Robe Lake Ecosystem Restoration
Feasibility Study
Appendix C: Environmental | DRAFT
Valdez, Alaska

U.S. Army Corps
of Engineers
Alaska District

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1.0   INTRODUCTION

1.1.   Project Site Description and History

This document is the Environmental Appendix for the Robe Lake Ecosystem Restoration feasibility study authorized under the Continuing Authorities Program (CAP) Section 206 of the Water Resources Development Act (WRDA) of 1996 (33 U.S.C. §2330), as amended. This study was requested by the City of Valdez and the Native Village of Tatitlek (the non-Federal sponsors), in response to conditions that have led to a degraded aquatic ecosystem at Robe Lake, in Valdez, Alaska.

Robe Lake is located within the northern portion of Prince William Sound (Figure 1A) in southcentral Alaska and lies within the city limits of Valdez (Figure 1B). Robe Lake is the largest freshwater lake in the Valdez area, with three tributary streams: Brownie Creek, Deep Creek, and Old Corbin Creek. Robe Lake empties into Robe River, which then flows under the Richardson Highway into the Lowe River (Figure 2).

In the 1950s a gravel berm was constructed on Corbin Creek, which heads at the terminus of Corbin Glacier, to divert flow and prevent flooding and washout of the Richardson Highway. Prior to this diversion, the main channel of Corbin Creek originally flowed into Robe Lake (Figure 3). Currently, Corbin Creek is a tributary of Valdez Glacier Stream and does not flow into Robe Lake (Figure 2). Corbin Creek's historic channel is now known as Old Corbin Creek, a relic channel with minimal flow.
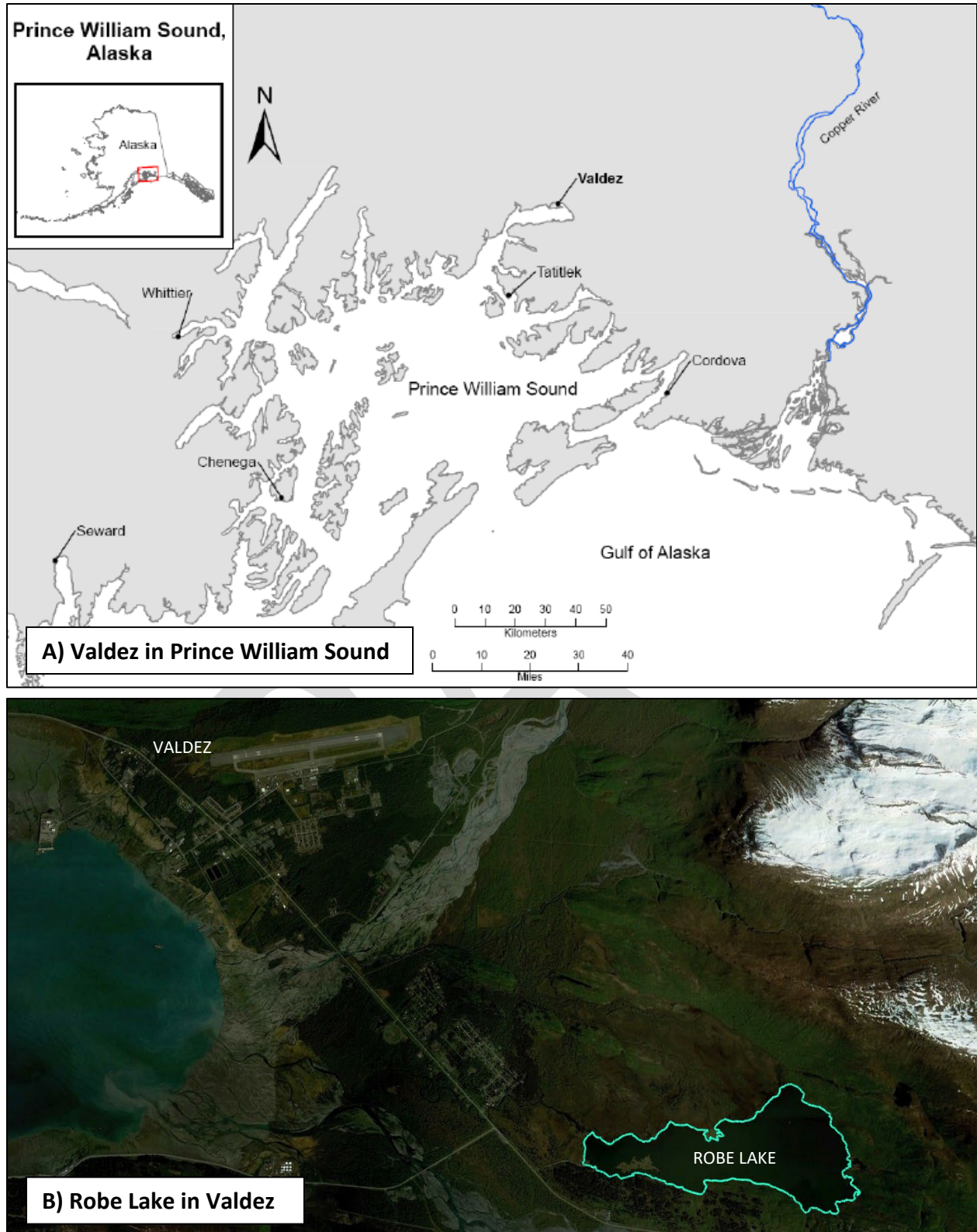
Figure 1. Vicinity map of Robe Lake and surrounding Valdez area.

