Salinas Lagoon Seining Report

Fall 2024

Submitted To:
Monterey County
Water Resources Agency

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Executive Summary

In fulfillment of the monitoring recommendations put forth in the 2009 draft Biological Opinion on sand bar management (NMFS 2009), FISHBIO conducted fish community and water quality sampling of the lower Salinas River and Lagoon on October 22, 2024. This sampling event occurred 39 days after the sandbar closed on September 13, 2024. Prior to September 13, the sandbar had remained breached, subjecting the lagoon to tidal influence and seawater inflow and provided opportunities for fish migration to and from the marine environment. As is regularly observed in the system, shifts in lagoon bathymetry resulting from sediment deposition necessitated some deviation from previous sampling locations. However, with adjustments to sample locations based on availability of suitable habitat, the field crew was able to perform seine hauls in 14 sites, nine of which were identical to those sampled in previous years.

In total, 10 species of fish were captured via seine sampling. Relatively high catch-per-unit-effort (CPUE; average = 41.5 fish/net haul) suggests a lower density of fish were present in the lagoon than the densities observed in fall 2023 sampling, but this CPUE was similar to fall sampling events prior to 2023. Notably, inland silversides were the most frequently captured fish with a CPUE of 18.9, which was the highest recorded for this fish since fall sampling began. Additionally, species diversity was relatively low in October 2024 compared to previous years and, in many sites, only one species was observed.

Notably, no striped bass (*Morone saxatilis*) were captured during this sampling event, which is the second time they were not detected in a fall sampling event since 2010. Striped bass were, however, noted in eDNA samples.

Analysis of 12 eDNA samples revealed that all species observed in the seine catch were detected with eDNA, in addition to ten fish species not observed in the seine catch: jacksmelt (*Atherinopsis californiensis*), California grunion (*Leuresthes tenuis*), northern anchovy (*Engraulis mordax*), white sucker (*Catostomus commersonii*), western mosquitofish (*Gambusia affinis*), arrow goby (*Clevelandia ios*), tidewater goby (*Eucyclogobius newberryi*), Chinook salmon (*Oncorhynchus tshawytscha*), and striped bass (Morone saxatilis). Unassigned sequences belonging to the genus *Sardinops* were detected as well.

No steelhead (*Oncorhynchus mykiss*) were detected in seine, hoop net, or eDNA samples collected during this sampling event. However, water quality data indicate that abiotic factors were not limiting for rearing juvenile steelhead or migrating adult steelhead, as temperatures and dissolved oxygen levels remained well within suitable ranges for the species.

Background

Monterey County Water Resources Agency (MCWRA) has played a leading role in monitoring and managing the Salinas Lagoon since 1996, when the organization adopted the Salinas River Lagoon Management and Enforcement Plan (MEP) that was developed by the multi-stakeholder Salinas River Task Force. Since that time, the recommended measures included in the MEP have primarily been implemented by MCWRA, its contractors, and the U.S. Fish and Wildlife Service (USFWS). The Salinas River Lagoon project area described in the MEP includes the lower portion of the river from the sandbar, which seasonally separates the river from Monterey Bay, to approximately two miles upstream.

Beginning in 2002, MCWRA implemented a Lagoon Monitoring Program, which was updated in 2010 to incorporate the recommendations of the National Marine Fisheries Service (NMFS) draft Biological Opinion for sandbar management (NMFS 2009). These changes were intended to mitigate potentially negative effects on lagoon-rearing steelhead (*Oncorhynchus mykiss*) belonging to the federally Threatened South-Central California Coast Distinct Population Segment (USFWS 1997). One component of this draft Biological Opinion was a requirement for sampling the fish community in the lower river in the spring and summer, in addition to the fall samples that MCWRA had been collecting. Samples were collected by Hagar Environmental Science in the spring, summer, and fall of 2011, 2012, and 2013, and spring of 2014. Fish community and water quality sampling resumed in the fall of 2020 with surveys conducted by FISHBIO. Sampling has since been conducted in the spring of 2021 and 2022, the spring and fall of 2023, and the spring and fall of 2024, the latest of which is described in this report. In total, Salinas Lagoon seine sampling has been conducted 26 times since sampling began in 2002 (eight spring events, four summer events, and 14 fall events: see Table A1 in Appendix).

The fish community composition in the lagoon is largely dependent on water quality and habitat conditions, which fluctuate in response to freshwater inflow from the Salinas River and the timing and duration of lagoon connectivity with the ocean. The early winter of 2023/2024 was drier than average in Salinas (Figure 1), with 66% of normal precipitation (2.62 inches) in Salinas during the first quarter of the 2024 water year (October through December 2024; MCWRA 2024a). Conditions became significantly wetter than average through the spring, with 117% of average rainfall in Salinas during the second quarter (January through March 2024; MCWRA 2024b). Precipitation decreased but was still above average for the third quarter (April through June 2024; MCWRA 2024c) at 118% of average cumulative rainfall in Salinas (14.74 inches). Finally, little precipitation (0.09 inches) was recorded in the fourth quarter but remained at 118% of average cumulative rainfall in Salinas (Figure 1; MCWRA 2024d). Notably, water years 2023 and 2024 represent the first two back-to-back wet years that have occurred since lagoon monitoring began.

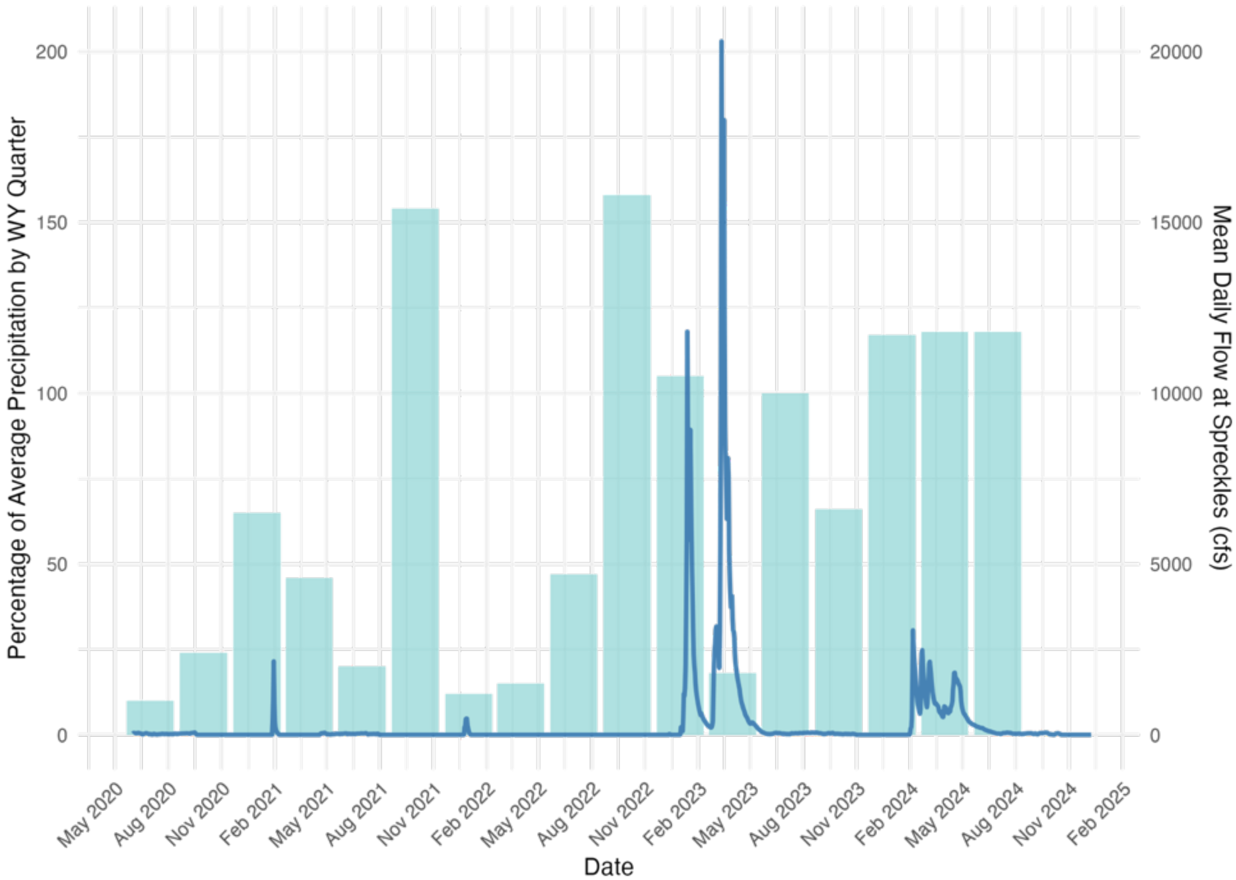

Figure 1. Bar plot depicting precipitation measured at the Salinas Airport as a percentage of average (i.e., that expected in a "normal" water year) by water year quarter, overlaid with a line plot of mean daily flow (in cfs) as measured at the Spreckles gauge (USGS gauge #11152500). Note that precipitation data have only been published up through the fourth quarter of water year 2024 (MCWRA 2024a).

