

# RESEARCH/PD ANNUAL REPORT - PROGRESS REPORT

2015 annual report - progress

Lorenz Hauser

Shifting baselines in Puget Sound: population abundance of Pacific herring and its use by Native Americans over the millennia

R/HCE-3

Submitted On: 04/29/2016 05:45:46 PM

## METRICS & MEASURES

Metric/Measure	Value	Note
Acres of coastal habitat	0	
Fishermen and seafood industry personnel	0	
Communities - economic and environmental development	0	
Stakeholders - sustainable approaches	0	
Informal education programs	200	Discover Science Weekend
Stakeholders who receive information	300	WA: Puget Sound Anglers Club, Port Gamble S'Klallam members, San Juan Island Community Members (Sea Doc Society) BC: Haida Community Members, Heiltsuk Community Members discover science weekend (200)
Volunteer hours	100	co-PI Kopperl's time, Sampling effort (various BC citizen scientists collecting samples), Lab members (Discover Science Weekend, MESA outreach) Marta Branch (helped set up interviews), Port Gamble S'Klallam Community Members (archaeological excavation at Port Gamble) (200) KL - COUNTING 100 (NOT LAB MEMBER TIME)
P-12 students reached	50	Kids attending Discover Science Weekend at the Seattle Aquarium and High School students enrolled in Seattle MESA Saturday Academy (KL NOT DOUBLE-COUNTING BETWEEN PROJECTS)
P-12 educators	0	

## REQUESTED INFORMATION

### Publications

No **Publications** information reported

### Students Supported

**Eleni Petrou** (Continuing Student)

elpetrou@uw.edu  
University of Washington, Aquatic and Fishery Sciences

**Field of Study:**  
**Advisor:**  
**Degree Type:** PhD  
**Degree Year:** 2018

**Student Project Title:**

**Involvement With Sea Grant This Period (capstone, fellow, intern, etc.):**

**Post-Graduation Plans (employer, grad school, etc.):**

**Was this thesis/dissertation supported by Sea Grant?:** Yes

**Thesis / Dissertation:**

**New or Continuing?:** continuing

**Degree awarded this reporting period?:** No

**Financially supported?:** Yes

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**Matthew Skirvin** (Continuing Student)  
**matthew.skirvin@gmail.com**  
**University of Washington, Biology**

**Field of Study:**  
**Advisor:**  
**Degree Type:** BS  
**Degree Year:** 2015

**Student Project Title:** Bioinformatics detection of DNA contamination from RAD sequence data

**Involvement With Sea Grant This Period (capstone, fellow, intern, etc.):**

**Post-Graduation Plans (employer, grad school, etc.):** job with computer gaming company

**Was this thesis/dissertation supported by Sea Grant?:** No

**Thesis / Dissertation:**

**New or Continuing?:** continuing

**Degree awarded this reporting period?:** Yes

**Financially supported?:** Yes

## Narratives

**Herring project report 2015**  
**Uploaded File:** [Project\\_Report\\_2015.pdf](#)

## Partners This Period

**Dept of Archaeology, Simon Fraser University**  
**Types:** Academic Institution

**Scale:** INTERNATIONAL

**Notes:** Co-PIs, anthropology, ancient DNA work.

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**University of British Columbia**

**Types:** Academic Institution

**Scale:** INTERNATIONAL

**Notes:** Lead in collaborating NSERC Program

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**Dept of Anthropology, University of Oregon**

**Types:** Academic Institution

**Scale:** INTERNATIONAL

**Notes:** Lead in collaborating NSF program

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**Port Gamble S'Klallam Tribe**

**Types:** Government

**Scale:** Tribal

**Notes:** Sampling, Discussion of TEK

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**Suquamish Tribe**

**Types:** Government

**Scale:** Tribal

**Notes:** Archeology, collaborator, providing TEK and access to historical samples

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**Washington Department of Fish and Wildlife**