A) shows the location of Valdez within Prince William Sound, Alaska; B) shows the location of Robe Lake within the Valdez area.
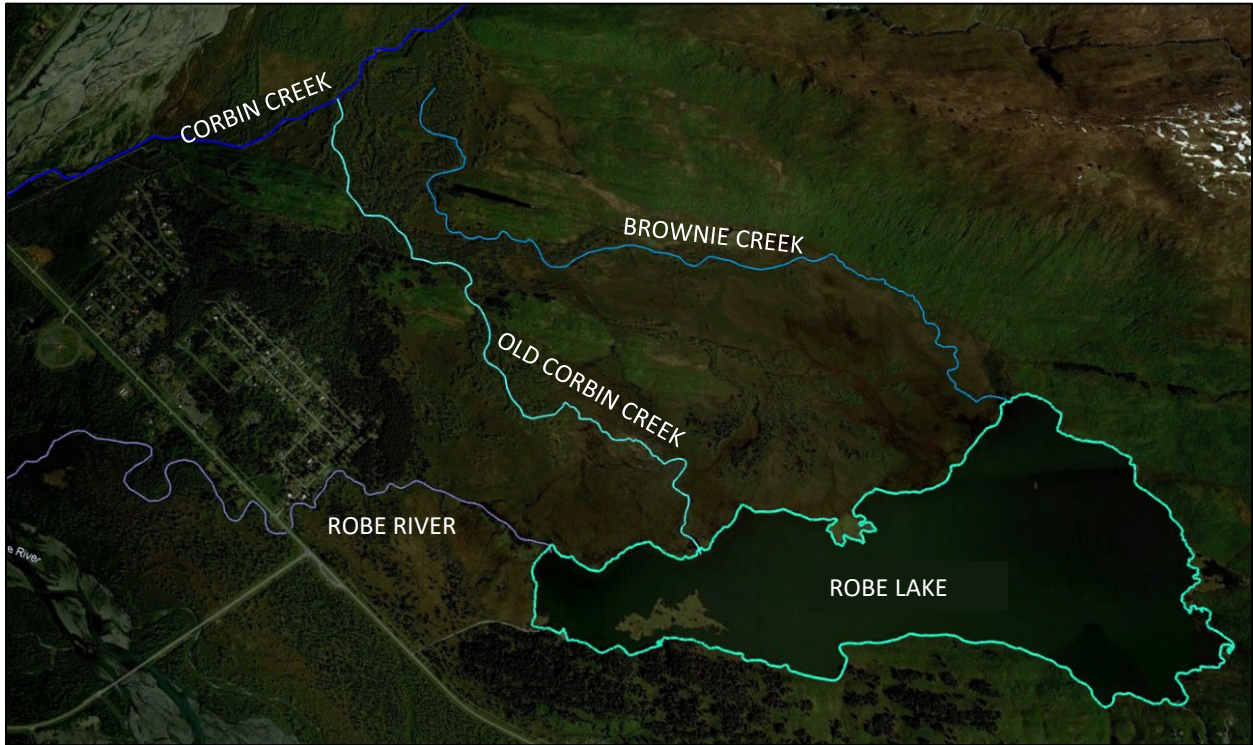
Figure 2. Current imagery of Robe Lake and the surrounding area.

