ERP Proposal: Native Fish Predation

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Proposal No.	Region

(Pages A13-A18)

Section 1: Summary Information

1. Project title:	Linking habitat and spatial variability to native fish predation
2. Applicant name:	The Regents of the University of California
3. Contact person:	Bernie May
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9. Agency Type:	Federal Agency ☐ State Agency ☐ Local Agency ☐ Nonprofit Organization ☐ University (CSU/UC) ☒ Native American Indian Tribe ☐
10. Certified nonprofit organization:	Yes ☒ No ☐
11. New grantee:	Yes ☒ No ☐
12. Amount requested:	$730,307
13. Total project cost:	$730,307
14. Topic Area(s):	Primary: Non-native Invasive Species Secondary: At-Risk Species Assessment; Harvestable Species Assessment; Estuary Foodweb Productivity
15. ERP Project type:	Research
16. Ecosystem Element:	Primary: Invasive Aquatic Organisms Secondary: Bay-Delta Aquatic Foodweb; Essential Fish Habitats; Predation and Competition; Freshwater Fish Habitats
17. Water Quality Constituent:	N/A
18. At-Risk species benefited:	Delta smelt; longfin smelt; Sacramento splittail; Central Valley Chinook salmon (spring-, winter-, and fall-run ESUs); Central Valley steelhead ESU; green sturgeon
19. Project objectives:	Genetic assays will be used to understand spatial and temporal variability in predation impacts on native and non-native fishes in the northern Delta. Bioenergetics modeling will estimate consumption of Chinook salmon by striped bass among different ecosystems.
20. Time frame:	09/01/2011 – 08/31/ 2014. Project duration is three years, with two years of field sampling (Fall 2011 – Spring 2013) and a third year for data analysis, reporting, and manuscript preparation.

Section 2: Location Information

1. Township, Range, Section: and the 7.5 USGS Quad map name.	Study will cover Liberty Island, Courtland, Rio Vista, and Isleton 7.5 USGS Quad maps
2. Latitude, Longitude (in decimal degrees, Geographic, NAD83):	38.3421 – 38.1310 N, -121.5270 – -121.6952 W
3. Location description:	Our study will be conducted in Liberty Island, the Sacramento Deep Water Ship Channel, Miner Slough, Steamboat Slough, Georgiana Slough, and the Sacramento River (from Rio Vista to Walnut Grove).
4. County(ies):	Solano, Sacramento
5. Directions:	From the Rio Vista municipal boat launch, travel upstream to confluence with Cache Slough. To reach Georgiana Slough, turn right and continue up the Sacramento River for 20 km and turn right. To visit north delta sites, turn left into Cache Slough and continue to Steamboat Slough (1 km, right), Miner Slough (7 km, right), Sacramento Deep Water Ship Channel (7.5 km, right), and Liberty Island (8.5 km, right).
6. Ecological Management Region:	Bay Delta
7. Ecological Management Zone(s):	Sacramento-San Joaquin Delta
8. Ecological Management Unit(s):	North Delta and East Delta
9. Watershed Plan(s):	N/A
10. Project area:	This study covers 45 miles of rivers and sloughs, spanning channel widths of 130 – 6,000 feet.
11. Land use statement:	Many areas adjacent to the study site have floodplain easements, and consist of wetland mitigation projects and restoration efforts. Many other areas are listed in the Bay Delta Conservation Plan for future tidal marsh and floodplain restoration efforts. Additionally, there are agricultural and grazing lands in the immediate area.
12. Project area ownership:	% Private___0____ % State___70___ % Federal___30___ *Enter ownership percentages by type of ownership.*
13. Project area with landowners support of proposal:	N/A

Section 3: Landowners, Access and Permits

1. Landowners Granting Access for Project: (Please attach provisional access agreement[s]). All sampling locations will be accessed via publicly-accessible boat launch areas, and sampling will be conducted within navigable water ways. Thus, it will not be necessary to obtain landowner access permits.	
2. Owner Interest: N/A	
3. Permits:	Sampling will require a federal Section 10(a)(1)(A) ESA permit for permission to conduct sampling in areas where incidental take of winter-run and spring-run Chinook salmon, Central Valley steelhead, and green sturgeon are possible. DWR is already in consultation with the National Marine Fisheries Service to acquire this permit. In addition, Department of Fish & Game-issued Scientific Collecting Permits

	will be necessary for the field sampling. Louise Conrad and Brian Schreier have already obtained Scientific Collecting Permits, which will be amended to include the proposed sampling protocol after the federal permit is obtained. Additionally, an MOU will be required for CESA-protected species, and this will also be obtained after securing a federal permit.
4. Lead CEQA agency:	N/A
5. Required mitigation:	Yes ☐ No ☒

Section 4: Project Objectives Outline

1. List task information:

Goal 1: Endangered and Other At-risk Species and Native Biotic Communities

The proposed study will directly address two objectives of this goal including:

- *Objective 1: Aiding in the recovery and long-term persistence of Central Valley winter-, spring- and fall/late fall-run Chinook salmon ESUs, Central Valley steelhead ESU, green sturgeon, delta smelt, longfin smelt, and Sacramento splittail*

  Predation by non-native predators, such as largemouth bass and striped bass, has been identified as a significant stressor to BDCP-target fish species (BDCP, 2010). In fact, specific locations for the removal of invasive predators of Chinook salmon, steelhead, and splittail are included in the recent BDCP draft. The proposed project aims to identify patterns of habitat, spatial, and/or temporal variability that increase predation pressures for all of the threatened and at-risk species listed above. Detection of predation on specific prey species, and perhaps specific Chinook ESUs, will be conducted with a DNA-based approach, which has been successfully employed to sensitively detect predation in many aquatic environments (reviewed in King et al. 2008). The information gathered by the proposed project will inform current and future restoration strategies to ensure effective adaptive management of non-native predators and aid in the recovery of their native prey.