MCWRA can partially regulate the water level in the lagoon by releasing water through the lagoon outlet slidegate to the Old Salinas River. However, once the lagoon stage exceeds approximately six feet, MCWRA facilitates lagoon breaching to prevent flooding of crop fields and residences adjacent to the lower river (USFWS 2007). The lagoon was closed on September 13, 2024, and as of the time of seine sampling in October, it had been closed for a period of 39 days.

Methodology

Fish Community Sampling

The purpose of Salinas Lagoon sampling efforts is to capture any juvenile steelhead that may be rearing in the lagoon. Objectives include evaluating presence or absence, condition, relative abundance (i.e., CPUE), and distribution of juvenile steelhead in the Salinas Lagoon. In addition, the sampling is designed to provide data on the overall fish community and how that community changes over time in response to environmental conditions.

The downstream end of the Salinas lagoon is characterized by open, sandy, gradual beaches that are particularly suitable for beach seining (Figure 3). However, the highly mobile nature of the substrate in the lower lagoon, combined with high flows and tidal action, make this portion of the river a very dynamic area, and the configuration of the lower lagoon can change dramatically between sampling events. Some sites varied slightly from previous sampling periods and additional sites were added during sampling to account for this habitat variability. The upstream portion of the lagoon is characterized by steep banks and dense vegetation, limiting the number locations where seining is feasible (Figure 4). As such, upstream sampling sites have remained consistent since 2020.

FISHBIO field crews conducted seine sampling at 14 stations (0, 1, 2, 3, 4, 5, 5.5, 5.75, Alternate 7, 8, 9, 10, 11, and 12; Figure 2). Seining was conducted using a 100-foot beach seine with ¼ inch mesh. The seine was deployed via inflatable raft in a semi-circle a short distance from shore and crew members pulled the seine onto shore, ensuring the float line stayed above the surface while keeping the lead line as close to the substrate as possible. These protocols and the dimensions of the net meant that the maximum area sampled by each seine haul was approximately 3,520 ft^2 (~327 m^2), although the true value was less than this due to the presence of obstacles and variations in wind direction that shifted the net.

Once the seine was pulled onto shore, crews quickly processed captured fish by placing specimens to be measured in aerated recovery buckets and counted extremely abundant species before releasing them. Once all fish were removed from the net, crews applied the standard protocol of recording fork and total length data on at least 20 individuals of each captured species before plus-counting any remaining individuals.

In addition to beach seining, hoop-style fyke nets were deployed as a means of passively sampling the fish community. The intention of including this additional gear was to obtain a more complete representation of the fish community present in the sampling stations by increasing the odds of capturing fish that may be inefficiently sampled with seine nets (e.g., larger bodied and strong-swimming species). In total, two hoop nets were set in the vicinity of Station 11 (Figure 2), one facing upstream and one facing downstream. Both nets were placed for a full tidal cycle during flood tide at approximately 16:00 on October 22 and recovered the next morning at approximately 09:30.

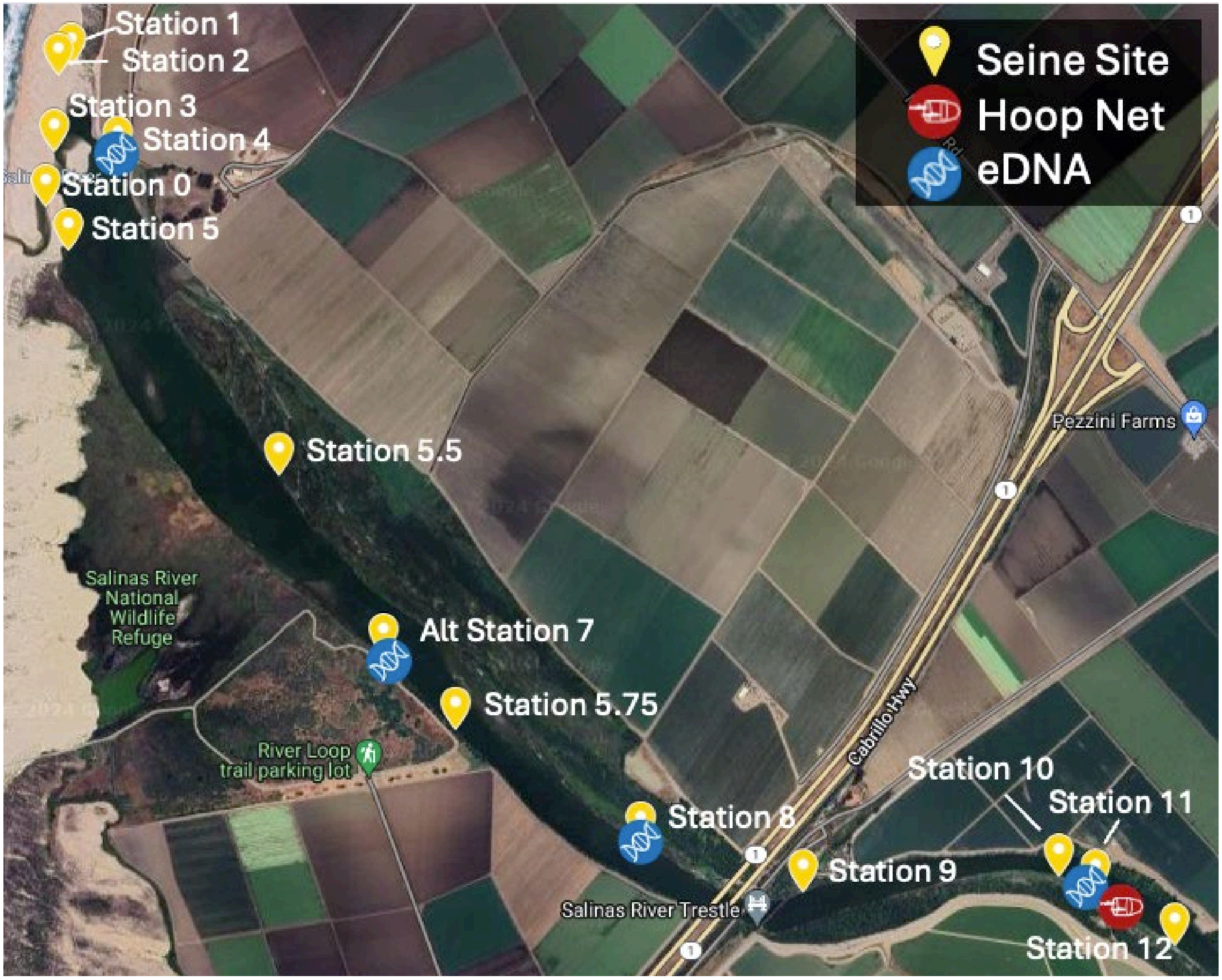

Figure 2. Stations sampled by FISHBIO in October 2024. Interactive map with data on species detected is available at https://bit.ly/salinas_lagoon_october_24

Figure 2. Seining near the mouth of the closed Salinas Lagoon on October 22, 2024.

Figure 4. Retrieving a 100-ft beach seine during sampling on October 22, 2024.

Water Quality Sampling

After fish processing was completed, crews collected water quality data using a YSI water quality meter in the sampled area. Staff used the YSI to measure temperature (˚C), specific conductivity (µS/cm at 25˚C), conductivity (µS/cm), salinity (parts per thousand; ppt), and dissolved oxygen (mg/L) at the surface.

eDNA Sampling

A total of 12 eDNA samples were collected at four locations as part of this monitoring effort (Sites 4, 7, 8, and 11; Figure 2). All samples were collected with single-use aquatic eDNA kits (Jonah Ventures, Boulder, Colorado). These self-contained kits include nitrile gloves, a 60-mL syringe, a 5-µm filter cartridge, and a 1-mL syringe of Longmire's solution to stabilize captured DNA for storage and transport. Three samples were collected at each of four sites ranging from the Old Salinas River slidegate (Station 4) to the second furthest upstream sample site (Station 11; Figure 2). Samples were collected in triplicate at each site to increase the total volume of water sampled (and thereby increase eDNA detection probability for rare species) and to allow for replicability to improve confidence in the validity of results.