The boundaries of the tributaries Old Corbin Creek and Brownie Creek, perimeter of Robe Lake, and the outflow of Robe River are highlighted.
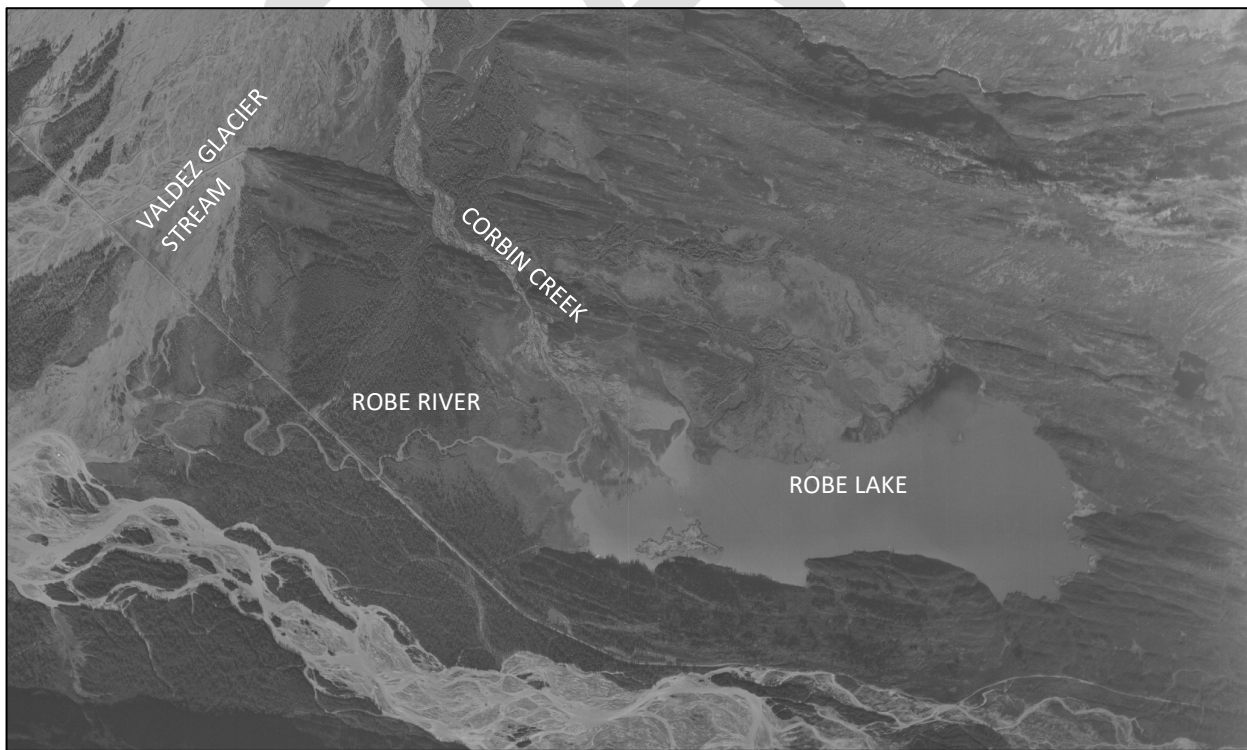
Figure 3. Historic imagery of Robe Lake and the surrounding area.

Robe Lake supports stocks of various anadromous fish species and is an important salmon (*Oncorhynchus* spp.) spawning and rearing site in the Valdez area. However, the berm constructed to re-direct the flow of Corbin Creek has altered the ecology and watershed dynamics of the lake. The loss of cold, turbid, glacial flow input from the Corbin Creek tributary has facilitated an overgrowth of macrophytes. The overgrowth of macrophytes have reduced the available rearing and spawning habitat for salmonid species.

Valdez Fisheries Development Association (VFDA) has a long history of maintaining salmonid spawning habitat within the Robe Lake watershed. VFDA has conducted mechanical weed harvesting of excess macrophytes since the 1990s. However, mechanical harvesting of excess macrophytes has a high operational cost, is time-consuming, and has limited overall success.

1.2. Problem

At Robe Lake, human induced hydrologic impacts resulting from a diversion of Corbin Creek have resulted in broad scale effects. The loss of cold, turbid, glacial flow from the Corbin Creek tributary has led to an excessive overgrowth of macrophytes. The macrophytes have impacted salmonid habitat by reducing available rearing and spawning habitat. Current mitigation requires mechanical harvesting of excess macrophytes. Mechanical harvesting of excess macrophytes has a high operational cost and is time-consuming.

2.0   ENVIRONMENTAL REPORTS

2.1. Macrophyte Identification

The loss of cold, turbid, glacial flow from the Corbin Creek tributary has led to the excessive overgrowth of macrophytes in Robe Lake. The macrophytes have impacted salmonid habitat by reducing available rearing and spawning habitat. Historical studies assessing the habitat at Robe Lake did not identify the problematic macrophytes to species (Koenings et al., 1987; Inter-Fluve et al., 2021). To provide a comprehensive analysis of the existing conditions at Robe Lake, we conducted a field survey to identify these macrophytes to species. Having a species-level identification provides an opportunity to examine individual tolerances with respect to changes in environmental conditions.

2.1.1. Archived Macrophyte Specimens

USACE Alaska District received frozen macrophyte specimens from Valdez Fisheries Development Association in March 2022. Three distinct macrophyte species were present in the shipment, though the collection date and locality of the specimens was unknown (Figure 4). Specimens were thawed to room temperature, and then mounted on archival paper. Specimens were then pressed and dried for further identification by a qualified botanist within USACE Alaska District. For identification efforts, the field guide *Introduction to Common Native and Potential Invasive Freshwater Plants in Alaska* (Morgan and Sytsma, 2009) was used as a key.

Figure 4. Photographs of frozen specimens of macrophytes.

Species identified from left to right: common mare's-tail (*Hippuris vulgaris*), white-stalked pondweed (*Potamogeton praelongus*), and whorl-leaf watermilfoil (*Myriophyllum verticillatum*).

