Evaluating eDNA as a tool to assess recolonization of a rare species: opportunities and constraints

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Challenges in recovery planning

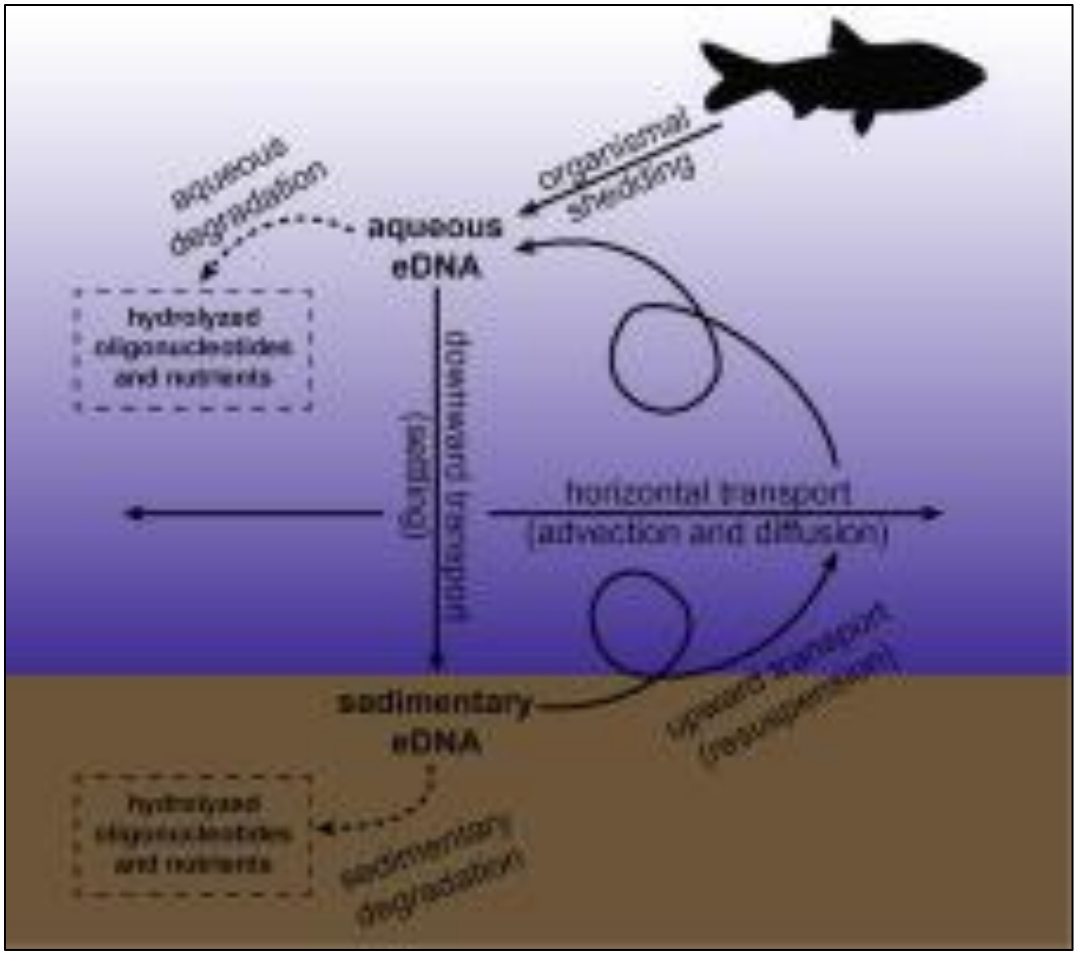
- Key data:
  - Current spawning distribution
  - Methodology to assess recolonization

- Existing methods to assess spawning are limited:
  - Visual surveys underestimate spawner abundance due to poor visibility, high flows, complex or deep habitat, turbidity
    - Example: weekly spawn surveys done in large river near reintroduction sites, no chum found, next spring, chum fry caught in screw trap
  - Traps ineffective because frequent floods during spawning
  - Low abundance, so effort to detect rare spawners is time consuming and cost prohibitive