- *Objective 3: Enhance and/or conserve native biotic communities in the Bay-Delta estuary and its watershed, including abundance and distribution of native resident estuarine and freshwater fish assemblages*

  The proposed project will contribute to our understanding of the predator-prey dynamics of native fishes and how they differ from non-native fishes across variable landscapes. The information gathered will thus help to promote more effective conservation strategies to benefit native fish communities. Moreover, our field sampling component will help to fill a current void in fishery monitoring efforts by tracking the abundance and distribution patterns of many high-profile predator species, including the native Sacramento pikeminnow, in the north Delta.

2. Additional objectives:

Goal 2: Ecological Processes

- *Objective 2: Increase estuarine productivity and rehabilitate estuarine food web processes to support the recovery and restoration of native estuarine species and biotic communities*

  Understanding current food web dynamics and the factors contributing to non-native predation on native prey will enable future restoration actions to create habitat that better supports and protects native estuarine fishes from non-native predators. The bioenergetics model will examine spatial and temporal processes between striped bass predators, Chinook salmon prey, and their environment in order to increase Chinook salmon productivity. Bioenergetics models have been used with considerable predictive success in the past to identify functional links between abiotic and biotic factors that contribute to changes in species productivity, including consumption from predator populations (reviewed in Hansen et al. 1993).

Goal 3: Harvested Species

- *Objective 1: Enhance fisheries for salmonids, white sturgeon, and native cyprinid fishes*

  Promoting conditions that reduce non-native predation of Chinook salmon, steelhead, and, to a lesser degree, Sacramento splittail and white sturgeon will directly enhance the fisheries for these species. Additionally, by comparing conditions that increase native pikeminnow predation relative to non-native bass predation, future restoration actions can be developed to favor both native prey and predators.

Goal 4: Habitats

- *Objective 1: Restore large expanses of all major habitat to support recovery of native species and biotic communities and rehabilitation of ecological processes*

  Identifying the habitat types that benefit native predator and prey fishes will enable more effective and efficient habitat restoration.

Goal 5: Nonnative Invasive Species

- *Objective 7: Limit the spread or, when possible and appropriate, eradicate populations of non-native invasive species through focused management efforts*

  Results from the proposed study will determine particular "hotspots" of predation for at-risk native species. The information obtained will include the predatory species most commonly consuming at-risk prey, the specific prey species being consumed, and where this predation is occurring in the north Delta. Therefore, local eradication of particular predators will be possible and this effort may benefit native species. Since we will also determine predation prevalence for non-native prey (Wakasagi smelt and Mississippi silverside), decisions regarding eradication can balance the benefit of reduced predation on native prey species with the potential increase in abundance of non-native prey species.

3. Source(s) of above information:

BDCP Working Draft (2010) Available at http://baydeltaconservationplan.com/Home.aspx

Hansen, M.J., D. Boisclair, S.B. Brandt, S.W. Hewett, J.F. Kitchell, M.C. Lucas, J.J. Ney (1993) Applications of bioenergetics models to fish ecology and management: where do we go from here? *Transactions of the American Fisheries Society* 122: 1019-1030.

King, R.A., D.S. Read, M. Turagott, and O.C. Symondson (2008) Molecular analysis of predation: a review of best practice for DNA-based approaches. *Molecular Ecology* 17: 947-963.

Section 6: Project Tasks and Results Outline

1. Detailed Project Description.

The effect of predation on native fishes in the Sacramento – San Joaquin Delta (Delta) has been identified as a major stressor to declining native fish populations (Bay Delta Conservation Plan, BDCP, 2010). While predation is a universal process for biota of nearly all trophic levels, a primary concern for native fishes in the Delta is that predation pressure from introduced, highly effective predators such as striped bass (*Morone saxatilis*), largemouth bass (*Micropterus salmoides*), and smallmouth bass (*Micropterus dolomeiu)* may limit population recovery or even exacerbate species' declines (Baxter et al., 2010). While the original cause of these declines is likely rooted in large-scale changes in habitat conditions (extensive wetland reclamation, channel dredging, dam construction on freshwater inputs to the system, and installation of powerful pumping operations that alter hydrodynamic patterns), these changes have modified conditions to favor abundance of these introduced predators, while decimating suitable habitat for native fishes (Brown and Michniuk, 2007; Sommer et al., 2007). In fact, several native species are listed under the federal Endangered Species Act (ESA) as endangered (Central Valley winter-run Chinook salmon, *Oncorhynchus tshawytscha*), threatened (Central Valley spring-run Chinook salmon; steelhead trout, *Oncorhynchus mykiss*; Delta smelt, *Hypomesus transpacificus*; green sturgeon, *Acipenser medirostris*) or a species of concern (fall and late-fall runs Central Valley Chinook salmon). Moreover, other species are not listed but have precipitously declined in number from historic levels, such as Sacramento splittail, (*Pogonichthys macrolepidotus*; Moyle et al., 2004), white sturgeon (*Acipenser transmontanus*; Fish, 2010); longfin smelt, (*Spirinchus thaleichthys;* Sommer et al., 2007). Thus, emerging conservation plans for the Delta prescribe extensive habitat restoration designed to favor native species while discouraging non-native predators (BDCP, 2010; Ecological Restoration Plan (ERP) Conservation Strategy, 2010; Delta Vision Strategic Plan, 2008), as well as aggressive predator removal programs targeting "predation hot spots" during periods when listed species are present (e.g. section 3.4.4.4, BDCP, 2010).