Data Analysis

Data collected during this sampling effort were added to the database of compiled Hagar Environmental Science and FISHBIO data that was developed in 2021 and has been updated each year since. To ensure comparability with data from Hagar Environmental Science, all data were standardized to individuals captured per seine haul. Cumulative and species-specific CPUE was then calculated for the October 2024 sampling event. Data collected during the October 2024 sampling event were also analyzed for species diversity at each sampling location using the Shannon-Weiner Diversity Index.

Results

Fish Community Sampling

Seine Catch

A total of 624 fish representing 10 different species were captured via seine in October 2024 (Table 1). Total CPUE was 36% and 59% lower than that observed in spring 2024 and fall 2023, respectively, but was comparable to that observed in the preceding fall sampling event of 2020 (Table 1). Species-specific CPUE data from past summer and spring sampling events are also presented in the Appendix for comparison (Tables A2 and A3). Total species richness was the same as the past two fall sampling events, which also saw the capture of 10 species, but was lower than the 14 species captured in spring of this year. Notably, three non-native species were observed (threadfin shad, inland silverside, and yellowfin goby), and the other seven species detected were native. As in all fall sampling events since 2002, no *O. mykiss* were observed. The species with the highest CPUE was the nonnative inland silverside, at 18.9 individuals/seine haul.

In terms of diversity, Shannon-Weiner Diversity Index values ranged from 0.00 at stations 0, 3, 5.5, 5.75, and 11 to a high of 1.33 at station Alt 7, with a mean across all sites of 0.47 (Figure 6). There was no clear trend of diversity indices increasing or decreasing with distance from the mouth of the lagoon, though there were more sites with no diversity lower in the lagoon. Rather, the diversity detected at each station appeared to be contingent upon the habitat present at that location.

Table 1. Cumulative and species-specific catch per unit effort (CPUE) across the 14 fall sampling events from 2002 to 2024. Note that CPUE is calculated using a single seine haul as the unit of effort. Non-native species are indicated by bolded common and scientific names. Horizontal lines separate the species by family.

	Date	**Oct-02**	**Oct-03**	**Oct-04**	**Oct-05**	**Oct-06**	**Oct-08**	**Oct-09**	**Oct-10**	**Oct-11**	**Oct-12**	**Oct-13**	**Oct-20**	**Oct-23**	**Oct-24**
	Total Seine Hauls	9	17	5	17	9	8	12	12	16	17	12	8	11	10
Common Name	**Scientific Name**														
Pacific herring	*Clupea pallasii*	0.7	0	6.6	62.9	0.3	194.1	4.4	41.6	56.4	0	0.2	0	2.73	10.5
Threadfin shad	***Dorosoma petenense***	0.2	4.8	27.8	0	0	12.9	0	0	0	0	5.1	29.88	0	1.8
Common carp	***Cyprinus carpio***	0.1	0.3	12.6	3.6	0	0	0.1	0	0	0	0.2	0	0	0
Goldfish	***Carassius auratus***	0	0	0	0	0	0	0	0	0	0	0	0.13	0	0
Hitch	*Lavinia exilicauda*	30.4	67.6	180	36.7	0.1	20.3	8.5	6.1	0.8	0	0.6	4.13	0.09	0.6
Sacramento blackfish	*Orthodon microlepidotus*	0	3.2	1.4	18.1	0.1	0.6	0	30.3	0	0	0.1	0	0	0
Sacramento pikeminnow	*Ptychocheilus grandis*	0	0.1	0	0	0	0	0	0	0	0	0	0	0	5.2
Sacramento sucker	*Catostomus occidentalis*	3.8	13.8	90	18.1	0	0.1	0.1	3.1	0	0	0.1	0.25	0	0
Topsmelt	*Atherinops affinis*	0	0	7	0	44.6	10.4	11.2	12.7	21.3	0	0	0	87.55	0
Chinook salmon	*Oncorhynchus tshawytscha*	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0
Steelhead	*Oncorhynchus mykiss*	0	0	0	0	0	0	0	0	0.1	0	0.1	0	0	0
Western mosquitofish	***Gambusia affinis***	0	0.1	640	6.1	0	0	0	0.9	0	0.4	0.1	0	0	0
Inland silverside	***Menidia beryllina***	0	0	0	0	0	0	0	0	0	0	0	0.38	0.18	18.9
Pacific staghorn sculpin	*Leptocottus armatus*	0.6	0.4	1	0.8	0	1.5	0.9	0.5	0.2	0.1	0.3	0.13	0	0.9
Prickly sculpin	*Cottus asper*	0.1	0.4	5.4	0.1	0	0.3	0.2	1.9	0.4	0.4	0.5	1.13	7.73	0.1

Unidentified sculpin	*Cottidae*	0	0	0	0	0	0	0	0	1.7	0	0	0	0	0
Threespine stickleback	*Gasterosteus aculeatus*	54.3	47	59.8	16.9	0	8.5	6.8	31.7	0.1	3.5	37.5	1	3.27	2.7
Shiner surfperch	*Cymatogaster aggregata*	0	0	0	0	0	4.5	0.6	0	0.7	0	0	0	0	0
Striped bass	*Morone saxatilis*	0	0	0	0.4	0	0	0.1	0	0.7	0.2	0.7	0.5	0	0
Bluegill Sunfish	***Lepomis macrochirus***	0	0	0	0	0	0	0	0	0	0	0	0	0.27	0
Arrow goby	***Clevelandia ios***	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0
Tidewater goby	*Eucyclogobius newberryi*	0	0	0	0	0	0	0	0	0	0	0.2	0	0.45	0
Yellowfin goby	***Acanthogobius flavimanus***	0	0	0	0	0	0	0	0	0	0	0.3	11.38	0.09	0.3
Starry flounder	*Platichthys stellatus*	0.1	0	0	0.9	0	0.5	0.7	0.1	0.2	0	0	0	0.09	0.5
	Total CPUE	90.4	137.7	212.6	164.6	45.1	253.7	33.7	129	82.6	4.6	46	48.91	102.45	41.5
	Native Species	8	7	8	9	4	10	10	9	11	4	10	5	7	7
	Non-Native Species	2	3	3	2	0	1	2	2	0	1	4	5	3	3
	Number of Species	10	10	11	11	4	11	12	11	11	5	14	10	10	10

*Whereas in previous years and the current year, a 100-foot beach seine was used for lagoon sampling, October 2023 sampling used a 200-foot seine. Therefore, CPUE values between 2023 reflect a larger area sampled per net haul, and caution should be exercised in comparing these values to those observed in previous years.

Figure 5. Left- and right-eyed starry flounder (*Platichthys stellatus*) captured during beach seining on October 22, 2024.