- Environmental DNA (eDNA) may be effective tool to identify presence/ absence

eDNA

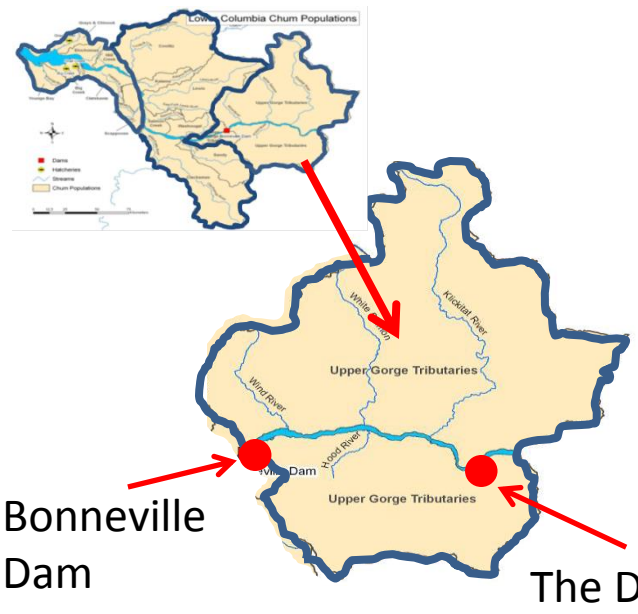
- Forensics technique to identify chum salmon DNA present in water
- Can be found up to 1 km downstream from source over two week period
- Requires genetic marker specific to species of interest

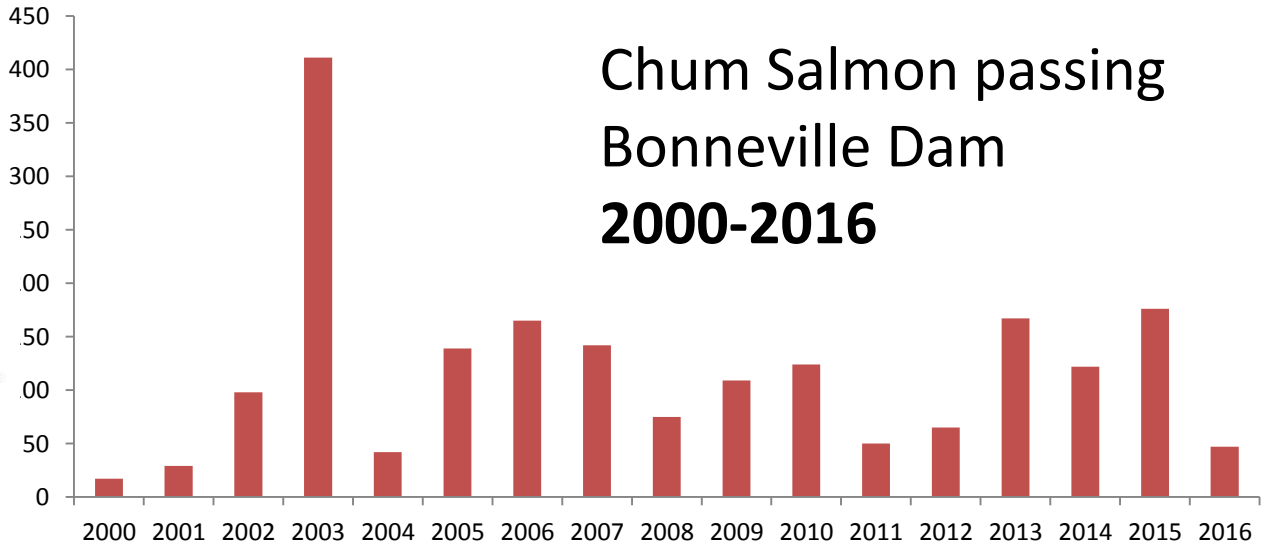


Objectives

1. Test and refine Chum Salmon marker
2. Identify spawning distribution in **Upper Gorge** recovery population

Where do they spawn?