As recently highlighted in the Interagency Ecological Program (IEP) Pelagic Organism Decline Work Team's

Synthesis of Results (Baxter et al., 2010), quantitative estimates of the impact of predation on native fish populations are largely non-existent. Knowledge of the spatial variability in predation in key areas still inhabited by native fish is extremely limited (but see Nobriga and Feyrer 2007, 2008), let alone an understanding of how predation pressure varies with habitat conditions. An understanding of environmental factors that promote or discourage predation, as well as specific locations to target for predator removal, will be critical to guide successful habitat restoration actions.

This study will provide essential, quantitative information for future restoration and predator removal efforts by examining the incidence of predation on Chinook salmon, steelhead trout, Delta and longfin smelt, white and green sturgeon, and Sacramento splittail by striped bass and largemouth bass as well as the native piscivore, Sacramento pikeminnow (*Ptychocheilus grandis*), across migration corridors and habitats of the north Delta (Fig. 1). This region of the Delta is considered a refuge for many native fish species, contains key migration corridors for Chinook salmon, steelhead, Delta smelt, longfin smelt, splittail, white sturgeon, and green sturgeon, and is also a major target for future tidal marsh restoration (BDCP, 2010). In addition, there is concern that planned installation of new pumping operations on the Sacramento River in the north Delta will attract predators to this region, potentially counter-acting benefits of habitat restoration (DRERIP Evaluation of BDCP Conservation Measures, Appendix F, 2009). However, no baseline data are available on current predation levels for this region of the Delta. This study will fill this critical gap and thus facilitate evaluation of the effects of proposed restoration actions.

Some background data on variable survival rates across migration corridors are available, though reduced survival in some reaches have not yet been explicitly linked to predation. For Chinook salmon, the probability of surviving emigration to the Pacific Ocean through the Delta varies with the specific migration route (Perry et al., 2010). An outmigrating salmon can travel via the Sacramento River all the way to the confluence with the San Joaquin River or through secondary channels such as Miner, Steamboat, or Georgiana Sloughs. Other migration routes include the Yolo Bypass (given inundation via the Fremont Weir), or deviations from major through-channels into flooded island habitat (e.g. Liberty Island) or alternative major waterways (e.g. Sacramento Deep Water Ship Channel). Among all of these possibilities, a salmon's chances of survival will vary with different hydrologic conditions, water project operations, food availability, and relative predator densities (Perry et al., 2010, Brandes & McLain, 2001). In addition to Chinook salmon, other native fishes are using the same habitats in the north Delta: steelhead smolts migrate through the same area, longfin smelt move upstream to spawn, and Delta smelt and Sacramento splittail rear and spawn in various locations in the north Delta during winter and spring months (Moyle, 2002).

One of the chief reasons for the paucity of quantitative predation studies in the Delta is that detection of predation of rare species (e.g., ESA-listed) in predator diets via traditional visual examination is extremely costly and time intensive: small, soft-rayed fishes are often too degraded in stomach contents for positive identification, and very large sample sizes are required to find any evidence of predation events. However, recently developed genetic approaches in which highly sensitive assays are used to detect the presence of target species' DNA in predator stomach contents have dramatically enhanced detection rates (King *et al.,* 2008, Braley *et al.,* 2010). Such an assay has already been successfully used to detect predation of larval Delta smelt in the stomach contents of Mississippi silversides (*Menidia beryllina*; Schreier and Baerwald, unpublished data). Parallel assays for introduced silversides and Wakasagi smelt (*Hypomesus nipponensis*) have also been developed, and these will be used for stomach content analyses in this study to allow for a comparison of native and non-native fish predation prevalence across a broad range of habitats. In addition, we will develop new genetic assays for additional native fish species (Chinook salmon, potentially identified to each Evolutionary Significant Unit (ESU); steelhead, Sacramento splittail, white sturgeon, green sturgeon, and longfin smelt) to examine predation-prey dynamics for many at-risk fish species found in the north Delta. Identification of Chinook salmon prey to the ESU-level will enable us to determine potential differences in predator-prey dynamics between run types.

The results from the genetic assay for predation of Chinook salmon will be used to inform a striped bass bioenergetics model in order to develop estimates for broader population impacts of striped bass predation on each ESU. Bioenergetics models are widely used to estimate predator consumption rates and develop estimates for impacts of predation on prey species (Brandt & Hartman, 1993). A bioenergetics model for striped bass has already been developed (Loboschefsky et al., in review) and can readily be applied to answer specific questions (e.g. spatial variability). The application of a bioenergetics model to estimate the predator response to relatively

rare prey is often limited due to low detection rates of predation events; however, our use of the genetic assay will make this approach much more feasible, as the sensitivity of the genetic assay will increase our detection rates significantly. In this study, we have chosen to limit the bioenergetics modeling component to the striped bass predator and Chinook salmon prey because striped bass are likely to be the most numerous predators in our sampling locations and salmon are likely to be the most numerous native prey species of interest. In addition, Chinook salmon survival probabilities for specific reaches along migration routes in the north Delta have already been developed from acoustic telemetry studies (Perry *et al.* 2010); yet, mechanisms for variation in survival (e.g. varying predation rates) have not been identified. For other prey species, and largemouth and pikeminnow predator species, comparing the incidence rate of predation across habitats and migration corridors will still be invaluable quantifications of spatial variability in predation risks.