Archived specimens were identified to species, or the lowest possible taxon based on physical characteristics. The three aquatic macrophyte species were identified as whorl-leaf watermilfoil (*Myriophyllum verticillatum*), white-stalked pondweed (*Potamogeton praelongus*), and common mare's-tail (*Hippuris vulgaris*).

2.1.2. Field Survey of Old Corbin Creek

Results of the field survey conducted in May 2023 found that macrophyte species within Robe Lake were not fully in green up. However, various species of sedge (*Carex* spp.) and common mare's-tail (*Hippuris vulgaris*) were present along the shoreline.

To assess site conditions within the project area, Alaska District biologists and archaeologists surveyed Old Corbin Creek. At the time of the survey, stream flow was present in Old Corbin Creek due to the high discharge of meltwater and spring runoff. The active channel of Old Corbin Creek did not have high velocity flow. Cobble clast gravel stream beds were only observed in areas of Old Corbin Creek with higher velocity of flows (i.e., at the culverts along the ALPETCO trail system; Figure 5). In areas of low flow, standing water was present and stream beds were occluded with organic matter and sediment deposition (Figure 6).

Figure 5. The Old Corbin Creek culverts on the ALPETCO trail system.

Figure 6. Area of low flow and standing water along Old Corbin Creek.

The gravel berm along Corbin Creek was observed to be overgrown with shrubs and understory vegetation, namely willow (*Salix* spp.), alder (*Alnus* spp.), and devil's club (*Oplopanax horridus*). Areas of the berm with well-drained soils supported stands of cottonwood (*Populus* spp.) and spruce (*Picea* spp.), a typical habitat observed on alluvial floodplains within the boreal forest (Figure 7). Sections of the berm were observed to be eroded away, as was evident by the Light Detection and Ranging (LIDAR) imagery (See the Hydrology and Hydraulics Appendix).

Figure 7. Photographs of the gravel berm along Corbin Creek.

2.1.3. Site Visit to Observe Weed Harvesting Efforts at Robe Lake

In August 2023, Alaska District biologists conducted a site visit to Robe Lake to observe weed harvesting efforts and to confirm that no invasive aquatic vegetation was present in Robe Lake. Biologists rode on the mechanical weed harvester with VFDA staff to identify macrophyte species being harvested from various areas of Robe Lake, and to assess the magnitude of harvest (Figure 8). No invasive species were observed during this site visit, and the three macrophyte species sent as specimens from VFDA: common mare's-tail (*Hippuris vulgaris*), white-stalked pondweed (*Potamogeton praelongus*), and whorl-leaf watermilfoil (*Myriophyllum verticillatum*) were the most abundant species being harvested at Robe Lake.

Adult pink salmon (*Oncorhynchus gorbuscha*) were observed in Robe Lake, migrating up Old Corbin Creek and Brownie Creek to spawn. Juvenile coho salmon (*Oncorhynchus kisutch*) were observed during weed harvesting efforts, most often occurring near the outflow of Old Corbin Creek and Brownie Creek. Three-spined sticklebacks (*Gasterosteus aculeatus*) were also observed in high densities, often being caught up in the harvested whorl-leaf watermilfoil (*Myriophyllum verticillatum*). Freshwater mussels (*Anodonta* spp.) were also observed in large numbers in shallow margins of Robe Lake with a large proportion of *Equisetum*.

Figure 8. Mechanical weed harvesting at Robe Lake by VFDA.

VFDA estimates that more than 50 tons of macrophytes are harvested from Robe Lake every year. Harvesting efforts are limited in duration, and only occur during the summer months (from June to August). VFDA concentrates harvesting efforts to occur outside of the spawning window for returning salmon.

2.2. Environmental DNA (eDNA)

An emerging method that improves detection of many aquatic species is environmental DNA (eDNA); which determines the presence of a species based on the collection, extraction, and amplification of DNA from the environment (Ficetola et al., 2008; Laramie et al., 2015). Sources of eDNA can include sloughed cells, feces, and bodily secretions. eDNA can be obtained from various environmental samples and reveals important information about present and past biodiversity within an ecosystem (Shu et al., 2020). For fish species, investigations into their distribution and ecology are often hindered by the challenge and complexity of working in these aquatic ecosystems (Goldberg et al., 2011). However, detection of eDNA within aquatic ecosystems is a reliable and cost-effective method for determining the distribution of various fish species (Jerde et al., 2011; Thomsen et al., 2011; Shu et al., 2020).

2.2.1. Field Collection

Given that eDNA sampling occurred mid-winter in November, sampling was limited to locations that were assessable with open water (Figure 9). For eDNA collection 1-Liter water samples were collected at two site locations (Figure 10). At each sampling location, three replicate samples were taken to detect any potential inconsistencies in our filtering techniques or downstream metagenomic library preparation. Collected water samples were filtered through a Thermo Scientific™ Nalgene™ 250 milliliter single use analytical funnel with a 47 millimeter diameter cellulose nitrate filter with a 0.45 micrometer pore size. A manual, hand driven vacuum pump was used to filter samples following procedures outlined in Protocol #1 of Laramie et al., 2015. Cross-contamination was mitigated for by disinfecting surfaces and instruments with 10% bleach solution and then rinsing with distilled water between processing replicates from different field sites. In addition to the three replicate samples collected at each field site, a negative control containing only distilled water was filtered to ensure our methods were effective in mitigating cross-contamination.