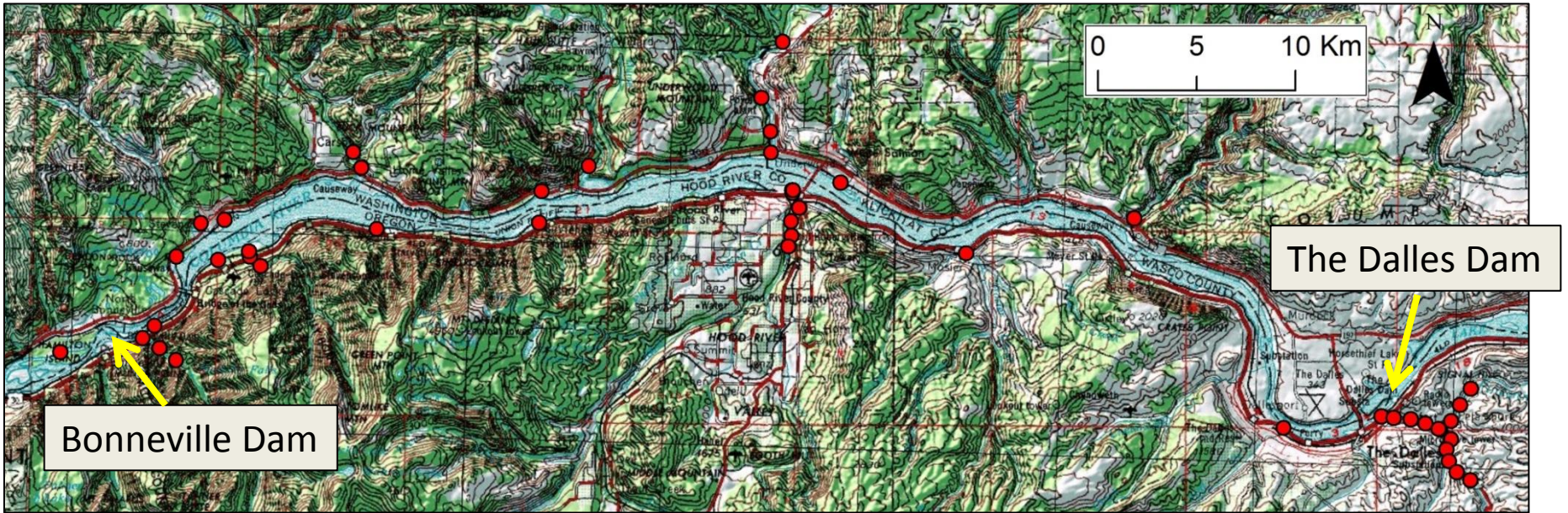




Chum Salmon passing Bonneville Dam
2000-2016

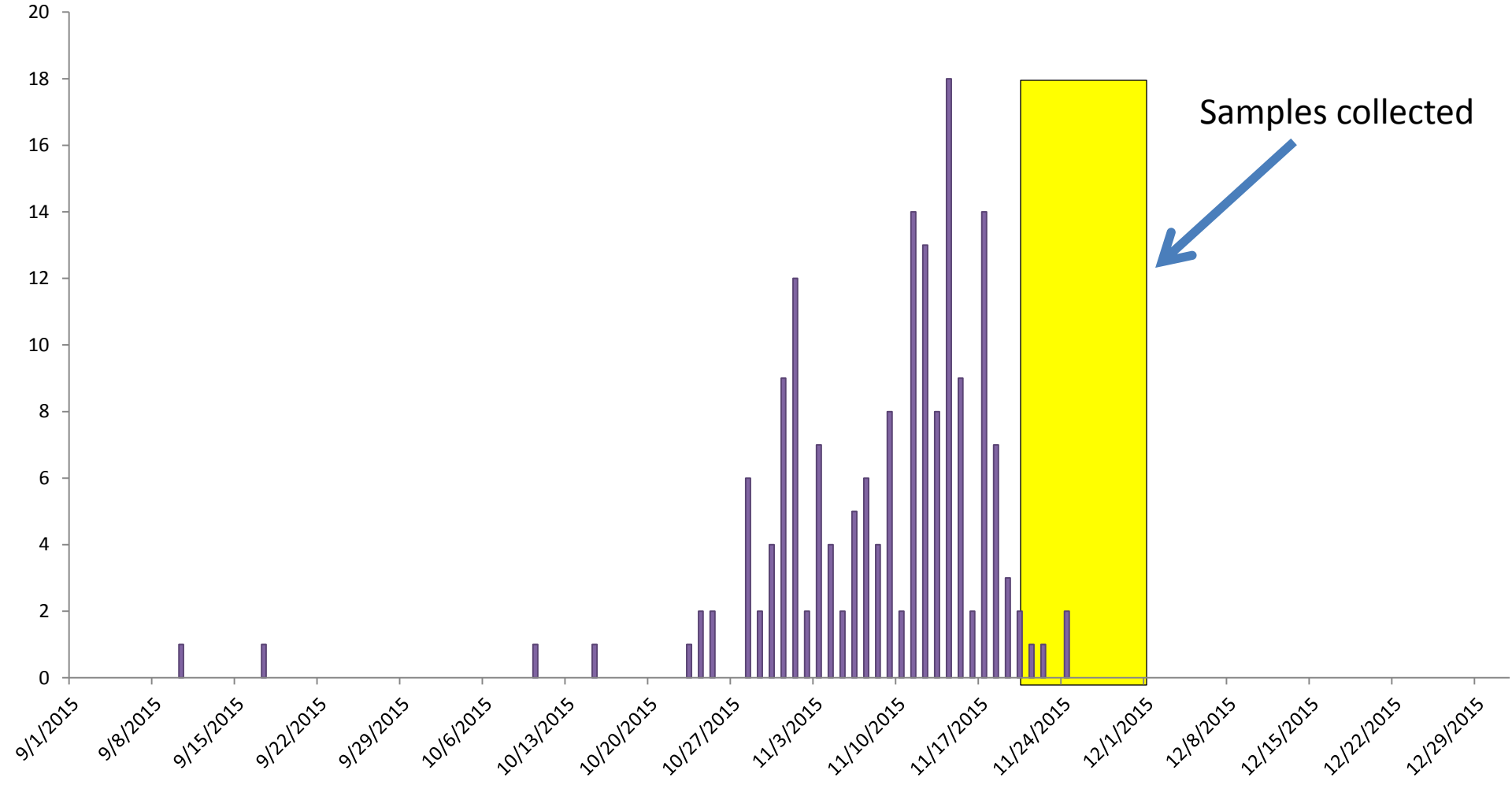
Methods

- **Marker testing:**
  - Collected tissue from Chum Salmon and co-occurring salmonids
  - Tested that marker only amplified Chum Salmon DNA
- **Spawning distribution: sample design**
  - Sample every 1 km in potential chum streams (based on gradient)
  - Four control (known positive) samples



Methods

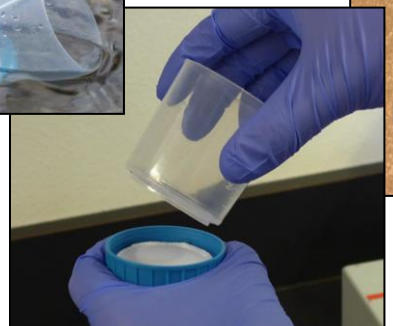
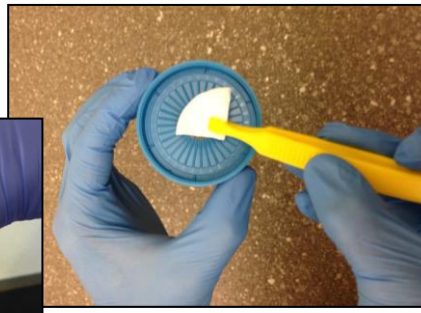
- **Spawning distribution: sample design (continued)**
  - Samples collected after peak migration over Bonneville



