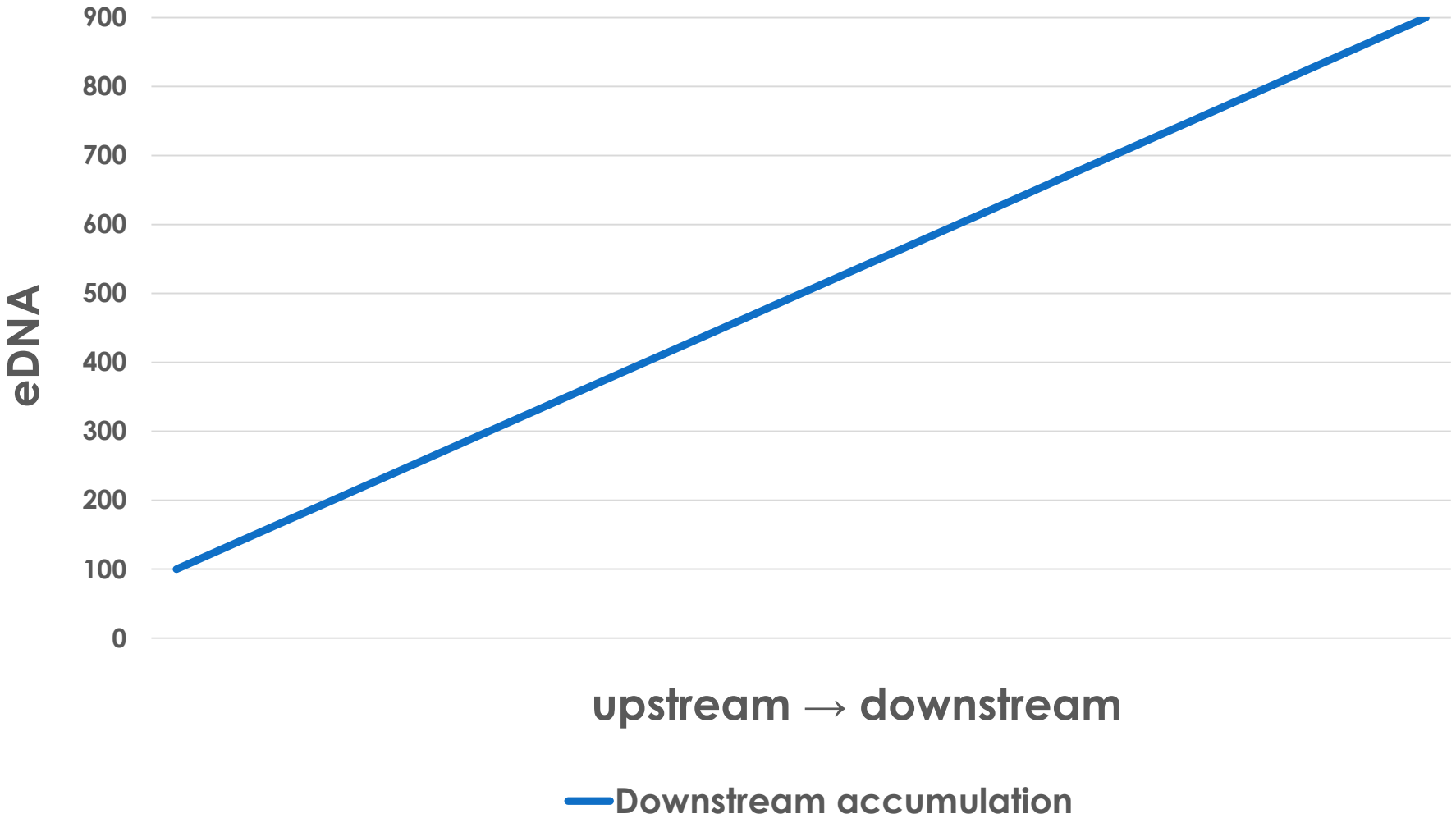
North Fork of the Teanaway River

Bull trout eDNA sampling

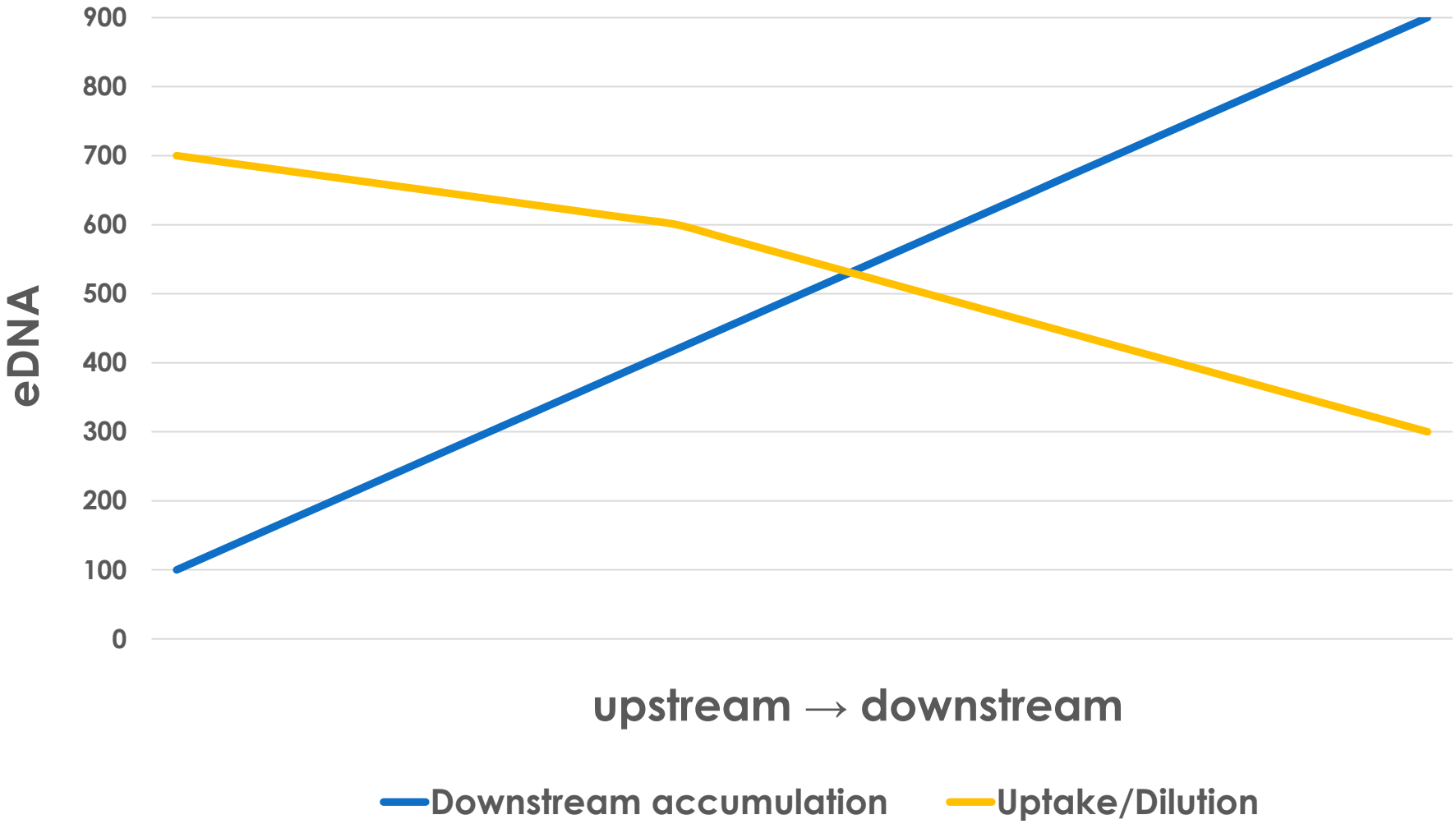
- 2012: 2 sites
- 2013: 7 sites + 5 sites downstream from probable redd

