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

Kris Homel, Ph.D.
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

Bonneville Dam
The Dalles Dam
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
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
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

![Flowchart]

- Send samples to RMRS
- Science!
- Receive results
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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