Methods

- **Spawning distribution: field methods**
  - Filter 5 liters using 1.5 micron glass microfiber filters
  - Used filter preserved in silica beads in labeled ziploc bag, stored in freezer until sent to lab
  - Precautions to not contaminate site or samples
  - Protocol: Carim, K.J., T. Padgett-Stewart, T. M. Wilcox, M.K. Young, K.S. McKelvey, and M.K. Schwartz. 2015. Protocol for collecting eDNA samples from streams. U.S.D.A> Forest Service, National Genomics Center for Wildlife and Fish Conservation. V 2.3



Methods

- **Spawning distribution: lab methods**
  - Samples processed by the U.S.F.S. Rocky Mountain Research Station National Genomics Center for Wildlife and Fish Conservation

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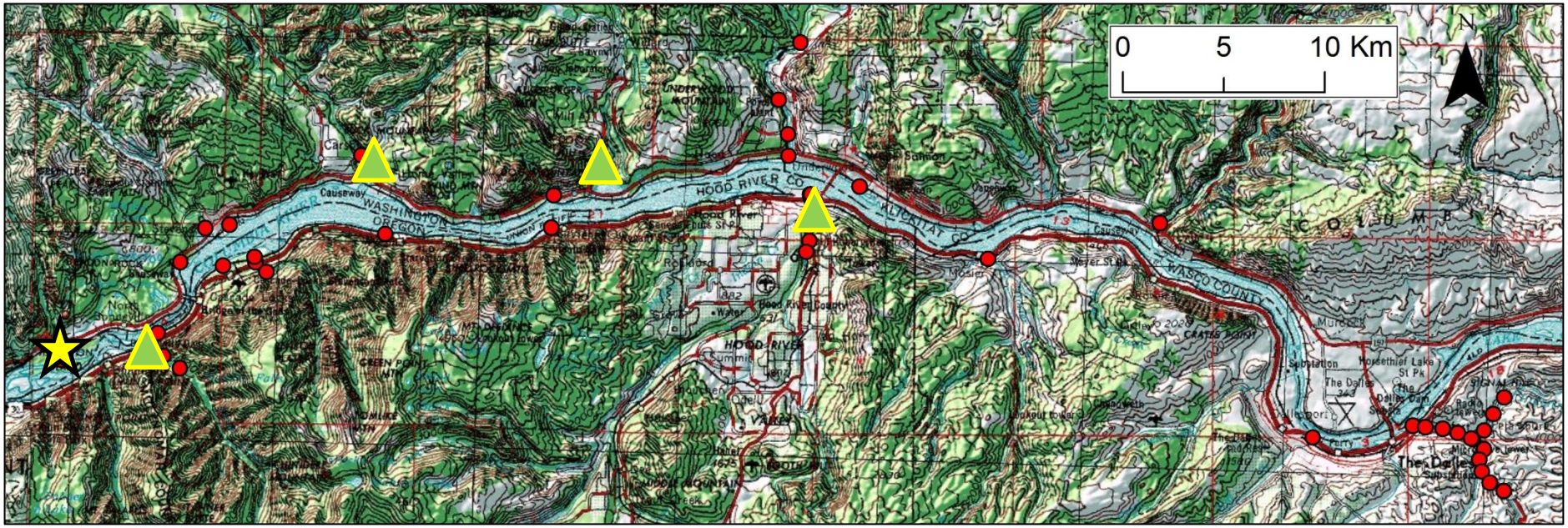
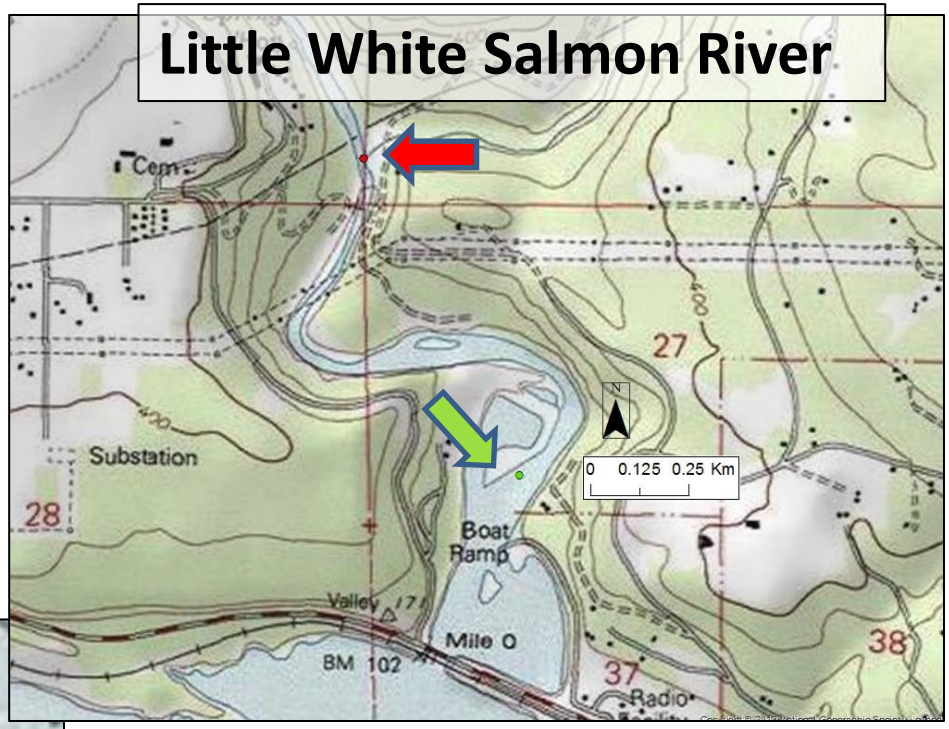
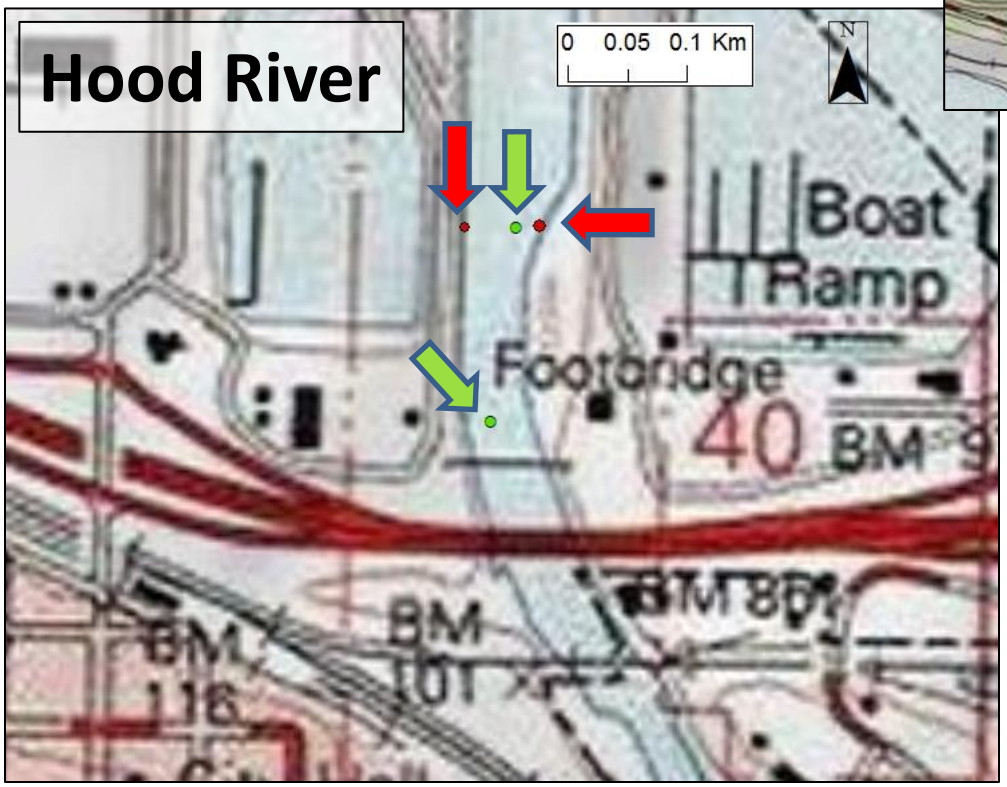
Results