Figure 9. Site conditions at Robe Lake during eDNA sampling.

Sampling for eDNA occurred on November 2nd, 2022 when the lake was nearing freeze-up.

2.2.2. Molecular Analysis

Samples were sent to the U.S. Army Engineer Research and Development Center's Genetics Reconnaissance Team (Environmental Processes Branch, Environmental Laboratory; CEERD-EPP) for DNA extraction, sequencing, and bioinformatic analysis. Extractions followed a modified cetyltrimethylammonium bromide (CTAB) protocol outlined in Doyle and Doyle, 1987. Two metabarcoding primers were chosen, MiFish-U (Miya et al., 2015) and AKOncCytB (Menning et al., 2020). MiFish-U is a universal primer that targets the 12S-rRNA gene and possesses robust detection potential across numerous freshwater and marine fish taxa. However, MiFish-U exhibits low discriminatory power among salmonid species (Polanco et al., 2021; Miya et al., 2020). Thus, the AKOncCytB metabarcoding primer specifically designed for detection and discrimination of salmonid species in the cytochrome-B gene was used in conjunction with MiFish-U. The combined use of multiple primer pairs targeted for more than one gene marker (e.g., 12S-rRNA and cytochrome-B) is recommended to improve classification, reduce primer bias and false negatives, and better perform community-level analyses (Xiong et al., 2022).

High throughput sequencing (HTS) libraries were generated for both markers for each sample using recommended library preparation protocols (Bourlat et al., 2016). Quality assurance and control (QA/QC) measures, specifically negative controls were incorporated into DNA extraction and HTS workflow to detect any potential issues with contamination. A positive control was included in early stages of the HTS workflow to ensure successful amplification. For the positive control, water filtrate samples from aquarium tanks containing only zebrafish (*Danio rerio*) were used. Zebrafish are found within the subfamily *Danioninae* of the family *Cyprinidae*. The only fish found within *Cyprinidae* in Alaska is the lake chub (*Couesius plumbeus*) from the subfamily *Leuciscinae*. Thus, with only one distantly related species in Alaska, any sample cross-contamination from the zebrafish eDNA positive controls should not pose a challenge to accurate identification of eDNA from Alaskan fish. Marker libraries from half of the samples were combined for the first sequencing run on an Illumina MiSeq, using V2 500 cycle kits. A run of combined marker libraries for the remaining (i.e., second half) of samples was then conducted using the same protocols.

2.2.3. Bioinformatics

Resulting raw sequence data was concatenated across the two HTS runs. These data were processed following the MiFish bioinformatics pipeline (version 3.87, Sato et al., 2018; Zhu et al., 2023). In short, low-quality bases and adapters were removed. Resulting paired-end reads were then merged, and erroneous reads and primers were removed. Unique sequence reads, or amplified sequence variants (ASVs), were identified and ASV read counts for each sample were calculated. Species-level taxonomic assessment was preformed using a sequence similarity search against available references on the MitoFish mtDNA database. For reads generated by the AKOncCytB marker, low-quality bases and adapters were removed. A matrix of error rates for forward and reverse reads were created. These error rates were used to denoise the reads. Denoised reads were merged to create ASVs. ASVs were assigned to species based on the best observed match at greater than 97% sequence identity to salmonids in a database created of all NCBI (National Center for Biotechnology Information) sequences (as of 7 February 2023) associated with the cytochrome-B region of 18 salmonid species present in this region of Alaska (courtesy of D. Menning, US Geological Survey Alaska Science Center). Following this initial ASV classification via the MiFish and Menning databases, classifications were further curated by identifying ASVs with equivalent sequence matches (i.e., identical E-value scores) to more than one taxon. These ASVs were entered into BLASTn (Basic Local Alignment Search Tool, nucleotides) searches against the entire NCBI GenBank DNA sequence archive. In cases where only one of the equivalent matches (in GenBank) was known to occur in Alaskan waters, the ASV was assigned to that taxon. In cases where more than one of the equivalent matches was known to occur in Alaskan waters, the ASV was assigned to a genus or subfamily, depending on the phylogenetic breadth of the matching sequences. In cases where the best observed sequence match for an ASV was between 95% to 97%, the ASV was assigned to the genus containing the best match (or matches). Original sequence data have been deposited on the NCBI Sequence Read Archive (SRA) under BioProject number PRJNA950049 (Table 1).