- No detections

eDNA in streams: longitudinal

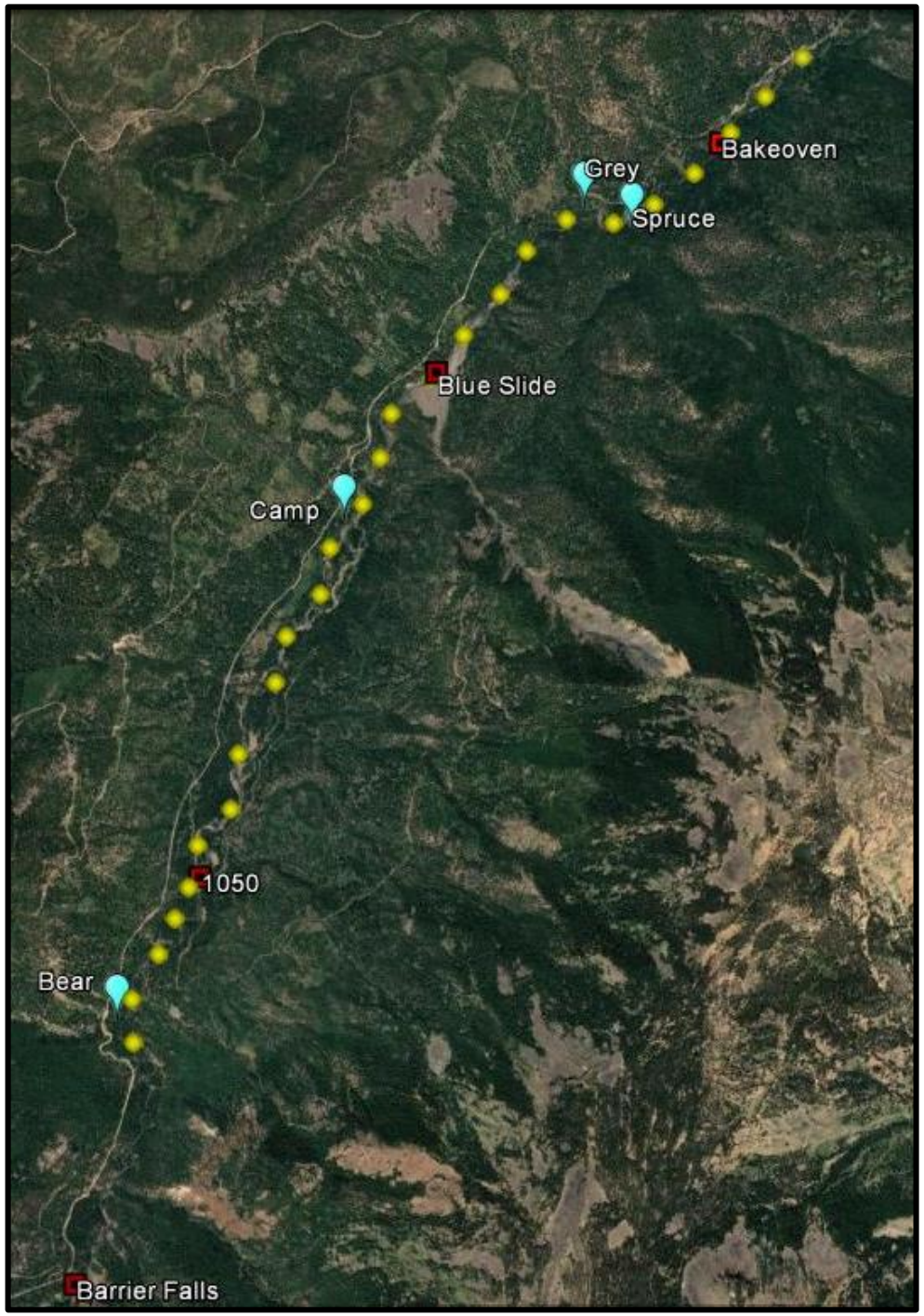


eDNA in streams: longitudinal

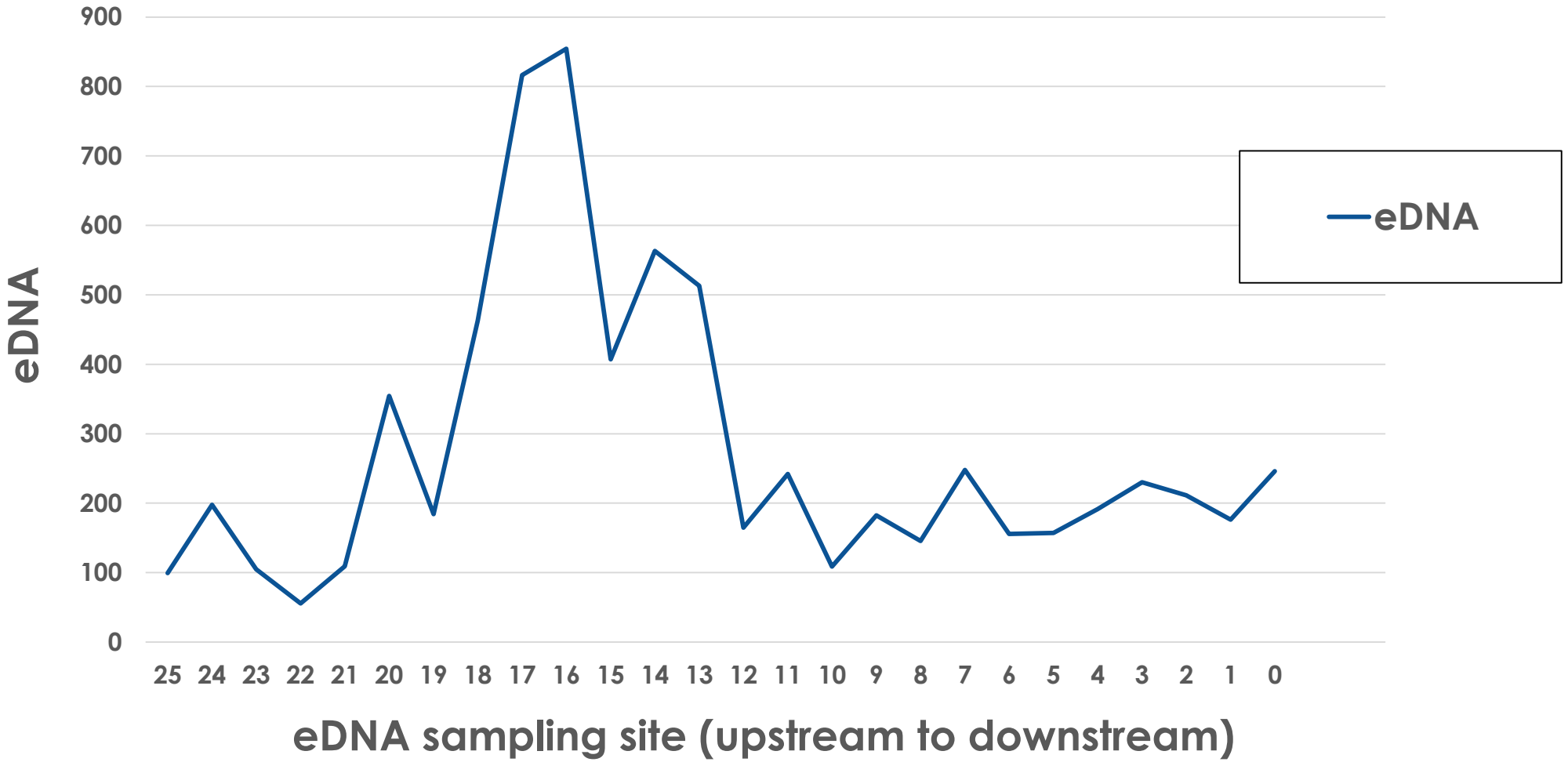


South Fork Tieton

- 26 mainstem sampling sites
  - 400 m segments
- 4 tributaries
- 4 samples/site (1 L samples)
- October 24-25, 2015