**Types:** Government

**Scale:** STATE

**Notes:** Sampling, Collaboration on DoE funded project on Port Gamble herring

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**Puyallup Tribe**

**Types:** Government

**Scale:** Tribal

**Notes:** Access to tribal samples

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**Heiltsuk First Nation, BC**

**Types:** Government

**Scale:** Tribal

**Notes:** Traditional Ecological Knowledge, Sampling

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**Haida First Nation, BC**

**Types:** Government

**Scale:** Tribal

**Notes:** Traditional Ecological Knowledge, sampling

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**Hakai Network**

**Types:** NGO

**Scale:** INTERNATIONAL

**Notes:** Collaboration on Ecosystem Based Management

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**Q'UI-Lhanumtsun Aquatic Resources Society**

**Types:** NGO

**Scale:** INTERNATIONAL

**Notes:** Sampling

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**Fisheries and Oceans Canada (DFO)**

**Types:** Government

**Scale:** INTERNATIONAL

**Notes:** Samples

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**University of Washington, Burke Museum of Natural History and Culture (UW)****Types:** Academic Institution**Scale:** STATE**Notes:** Provision of bone samples**Alaska Fisheries Science Center (US DOC, NOAA, NMFS)****Types:** Government**Scale:** STATE**Notes:** Sharon Wilde, provision of samples from Alaska**San Juan County Marine Resources Committee, Northwest Straits Commission****Types:** NGO**Scale:** REGIONAL**Notes:** Contact with traditional knowledge holders, outreach

## STANDARD QUESTIONS

**Impacts and Accomplishments****(1)**

<b>Type</b>	<b>accomplishment</b>
<b>Title</b>	Washington Sea Grant-funded researchers develop lab protocols for eliminating contamination in next-generation genetic sequencing
<b>Relevance</b>	Next-generation genetic sequencing is a key tool in research such as a current Washington Sea Grant effort to chart changes in the local abundance of Pacific herring, an important food and forage fish. Contamination is a major issue in such sequencing because it is difficult to detect and may have serious impacts on downstream analysis. Samples collected at spawning sites, such as herring fin clippings, are particularly prone to contamination by sperm.
<b>Response</b>	Washington Sea Grant-funded researchers developed and optimized lab protocols for removing contamination without damaging DNA quality or quantity.
<b>Results</b>	Tests with contaminated, decontaminated and clean samples demonstrated the effectiveness of the decontamination approach. This protocol will be particularly useful for herring sampled at spawning beaches, but can also be used for other applications.
<b>Recap</b>	Washington Sea Grant-funded researchers developed a new decontamination protocol for next-generation sequencing, a vital tool in ongoing herring studies and other research.
<b>Comments</b>	
<b>Primary Focus Area</b>	Healthy Coastal Ecosystems
<b>Secondary Focus Areas</b>	Sustainable Fisheries and Aquaculture, Resilient

<b>Secondary Focus Areas</b>	Communities and Economies
<b>Goals</b>	Ocean and coastal resources are managed using ecosystem-based approaches. Coastal communities and economies are vibrant and resilient.
<b>Partners</b>	Alaska Fisheries Science Center (US DOC, NOAA, NMFS) Department of Archaeology, Simon Fraser University (SFU) Fisheries and Oceans Canada (DFO) Haida First Nation, BC Hakai Network Heiltsuk First Nation, BC Port Gamble S'Klallam Tribe Puyallup Tribe Q'UI-Lhanumutsun Aquatic Resources Society San Juan County Marine Resources Committee Suquamish Tribe University of British Columbia University of Oregon, Department of Anthropology (UO) University of Washington, Burke Museum of Natural History and Culture (UW) Washington Department of Fish and Wildlife
<b>PI Draft</b>	<p>* Type accomplishment * Title Washington Sea Grant funded research provides protocols to remove contamination in samples used for next generation sequencing * Relevance Contamination is a major issue in next generation sequencing, because it is difficult to detect and may have major impacts on downstream analysis. Samples collected at spawning sites, such as herring fin clippings, are particularly prone to contamination because of contamination with sperm. * Response Washington Sea Grant funded researchers developed and optimized protocols that remove contamination without impacting DNA quality and quantity * Results Tests with contaminated, decontaminated and clean samples demonstrated the effectiveness of the decontamination approach. The protocol will be particularly useful for herring sampled at spawning beaches, but can also be used for other applications * Recap Washington Sea Grant funded researchers develop a new decontamination protocol for next generation sequencing approaches. Comments Primary Focus Area Sustainable Fisheries and Aquaculture Secondary Focus Areas Healthy Coastal Ecosystems Goals Ocean and coastal resources are managed using ecosystem-based approaches., Fisheries are safe, responsibly managed and economically and culturally vibrant. Partners</p>