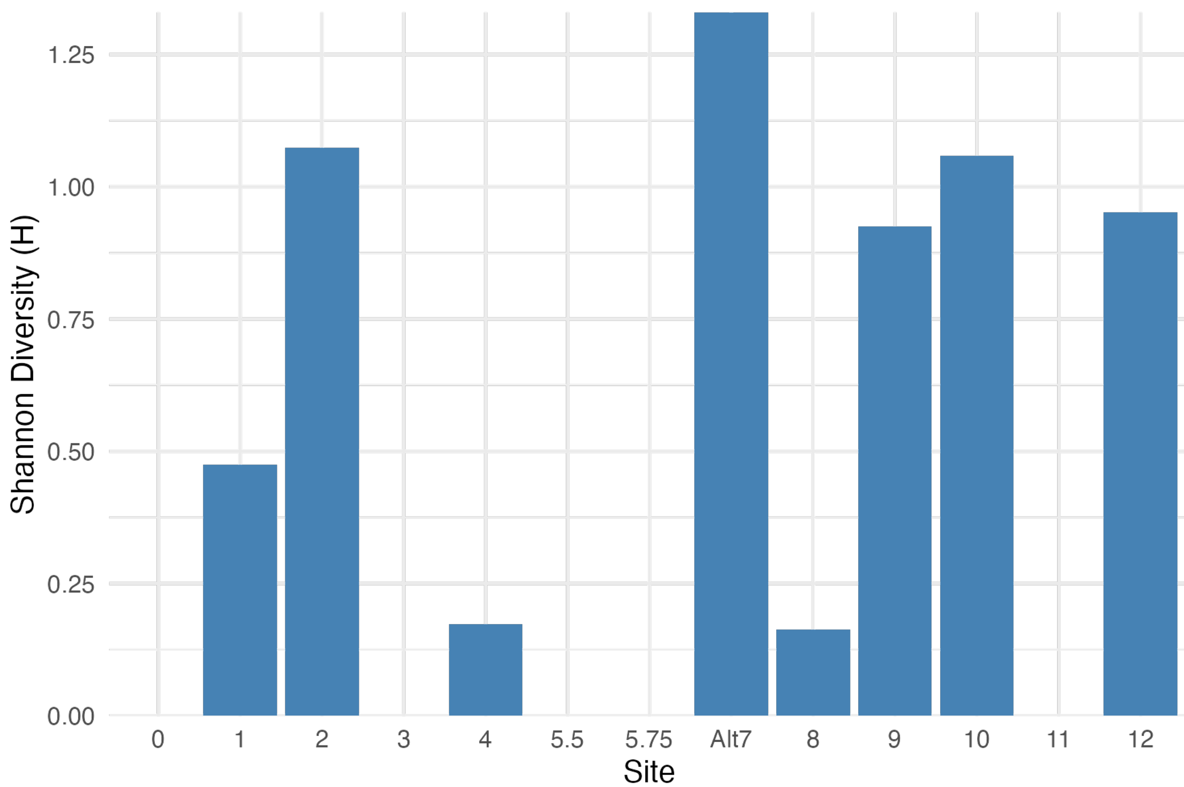

Figure 6. Shannon-Weiner Diversity (H') by site, ordered from downstream to upstream of sites sampled during the fall 2024 sampling event.

Hoop Net Catch

The two hoop nets captured only one species (Table 2), hitch, which was also represented in the seine catch. However, the hoop nets captured larger fish, as the mean total length of fish captured in the hoop nets was 201.9 mm, compared to a mean total length of 118.5 mm for fish captured by the seine net.

Table 2. Total catch of the two hoop nets deployed in the upstream reaches of the Lagoon (Station 11).

Net	Family	Common Name	Species	Total Length (mm)
Trap facing downstream	Cyprinidae	Hitch	*Lavinia exilicauda*	180
	Cyprinidae	Hitch	*Lavinia exilicauda*	210
	Cyprinidae	Hitch	*Lavinia exilicauda*	184
	Cyprinidae	Hitch	*Lavinia exilicauda*	195
Trap facing upstream	Cyprinidae	Hitch	*Lavinia exilicauda*	234
	Cyprinidae	Hitch	*Lavinia exilicauda*	205
	Cyprinidae	Hitch	*Lavinia exilicauda*	205

Environmental DNA

A total of 12 eDNA samples were collected in the lagoon at four locations. Sample volumes ranged from 180 mL to 240 mL due to variation in turbidity across sites that led to faster clogging of the filter in more turbid areas. Whereas eDNA samples collected in 2022 were analyzed using qPCR for the detection of a single species (*O. mykiss*), samples collected from May 2023 onward have been subjected to metabarcoding using MiFish 12S primers, allowing for the detection of multiple species. All samples were submitted to Jonah Ventures for analysis (detailed laboratory methodology is provided in the Appendix).

Seventeen fish, two birds, and one mammal were identified to the species level in the 12 eDNA samples collected. Of the 17 fish species, ten were not detected in either the seine or hoop net samples and they included jacksmelt, California grunion, sardine, northern anchovy, white sucker, western mosquitofish, arrow goby, tidewater goby, Chinook salmon, and striped bass (Table 3). As in previous years, eDNA sampling did not detect *O. mykiss* DNA at any of the sampled locations.

Environmental DNA detected sardines to the genus level at one site. While Pacific sardines (*Sardinops sagax*) are native to the California coast, recent work has identified the presence of Japanese sardines (*Sardinops melanosticta*) in California, including in Monterey Bay (Longo et al. 2024), which the Salinas Lagoon empties into. Thus, it is most likely that this detection identified a Pacific sardine, though identification only to the genus level and potential presence of Japanese sardine in the Monterey Bay confounds further conclusion about the source of the DNA.

Table 3. Environmental DNA samples and detection results. Each site includes combined results from three replicate eDNA samples. Green cells indicate positive directions, whereas red cells indicate no detection. Species not detected in hoop net or seine samples are highlighted in yellow.

Family	Common Name	Station 4	Station 7	Station 8	Station 11
Atherinopsidae	Jacksmelt	x			
	California Grunion	x			
	Inland Silverside*	x	x	x	x
Clupeidae	Pacific Herring	x	x	x	x
	Threadfin Shad			x	x
	Sardine Sp.	x			
Engraulidae	Northern Anchovy	x	x		
Catostomidae	White Sucker				x
Leuciscidae	Hitch	x	x	x	x
Poeciliidae	Western Mosquitofish			x	x
Gobiidae	Yellowfin Goby	x	x	x	x
	Arrow Goby	x			
	Tidewater Goby				x
Cottidae	Pacific Staghorn Sculpin	x	x	x	
Gasterosteidae	Threespine stickleback	x	x	x	x
Salmonidae	Chinook Salmon	x			
Moronidae	Striped Bass	x	x		
	Total Species Detected	13	8	8	9

*The detected inland silverside sequences were assigned only to the genus level, but inland silverside is the only species in this genus likely to be present to be in the system, allowing for inference of species-level ID.

Water Quality Sampling

Water quality sampling during the seining survey revealed an expected, though somewhat minimal, gradient of decreasing salinity with increasing distance from the ocean. Persistent freshwater inflow appeared to maintain low-salinity conditions (0.5 ppt to 1.3 ppt) at every sampling location (Table 4). Dissolved oxygen concentrations were relatively high, exceeding 6.3 mg/L at all monitored locations, which is likely attributable to a combination of algal photosynthesis and continuous mixing of the water column due to freshwater inflow and tidal action. Conditions encountered during field sampling were well within the environmental tolerances of the native fish species in the Salinas River Basin, including listed species like steelhead and tidewater goby.

Table 4. Summary of water quality parameters collected concurrently with beach seining on October 22 2024.

Station	Temp (ºC)	Dissolved Oxygen (mg/L)	Salinity (ppt)	Conductivity (µS/cm)
0	15.8	7.84	1.24	1960
1	15.8	7.8	1.26	1,999
2	16.4	7.45	1.02	1,986
3	16.1	6.31	1.3	2,096
4	15.9	7.7	1.23	1,966
5	15.5	7.14	1.27	2,461
5.5	17.7	9.1	1.04	1,756
5.75	17.7	6.34	0.86	1,465
Alternative 7	17.9	8.04	0.91	1,541
8	18.1	6.51	0.67	1,164
9	18.2	8.04	0.55	1,002
10	18.1	9.78	0.51	886
11	18.1	9.79	0.51	1,020
12	18.1	10.63	0.5	898

Species Discussion

The sampling in October of 2024 is a snapshot of the fish community following a period of 39 days of disconnection from Monterey Bay, which represents a relatively short period of time of closure after an extended period of connectivity with the ocean that spanned from January to September 2024. Habitat conditions in the lagoon and its connectivity with the marine environment tend to drive patterns in the observed fish assemblage. Changes in environmental conditions between June 2024 and October 2024 led to noticeable differences in the fish community assemblage. In the sections below, we provide a discussion of key species observations and any potential implications for lagoon use by rearing juvenile steelhead.

Native Species

Native species represented the majority of fish observed during October 2024, but the proportion was still not as high as was observed in June 2024. Given the more freshwater conditions observed during the fall, many brackish species were absent from sampling. For example, topsmelt were absent from seine and hoop net hauls in the fall, in contrast to the spring 2024 survey. Topsmelt appear to undergo boom-and-bust cycles in the lagoon, showing up in extremely high abundances some years and being completely absent in others. Pacific staghorn sculpin also decreased in abundance from the spring to the fall. This species is generally very abundant in the sites near the mouth of the lagoon; however, many of those sites had relatively low abundance of fish in fall 2024, with very few fish (and few species) observed overall (Figure 7). One fish that did increase in abundance compared to the spring sampling effort in 2024 was Pacific herring. This species also appears to undergo boom-and-bust cycles within the lagoon, likely driven by ocean conditions.

There are no notable trends between observed diversity and site location. However, there may be some effect of a microclimate within the lagoon occurring, explaining the low or absence of diversity observed in sites 0, 11, and 3 through Alt7. Site 5.75, located near the middle of the lagoon, had by far the highest CPUE of all sampling locations, but it is hard to draw any conclusions as to habitat conditions that may have contributed to this catch, as it appeared to exhibit similar conditions to other nearby sites (Figure 7).