Specifically, our investigation will address the following questions:

1) How do consumption rates compare between targeted native (Sacramento splittail, Chinook salmon, steelhead, Delta smelt, longfin smelt, green sturgeon, and white sturgeon) and non-native fishes (Mississippi silversides, Wakasagi smelt) in the north Delta region?
2) Does the incidence rate of predation of native and non-native species vary seasonally, and/or with respect to habitat conditions and migration routes?
3) How long after consumption is Chinook salmon DNA detectable in striped bass stomach contents using a genetic assay?
4) Do striped bass consumption rates for three ESUs (winter-, spring-, fall-run) of Chinook salmon vary across migration routes?

To address these questions, we have developed a study plan that will build on existing collaborative work between the Aquatic Ecology research group at the California Department of Water Resources (CDWR), the Genomic Variation Laboratory (GVL) at the University of California, Davis (UC Davis), as well as molecular ecologists and fisheries biologists at Cramer Fish Sciences (CFS). In a two-year effort sponsored by the Interagency Ecological Program (IEP), these groups have already partnered to develop the genetic assays for Delta smelt, Mississippi silversides, striped bass, and largemouth bass, and successfully applied it to wild-caught predators.

In the expanded effort that we proposed here, our objectives will be to sample striped bass, largemouth bass, smallmouth bass, and pikeminnow predators via gill netting in specific reaches of the Sacramento River, Steamboat Slough, Miner Slough, and Georgiana Slough with previously determined Chinook salmon survival probabilities (Perry *et al.*, 2010). To encompass as much habitat variation as possible, we will also sample predators in the southern portion of Liberty Island, the Sacramento Deep Water Ship Channel, and the toe drain of the Yolo Bypass (Fig. 1), characterizing habitat conditions at every location. To coincide with native fish migration periods, and to minimize catch of upstream migrating ESA-listed adult salmonids, sampling will take place in early winter and early spring months (December -January and April). This field effort will be led by biologists from CDWR. Whole stomachs will be dissected from predators for genetic assays to be conducted at the GVL, where molecular ecologists from GVL and CFS will develop new genetic assays and determine presence of target species in stomach contents. This joint field and laboratory effort will be conducted for two years in order to analyze results from different flow regimes and assess temporal stability of predation patterns. To aid in interpretation of salmonid predation detection from the genetic assay, and to inform the bioenergetics modeling component, it will be necessary to determine the rates of detection in striped bass stomach contents over a digestion time course (Question 3). Thus, laboratory trials to be carried out at the Center for Aquatic Biology and Aquaculture (CABA, UC Davis) will sample striped bass stomach contents at progressive intervals after a discrete feeding event of hatchery origin salmon. This project component will be especially informative for our final element, which will use an existing bioenergetics model for striped bass to assess spatial variability in striped bass consumption of winter, spring, and fall-run ESUs of Chinook salmon (Question 4). Here, we will draw on modeling expertise from CFS by applying the Delta Passage Model (DPM, Cavallo et al., 2011) to estimate abundance of Chinook salmon during field sampling periods and determine predator consumption rates. The bioenergetics model will then be leveraged to estimate potential impacts of striped bass predation across the suite of salmon migration corridors.

2. Background and Conceptual Models

Study Location

The Delta is vast network of tidally influenced channels and open water sites receiving inputs from the Sacramento and San Joaquin Rivers. The northern Delta consists of sloughs, deep channels, seasonal floodplains, and flooded islands. Hydrodynamics in this area are dominated by both tides and flow inputs from the Sacramento River, via the Yolo bypass floodplain during high flows, or through Steamboat and Cache sloughs. Habitats are diverse and include channels with rip-rapped banks, extensive beaches, small tule islands, and patchily vegetated riparian zones, floodplains, as well as flood islands. Due mainly to large, shallow-water areas (i.e. Liberty Island), the north Delta is characterized by relatively higher turbidities compared to other parts of the Delta system.

Many native fishes utilize the north Delta's habitats either as migration corridors or as spawning and rearing habitat, including Chinook salmon (Sommer et al. 2001) and Sacramento splittail (Sommer et al., 2002). Additionally, the north Delta area appears to be of significant importance to the threatened delta smelt, both for spawning (Bennett, 2005) and resident adults (Sommer, CDWR, pers. comm.). However, the same area serves as a migration route for adult striped bass on their way to spawning areas in the upper Sacramento River (Moyle, 2002). The area is also inhabited by largemouth and smallmouth bass, whose abundance in the area has increased significantly in recent decades (Brown and Michniuk, 2007). In addition, previous Delta-wide piscivore sampling efforts yielded the greatest catch of Sacramento pikeminnow in the Liberty Island area and Sacramento River (Nobriga and Feyrer, 2007). While all of these predator species exist in the north Delta region, their abundance varies between habitat types: largemouth bass are typically considered common along the shoreline and are associated with submerged vegetation (Brown and Michniuk, 2007), while striped bass and pikeminnow are more abundant in the open water. Like the predators, prey species will also vary in abundance across habitats, as well as seasonally. This spatial and temporal variation in abundance for both predators and the possible effects of habitat on predator foraging efficiency make prediction of predation rates for individual prey species very difficult. This project will help fill this information gap by collecting predation data across a range of habitat types and implements a modeling approach to estimate impacts of striped bass predation for Chinook salmon.

