

Alaska Sustainable Salmon Fund Statement of Work

I. Project Title: Estimating Escapement of Chilkat River Chinook Salmon Using Transgenerational Mark-Recapture

II. Project Number: 54018

III. Principal Investigator

Megan V. McPhee, Associate Professor of Fisheries
University of Alaska Fairbanks
17101 Point Lena Loop Road
Juneau, AK 99801
907-796-5464
mvmcphee@alaska.edu

Co-Principal Investigator

Kyle Shedd, Fisheries Geneticist II
Alaska Department of Fish and Game
Division of Commercial Fisheries
Gene Conservation Laboratory
333 Raspberry Road
Anchorage, AK 99518
907-267-2531
kyle.shedd@alaska.gov

IV. Project Period: 8/15/21 - 8/14/23

V. AKSSF Objective: Escapement **PCSRF Objective:** RM&E

VI. Project Description

1. Synopsis

Chilkat River Chinook salmon have historically been a central stock for subsistence (including customary and traditional) harvest by residents of the Haines region in Southeast Alaska. Recent declines in productivity and failure to meet escapement goals have led to this population being listed as a “stock of management concern” by the State of Alaska and have curtailed subsistence harvest in recent years. This project will estimate escapement of Chilkat River Chinook salmon abundance by implementing an emerging method called “transgenerational mark-recapture” (tGMR) where marking and recapturing is accomplished via genotypic identification of spawners and their offspring. Simulations will be used to assess assumptions and mitigate for potential biases in tGMR, which will help guide future tGMR projects.

2. Introduction

Estimating the number of spawning adults in a population is a fundamental but difficult task for fishery managers. This task is manageable for Pacific salmon stocks, which can be enumerated through visual or sonar counts as they migrate homeward through relatively small sampling areas. Still, escapement monitoring requires intensive sampling across the return migration, often in remote locations, and is subject to changing environmental conditions (e.g., strong winds, high turbidity) that can reduce data quality. Therefore, methods that can increase the efficiency and accuracy of escapement monitoring would be highly beneficial, particularly during times of shrinking budgets for fisheries monitoring.

A recent advance in population monitoring is the use of genetics in mark-recapture methods. Specifically, genotypes can be used to mark individuals, and sampling those individuals' offspring (identified by comparing juvenile to adult genotypes) can be treated as 'recapturing' those focal individuals. A specific variant of this approach, tGMR, has been developed for semelparous Pacific salmon. Event 1 in tGMR is genetic sampling of adult spawners, and event 2 is genetic sampling of their offspring in the following year. Parent-offspring pairs are inferred by assigning juveniles to parents based on their genotypes, and so both 'recaptured' (assigned parent-offspring pairs) and 'unmarked' (unsampled parents of unassigned offspring) adults are identified with the juvenile samples. These data are used in Peterson mark-recapture models to estimate the size of the adult spawning population.

Chinook Salmon from the Chilkat River in Southeast Alaska are currently being genetically sampled by Alaska Department of Fish and Game (ADF&G) with the aim of applying tGMR to estimate escapement. Unlike traditional mark-recapture projects, the methods used to evaluate tGMR assumptions are not fully understood. There are several aspects of salmon life history and catchability that could lead to non-independence in capture probabilities in the two sampling events of tGMR including biases, such as correlations among adult size, catchability, and number of juveniles produced. Therefore, in addition to producing a tGMR population estimate, a secondary goal of the project is to evaluate potential biases in tGMR estimates under a range of scenarios using simulation analysis, and to develop methods to test the core assumptions of tGMR. If tGMR proves to be successful for estimating escapement of Chilkat River Chinook salmon, this method could be extended to other Alaskan salmon stocks that lack intensive monitoring programs for more efficient and precise escapement monitoring.

