Alaska eDNA Workshop April 1, 2019

Themes and Takeaways

Applying eDNA methods:

- EDNA data is generally more useful and interpretable when collected in conjunction with traditional sampling methods. Pilot studies and validation of eDNA findings are critical for successful projects and avoiding false positives.
- Interpreting data requires lots of knowledge about local conditions that might affect sources, persistence of eDNA in the environment, and contamination. For water samples, understanding the hydrology of the system is critical (where's the water coming from and how much dilution is happening).
- Usefulness of eDNA techniques depends on study questions and needs, limitations of other sampling techniques.

Cost:

- Cost and effort of an eDNA project depend on availability of appropriate primers. Check with labs and the literature for options. If primers are available, the cost of the project will be much lower.
- Metabarcoding may be useful for many different applications – collaborating and sharing analytical costs of the same samples can be an effective way to lower individual project costs.

Invasive Species:

- Ora Russ presented information about some preliminary studies that FWS is doing to explore early detection of Elodea and pike eradication monitoring.
- Trey Simmons presented his efforts (with USGS lab) to monitor for a suite of potential invasive species in National Parks using a metabarcoding approach.

Abundance:

- Dave Tallmon and Meredith Pochardt presented results of studies with that successfully linked eDNA data and fish abundance (salmon and hooligan, respectively). More studies are needed to explore how successful these approaches will be in other systems.

Habitat Mapping

- Brooke Penaluna presented some preliminary results of their work to establish end-of-habitat for coastal cutthroat trout in WA and OR with eDNA and electrofishing methods. In some cases, eDNA seems to be more sensitive at low fish densities.
- Jeff Falke presented Allison Matter's research on juvenile Chinook habitat distribution in the Chena watershed. Sampling targeted sub-watersheds with a range of predicted habitat quality, based on preliminary intrinsic potential models.

Data Sharing:

- The USGS is adding eDNA data to their publicly searchable database.
- There is interest in exploring other options for AK researchers to share their work, including primers and results.

Resources identified during the meeting

Workshop Presentations (with links to website archive at https://seakfhp.org/edna-in-alaska-1-day-workshop-april-1-2019/)

Session 1. Primer on science status of eDNA, considerations for Alaska

eDNA Primer & USFWS Perspectives – Ora Russ (USWFS Genetics Lab)

An Ecologists Guide to eDNA: Examples from Oregon – Brooke Penaluna (USFS, PNWRS)

eDNA at AFSC: Environmental DNA at the Alaska Fisheries Science Center – Chris Kondzela (NOAA Genetics Lab)

Alaska Department of Fish and Game's Anadromous Waters Catalog and Position on eDNA Sampling Methods – J Johnson (ADFG AWC), Chris Habicht (ADFG Genetics Lab)

ADFG Anadromous Waters Catalog Information

ADFG AWC Guidelines and Position on eDNA Sampling

Session 2. Field applications utilizing eDNA sampling

Auke Creek Salmon eDNA – David Tallmon (UAS)

Using Environmental DNA to Monitor Eulachon (Thaleichthys pacificus) Abundance Northern Southeast Alaska (aka hooligan, Saak) – Meredith Pochardt (Takshanuk)

Identifying distribution boundaries at the upper extent of fish in forested streams with electrofishing and eDNA – Brooke Penaluna (USFS, PNWRS)

A Rapid Assessment Method to Estimate the Distribution of Juvenile Chinook Salmon (Oncorhynchus tshawytscha) in Tributary Habitats Using eDNA and Occupancy Estimation – Jeff Falke (UAF) for Allison Matter (see additional publication resource noted below)

Using eDNA (single species qPCR assays) for aquatic invasive species in Alaska – Ora Russ (USFWS Genetics Lab)

Multispecies/Metabarcoding with eDNA – Damian Menning (USGS)

Using metabarcoding of eDNA for detection of multiple aquatic invasive species (AIS) – Trey Simmons (NPS)

eDNA Resources

- Washington State University eDNA Resources Hub: https://www.ednaresources.com/
- The Rangewide Bull Trout eDNA Project https://www.fs.fed.us/rm/boise/AWAE/projects/BullTrout_eDNA.html