South Fork Tieton



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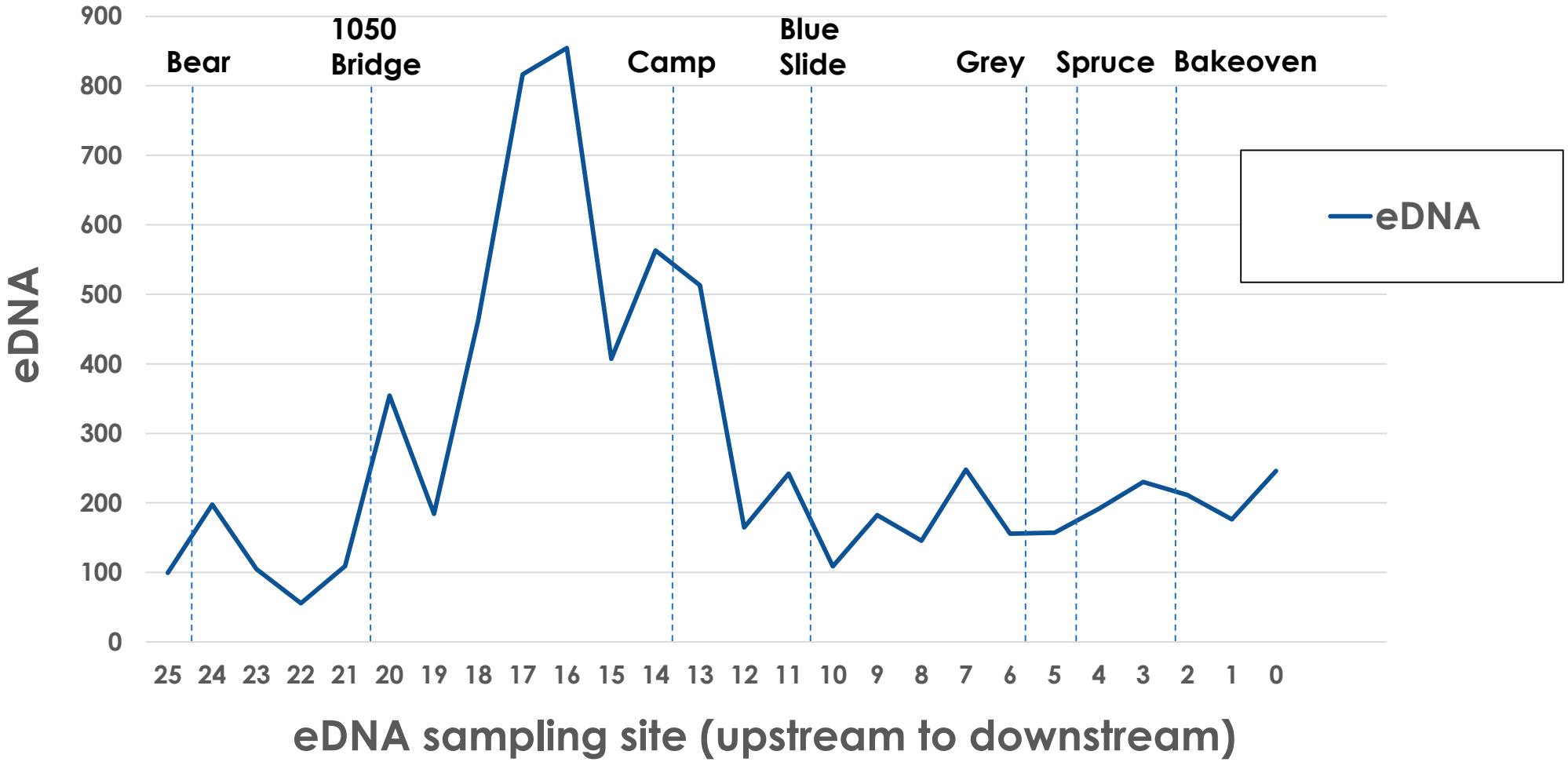