3. Location
Chilkat River: 59.267627, -135.651157
4. Related Projects
None

VII. Objectives

- **Objective 1:** Estimate escapement of Chilkat River Chinook salmon in 2020 using transgenerational mark-recapture (tGMR)

- **Objective 2:** Compare tGMR estimates to those derived from traditional mark-recapture
- **Objective 3:** Use simulation models to assess tGMR assumptions and develop methods to test for potential violations

VIII. Methods

The field data and traditional mark-recapture estimate to be used in this project are generated as part of ADF&G's regular monitoring activities on the Chilkat River. A traditional two-sample mark-recapture for closed population estimate of spawner abundance will be conducted. Returning adult Chinook salmon are sampled in early summer by drift gillnet and fishwheel in the lower river during event 1, marked by opercular punch, and released. The second sampling event takes place in late summer/early fall in the major spawning reaches of the drainage, where field crews use a variety of methods in order to sample as many individuals as possible. For the purposes of tGMR, tissue samples (pelvic fin clips) will be collected from all adults captured during event 1 and all unmarked adults captured during event 2. The second sampling event for the tGMR estimate will be of offspring, sampled as parr in autumn of 2021 during ADF&G's regular monitoring activities. Tissue samples will be taken from all incidental parr mortalities, and DNA collections will be supplemented by mucus swabs of live parr in order to achieve target sample sizes.

Adult and parr tissue and mucus samples will be sent to the ADF&G Gene Conservation Lab for DNA extraction and genotyping. Laboratory personnel will genotype each sample at 299 SNP loci using the 'genotyping in thousands' (GTseq) method including a standard quality-control/quality assurance protocol. Relationships between sampled adults and parr will be identified using two methods. First, parent-offspring pairs will be identified by maximum likelihood based on Mendelian inheritance. Second, a full pedigree will be reconstructed based on genotypes of parr and sampled parents; unsampled parents will be inferred from identified sibling parr. This method allows inference of the total number of sampled and unsampled parents contributing to the observed juvenile genotypes, which is used in downstream tGMR calculations using the hypergeometric distribution.

This project will implement tGMR using two different methods, following the methods outlined in Rawding et al. (2014): the binomial Lincoln-Petersen method and the hypergeometric estimator. The binomial estimator allows sampling with replacement and estimates the adult population size based on the number of adults genotyped ("marks"), the number of parr sampled multiplied by two ("captures"), and the number of parr assigned to genotyped parents ("recaptures"). The hypergeometric estimator uses sampling without replacement (i.e., only the first 'sampling' of a parent by a genotyped parr is considered) and relies on the estimate of the number of unsampled (inferred) parents produced by the pedigree reconstruction. In this case, the number of adults genotyped still constitute the "marks", but "captures" are the number of unique parents inferred from the offspring, both sampled and unsampled, and "recaptures" are the number of unique parents assigned to offspring.

Simulations will be used to address a range of possible demographic and sampling scenarios that could violate the tGMR model assumptions and bias adult population size estimates. Such violations could arise, for example, if adult sampling is size-selective and if reproductive success (i.e., family size) is also correlated with size. Existing literature on the phenotypic correlates of reproductive success in Chinook salmon will be reviewed to come up with a range of biologically plausible parameter values for variable family size. The long-term monitoring data from the Chilkat River will be used to compare the body size of adult catch among capture method and sample date to infer plausible size-selectivity parameters. Simulation models will be used to generate plausible tGMR samples from known population sizes. These simulated samples will then be used to evaluate tGMR estimates and compared to the known population size in order to evaluate the direction and magnitude of bias under varying scenarios. Results from the simulation analyses will be used to better understand the tGMR model and develop recommendations on how to test for potential violations.

IX. Benefits

Accurate and efficient enumeration of salmon populations is essential for assessing the status of salmon populations, including monitoring declines as well as recovery. Since the listing of Chilkat Chinook as a “stock of management concern”, subsistence harvest has been severely restricted. This project develops methods that may enhance the efficiency, accuracy, and precision of abundance estimates for Chilkat Chinook. The project will also provide widely applicable benefits to many stocks of salmon by refining our understanding of the extent of, and how to mitigate for, potential biases in the tGMR method. Moreover, if the tGMR methodology can be validated, it could be used as a cost-effective tool to estimate spawning abundance on wild salmon populations in Southeast Alaska lacking robust assessment tools.

X. Products, Milestones, and Timelines

Note: Prior to and alongside this project, ADF&G will conduct adult genetic sampling and traditional mark-recapture sampling (summer 2020), genetic sampling (fall 2021), and genotyping (winter 2021-2022) with other funding.