Conceptual Model

Despite a lack of predation studies in the Delta, some previous data on predation patterns for invasive predators, as well as the basic structure of bioenergetics models used to estimate predation effects on specific prey, provide a framework for a conceptual model to guide expectations for this study. In order to apply bioenergetics models to estimate predation impacts on a particular prey, one must have knowledge of prey and predator abundances, temperature conditions, predator growth rate, and the proportion of the predator's total diet occupied by the target prey species. The latter item relates to a question of key interest to this study: given some overlap in range between predators and their fish prey, plus current environmental conditions, how much do predators focus on these native fishes to satisfy their metabolic demand, as opposed to other, non-native, prey species? This consumption demand of predators to prey can be defined as the 'functional response', or the probability of prey occurring in the predator stomachs as a function of prey density.

Nobriga & Feyrer (2008) described diet composition of striped bass in the Delta and demonstrated their functional response to Mississippi silversides, threadfin shad (*Dorosoma petenense)*, and decapod shrimp. This work, in addition to key background predation experiments conducted on the east coast on striped bass (Hartman, 2000), lead to two principles that structure the shape of the striped bass functional response to prey:

(1) The probability of consuming a given prey species increases with the density of the prey.
(2) The probability of consuming a given prey species varies as function of the size of the prey relative to the average size of the predator.

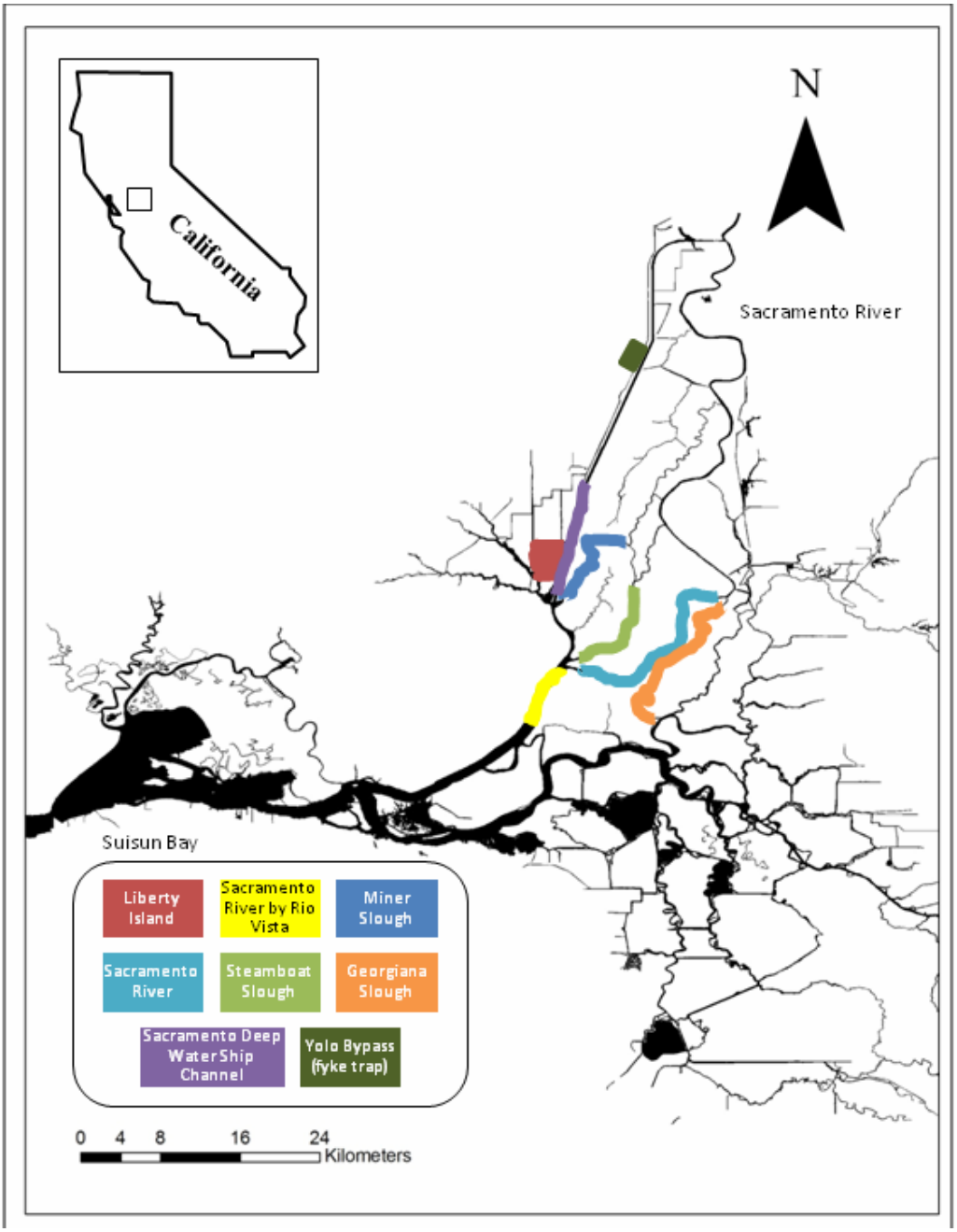

Figure 1. Map of sampling locations within the Sacramento-San Joaquin Delta.