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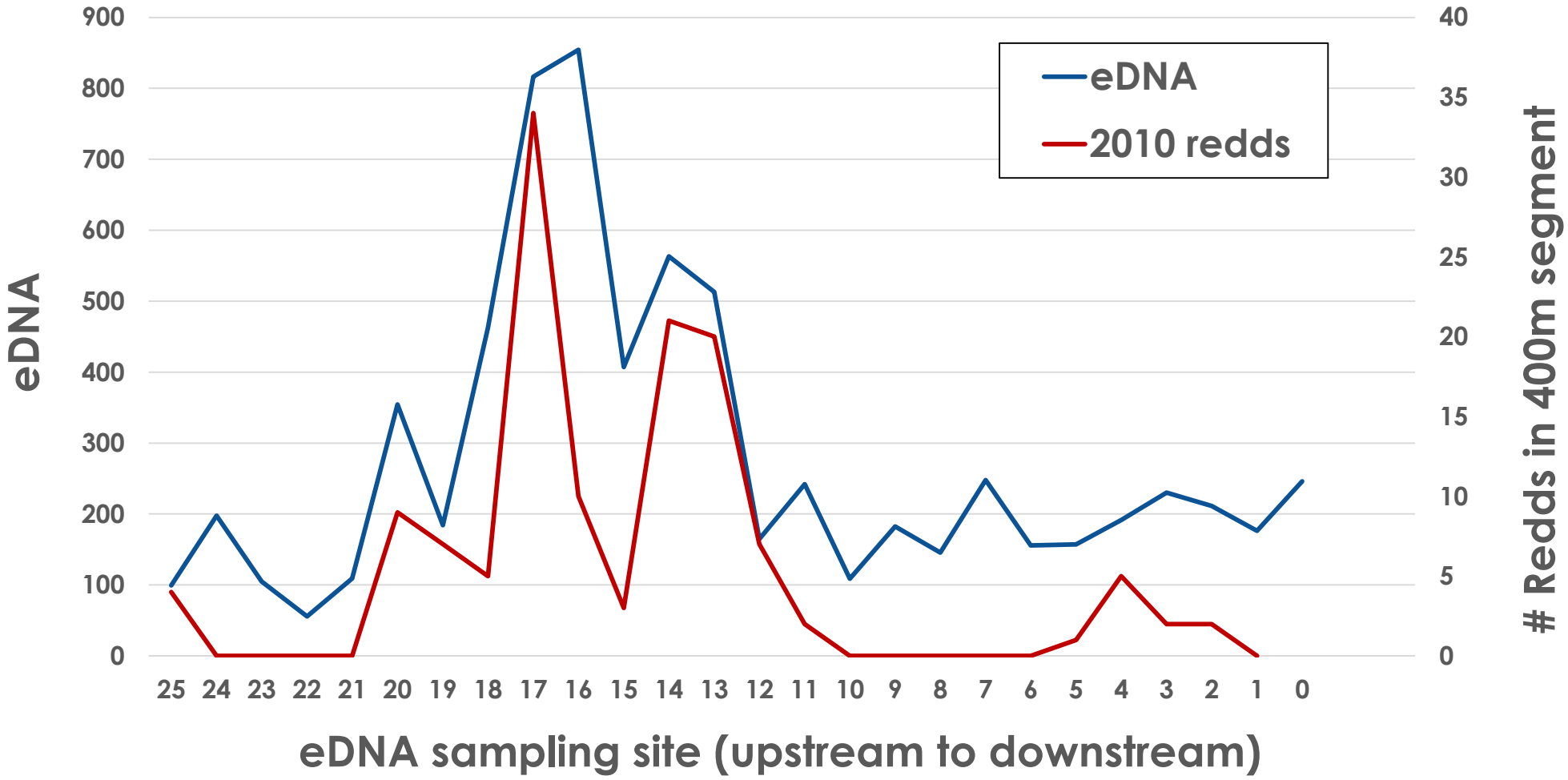
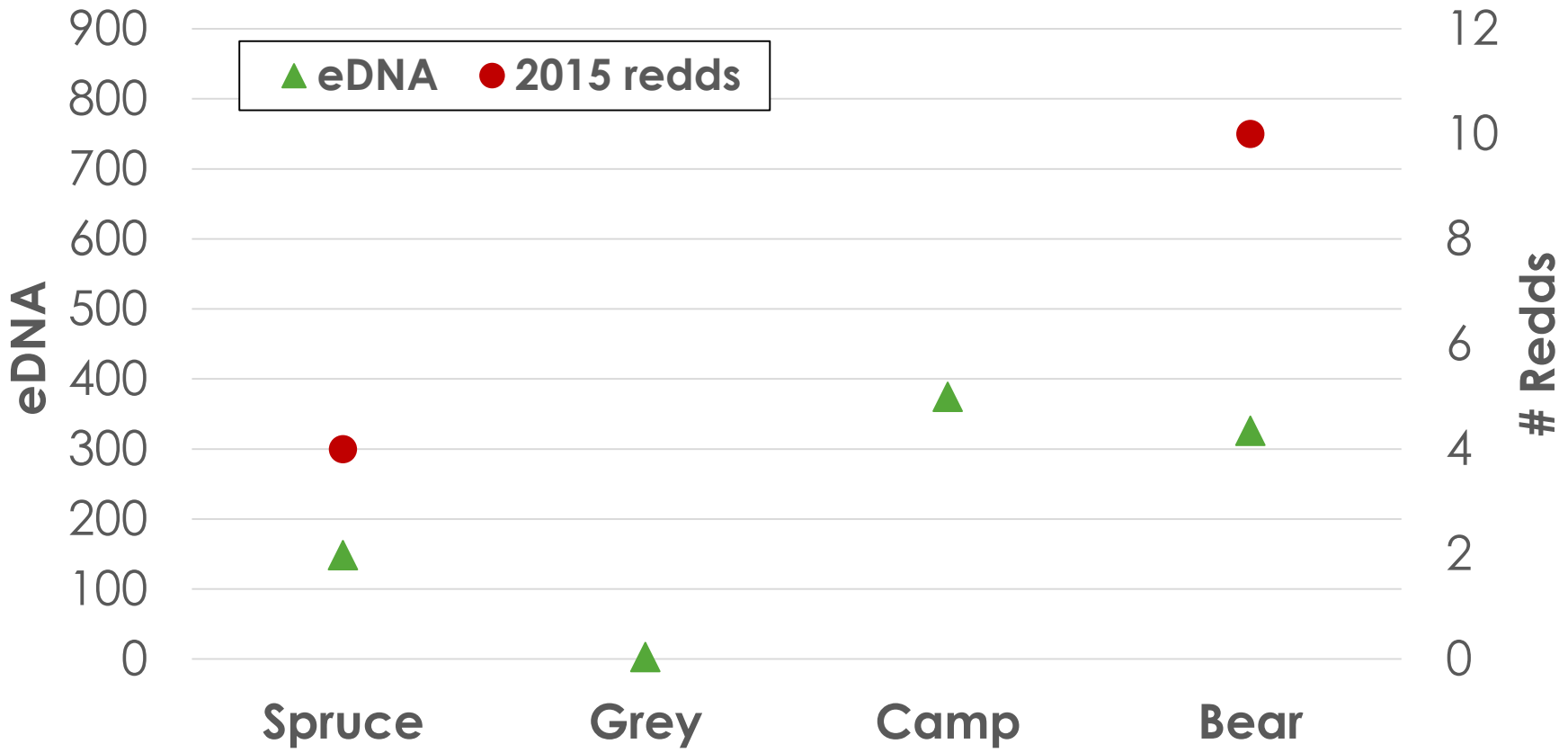