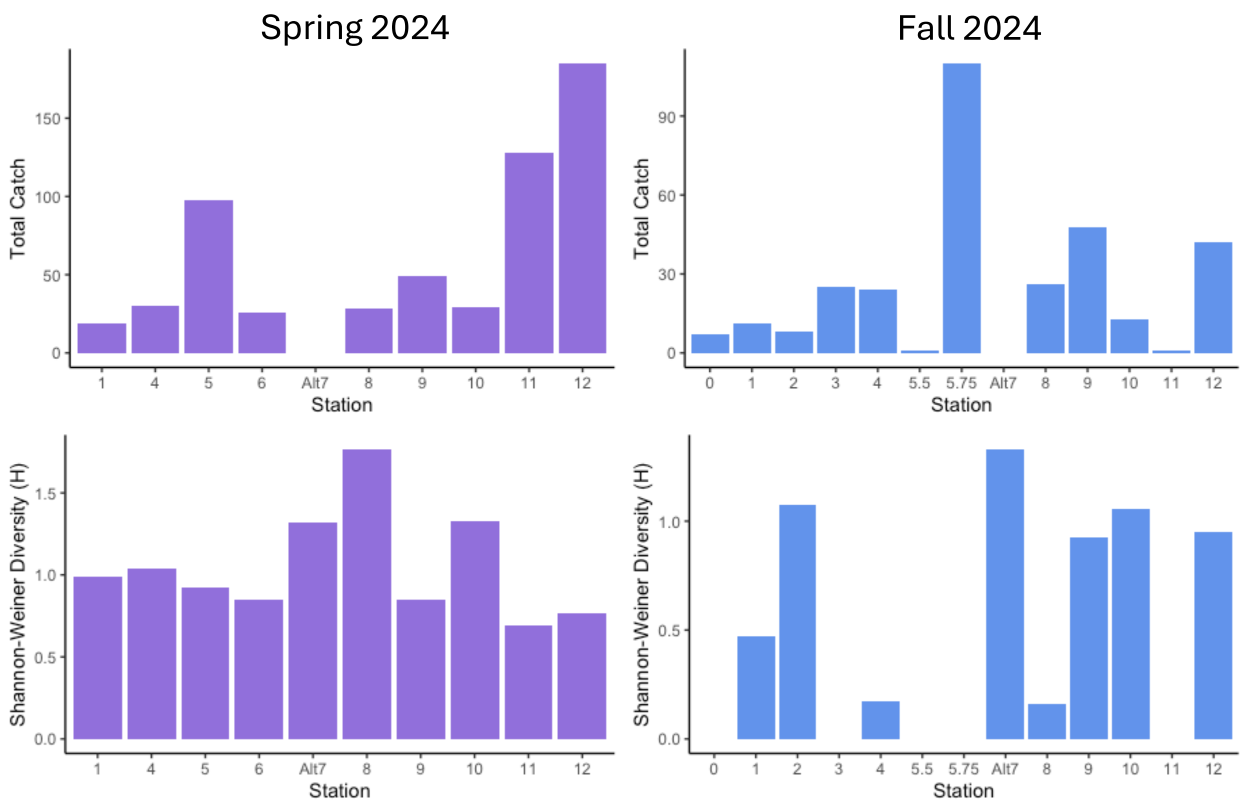

Figure 7. Total catch and Shannon-Weiner diversity index at each sampling site during June and October 2024.

Juvenile steelhead are rarely detected in the lagoon, appearing in only five of the past 24 surveys that occurred since 2002 (Table 1, and Tables A2 and A3 in Appendix). They were last detected during the seining effort in October 2013, and they have not been captured in any of the seining efforts conducted by FISHBIO since 2020. No steelhead were found during the October 2024 sampling event, despite two years with above normal rainfall and ample freshwater flow in the river. Monitoring of *O. mykiss* across the Salinas Basin indicates a small but persistent population, but the chances of detecting any individuals in the lagoon will likely remain minimal given their rarity. Water quality data suggest that abiotic factors such as dissolved oxygen and water temperature have remained within a range suitable for rearing juvenile steelhead, and it is likely that biotic factors and overall population trends – rather than water quality – play a more significant role in reducing juvenile steelhead lagoon use.

Nonnative Species

Inland silverside and yellowfin goby were the only nonnative species observed in seining and hoop net surveys. Inland silverside were observed at higher abundances than previously recorded with CPUE during this survey, being several orders of magnitude higher than in any previous survey during spring, summer, or fall. Inland silversides were observed primarily in the lower lagoon where they constituted most of the overall catch and had the highest CPUE among all fish caught in this survey. A total of 258 inland silverside largely outnumbered any other species captured with the next closes catch being Pacific herring at 158 individuals and Sacramento pikeminnow at 78. The high number of inland silverside is likely due to the low salinity measured across the Salinas Lagoon due to releases and rains prior to the sampling event. Compared to Fall 2023 sampling, salinity was 70-80% lower across the lagoon and variability among sites was lower than earlier in the year (0.5 ppt to 1.3 ppt in fall compared to 0.89 ppt to 21.82 ppt in spring 2024). As salinity increases, the number of inland silverside observable in the Salinas Lagoon is expected to decrease. Yellowfin goby were also observed in October 2024 sampling but at a much lower rate than inland silversides and only at sites higher up in the lagoon than inland silversides. Notably, striped bass were not captured during seining which is relatively rare, although it did also occur in the fall of 2023.

Conclusions

The Salinas Lagoon is a dynamic system that is marked by sudden, dramatic shifts in depth, discharge, and water quality, and associated shifts in the composition of the aquatic community. Historically, this system had an extensive floodplain that was seasonally inundated, and estimates suggest that the area of open water in the lagoon was much larger, with an estimated size of approximately 340 acres in the early 20th century (NMFS 2007). This expansive wetland likely provided rearing habitat for juvenile steelhead throughout the year. Disconnection of this former wetland habitat, management of the lagoon level to protect agricultural fields and residences, reductions in discharge due to water operations, and the introduction of invasive predators (i.e., striped bass) have reduced the suitability of the Salinas Lagoon for rearing steelhead and other native species.

The prevalence of a native-dominated fish community in the Salinas Lagoon is likely a result of two years of above-normal rainfall and increased freshwater flows in the Salinas River as well as prolonged periods of lagoon connectivity with the ocean. The Salinas Basin has experienced two prolonged droughts over the last decade, and conditions during this time likely favored nonnative fish, many of which thrive in the warm, static conditions which were prevalent in the lagoon and farther upstream. Conditions over the last two years are likely more reflective of historical norms and may have favored native fish in both the estuarine and freshwater environments.

The results of the eDNA sampling conducted during this lagoon survey indicated further community diversity that was not captured in seine and hoop net sampling events. The detection of four marine species – jacksmelt, California grunion, northern anchovy, and arrow goby – suggest a greater degree of marine influence on the lower lagoon, which aligns with the continued connectivity that occurred from January to September. Detection was high compared to June 2024 eDNA sampling, suggesting that performance of eDNA collection, amplification, quantification, and identification methods performed better in October 2024 sampling, however, it is difficult to say what conditions may have contributed to this success. The detection of ten species that were not physically captured or observed in the lagoon during seine and hoop net surveys continues the trend of eDNA detecting additional diversity that physical capture surveys have missed. Incorporating these additional sampling strategies into the lagoon surveys in recent years has greatly increased our ability to detect a more accurate sample of the fish community. The use of eDNA sampling in the standard lagoon sampling protocol starting in 2022 has provided further evidence that steelhead are either not present or are very rare in the lower river, and the use of metabarcoding analysis in 2023 and 2024 has demonstrated the value of this approach for detecting species that may elude capture in traditional gears such as seines. Notably, the use of hoop nets since 2023 has also provided more data on larger species that may elude capture by seine nets, including predatory species like Sacramento pikeminnow. The continued capture of larger fish in the hoop nets and new species detections via eDNA highlight the value of a mixed-gear approach for capturing a more complete representation of the fish community in the Salinas Lagoon.

Based on observations in the field over the past three years of sampling by FISHBIO crews, beach seining is of variable efficiency across the sample stations, and changes in river morphology and the presence of debris can make it highly inefficient in certain locations as site conditions change. This is particularly true in many of the upstream sites, where dense vegetation and abundant debris often impede efficient seining and necessitate annual adjustment of sample stations. More strategic and extensive deployment of passive gears like the hoop nets, as well as the inclusion of other gears that are less hindered by the presence of debris (e.g., round haul net), may greatly improve the ability of surveyors to capture a representative sample of the fish community. As such, development of a more comprehensive, multi-gear sampling protocol would be a worthwhile endeavor for ongoing lagoon monitoring.