2.2.4. Taxonomic Assessment Results

Taxonomic assessment of the freshwater community within Robe Lake and the Robe River using eDNA detected a range of fish species (Table 2). In general, eDNA data detected the presence of

three salmonid species at both site 1 and site 2. These salmonid species were coho salmon (*Oncorhynchus kisutch*), sockeye salmon (*Oncorhynchus nerka*), and Dolly Varden (*Salvelinus malma*). Three-spined stickleback (*Gasterosteus aculeatus*) was only detected at site 1. The relatively limited range of fish species detected in eDNA is likely due to the sampling date occurring during winter months. If resampling of these sites had taken place to account for changes in species composition over time, we suspect that a greater diversity in species would have been detected.

The presence of some birds and one mammal were also detected in eDNA samples (Table 2). Though the detection of birds and mammals was not the focus or aim of the eDNA analysis, incidental amplification of non-target taxa are inevitable (Ritter et al., 2022). Bird species detected included a diverse range of waterfowl, i.e., mallard (*Anas platyrhynchos*), common goldeneye (*Bucephala clangula*), and white-winged scoter (*Melanitta deglandi*). In addition to waterfowl, American crow (*Corvus brachyrhynchos*) and bald eagle (*Haliaeetus leucocephalus*) were detected at site 1. The only mammal detected was coyote (*Canis latrans*) at site 1. These incidental detections of non-target taxa within eDNA data do provide some insight into the bird and mammal species that may be present within the Robe Lake watershed. However, given the molecular and bioinformatic approaches used, the interpretation of the presence and absence of non-target taxa within eDNA data warrants caution.

Figure 10. Sampling sites for eDNA at Robe Lake.

Sampling occurred on 2 November 2022. Site 1 (pink icon, 1) was located near the culvert on the unnamed tributary flowing into Robe Lake. Site 2 (pink icon, 2) was located directly upstream from the two 12.75 ft. Robe River culverts located under the Richardson Highway.

Table 1. Voucher information for eDNA samples.

Original sequence data have been deposited on the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA). Samples with too low of read count to be given an SRX accession number are denoted with the BioSample SAMN number. All reads are available under BioProject number PRJNA950049.

Site	Replicate	Date	Location	Latitude (°N)	Longitude (°W)	SRA Number (MiFish-U)	SRA Number (AKOncCytB)
1	1	2-Nov-22	Robe Lake	61.084981	-146.178082	SRX19877860	SRX19877870
1	2	2-Nov-22	Robe Lake	61.084981	-146.178082	SRX19877861	SRX19877871
1	3	2-Nov-22	Robe Lake	61.084981	-146.178082	SRX19877865	SRX19877872
2	1	2-Nov-22	Robe Lake	61.090598	-146.200507	SRX19877866	SRX19877862
2	2	2-Nov-22	Robe Lake	61.090598	-146.200507	SRX19877867	SRX19877863
2	3	2-Nov-22	Robe Lake	61.090598	-146.200507	SRX19877868	SRX19877864
method blank	-		N/A	-	-	SRX19877869	SAMN33969587

N/A – Not Applicable.

Table 2. Species detected with eDNA.

Sequences with low taxonomic resolution were classified to the lowest taxon given percent sequence identity. As a taxonomic assessment, species were sorted by scientific name rather than common name to improve clarity of eDNA results. Original raw sequence data are archived on the NCBI SRA under BioProject number PRJNA950049. Species illustrations for avian taxa were obtained from individual species profiles on Birds of the World; photographs of fish species were obtained from Johnson et al., 2015.

Species	Scientific Name	SITE 1	SITE 2
Mallard	*Anas platyrhynchos*	.	.
unidentified dabbling duck	*Anas sp.*	.	.
Bufflehead	*Bucephala albeola*		.
Common goldeneye	*Bucephala clangula*	.	.
Coyote	*Canis latrans*	.	
American crow	*Corvus brachyrhynchos*	.	
Tundra swan	*Cygnus columbianus*		.
Three-spined stickleback	*Gasterosteus aculeatus*	.	
Bald eagle	*Haliaeetus leucocephalus*	.	
White-winged scoter	*Melanitta deglandi*	.	.
Common merganser	*Mergus merganser*	.	
Coho salmon	*Oncorhynchus kisutch*	.	.
Sockeye salmon	*Oncorhynchus nerka*	.	.
Dolly Varden	*Salvelinus malma*	.	.
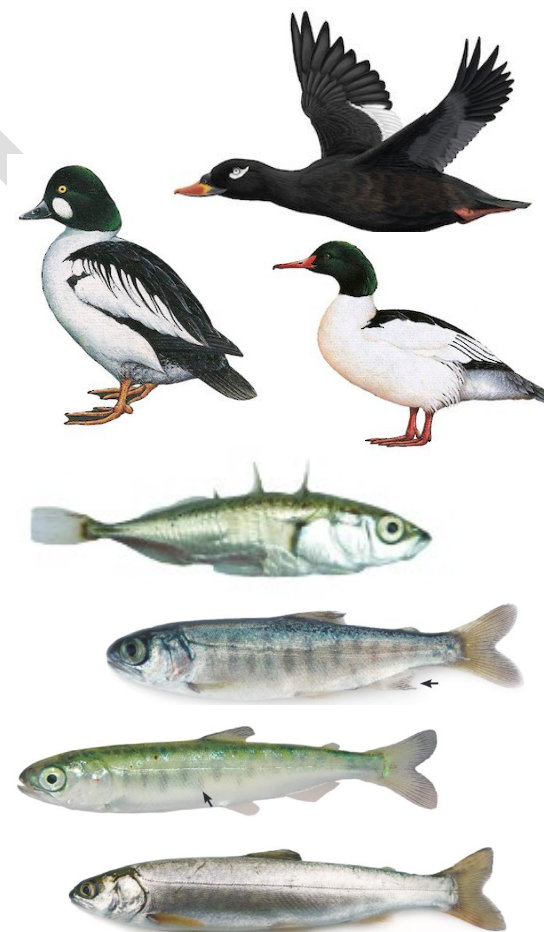
2.3.   General Salmonid Habitat Model