The first principle is logical: the higher the densities of a given prey item, the more likely it is are to be the target of the surrounding predators. The second principle is also logical and rests on the observation that predators of different sizes will focus on prey of different sizes. For example, Nobriga and Feyrer (2008) observed a negative relationship between the likelihood of Mississippi silverside occurrence in striped bass diet and the striped bass fork length. In contrast, the likelihood of predation of threadfin shad, a larger-bodied fish than Mississippi silversides, increases with the length of striped bass predators (Fig. 3, in 'Approach and Scope of Work', Task 4). Conceptualized shapes for these two predator functional responses for both small and large-bodied prey are illustrated in Figure 2. Based on knowledge of seasonal variation in abundance and average body size of prey species, we have formulated specific hypotheses for the functional response of predators for each prey species (Table 1). These hypotheses are based on a predator size range of 200 – 600mm, based on the gill net mesh sizes to be used for field sampling. Seasonal variation in relative prey abundance is based on typical migration and spawning periods for each species (Moyle, 2002), as well as abundance data for the north Delta region from monthly beach seining efforts conducted by the US Fish and Wildlife Service (USFWS) since the mid-1970s (USFWS, unpublished data). Hypotheses outlined in Table 1 reflect predictions for how the predator functional response should compare for each species across sampling months (December-January vs. April), and between prey species.

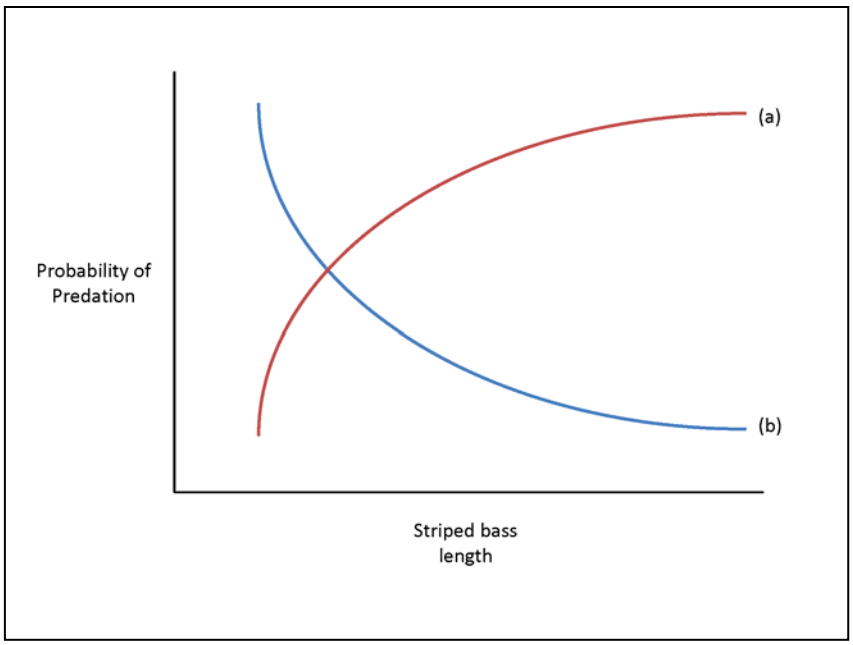

Figure 2. Hypothetical graph of striped bass fork length vs. the probability of a predation event on a particular prey item. (a) represents the curve expected for large prey items and (b) represents the curve expected for small prey items. Adapted from results in Nobriga & Feyrer (2008).

Ideally, abundance data would be available for each prey species for each of our sampling locations such that we could compare the predator functional response for each species across habitats. However, prey abundance data is not available at such a high spatial resolution. The USFWS beach seine data, as well as other ongoing IEP-sponsored monitoring efforts (e.g., USFWS Sacramento trawl and CDFG Spring Kodiak trawls for smelt abundance), will provide estimates of regional abundance levels for each prey species and we will be able to develop and compare predator functional responses between species for the north Delta region as a whole. Using these abundance estimates for the north Delta region and the functional responses of predators, we will also produce estimates for the region-wide impact of predation on these listed species. For each sampling location, our results will provide specific incidence rates of predation for each species (# predators with positive detections for target species/ total # predator stomachs processed), allowing us to compare this incidence rate varies with respect to habitat conditions or migratory route (Question 2, in 'Project Description'). In addition, we will develop a more sophisticated analysis for Chinook salmon in order to address spatial variation in predation with respect to habitat. The DPM (Cavallo et al., 2011) will be used to estimate relative abundance of Chinook salmon at each sampling location in order to compare predator functional responses and predation impacts between salmon migration routes (Question 4, in 'Project Description').

Table 1. Expected life-stage, size range, and abundance for each prey species for which we will have an assay. Values under "Predator:Prey Size Ratio Curve" correspond to curves in Figure 2. Estimated likelihood of detection refers to how frequently we expect to see these prey items in the assay results from predator stomach contents, and largely reflect the relative abundance of each prey species.