- Marker successfully amplified only Chum DNA
- All control sites were positive ★
- Chum DNA found in four streams ▲
  - Eagle Creek, Hood River (OR)
  - Wind River, Little White Salmon River (WA)



- Large river sampling is feasible
- Thalweg sampling is a challenge
- Can use results to refine upstream sample extent





- Sample location matters
- Sample date matters
- Presence-only sampling
- Required repeat sampling to detect chum

Discussion

- To apply eDNA to assess recolonization:
  - Need explicit sample framework to address spatio-temporal variability of spawning
    - which streams sampled and when
  - Need to statistically assess sampling requirements in large rivers vs. small streams
    - e.g., model where DNA might be detectable relative to hydrology and DNA release point
  - Need more information on how environmental conditions affect persistence and detectability of DNA
  - Need to understand whether surveyors/ anglers are a source of contamination (i.e., false positives)

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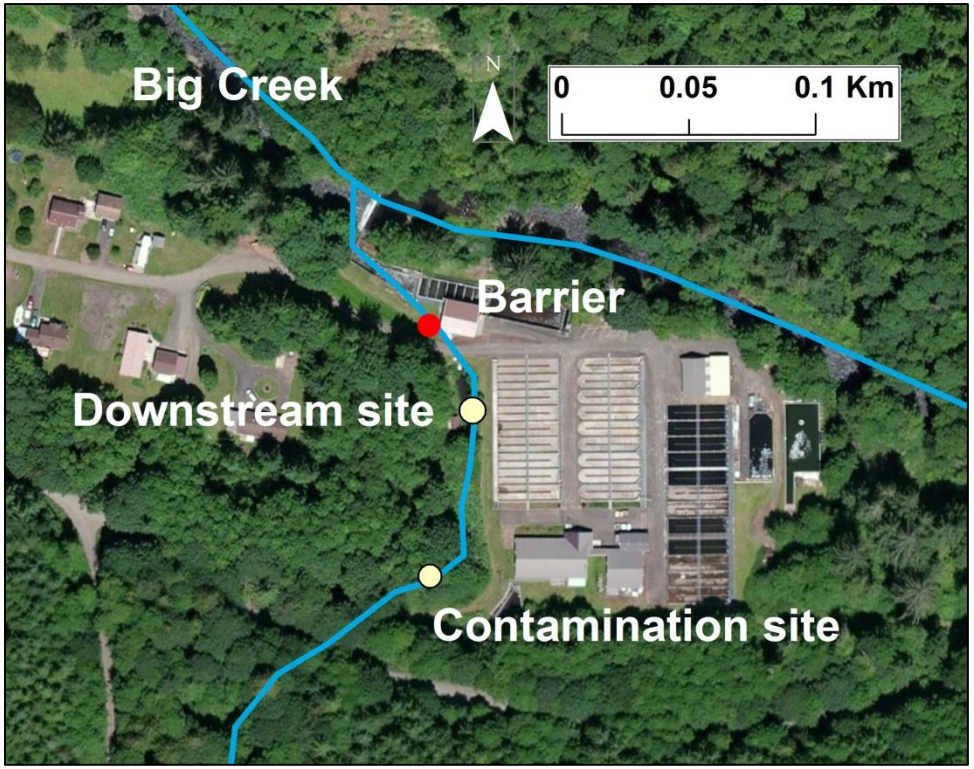
Tested contamination

- **Contamination:**
  - Canvas waders and felt-soled boots
  - Steps in tub with carcass and water
  - Enters and remains in stream until “during” sample complete



Sample design:

Day 1: Pre-sampling (is DNA present)

During sampling (1 m d/s of contamination site)

After sampling (1 m d/s of site; 10 min after)

After sampling (75 m d/s of site; 30 min after)