South Fork Tieton



eDNA in streams: cross-section

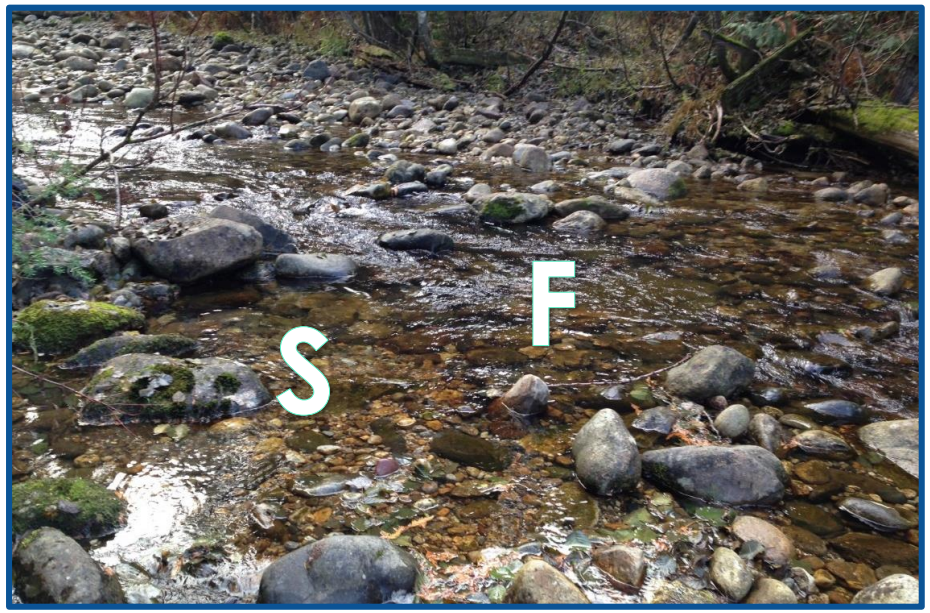
Where to sample?

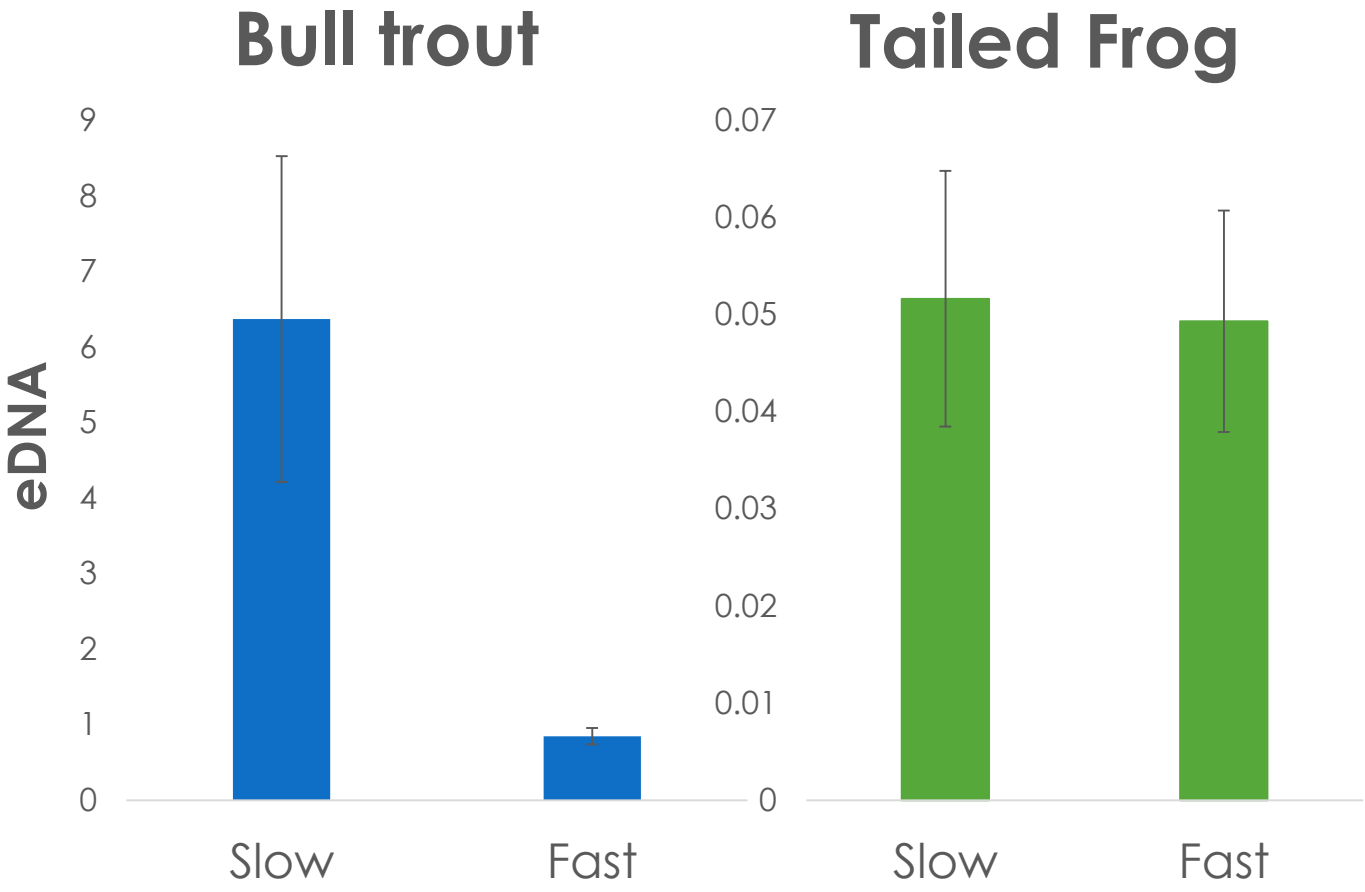
- High density sampling:
- 3 bull trout streams, 5 transects per stream

eDNA in streams: cross-section

Where to sample?