Salmonid species are critically important in freshwater, estuarine, and marine ecosystems. In Alaska, salmon are a key natural resource that have high economical, commercial, and subsistence value. Robe Lake is an important salmon (*Oncorhynchus* spp.) spawning and rearing site in the Valdez area. Therefore, restoration alternatives must be evaluated within the context of changes in habitat suitability for salmonid species. Improving the quality of existing salmonid habitat within Robe Lake is a planning objective that must be met.

The *General Salmonid Habitat Model* was developed by the U.S. Army Corps of Engineers Research and Design Center (ERDC) to assist in the plan formulation process for ecosystem restoration and mitigation projects (Herman et al., 2018; Herman et al., 2019a; Herman et al., 2019b). The certified model generates relative differences in habitat quality between proposed alternative future scenarios. The model is scalable, meaning various parameters may be measured at different landscape scales (i.e., tributary vs. watershed). This model is appropriate for use in any planning project focused on the restoration of streams, rivers, and estuaries, because the parameters are measures of ecosystem level structure, function, and process.

Model parameters were developed to capture primarily physical characteristics of anadromous fish habitat, particularly salmon species, that play critical roles in the suitability of the environment (Table 3). The goal of using this model is to distinguish changes in salmon habitat suitability between restoration alternatives using the criteria of acceptability, completeness, effectiveness, and efficiency.

Table 3. Parameter definitions the *General Salmonid Habitat Model*.

Asterisks (*) indicate parameters that were modified in collaboration with model authors to be optimized for the Robe Lake ecosystem.

PARAMETER	DEFINITION
CHANNEL	Diversity of in-stream habitat types that result from the shape and geomorphic contours of a channel. This parameter represents diversity of in-stream habitats.
POOLS, RIFFLES, AND RUNS	Relationship of specific in-stream features (i.e., pools) to the quality of anadromous fish habitat. The appropriate way to measure this parameter is to measure the amount of area each feature covers within a reach and calculate the ratio of area of features.
FLOODPLAIN FEATURES	Floodplain includes the following features: wall-based ponds, oxbows, wetlands, and others. As a floodplain is restored, the number of different habitat features available increases, and the quality of habitat increases.
LOGITUDIONAL CONNECTIVITY	The ability of an organism to access areas within a watershed network. Barriers to movement create disconnected habitat. Barriers to movement may manifest during different times of the year.
LATERAL CONNECTIVITY	The ability of organisms to access habitat adjacent to stream and river reaches within floodplain and surge plain areas. Lateral connectivity is driven by river fluctuations that allow access to floodplain habitat during portions of the year. Lateral connectivity is impacted when barriers (i.e., levees) no longer allow species to access floodplain habitat.
EDGE COVER (1)*	Percent vegetated cover within the riparian buffer (e.g., can be native or non-native or a mix) is positively correlated with suitable aquatic habitat. Modified parameter for lake system to reflect negative effect on habitat suitability with overgrowth of macrophytes within the littoral buffer.
EDGE COVER (2)	Percent vegetated with native species cover within the riparian buffer. A response curve exhibiting a mostly linear relationship with percent cover in the riparian buffer area and a plateau of suitability around 75% cover.
WOODY DEBRIS TRIBUTARY (1)	Number of woody debris pieces found within the bankful width of a reach. The tributaries are measured as the average number of pieces of woody debris per square meter within the bankful width of the reach.
SEDIMENT	The measurement of this parameter would be an average visual assessment of the area of concern to decide whether a project along a tributary or mainstem is accreting or eroding.
GENERAL TEMPERATURE (1)	Describes the general range of water temperature and its associated habitat suitability. As temperature increases from the expected low of 15°C to greater than 25°C, the suitability of habitat decreases.
BIOENERGETICS TEMPERATURE (2)*	Describes the predicted performance of individuals in terms of successful migration, breeding, and rearing (e.g., bioenergetics).There is an optimum range of bioenergetics that sits around 10°C, anything lower or higher is not as suitable. Measurement is a mean, but the timing and duration of measurement may vary with project.
SURVIVAL TEMPERATURE (3)	Anadromous fish are expected to survive temperatures between 0°C to 25°C; anything greater than 25°C is considered lethal to most life stages and in most landscape units.