			Relative Abundance in north Delta		Predator:Prey Size Ratio Curve		Estimated Likelihood of Detection	
Species	**Life-stage**	**Size Range**	**Dec-Jan**	**April**	**Dec-Jan**	**April**	**Dec-Jan**	**April**
Delta smelt	Adult	70 – 90 mm[a]	Moderate[d]	Moderate[d]	(b)	(b)	Low	Low
Longfin smelt	Adult	90 – 150 mm[a]	Very low[d]	Low[d]	(a)	(a)	Very low	Very low
Sacramento splittail	YOY	20 – 110 mm[a]	n/a[d]	High[d]	-	(b)	Low	High
	Juvenile	110 – 170 mm[a]	Very low[d]	Low[d]	(a)	(a)		
	Sub-adult	170 – 250 mm[a]	Low[d]	Low[d]	(a)	(a)		
Fall-run Chinook	YOY	30 – 90 mm[b]	High[d]	Moderate[d]	(b)	(b)	High	Moderate
	Juvenile	150 – 270 mm[b]	Very low[d]	n/a[b]	(a)	-		
Late fall-run Chinook	YOY	30 – 40 mm[b]	n/a[b]	Low[d]	-	(b)	Low	Low
	Juvenile	80 – 250 mm[b]	Low[d]	Very low[d]	(a)	(a)		
Winter-run Chinook	YOY	40 – 240 mm[b]	Low[d]	Very low[d]	(a)	(a)	Low	Very low
Spring-run Chinook	YOY	40 – 120 mm[b]	Low[d]	Moderate[d]	(b)	(b) & (a)	Low	Moderate
Steelhead	Juvenile	100 – 300 mm[a,d]	Low[d]	Low[d]	(a)	(a)	Low	Low
Green sturgeon	YOY	20 – 40 mm[c]	n/a[c]	Very low[c]	-	(b)	Very low	Very low
	Juvenile	200 – 700 mm[a]	Very low[c]	Very low[c]	(a)	(a)		
White sturgeon	YOY	20 – 60 mm[c]	n/a[c]	Low[c]	-	(b)	Low	Low
	Juvenile	120 – 300 mm[a]	Low[c]	Low[c]	(a)	(a)		
Mississippi silverside	Adult	50 – 90 mm[a]	High[d]	High[d]	(b)	(b)	High	High
Wakasagi smelt	Adult	70 – 120 mm[a]	Low[d]	Very low[d]	(b) & (a)	(b) & (a)	Low	Very low

[a]Moyle 2002
[b]Fisher size at date criteria for the Bay-Delta Region
[c]Drauch-Schreier, pers. comm.
[d]USFWS beach seine data for north Delta stations (1995-2010)

3. Approach and Scope of Work

Task 1: Predator Sampling.

Task Leads: Brian Schreier, Louise Conrad, CDWR
Assistance: CDWR technical staff, and Gregg Schumer, Brad Cavallo, CFS

The purpose of this task is to collect the predators and extract the predators' stomachs to be used for genetic determination of presence or absence of target prey species (Task 2). During sampling, habitat and environmental conditions at each site will be characterized in order to relate the results from the genetic assays to location and habitat. Sampling sites will span seven different areas of the north Delta (Fig. 1). Four potential migration corridors for out-migrating Chinook smolts will be sampled, including Steamboat Slough, Miner Slough, Georgiana Slough, and the Sacramento River. Additionally, predators will be sampled from Liberty Island and the Sacramento Deep Water Ship Channel (DWSC). Finally, samples will be collected from the lower Sacramento River downstream of the confluence of Steamboat Slough but upstream of Rio Vista, CA. Sampling will not be conducted within 2 km of the upstream and downstream extents of each sampling reach to create separation between the different sampling areas.

Within each of seven sampling areas, ten stations will be chosen at random. All stations will be sampled once in December or January (as early as possible in the winter season, but after the first flush event has occurred) and again in April, with sampling to be repeated during winter/spring 2011-2012 and 2012-2013. All stations will be sampled over the course of 15 days for each sampling period, and over the course of the entire study each station will be sampled four times. Target predator species will include age-1+ striped bass, largemouth bass, smallmouth bass, and Sacramento pikeminnow.

At each station, predators will be sampled using gill nets (60 m x 2 m; randomized panels of 63.5, 76.2, 88.9, 101.6, 127, and 152.4 mm stretch mesh). Gill nets will be set for 45 minutes with one set per station. The orientation of the net to shore will be randomized between perpendicular (70% of sets) and parallel (30% of sets), so as to effectively sample all targeted predator species. All fishes collected in the gill nets will be identified to species and their fork length measured to the nearest millimeter. Samples will be collected between dawn and dusk, across all tidal stages. Estimated sample sizes and size ranges for each predator species are provided in Table 2. Water quality parameters (temperature, pH, electrical conductivity, turbidity, and dissolved oxygen), secchi depth, water depth, GPS coordinates, and tide/current conditions will be recorded at each set. Environmental variables (depth, presence of submerged or floating aquatic vegetation, bank and substrate type) will also be recorded at each of the sampling locations in order to relate predation rates to habitat.

Table 2. Expected sample size and size range for each targeted predator species.

Species	Expected Sample Size	Expected Fork Lengths
Striped bass	1000	200 – 600 mm
Largemouth bass	100	200 – 500 mm
Smallmouth bass	100	200 – 400 mm
Pikeminnow	200	250 – 700 mm

All reasonable measures will be taken to limit take and harm to adult salmonids and sturgeon during gill net sampling. While the net is fishing, crew members will actively monitor the net for salmonids and sturgeon catch and any individuals observed will be immediately removed. Crew members will also observe the immediate area for signs of sea lion activity, and if any are observed that sampling area will be abandoned for two days. Additionally, if any listed salmonids or sturgeon are captured during the course of sampling, that entire sampling area will be abandoned for two days to allow for ESA-listed species to move through the system. Salmonids and sturgeon will be brought aboard by supporting their bodies with the net, and individuals caught by their gills will be removed by cutting net strands to avoid any unnecessary trauma to the fish. A recovery tub equipped with air bubblers will be kept onboard the sampling vessel to allow for salmonids and sturgeon to recover before their release back into the wild. To facilitate quick processing of non-target and ESA-listed species, all fish will be removed from the net before processing of

predators begins.

All potential predators of native fish will have their stomachs and intestines preserved for genetic analysis. Predators will have their guts dissected out immediately after capture using DNA-sterile protocols (bleaching and rinsing of all instruments and work surfaces). Predator guts will then be preserved in 80% ethanol and stored on dry ice until transferred to the GVL at UC Davis for genetic analysis.