- Thalweg vs. pools

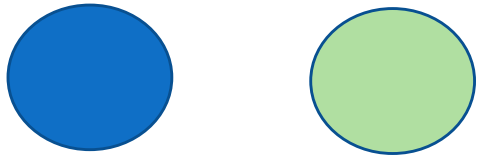




Fall vs. spring run analysis

- Some taxa do not have genetic fixed differences, instead varying by frequency

Fixed difference:



Taxon 1 Taxon 2

Frequency-based difference:

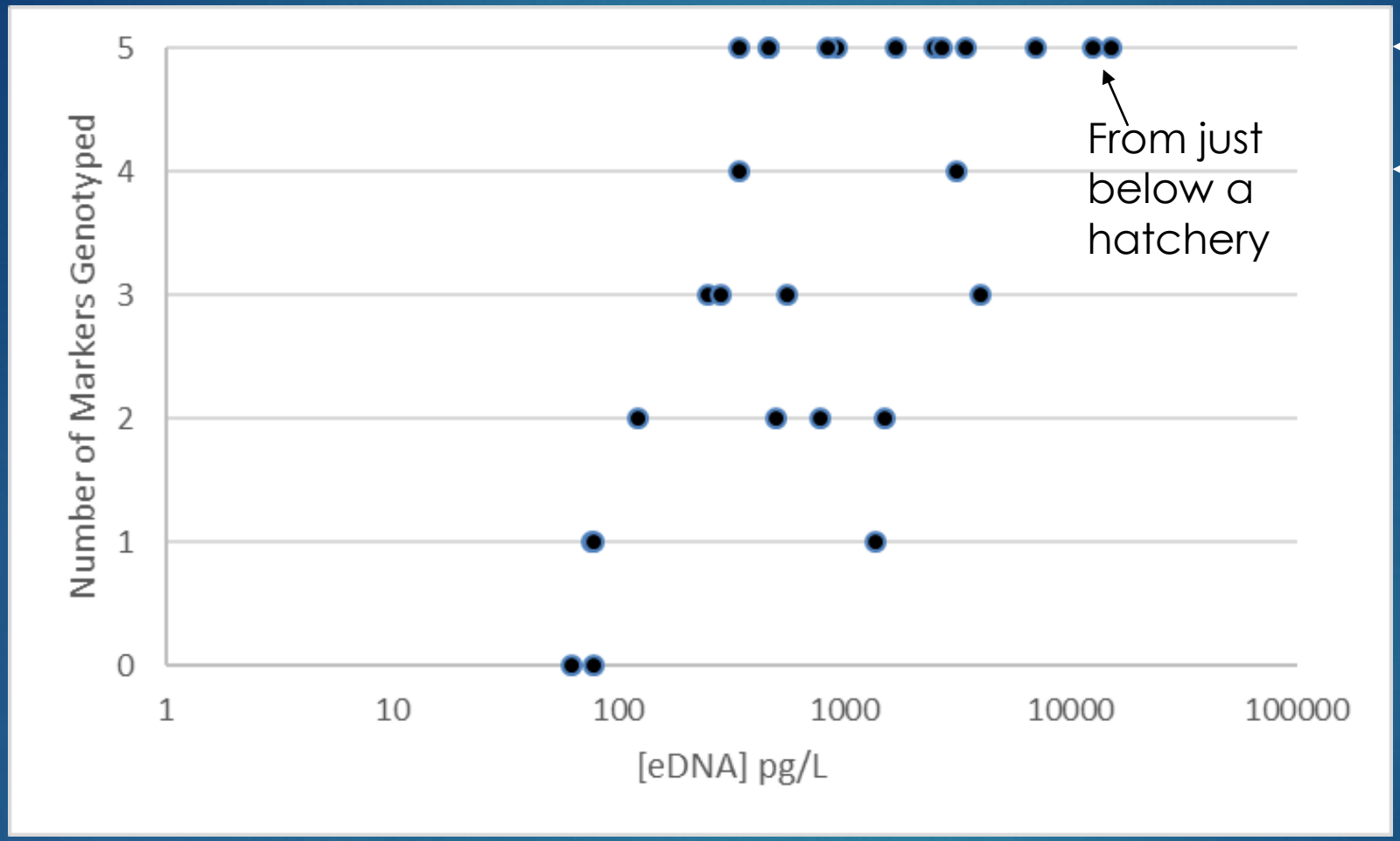
Taxon 1 Taxon 2

These are a challenge for eDNA assays because we need information from nuclear genes (much more rare than mitochondria)

Fall vs. spring run analysis

- Through collaboration with CRITFC (Shawn Narum), we identified 5 SNPs that only amplified Chinook DNA
- Statistically, an assignment to fall or spring run can be made with 4 of these SNPs
- However, if both alleles (A/G) are present but we only pick up one, that will give a false signal.
- How much Chinook eDNA do we need to correctly assign a run?