**Tools, Technologies, Information Services / Sea Grant Products**

No **Tools, Technologies, Information Services / Sea Grant Products** information reported

**Economic Impacts**

No **Economic Impacts** information reported

## Community Hazard Resilience

No Community Hazard Resilience information reported

### Meetings, Workshops, Presentations

(1)

<b>Type of Event</b>	Public or professional presentation
<b>Description</b>	Petrou EL, Lepofsky D, Yang D, Kopperl R, Hauser L. (November 2015). Shifting baselines in the Pacific Northwest: the story of Pacific herring. Oral presentation. Graduate Student Symposium of the University of Washington's School of Aquatic and Fishery Sciences, Seattle, WA, USA
<b>Event Date</b>	11-19-2015
<b>Number of Attendees</b>	60

(2)

<b>Type of Event</b>	Public or professional presentation
<b>Description</b>	Petrou EL, Yang D, Lepofsky D, Kopperl B, Hauser L. An interdisciplinary investigation of shifting baselines in the socio-ecological system of Pacific herring and Salish Sea peoples. Oral presentation. May 2015, Annual Meeting of the Society of Ethnobiologists, Santa Barbara, CA, USA.
<b>Event Date</b>	05-08-2015
<b>Number of Attendees</b>	30

(3)

<b>Type of Event</b>	Public or professional presentation
<b>Description</b>	Petrou EL, Yang D, Lepofsky D, Kopperl B, Hauser L. A coastwide analysis of Pacific herring population structure. Oral presentation. August 2015, Annual Meeting of the American Fisheries Society, Portland, OR, USA.
<b>Event Date</b>	08-18-2015
<b>Number of Attendees</b>	50

(4)

<b>Type of Event</b>	Public or professional presentation
<b>Description</b>	Hauser L. Pacific herring in space and time: insights from next generation sequencing. Invited Seminar, Department of Zoology, Nelson Mandela Metropolitan University, South Africa

<b>Event Date</b>	03-16-2015
<b>Number of Attendees</b>	40

(5)

<b>Type of Event</b>	Public or professional presentation
<b>Description</b>	Hauser L, Jimenez-Hidalgo I, Lowry D, Stick K, Lindquist A (2015) Dynamic population structure of Pacific Herring in Puget Sound
<b>Event Date</b>	08-18-2015
<b>Number of Attendees</b>	30

(6)

<b>Type of Event</b>	Public or professional presentation
<b>Description</b>	Hauser L (2015) Pacific Herring in Space and Time: scientific evidence for population structure in a highly dynamic species. Herring Summit, Vancouver
<b>Event Date</b>	06-09-2015
<b>Number of Attendees</b>	60

### Leveraged Funds

(1)

<b>Purpose</b>	Shifting baselines in Puget Sound: population abundance of Pacific herring and its use by Native Americans over the millennia - graduate student support
<b>Source</b>	NSF
<b>Amount</b>	36000
<b>Start Date</b>	02-01-2015
<b>End Date</b>	01-31-2016

(2)

