The rapid, range-wide, eDNA-based assessment of Bull Trout distributions: Wenatchee River basin

State(s): Washington
Managing Agency/Organization: Wild Fish Conservancy
Type of Organization: Nonprofit Organization
Project Status: Underway
Project type: WNTI Project
Project action(s): Watershed or Population Assessment, Watershed Planning
Trout species benefitted: Bull Trout
Population: Wenatchee River Basin

Project summary:

The Bull Trout is an ESA-listed species that relies on cold stream environments across the Northwest and is expected to decline with climate change. Resource managers are charged with assessing Bull Trout populations across their range, but monitoring this species is difficult and costly, thus many potential habitats have rarely or never been sampled and the status of some populations is uncertain. To reduce this uncertainty (and the regulatory gridlock that can arise), we propose to assess the distribution of juvenile Bull Trout in the U.S. by using inexpensive, reliable environmental DNA (eDNA) sampling. For this proposal, the project area is the Wenatchee River basin.

Problem the Project Addresses:

Though once abundant, Bull Trout have declined in many locations from an array of factors, primarily habitat degradation, population isolation, and nonnative species invasions (USFWS 2015). This species is also the most thermally restricted salmonid in the Northwest—over 90% of juvenile Bull Trout observations are in streams with mean August water temperatures < 11°C (Isaak et al. 2015)—and there is recent evidence of range contraction in response to climate change (Eby et al. 2014). Federal listing mandates that agencies have reliable and precise information about the distribution of Bull Trout in thousands of streams, but Bull Trout surveys are expensive because the fish are often rare and difficult to collect (USFWS 2008). Consequently, many potentially or historically occupied habitats have been sampled infrequently or not at all. The uncertainty about Bull Trout distributions comes at a cost; agencies may not be able to efficiently target their limited conservation resources, may forego or delay land management critical for other objectives, and may even avoid monitoring populations because of the added burden of obtaining sampling permits.

To overcome some of that uncertainty, Rocky Mountain Research Station scientists recently developed the Climate Shield habitat occupancy model, which predicts the probability of juvenile Bull Trout presence in 5,332 potential natal cold-water habitats across the northwestern U.S. The fish and temperature data used to develop the model were crowd-sourced, provided by hundreds of biologists working for dozens of resource agencies and collected from thousands of sites. The Climate Shield model accurately predicted those cold-water habitats likely to support juvenile Bull Trout (78% classification accuracy), and made robust projections about those areas likely to remain as suitable habitat under moderate and extreme climate change scenarios. This model can act as a guide to make population surveys more efficient, but applying traditional sampling methods like electrofishing or snorkeling to the thousands of potential Bull Trout habitats
is logistically impossible. What biologists need is a method that provides precise, robust information about the presence of Bull Trout that can be collected quickly and at low cost across the entire range of this species. This goal is now attainable because of advances in environmental DNA (eDNA) sampling in streams i.e., the collection of DNA released by a target species into the water. Researchers at the U.S. Forest Service's National Genomics Center for Wildlife and Fish Conservation (NGCWFC) have pioneered developments in this field—including the first reliable eDNA assay for salmonid fish species, and the first that distinguishes Bull Trout from other species of char (Wilcox et al. 2013, 2014). They have also developed a field-proven eDNA sampling protocol that enables one person to collect sample in only 15 minutes (Carim et al. 2015). Species detection with eDNA is remarkably sensitive—in earlier research, 100% detection efficiency of target species was achieved despite order-of-magnitude changes in stream discharge (Jane et al. 2014). Subsequent field experiments indicate that detection probability of a single trout in 100 m of stream exceeds 85%, an efficiency several-fold better than one-pass electrofishing yet is less costly to obtain (Wilcox et al. in review). Collected samples are easily stored while in the field and can be processed rapidly in the lab. This protocol—used to guide collections of over 3,000 samples— has

been adopted by biologists from partner agencies in most western states, on projects ranging from population inventories to gauging the effectiveness of chemical treatments or electrofishing to remove nonnative species. Often, an entire 6th-code subwatershed (~20– 30 km of stream) can be sampled by a single person in one day, and because it involves filtering water, permitting is not an issue.

Bull Trout have been a focus of these eDNA surveys. The initial studies have been directed at precisely delineating the distribution of Bull Trout within select watersheds, as well as confirming their absence from potential habitats and discovering previously unknown populations (Figure 2; McKelvey et al. in press). In 2015, NGC scientists coordinated with partners to pair predictions of juvenile Bull Trout habitat occupancy from the Climate Shield model with an optimized eDNA sampling protocol to completely inventory potential juvenile Bull Trout habitats throughout two 4th-code river basins, the St. Joe in Idaho and the Upper Clark Fork in Montana, as well as begin inventories in the Boise, Boise-Mores, North-Middle Forks Boise, South Fork Boise, Payette, North Fork Payette, South Fork Payette, South Fork Salmon, and Upper Salmon in Idaho, the Middle Clark Fork in Montana, and the Upper Deschutes in Oregon. In 2016–2018, the objective is to extend this sampling to the entire range of Bull Trout in the U.S.

Objectives:

In 2016, this project will complete an eDNA-based inventory of juvenile Bull Trout habitats in the Wenatchee River basin. Locations to be sampled will include those predicted to be suitable for juvenile Bull Trout by the Climate Shield model, those designated as critical spawning and rearing habitat by the U.S. Fish and Wildlife Service, and those with historical observations of juvenile or spawning Bull Trout for which there are no recent surveys. Areas well-surveyed using other methods need not be sampled, unless desired by agency personnel. These surveys will precisely delineate the distribution of juvenile Bull Trout in this river basin, are likely to discover previously unrecognized spawning and rearing areas, and will remove uncertainty about whether historically occupied habitats still support juvenile Bull Trout. Moreover, these data, in combination with eDNA sampling from the rest of the historical range of Bull Trout, will be used to refine the accuracy of the Climate Shield model to provide even more spatially explicit and accurate predictions of occupied habitats and projections of habitats likely to remain suitable under various climate change scenarios.

Project proponents will construct an eDNA sampling template from the Climate Shield model for the Wenatchee River basin. Habitats will be sampled at 1-km intervals, which produces robust estimates of habitat occupancy in Bull Trout spawning and rearing habitats (McKelvey et al. in press). The sampling protocol will follow Carim et al. (2015). Laboratory analyses will follow Wilcox et al. (2013) and McKelvey et al. (in press).

Partners:

- Wild Fish Conservancy
- U.S. Forest Service, Rocky Mountain Research Station
- U.S. Fish and Wildlife Service

Project Monitoring:
Project stages consist of eight steps: 1) Develop an eDNA point template; 2) Work with project partners to refine the template (current estimate, 561 sites); 3) Train partners to conduct eDNA sampling; 4) Perform the eDNA sampling at identified sites; 5) Return samples to the National Genomics Center for Wildlife and Fish Conservation (NGCWFC); 6) Catalog and analyze samples; 7)Tabulate results; and 8) Complete a project report with maps and data ready to be posted on ScienceBase. The stages are specific, quantifiable, and readily monitored.

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