Chinook SNPs from eDNA samples



Sample contribution from Matt Laramie

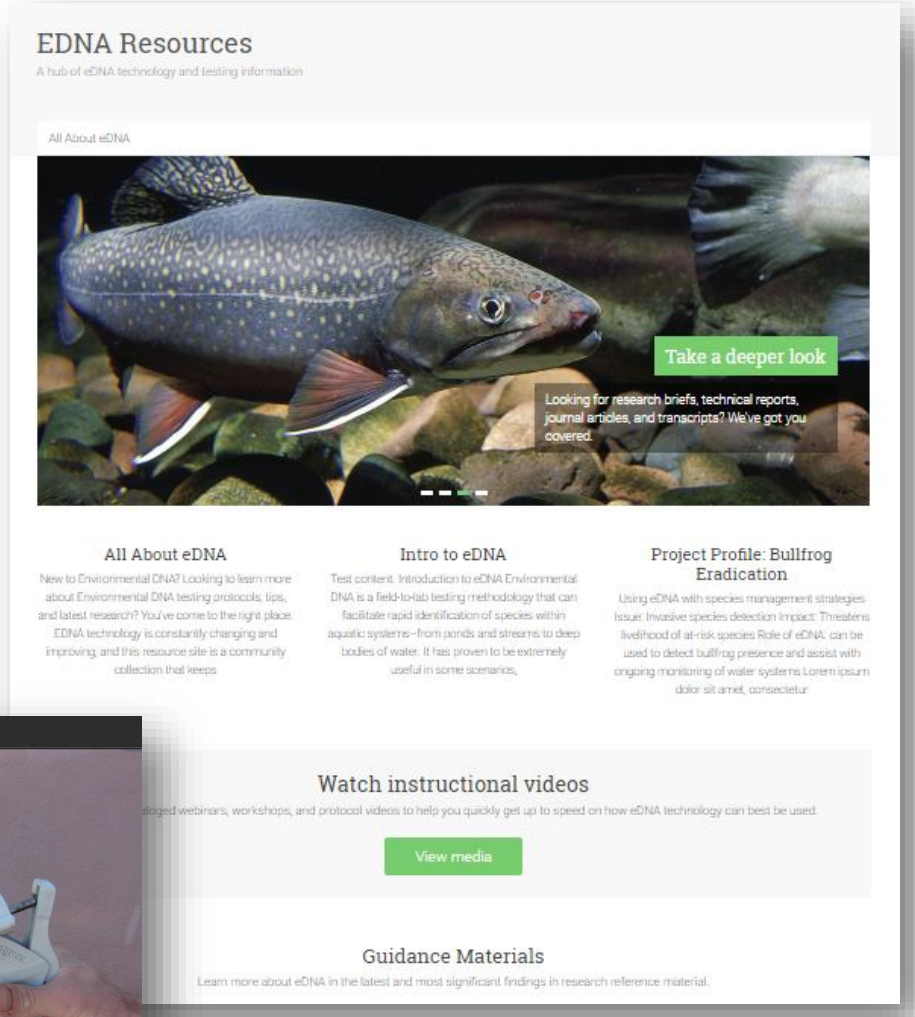
Figure 5-5. Relationship between Chinook eDNA concentration in sample replicate and the number of single nucleotide polymorphism markers that generated data for run-specific analysis. A minimum of 4 markers was required for run identification.

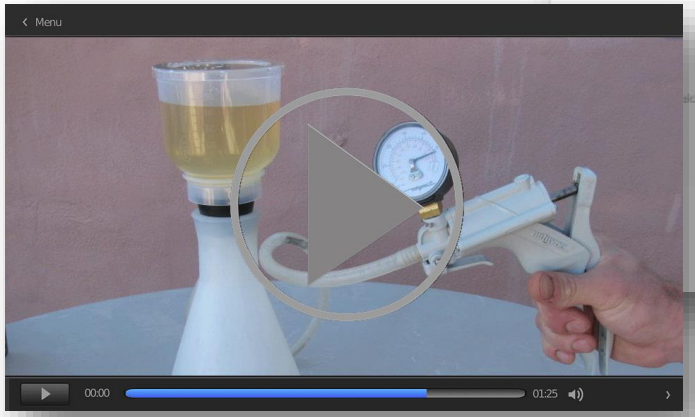
Summary

- eDNA concentration is related to where fish are (longitudinally and cross sectionally)
  - Laramie et al. 2015: longitudinal sampling in Methow
    - no accumulation, localized concentrations
  - Strobel et al. in press: Chinook and Coho redds
    - More eDNA of the species that made the redd, but mixed in water column
- New approaches for ESUs

eDNA online resource center

- Knowledge base
  - Intro to eDNA
  - Project profiles
  - Lessons learned
  - Links to research and commercial labs
- Guidance
  - Protocols
  - Technical details
- Community hub
  - Information exchange
  - Emerging technology

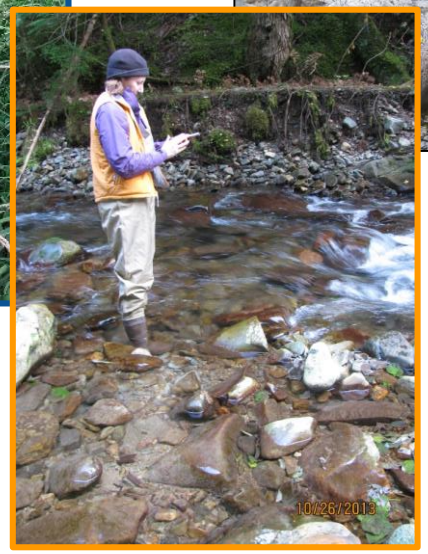




https://labs.wsu.edu/edna

@eDNAresources

Thank You



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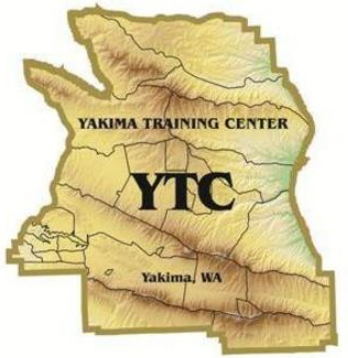
YAKIMA BASIN FISH & WILDLIFE RECOVERY BOARD



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