<b>Purpose</b>	Shifting baselines in Puget Sound: population abundance of Pacific herring and its use by Native Americans over the millennia - complementary study on population genetics of herring in British Columbia.
<b>Source</b>	NSERC
<b>Amount</b>	189333
<b>Start Date</b>	02-01-2015

<b>End Date</b>	01-31-2016
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# Shifting baselines in Puget Sound: population abundance of Pacific herring and its use by Native Americans over the millennia

Lorenz Hauser, Dana Lepofsky, Dongya Yang and Robert Kopperl

## Activities and Progress

### Sample Collection in 2015

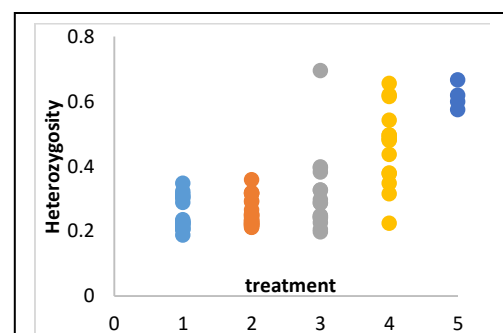
We coordinated sample collection with our research partners, the Washington Department of Fish and Wildlife and the Port Gamble S'Klallam Tribe. In 2015, spawning adults were collected from Port Gamble (N = 25), Similk Bay (N = 74), and Cherry Point (N = 100), WA. Newly hatched herring larvae (N = 200) were collected from Elliot Bay, WA. We also collected non-spawning herring from the USGS Marrowstone Research Station (N = 100) for use in a decontamination experiment (described below).

### DNA decontamination

Contamination continued to be an issue in 2015. Although a previous Sea Grant project developed a decontamination protocol for microsatellites (Mitchell et al. 2008), the effects of bleaching on next generation sequencing data was unclear. We therefore tested the efficiency and effect of decontamination in a controlled experiment using contaminated wild spawning herring as well as uncontaminated samples of juvenile herring from the USGS lab at Marrowstone (Paul Hershberger). Each sample was used directly as well as after bleaching as described in Mitchell et al. (2008). In addition, we created artificially contaminated samples by combining four uncontaminated samples in equal concentration. DNA was extracted from all samples, and screened at six microsatellite loci as well as prepared for RAD sequencing. Eight individuals were re-extracted to estimate genotyping error rates.

Microsatellite analyses showed that 25% of the samples collected from spawning adults displayed more than two alleles per microsatellite locus, suggesting that the samples were contaminated with sperm DNA. In contrast, only one sample had more than two alleles per locus after bleaching. None of the samples collected from juvenile herring had more than two alleles per microsatellite locus, confirming the absence of contamination.

RAD sequencing resulted in 6,208 loci in 82 samples (35 samples in control treatment, 35 samples in bleaching treatment, 4 contamination control samples, 8 replicated samples) in our data set. As expected, contaminated samples had higher heterozygosity than uncontaminated samples, at a level very similar to the artificially contaminated samples (Figure 1). Bleaching reduced the heterozygosity of contaminated samples to that of uncontaminated samples, but had negligible effects on uncontaminated sample heterozygosity. Furthermore, analysis of replicated extractions of juvenile herring showed that bleaching did not alter the genotypes: the genotype discrepancy rate was 3% between individuals exposed to different treatments, which is below the 5% commonly reported in the literature. We are now confident that our method (i) removes all or most of the contamination and (ii) does not affect the determination of



**Figure 1.** Individual heterozygosity calculated using 6,208 RAD loci. Each circle represents a different sample. Treatments are: 1: uncontaminated; 2: uncontaminated, bleached; 3: contaminated, bleached; 4: contaminated; 5: artificially contaminated.

genotypes significantly. These results will be verified with VerifyBamID (Jun et al. 2012), a program that estimates levels of contamination directly from RAD data.