- Oregon State University's OPENS lab is developing an autosampler that may be useful for eDNA sample collection http://www.open-sensing.org/opensampler
- new journal: Environmental DNA https://onlinelibrary.wiley.com/journal/26374943
- Critical considerations for the application of environmental DNA methods to detect aquatic species (Goldberg et al. 2016) https://besjournals.onlinelibrary.wiley.com/doi/full/10.1111/2041-210X.12595
- A Rapid-Assessment Method to Estimate the Distribution of Juvenile Chinook Salmon in Tributary Habitats Using eDNA and Occupancy Estimation (Matter et al. 2018) https://afspubs.onlinelibrary.wiley.com/doi/10.1002/nafm.10014
- ADFG invasive species in Alaska information and resources: http://www.adfg.alaska.gov/index.cfm?adfg=invasive.main
- Potential of Environmental DNA to Evaluate Northern Pike (Esoxlucius) Eradication Efforts: An Experimental Test and Case Study (Dunker et al. 2016) https://s3-us-west-1.amazonaws.com/akssfapm/APM_Uploads/2014/44168/.pdf/dunkeretal2016.pdf
- Validation of PCR-Based Assays and Laboratory Accreditation for Environmental Detection of Aquatic Invasive Species (ISAC White Paper 2012) https://www.doi.gov/sites/doi.gov/files/uploads/isac_pcr_white_paper.pdf
- Needle in a haystack? A comparison of eDNA metabarcoding and targeted qPCR for detection of the great crested newt (Triturus cristatus) (Harper et al. 2017) https://onlinelibrary.wiley.com/doi/pdf/10.1002/ece3.4013
- Bokulich NA, Subramanian S, Faith JJ, Gevers D, Gordon JI, Knight R, Mills DA, Caporaso JG (2013) Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. Nat Methods 10:57–59. https://doi.org/10.1038/nmeth.2276
- Greiman SE, Cook JA, Tkach VV, Hoberg EP, Menning SM, Hope AG, Sonsthagen SA, Talbot SL (2018) Museum metabarcoding: a novel method revealing gut helminth communities of small mammals across space and time. Int J Parasitol doi. https://doi.org/10.1016/j.ijpara.2018.08.001
- Longmire JL, Maltbie M, Baker RJ (1997) Use of "Lysis Buffer" in DNA isolation and its implication for museum collections. Museum of Texas Tech University https://www.biodiversitylibrary.org/item/242562
- Menning DM, Simmons T, Talbot S (2018) Using redundant primer sets to detect multiple native Alaskan fish species from environmental DNA. Conservation Genet Resour https://doi.org/10.1007/s1268 6-018-1071-7
- Taberlet P, Coissac E, Pompanon F, Gielly L, Miguel C, Valentini A, Vermat T, Corthier G, Brochmann C, Willerslev E (2007) Power and limitations of the chloroplast trnL (UAA) intron for plant DNA barcoding. Nucleic Acids Res 35(3):e14. https://doi.org/10.1093/nar/gkl938
- Taberlet P, Gielly L, Pautou G, Bouvet J (1991) Universal primers for amplification of three non-coding regions of chloroplast DNA. Plant Mol Biol 17: 1105-1109. https://doi.org/10.1007/BF00037152
- Zeglin LH, Wang B, Waythomas C, Rainey F, Talbot S (2016) Organic matter quantity and source affects microbial community structure and function following volcanic eruption on Kasatochi Island, Alaska. Env Micro https://doi.org/10.1111/1462-2920.12924

Next steps

- Continue communication among the group to share research, methods, results
    - Create a working group, quarry for interest

    - Piggy back on other in-person meetings like AFS, AWRA, Wildlife Society, others?
    - Create a listserv that people can use to query experts and share information
- Identify data sharing opportunities
    - Especially information about primers that exist for AK species
    - Results from AK studies
    - Can we develop or add to an existing database/portal?
- Prioritize monitoring, especially for invasive species
- Collaborate to access funding and use funding efficiently