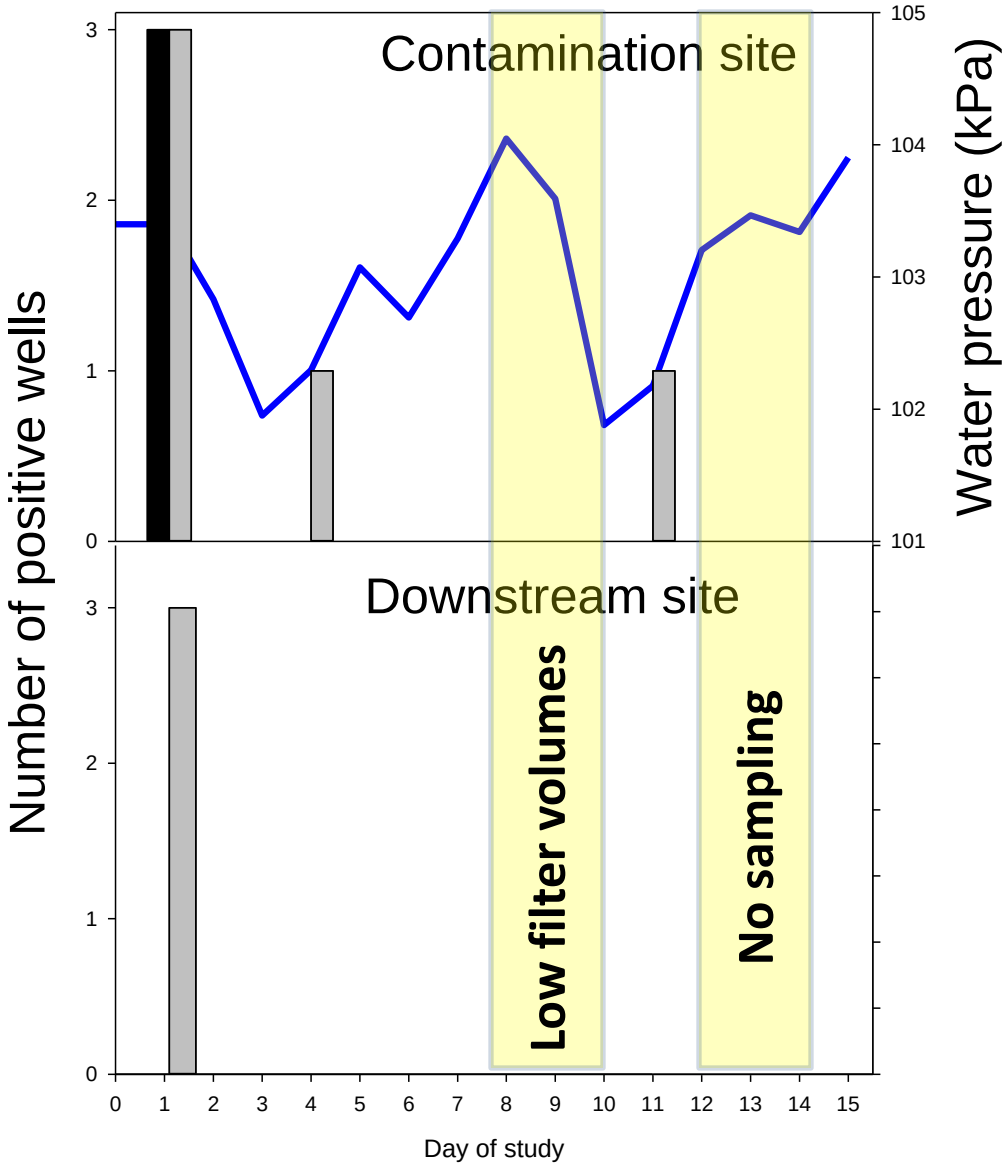
Day 2-11: Upper and lower sites sampled daily

Day 15: Upper and lower sites sampled

Preliminary results

- "Pre sampling" = --
- Day 1- both sites = +
- Day 4- upstream site = +
- Day 11- upstream site = +

- Positive detections appear to relate to hydrograph
- Implications for sampling in surveyed creeks:
  - After contamination day, DNA not detected 75 m downstream
  - DNA is detectable locally after 10 days



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