Literature Cited

Bollens, SM, and Sanders, AM. 2004. Ecology of larval Pacific herring in the San Francisco Estuary: seasonal and interannual abundance, distribution, diet, and condition." *American Fisheries Society Symposium*. American Fisheries Society.

[CDFW] California Department of Fish and Wildlife. 2019. California Pacific Herring Fishery Management Plan. https://wildlife.ca.gov/Fishing/Commercial/Herring/FMP

Fleming, K. 1999 Clupeidae. Pages 151-166 *in* J.J. Orsi, editor. Report on the 1980-1995 fish, shrimp, and crab sampling the San Francisco Estuary, California. California Department of Water Resources, Interagency Ecological Program, Technical Report 63, Sacramento, California.

Gaines, W. L. 1999. Monitoring biodiversity: quantification and interpretation (Vol. 443). US Department of Agriculture, Forest Service, Pacific Northwest Research Station.

Hagar Environmental Science. 2014. Salinas River Lagoon Monitoring Report.

Kumar, G., Farrell, E., Reaume, A.M., Eble, J.A. & Gaither, M.R. 2021. One size does not fit all: tuning eDNA protocols for high-and low-turbidity water sampling. Environmental DNA, 4, 167–180.

Longo, G.C., Minich, J.J., Allsing, N., James, K., Adams-Herrmann, E.S., Larson, W., Hartwick, N., Duong T., Muhling, B., Michael, T.P., Craig, M.T. 2024. Crosing the Pacific: Genomics reveals the presence of Japanese sardine (*Sardinops melanosticta*) in the California current large marine ecosystem. Molecular Ecology, 33,13pp.

[MCWRA] Monterey County Water Resources Agency. 2013. Salinas Valley Water Project Annual Fisheries Report. https://www.co.monterey.ca.us/home/showdocument?id=19052

[MCWRA] Monterey County Water Resources Agency. 2024a. Report on Salinas Valley Water Conditions for the First Quarter of Water Year 2023-2024. https://www.countyofmonterey.gov/home/showpublisheddocument/128888/638445393764330000

[MCWRA] Monterey County Water Resources Agency. 2024b. Report on Salinas Valley Water Conditions for the Second Quarter of Water Year 2023-2024. https://www.countyofmonterey.gov/home/showpublisheddocument/132642/638532728311800000

[MCWRA] Monterey County Water Resources Agency. 2024c. Report on Salinas Valley Water Conditions for the Third Quarter of Water Year 2023-2024. https://www.countyofmonterey.gov/home/showpublisheddocument/136804/638670929371900000

[MCWRA] Monterey County Water Resources Agency. 2024d. Report on Salinas Valley Water Conditions for the Fourth Quarter of Water Year 2023-2024. https://www.countyofmonterey.gov/home/showpublisheddocument/136802/638670927643830000

Michel, CJ, Smith, JM, Demetras, NJ, Huff, DD, and Hayes, SA. 2018. Non-native fish predator density and molecular-based diet estimates suggest differing impacts of predator species on juvenile salmon in the San Joaquin River, California. *San Francisco Estuary and Watershed Science* 16(4).

Moyle, P. B. 2002. Inland fishes of California: revised and expanded. University of California Press.

[NMFS] National Marine Fisheries Service. 2007. Biological Opinion: Monterey County Water Resources Agency, Salinas Valley Water Project in Monterey County, California. SWB/2003/2080.

[NMFS] National Marine Fisheries Service. 2009. Biological Opinion for Sandbar Breaching at the Mouth of the Salinas River. Southwest Region, Long Beach, California, December 21, 2009.

Nobriga, ML, and Feyrer, F. (2008). Diet composition in San Francisco Estuary striped bass: does trophic adaptability have its limits? *Environmental Biology of Fishes*, *83*(4), 495-503.

Sanches, T. M., & Schreier, A. D. 2020. Optimizing an eDNA protocol for estuarine environments: Balancing sensitivity, cost and time. *PLoS One*, *15*(5), e0233522.

Skinner, J. E. 1962. Anadromous fisheries. In: An historical review of the fish and wildlife resources of the San Francisco Bay area (J. E. Skinner, ed.), p. 57–93. California Bay-Delta Authority Science Program and the John Muir Institute of the Environment.

[USFWS] US Fish and Wildlife Service. 1997. Endangered and Threatened Species: Listing of Several Evolutionary Significant Units (ESUs) of West Coast Steelhead. *Federal Register* 62(159): 43937-43954.

[USFWS] US Fish and Wildlife Service. 2007. Biological Opinion on Issuance of Department of the Army Permits to the Monterey County Water Resources Agency for Construction of a Surface Water Diversion Structure in the Salinas River, Near the City of Salinas (Corps File Number 24976S) and for Breaching of the Salinas River Lagoon (Corps File Number 16798S) in Monterey County, California (1-8-06-F .54)

Appendix

Table A1. Temporal coverage of Salinas Lagoon sampling events from 2002 to 2024. Grey shading indicates that no sampling occurred during that year.

Year	Spring	Summer	Fall
2002	-	-	October
2003	-	-	October
2004	-	-	October
2005	-	-	October
2006	-	-	October
2007	-	-	-
2008	-	-	October
2009	-	-	October
2010	-	August	October
2011	May	August	October
2012	April	July	October
2013	April	July	October
2014	April	-	-
2015	-	-	-
2016	-	-	-
2017	-	-	-
2018	-	-	-
2019	-	-	-
2020*	-	-	October
2021*	April	-	-
2022*	May	-	-
2023*	May	-	October
2024*	June	-	October

*Sampling conducted by FISHBIO

Table A2. Cumulative and species-specific catch per unit effort (CPUE) across the four summer sampling events ranging from August 2008 to July 2013. Note that CPUE is calculated using a single seine haul as the base unit of effort. Non-native species are indicated by bolded common and scientific names.

		Date	**Aug 2010**	**Aug 2011**	**July 2012**	**July 2013**
		Total Seine Hauls	7	9	13	13
Family	**Common Name**	**Scientific Name**				
Clupeidae	Pacific herring	*Clupea pallasii*	35.70	0	0	0.80
	Pacific sardine	*Sardinops sagax*	0.10	0	0	0
Cyprinidae	**Common carp**	***Cyprinus carpio***	0.10	0	0	0.60
	Hitch	*Lavinia exilicauda*	134.10	4.10	16.20	4.50
	Sacramento blackfish	*Orthodon microlepidotus*	33.60	0	0.10	0.10
	Unidentified cyprinid	*Cyprinidae*	0.10	0	0	0
Catostomidae	Sacramento sucker	*Catostomus occidentalis*	45.90	0	2.60	1.10
Osmeridae	Topsmelt	*Atherinops affinis*	15.10	0	0	0
Salmonidae	Steelhead	*Oncorhynchus mykiss*	0	0.10	0	0
Poeciliidae	**Western mosquitofish**	***Gambusia affinis***	0	0.40	1.50	0.20
Cottidae	Pacific staghorn sculpin	*Leptocottus armatus*	33.30	0.60	0.90	0.80

	Prickly sculpin	*Cottus asper*	5.40	0.40	20	5.10
	Unidentified sculpin	*Cottidae*	0.30	0	0	0
Gasterosteidae	Threespine stickleback	*Gasterosteus aculeatus*	347.60	3.40	5.10	21.20
Embiotocidae	Shiner surfperch	*Cymatogaster aggregata*	13.40	0	0	0
Moronidae	**Striped bass**	***Morone saxatilis***	0.40	0	2.40	3.60
Centrarchidae	**Largemouth bass**	***Micropterus salmoides***	0	0	0	0.10
Gobiidae	**Yellowfin goby**	***Acanthogobius flavimanus***	0	0	0	4.60
	Unidentified goby	*Gobiidae*	0.50	0	0	0
Scorpaenidae	Unidentified rockfish	*Sebastes* sp.	0.20	0	0	0
Pleuronectidae	Starry flounder	*Platichthys stellatus*	0.90	0.10	0.10	0.10
		Total CPUE	666.70	9.10	30.90	42.80
		Native Species	15	6	7	8
		Non-native Species	2	1	2	5
		Total Number of Species	17	7	9	13

Table A3. Cumulative and species-specific catch per unit effort (CPUE) across the seven spring sampling events from 2011–2024. Note that CPUE is calculated using a single seine haul as the base unit of effort. Non-native species are indicated by bolded common and scientific names.