2.3.1. Caveats and Considerations

Throughout the implementation of using the General Salmonid Habitat Model to refine restoration alternatives, caveats and considerations were taken into account. For instance, the model was developed for stream and riverine restoration projects in Pacific Northwest ecosystems. Therefore, certain parameters in the model needed to be modified to fit the Robe Lake system, a lacustrine ecosystem in Alaska. To do this, we worked with authors of the model to optimize and modify two parameters. These two parameters were *Edge Cover (1)* and *Bioenergetics Temperature (2)*. The *Edge Cover (1)* parameter was modified to have a negative effect above a 45% cover threshold in the littoral buffer to capture unsuitability of macrophyte overgrowth. The *Bioenergetics Temperature (2)* parameter was shifted to encompass lower ideal temperatures for salmon species in Alaska (Weber Scannell, 1992).

2.3.2. Habitat Model Workshop

USACE Alaska District held a habitat modeling workshop on February 7th, 2023 to implement the General Salmonid Habitat Model. During the workshop, USACE Alaska District collaborated with other agencies to determine initial baseline and forecast parameter inputs. The goal of the workshop was to evaluate the restoration alternatives with respect to changes in habitat suitability indices given the parameter input. Each alternative was evaluated against each parameter; for both the tributary and watershed calculators. The results of this workshop were used to infer changes in habitat suitability for the Cost-Effectiveness and Incremental Cost Analysis (CE/ICA). The results of these data can be found in the Economic Appendix.

3.0   ENVIRONMENTAL CORRESPONDENCE

3.1.   Coordination and Consultation History

The following list of Federal agencies were contacted during the scoping period to solicit input on the scope of the impacts and resources affected by the proposed project (Table 4). These inquiries were in regard to environmental coordination under National Environmental Policy Act (NEPA) and the Fish and Wildlife Coordination Act (FWCA). No responses requesting to be a cooperating agency were received. All coordination letters can be found in the Correspondence Appendix.

Table 4. Federal agencies contacted during the scoping period.

Asterisks (*) indicate a response received but request to be a coordinating agency on the project was declined.

Agency	Nature of Inquiry	Postmarked Date	Response?
National Marine Fisheries Service (NMFS), Habitat Conservation Division	Coordination under FWCA	04 August 2022	No
U.S. Fish and Wildlife Service (USFWS), Conservation Planning Assistance	Coordination under FWCA	04 August 2022	No
Environmental Protection Agency (EPA), R10	NEPA Cooperating Agency Request	15 August 2022	No*
U.S. Fish and Wildlife Service (USFWS), Conservation Planning Assistance	NEPA Cooperating Agency Request	15 August 2022	No
National Marine Fisheries Service (NMFS), Habitat Conservation Division	NEPA Cooperating Agency Request	26 September 2022	No
Alaska State Historic Preservation Officer (SHPO)	Request for Concurrence on Determinations of Eligibility	11 August 2023	Pending
Alaska State Historic Preservation Officer (SHPO)	Request for Concurrence on Assessment of Effect	30 August 2023	Pending

The draft IFR-EA was made available for public and agency review. Substantial comments received during the public comment period and actions taken to involve the public and agencies will be compiled and appended in the Correspondence Appendix after the public release of this IFR-EA. Comments received will be addressed in the final IFR-EA.

3.2.   Environmental Compliance

Compliance with the following environmental laws, regulations, and EOs is required for the recommended plan under consideration. This project is anticipated to be in full compliance with all environmental laws, regulations, and EOs (Table 5).

Table 5. Status of environmental compliance.

Asterisks (*) indicate that full compliance will be attained upon the signing of the Finding of No Significant Impact (FONSI).

FEDERAL LAW	COMPLIANCE
Clean Air Act	Fully Compliant
Clean Water Act Section 404(b)(1)	In Progress
Endangered Species Act	Fully Compliant
Fish & Wildlife Coordination Act	Fully Compliant
National Environmental Policy Act	Partially Compliant *
National Historic Preservation Act	In Progress
Magnuson-Stevens Fishery Conservation & Management Act	Fully Compliant
Marine Mammal Protection Act	Not Applicable
Migratory Bird Treaty Act	Fully Compliant
Bald Eagle Protection Act	Fully Compliant
Executive Order 12898, Environmental Justice	Fully Compliant
Executive Order 13045, Protection of Children	Fully Compliant

STATE AND LOCAL LAWS	COMPLIANCE
Clean Water Act Section 401	In Progress
Alaska Statute 16.05.871- .45901 Anadromous Fish Act	In Progress
Alaska Statute 16.05.841 Fish Passage Act	In Progress

4.0   REFERENCES

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