- August-December 2021: Gather life-history and catchability data from literature for parameterization of simulations (Objective 3)
- April-June 2022: Conduct parentage analysis to assign juvenile samples to parents (exact timing depending on availability of genotypic data)
- June-August 2022: Conduct and compare tGMR (Objective 1) and traditional mark-recapture (Objective 2) estimates
- September-December 2022: Run simulations for Objective 3 and develop recommendations for evaluating tGMR assumptions
- January-May 2023: Finalize analyses and draft final report, peer-reviewed manuscript, and student MS thesis
- Spring 2023: Present results at the annual meeting of the Alaska Chapter of the American Fisheries Society
- Summer 2023: Student defense of MS thesis; final report submitted to AKSSF

XI. Project Budget

UAF Budget	Total
100 Personnel	\$77,464
200 Travel	\$2,291
300 Contractual	\$25,626
400 Supplies	\$0
500 Equipment	\$0
Subtotal	\$105,381
Expenses subject to indirect	\$80,231
600 Indirect	\$44,127
Total	\$149,508

UAF Budget Narrative:

Line 100: Personnel (\$77,464)

Megan McPhee will oversee the project, assist with analyses and manuscript preparation, and ensure timely submission of progress reports and final project deliverables: 40 hours in Year 1 and 80 hours in Year 2 @ \$49.47/hour (+2.5% yearly increase) + 18.4% leave reserve + 29.8% benefits = \$9,507.

A graduate student will assist in analyses (including parentage analyses, population estimates, and simulations), manuscript preparation, and presentations and will write a MS thesis based on the research conducted in this project over one academic year and a summer: 2,724 hours @ \$21.34/hour + 9.1% benefits (summer only) + \$5,841 student health care fees = \$67,957.

Salary table

	Hourly Wage	Leave Rate	Yearly Increase	Yr 1 Hours	Yr 1 Total	Yr 2 Hours	Yr 2 Total	Total Request
Megan McPhee	\$49.47	18.4%	1.025	40.0	\$2,401	80.0	\$4,923	\$7,324
Grad Stud/Academic	\$21.34	0.0%	1	696.0	\$14,853	696.0	\$14,853	\$29,706
Grad Stud/Summer	\$21.34	0.0%	1	696.0	\$14,853	696.0	\$14,853	\$29,706
TOTAL SALARIES AND WAGES					\$32,107		\$34,629	\$66,736

Benefits table:

		Yearly Increase	Year 1	Year 2	Total Request
Megan McPhee	29.8%		\$716	\$1,467	\$2,183
Grad Student/Academic Year	0.0%		\$0	\$0	\$0
Grad Student/Summer	9.1%		\$1,352	\$1,352	\$2,704
Graduate Student Health Insurance	\$2,637	1.07	\$2,822	\$3,019	\$5,841
TOTAL FRINGE BENEFITS			\$4,890	\$5,838	\$10,728

Line 200: Travel (\$2,291)

The graduate student will travel to Anchorage to attend the Alaska Chapter of the American Fisheries Society meeting or a similar conference venue to present the project:

- Airfare Juneau-Anchorage: \$605
- Lodging per diem: 5 days @ \$229/day = \$1,145
- Meals/incidentals per diem: 6 days @ \$70/day = \$420
- Ground transportation: \$121

Line 300: Contractual (\$25,626)

- Graduate student tuition: \$21,330
- Graduate student fees: \$3,820
- Conference registration: \$476

Line 600: Indirect (\$44,127)

UAF’s federally negotiated indirect rate through June 30, 2022, is 55% excluding, among other costs, tuition, equipment, and contractual costs in excess of \$25,000.

XII. Match Budget

UAF Match Budget	Total
100 Personnel	\$33,760
200 Travel	\$0
300 Contractual	\$0
400 Supplies	\$0
500 Equipment	\$0
Subtotal	\$33,760
600 Indirect	\$18,568
Total	\$52,328

UAF Match Budget Narrative:

Line 100: Personnel (\$33,760)

Megan McPhee will oversee the project, assist with analyses and manuscript preparation, and ensure timely submission of progress reports and final project deliverables: 214 hours in Year 1 and 214 hours in Year 2 @ \$49.47/hour (+2.5% yearly increase) + 18.4% leave reserve + 29.8% benefits = \$33,760.

Line 600: Indirect (\$18,568)

UAF’s federally negotiated indirect rate through June 30, 2022, is 55% excluding, among other costs, tuition, equipment, and contractual costs in excess of \$25,000.

XIII. References

Rawding, D. J., C. S. Sharpe, and S. M. Blankenship. 2014. Genetic-based estimates of adult Chinook Salmon spawner abundance from carcass surveys and juvenile out-migrant traps. *Transactions of the American Fisheries Society* 143:55–67.