		Date	**May 2011**	**April 2012**	**April 2013**	**April 2014**	**April 2021**	**May 2022**	**May 2023***	**June 2024***
		Total Seine Hauls	16	17	14	8	12	10	11	10
Family	**Common Name**	**Scientific Name**								
Petromyzontidae	Pacific lamprey	*Petromyzon tridentata*	0	0.1	0	0	0	0	0.1	0
Alosidae	**American shad**	***Alosa sapidissima***	0	0	0	0	0	0	0.1	0
Clupeidae	Pacific herring	*Clupea pallasii*	0	2.9	89.8	0	104.4	67.8	0	3.1
	Threadfin shad	***Dorosoma petenense***	0	0.1	0	0	0	0	0	0
Cyprinidae	**Common carp**	***Cyprinus carpio***	0	0.2	0	0	0	0	0	0
	Hitch	*Lavinia exilicauda*	8.3	11.8	6.5	0	0.1	0.1	2.1	26.0
	Sacramento blackfish	*Orthodon microlepidotus*	0.1	0.9	0	0	0	0	0	0
	Sacramento pikeminnow	*Ptychocheilus grandis*	0	0.10	0	0	0	0	0	11.6
Catostomidae	Sacramento sucker	*Catostomus occidentalis*	2.3	1.1	0.2	0	0	0	2.5	1.2
Osmeridae	Topsmelt	*Atherinops affinis*	0	0	0	0	1.1	2.3	0	6.4
Salmonidae	Steelhead	*Oncorhynchus mykiss*	0.1	0.1	0	0	0	0	0	0
Poeciliidae	**Western mosquitofish**	***Gambusia affinis***	0	0	0	0	0.1	0.7	0	0
Atherinidae	**Inland silverside**	***Menidia beryllina***	0	0	0	0	0.6	0	0	0
Cottidae	Pacific staghorn sculpin	*Leptocottus armatus*	5.3	0	15.9	0	15.5	18.8	0.5	7.4
	Prickly sculpin	*Cottus asper*	0.2	0.8	0	1.3	0.7	1.5	0.3	6.3
Gasterosteidae	Threespine stickleback	*Gasterosteus aculeatus*	0	6.6	1.9	10.4	0.3	48.5	0.1	0.3
Embiotocidae	Shiner surfperch	*Cymatogaster aggregata*	0.2	0.2	0	0	0	0	0	0.6
Moronidae	**Striped bass**	***Morone saxatilis***	0.3	2.4	0.6	0	0.1	0.1	0.7	0.6
Gobiidae	Tidewater goby	*Eucyclogobius newberryi*	0	0	0	7.3	0	0	0	0
	Yellowfin goby	***Acanthogobius flavimanus***	0	0	0.1	0	0.2	0.1	0	0
Scianidae	White croaker	*Genyonemus lineatus*	0	0	0	0	0.1	0	0	0
Scorpaenidae	Unidentified Rockfish	*Sebastes* sp.	0	0	0	0	0	0	0	0.1
Paralichthyidae	Speckled sanddab	*Citharichthys stigmaeus*	0	0	0	0	0.1	0.1	0	0.1
Pleuronectidae	Petrale sole	*Eopsetta jordani*	0	0	0	0	0	0	0	1.3
	Starry flounder	*Platichthys stellatus*	0.1	1.1	0	0	0	0	0	0.1
		Total CPUE	16.9	28.4	115	19	123.1	140	6.4	65.1
		Native Species	8	11	5	3	8	7	6	13
		Non-native Species	1	3	2	0	4	3	2	1
		Total Number of Species	9	14	7	3	12	10	8	14

*Whereas in previous years a 100-foot beach seine was used for lagoon sampling, May 2023 and June 2024 sampling used a 200-foot seine. Therefore, CPUE values from 2023 and 2024 reflect a larger area sampled per net haul, and caution should be exercised in comparing these values to those observed in previous years.

Environmental DNA Metabarcoding Methodology – Courtesy of Jonah Ventures

Sample Process
Sample barcodes were recorded and assigned a well within the 96 well plate or numbered extraction tube. A customized one-ton arbor press along with a removable leather punch was used to open the plastic casing of each filter. Once plastic casing was cut, sample barcodes were recorded and assigned a well within the 96 well plate or numbered extraction tube. The whole filter was removed and transferred to the extraction plate/tube using sterilized tweezers inside a laminar flow hood. The removable leather punch was sterilized between each eDNA filter. Plates or tubes were immediately processed or stored in -20C until the extraction process could be performed.

Extraction
Genomic DNA from samples was extracted using the DNeasy Blood & Tissue Kit (250) (Cat. No. / ID: 69506) according to the manufacturer's protocol. Whole (25mm or 47mm) filters were used for genomic DNA extraction. Genomic DNA was eluted into 200µl and frozen at -20°C.

PCR
Forward Primer: GTCGGTAAAACTCGTGCCAGC
Reverse Primer: CATAGTGGGGTATCTAATCCCAGTTTG
Primer reference: Miya et al 2015

Portions of hyper-variable regions of the mitochondrial 12S ribosomal RNA (rRNA) gene were PCR amplified from each genomic DNA sample using the MiFishUF and MiFishUR primers with spacer regions. Both forward and reverse primers also contained a 5' adaptor sequence to allow for subsequent indexing and Illumina sequencing. PCR amplification was performed in replicates of six and all six replicates were not pooled and kept separate. Each 25 µL PCR reaction was mixed according to the Promega PCR Master Mix specifications (Promega catalog # M5133, Madison, WI) which included 12.5ul Master Mix, 0.5 µM of each primer, 1.0 µl of gDNA, and 10.5 µl DNase/RNase-free H2O. DNA was PCR amplified using the following conditions: initial denaturation at 95C for 3 minutes, followed by 45 cycles of 20 seconds at 98C, 30 seconds at 60C, and 30 seconds at 72C, and a final elongation at 72C for 10 minutes. Added 11/2019.

Gel
To determine amplicon size and PCR efficiency, each reaction was visually inspected using a 2% agarose gel with 5µl of each sample as input.

PCR Amplicon Cleanup
Amplicons were then cleaned by incubating amplicons with Exo1/SAP for 30 minutes at 37C following by inactivation at 95C for 5 minutes and stored at -20C.

Barcoding PCR
A second round of PCR was performed to complete the sequencing library construct, appending with the final Illumina sequencing adapters and integrating a sample-specific,12-nucleotide index

sequence. The indexing PCR included Promega Master mix, 0.5 µM of each primer and 2 µl of template DNA (cleaned amplicon from the first PCR reaction) and consisted of an initial denaturation of 95 °C for 3 minutes followed by 8 cycles of 95 °C for 30 sec, 55 °C for 30 seconds and 72 °C for 30 seconds.

PCR Normal Pool

Final indexed amplicons from each sample were cleaned and normalized using SequalPrep Normalization Plates (Life Technologies, Carlsbad, CA). 25µl of PCR amplicon is purified and normalize using the Life Technologies SequalPrep Normalization kit (cat#A10510-01) according to the manufacturer's protocol. Samples are then pooled together by adding 5µl of each normalized sample to the pool.

Sequencing

Sample library pools were sent for sequencing on an Illumina MiSeq (San Diego, CA) at the Texas A&M Agrilife Genomics and Bioinformatics Sequencing Core facility using the v2 500-cycle kit (cat# MS-102-2003). Necessary quality control measures were performed at the sequencing center prior to sequencing.

Bioinformatics

Raw sequence data were demultiplexed using pheniqs v2.1.0 [1], enforcing strict matching of sample barcode indices (i.e, no errors). Cutadapt v3.4 [2] was then used remove gene primers from the forward and reverse reads, discarding any read pairs where one or both primers (including a 6 bp, fully degenerate prefix) were not found at the expected location (5') with an error rate < 0.15. Read pairs were then merged using vsearch v2.15.2 [3], discarding resulting sequences with a length of < 130 bp, > 210 bp, or with a maximum expected error rate [4] > 0.5 bp. For each sample, reads were then clustered using the unoise3 denoising algorithm [5] as implemented in vsearch, using an alpha value of 5 and discarding unique raw sequences observed less than 8 times. Counts of the resulting exact sequence variants (ESVs) were then compiled and putative chimeras were removed using the uchime3 algorithm, as implemented in vsearch. For each final ESV, a consensus taxonomy was assigned using a custom best-hits algorithm and a reference database consisting of publicly available sequences (GenBank [6]) as well as Jonah Ventures voucher sequences records. Reference database searching used an exhaustive semi-global pairwise alignment with vsearch, and match quality was quantified using a custom, query-centric approach, where the % match ignores terminal gaps in the target sequence, but not the query sequence. The consensus taxonomy was then generated using either all 100% matching reference sequences or all reference sequences within 1% of the top match, accepting the reference taxonomy for any taxonomic level with > 90% agreement across the top hits.