### Molecular work for population genetics of herring

Using the protocol we developed in the decontamination experiment, we cleaned fin samples taken from spawning adult herring from the following populations and sampling years: Port Gamble 2014, Quilcene Bay 2014, Similk Bay 2015, Cherry Point 2014, Port Orchard 2014, and Squaxin Pass 2014 (N = 48 individuals per population). DNA was of high quality for Squaxin Pass, Port Orchard and Similk Bay, but appeared highly degraded for the other samples, probably because of extended time between capture of herring and collection of tissue samples. Extracted DNA from these samples was delivered to the WDFW genetics lab and they are preparing DNA libraries for RAD sequencing.

### Ancient DNA of archaeological herring bones

Ancient DNA (aDNA) was extracted in Dongya Yang's aDNA laboratory at Simon Fraser University from ten herring prootic bones originating from the Burton Acres (45KI437) archaeological assemblage. Eight of the samples successfully amplified at the mitochondrial D-loop locus using PCR, and the resulting haplotypes matched previously published haplotypes for Pacific herring. These results indicate that we can successfully amplify ancient herring DNA from prootic bones.

### Interviews of herring fishers and tribal elders

From November 2014-May 2015, we conducted semi-directive interviews with 13 fishers who harvested herring in the Salish Sea. The semi-directive interview is considered a standard method to collect ethnographic information, in which the interviewer guides the discussion based on a list of topics, and the participant can skip or add topics based on their particular expertise. We chose to conduct interviews primarily with elders because they might have memories of herring abundance and spawning behavior predating the start of scientific surveys in the 1970's. Participatory mapping techniques (Huntington 2000) were used to identify where and when respondents fished, where they routinely encountered schools of herring, and where they observed herring spawning. Finally, respondents were prompted to describe the cultural and economic uses of herring and to discuss any trends they have observed over time. The interview topics were approved by the Human Subjects Division of the University of Washington.

The results presented here are from a preliminary analysis of the interview data, based on interview notes. Interview participants included commercial herring fishers, subsistence herring fishers, and recreational salmon fishers who used to catch herring for use as bait. The average participant age was 76 years, and ages ranged from 90 to 55 years. Interview participants included members of Native American Tribes (Lummi and Samish) and Indo-European inhabitants of coastal Washington State. Only one of the interview participants was a woman. All interview participants observed declines in the abundance of herring during their lifetimes. Qualitative ranking of herring abundance by decade revealed that older fishers reported declines in herring abundance earlier than younger fishers. This finding is consistent with shifting baselines in peoples' perception of herring abundance.

### Future work for 2016

#### Population genetics and ancient DNA

We are in the process of developing RAD libraries for sequencing to describe population structure of sampled herring populations. Using these sequence data, we will develop DNA markers that can distinguish between Cherry Point, Squaxin Pass, and the remaining populations in WA State. These

markers will be used to analyze ancient herring bones from the Burton Acres, Xaxtl'abish 1, Old Man House and Bay Street Shell Midden archaeological sites.

### Interviews

We will expand this research to cover a greater geographic area within Washington State, and to investigate whether there is spatial variation in observed trends of herring abundance and herring use. In addition, we will transcribe the interviews and code them for a full qualitative analysis. We are in the process of setting up additional interviews with members of the Suquamish Tribe.

### References

- Huntington, H. P. 2000. Using traditional ecological knowledge in science: methods and applications. *Ecological Applications* **10**:1270-1274.
- Jun, G., M. Flickinger, K. N. Hetrick, J. M. Romm, K. F. Doheny, G. R. Abecasis, M. Boehnke, and H. M. Kang. 2012. Detecting and Estimating Contamination of Human DNA Samples in Sequencing and Array-Based Genotype Data. *American Journal of Human Genetics* **91**:839-848.
- Mitchell, D., P. McAllister, K. Stick, and L. Hauser. 2008. Sperm contamination in archived and contemporary herring samples. *Molecular Ecology Resources* **8**:50-55.