References:

Galanti, Shasha and Gunsalus (2021). Pheniqs 2.0: accurate, high-performance Bayesian decoding and confidence estimation for combinatorial barcode indexing. BMC Bioinformatics 22.

Martin (2011), Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnet. journal 17.

Torbjørn et al. VSEARCH: a versatile open source tool for metagenomics. PeerJ 4 e2584 (2016).

Edgar and Flyvbjerg (2015), Error filtering, pair assembly and error correction for next-generation sequencing reads. Bioinformatics 31.

Edgar (2016), UNOISE2: improved error-correction for Illumina 16S and ITS amplicon sequencing. doi: https://doi.org/10.1101/081257.

Benson et al. (2005), GenBank. Nucleic Acids Res 33.

Data Management Plan

This data management plan is designed to ensure that project data are collected using peer–approved methods, undergo a quality control and accuracy assessment process, include metadata that meet CDFW's minimum standards.

The following documentation provides evidence of the methods and quality control procedures that were used to meet Grant Agreement requirements.

1. **Who collected the data:** Michael Hellmair, Dana Lee, Emily Jonagan, Marinn Browne
2. **When the data was collected:** October 2024
3. **Where the data was collected:** Salinas River Lagoon
4. **How the data was collected (description of methods and protocols):** Surveys conducted by FISHBIO used a four-person crew with a100 x 6-foot beach seine (1/4-inch mesh). No particular habitat type was preferentially targeted or favored for sampling; rather, approximately equidistant sampling locations were chosen to obtain an adequate overview of the spatial distribution of the fish community within the lagoon. During subsequent sampling events, initially selected locations were revisited. At each sampling location, one to two seine hauls were conducted. All fish captured during each survey, regardless of method, were identified to species, enumerated, and measured. All data sheets collected in the field were scanned (with electronic copies stored on a server) before the data was entered into a database. Prior to data analyses, the database underwent QA/QC procedures including being checked against field datasheets by two separate individuals. All datasheets were also stored as hard copies at the FISHBIO office.
5. **The purposes for which the data was collected:** Salinas Lagoon sampling is intended to assist in determining the presence and spatial distribution of *O. mykiss* in the lower Salinas River and Lagoon as well as understanding the composition and relative abundance of the overall fish community. Objectives include evaluating presence or absence, condition, relative abundance (i.e., catch per unit effort; CPUE), and distribution of *O. mykiss* and other species in the Salinas Lagoon.
6. **Definitions of variables, fields, codes, and abbreviations used in the data, including units of measure:** All species field codes are included below.
7. **The terms of any landowner access agreement(s), if applicable:** Not Applicable
8. **References to any related Department permits or regulatory actions:** Not Applicable
9. **Peer review or statistical consultation documentation:** All reports were reviewed by multiple parties, including the Grant recipient, and will also be published online and therefore subject to external peer review.
10. **Data licensing and disclaimer language:** All data is the property of Monterey County Water Resources Agency and is subject to their data licensing and disclaimer requirements.

Abbreviation Codes

Common Name	Species Code
American Shad	AMS
Bass Unknown	BAS
Bigscale Logperch	LP
Black Bullhead	BKB
Black Crappie	BKS
Blue Catfish	BLC
Bluegill	BGS
Brook Trout	BKT
Brown Bullhead	BRB
Brown Trout	BT
California Roach	CAR

Common Name	Species Code
Rainbow / Steelhead Trout	RBT
Red Shiner	RSN
Redear Sunfish	RES
Redeye Bass	REB
Riffle Sculpin	RFS
River Lamprey	RL
Sacramento Blackfish	SCB
Sacramento Perch	SP
Sacramento Squawfish	SASQ
Sacramento Sucker	SASU
Sculpin Unknown	SCP

Catfish Unknown	CAT
Channel Catfish	CHC
Chinook Salmon	CHN
Common Carp	C
Delta Smelt	DSM
Fathead Minnow	FHM
Golden Shiner	GSN
Goldfish	GF
Green Sturgeon	GST
Green Sunfish	GSF
Hardhead	HH
Hitch	HCH
Inland Silverside	MSS
Kern Brook Lamprey	KBL
Kokanee Salmon	KOS
Lamprey Unknown	LAM
Largemouth Bass	LMB
No Catch	NONE
Pacific Lamprey	PL
Pacific Brook Lamprey	BL
Pacific Staghorn Sculpin	PSS
Prickly Sculpin	PRS
Pumpkinseed	PKS

Stanislaus River Station	**Station Code**
Caswell State Park	ST004X
Caswell State Park – North Trap	ST004N
Caswell State Park – South Trap	ST004S
Oakdale Recreation Area	ST040X
Stanislaus Weir	ST031X
Calaveras River Station	**Station Code**
Shelton Rd.	CR028X
Merced River Station	**Station Code**
Gallo Ranch	ME041X
Hatfield Park – North Trap	ME002N
Hatfield Park – South Trap	ME002S

Condition Code	**Description**
1	Good
2	Fair (partial cell block)
3	Poor (total cell block)
4	No sample taken

Debris Code	**Description**
LIT	Light
MED	Medium
HVY	Heavy

Weather Code	**Description**
CLD	Cloudy
RAN	Rainy
CLR	Clear
NIT	Night

Shimofuri Goby	SHM
Smallmouth Bass	SMB
Speckled Dace	SPD
Splittail	SPLT
Spotted Bass	SPTB
Striped Bass	STB
Sturgeon Unknown	STG
Sunfish Unknown	SNF
Threadfin Shad	TFS
Threespine Stickleback	TSS
Tule Perch	TP
Unknown (Unid Juvenile Fish)	UNID
Unknown Centrarchid	CENT
Wakasagi	WAG
Warmouth	W
Western Mosquitofish	MQK
White Catfish	WHC
White Sturgeon	WST
Yellow Bullhead	YEB
Yellowfin Goby	YFG

Tuolumne River Station	**Station Code**
Grayson	TU005X
Grayson – North Trap	TU005N
Grayson – South Trap	TU005S
Waterford	TU030X
Tuolumne Weir	TU024X
Arroyo Seco River	**Station Code**
Arroyo Seco River	AS012X
Nacimiento River	**Station Code**
Nacimiento River	NR001X
Salinas River	**Station Code**
Upper Salinas	SR109X
Salinas Weir	SR003X

Mark Codes	**Description**
CFG**N**	Natural Origin
CFG**H**	Hatchery Origin
CFG*	Caudal Fin Green
CFR*	Caudal Fin Red
CFO*	Caudal Fin Orange
CFP*	Caudal Fin Pink
CFB*	Caudal Fin Blue
AFG*	Anal Fin Green
AFB*	Anal Fin Blue
TCR**	Top Caudal Fin Red
BCR**	Bottom Caudal Fin Red
DCB**	Double Caudal Fin Red
(*) Always indicate stock origin (H or N)	
(**) Indicate if mark is specific to location on fish (T or B or D)	

Gear Status	**Description**
0	Set trap
3	Check and raise trap

Invasive Species Prevention Plan

All field gear used in the Salinas Lagoon was properly disinfected following California Department of Fish and Wildlife Aquatic Invasive Species Disinfection/Decontamination Protocols prior to the start of fieldwork.

A detailed list of the relevant disinfection procedures and preventative measures that were used to prevent the spread of aquatic invasive species in the Salinas Watershed is listed below.

If equipment is used on the project that was previously working in another stream, river, lake, pond, or wetland within 10 days of initiating work, we implement one of the following procedures to prevent the spread of New Zealand Mud Snails and other aquatic hitchhikers:

(1) Remove all mud and debris from equipment (waders, nets, watercraft, etc.) and keep the equipment dry for 10 days. OR

(2) Remove all mud and debris from Equipment (waders, nets, watercraft, etc.) and spray/soak equipment with either a 1:1 solution of Formula 409 Household Cleaner and water, or a solution of Sparquat 256 (5 ounces Sparquat per gallon of water). Treated equipment must be kept moist for at least 10 minutes. OR

(3) Remove all mud and debris from equipment (waders, nets, watercraft, etc.) and spray/soak equipment with water greater than 120 degrees F for at least 10 minutes. OR (4) Remove all mud and debris from equipment (waders, nets, watercraft, etc.) and freeze equipment below 0 degrees F for at least 48 hours.