Task 2: Genetic Assay Development & Application.

Task Leads: Melinda Baerwald (GVL, UC Davis), Gregg Schumer (CFS), and Bernie May (GVL, UC Davis)
Laboratory Assistance: GVL technical staff

This task will address the following questions for each predator-prey interaction: a) does incidence of predation of at-risk species or non-native species vary with habitat or location, and average size of the predator?; and (b) do predator-prey interactions vary seasonally, and (c) are these changes correlated with prey species abundance and/or habitat or spatial attributes of sampling locations? This task will provide the results necessary to estimate regional-scale impacts of predation for native, listed species and will inform the bioenergetics modeling work that will compare consumption rates of Chinook salmon across migration corridors (Task 4). This task is contingent on completion of Task 1, which will provide the samples for genetic analysis.

Traditionally, visual identification of gut contents has been conducted to provide insight into food web dynamics. Degradation in the gut, however, typically limits the utility of visual identification to a short time span post-ingestion and is time-consuming, expensive, and prone to species bias (Symondson 2002, Schooley et al. 2008). Stable isotope analysis is an alternative method that has been used to examine predator-prey interactions but identification of prey down to the species level can be difficult or impossible due to considerable overlap in isotopic values (Carreon-Martinez & Heath 2010). Recently, genetic analysis has been increasingly used in food web studies for a wide range of taxa (reviewed in King et al. 2008), including freshwater fishes (Corse et al. 2010). Genetic identification of gut contents is capable of accurately distinguishing species and even specific lineages within species (King 2010). The use of genetic tools in diet studies has dramatically increased sensitivity over visual identification of gut contents (e.g., able to detect highly degraded prey) and is a comparatively rapid and inexpensive method (Symondson 2002).

We have previously developed PCR-based TaqMan assays capable of identifying Delta smelt, Wakasagi smelt, and Mississippi silverside DNA with 100% accuracy (no cross-species amplification) and high sensitivity (Baerwald et al., in press). The Delta smelt TaqMan assay can reliably detect as little as 0.1 picograms of Delta smelt DNA in the presence of silverside DNA. A feeding trial demonstrated that Delta smelt DNA can be consistently detected in silverside gut contents 9 hours post-ingestion and, in some instances, up to 36 hours post-ingestion. In addition to the already developed assays for Delta smelt, Wakasagi smelt, and Mississippi silverside, we are currently creating species-specific TaqMan assays for striped bass and largemouth bass. For this proposed study, we will create additional assays capable of accurately identifying another invasive predator species (smallmouth bass) and seven native species (Chinook salmon, steelhead, green sturgeon, white sturgeon, Sacramento splittail, pikeminnow, and longfin smelt). Similar to the steps undertaken for the already designed TaqMan assays, we will sequence several regions of the mitochondrial genome (e.g., Cyt-b, COI, 12S) for ~5 individuals collected throughout the core distributional range for each species. Sequence comparisons among both target and non-target species found in the Delta will enable us to identify species-specific polymorphisms. TaqMan assays will be designed and an additional ~40 individuals collected throughout the regional distribution range for each species will be screened using the developed assays to ensure consistent amplification. Additionally, to substantially reduce or eliminate the risk of false positives, all assays will be tested on other potentially co-occurring non-target fishes (N = 3-4 individuals/species) to verify that no cross-species amplification occurs. The sensitivity of each assay will also be assessed by a serial dilution series of increasingly lower amounts of target species DNA in order to determine the limit of detection. Tissue samples (e.g. fin clips) for genetic assay development have already been collected for the majority of regional fish species from existing monitoring efforts (e.g. Spring Kodiak trawl survey) or archives (e.g. CDFG Salmonid Tissue Collection Archive; UC Davis GVL Tissue Collection Archive). Use of tissue from federally listed species will commence only after all required permits have been obtained for this project.

As mentioned in the project description, it will be quite valuable to detect variable predation effects for specific Chinook salmon ESUs. To determine if diagnostic ESU-specific genetic assays can be developed for Chinook salmon, we will sequence regions of the mitochondrial (e.g., entire control region, COI) and nuclear (e.g., ITS-1, 18S,

near-diagnostic microsatellites) genomes using a screening panel of at least ten individuals per ESU collected from spawning locations throughout their distributional ranges. The continual reduction in sequencing costs combined with the existence of suitable samples in the CDFG Salmonid Tissue Collection Archive will make this a quick and inexpensive endeavor. Previously, Nielsen (1994) sequenced the terminal 3' end of the control region and found that haplotype frequency differences existed among the runs but did not identify diagnostic polymorphisms. Additionally O'Malley et al. (2007) identified run-type allele frequency differences at two candidate nuclear loci but also did not identify diagnostic differences. These two studies examined only three regions of the genome looking for run-specific differences so it is our hope that further exploration of the genome will enable run-specific assays to be developed. An inability to design run-specific diagnostic assays, however, does not preclude the use of existing microsatellite loci for individual assignment of prey back to each ESU. Garza et al. (2008) demonstrated that a small suite of microsatellite loci has a success rate of >95% when assigning Central Valley Chinook individuals back to their respective ESUs. This high assignment success, combined with the ability to detect nuclear microsatellite DNA in other gut content studies (DeWoody et al. 2001; Bowman et al. 2004) make it quite feasible that we will be able to identify the presence of distinct Chinook ESUs in the gut contents of predators. Additionally, amplification of highly variable microsatellite loci will make it possible to determine the minimum number of Chinook individuals found in each predator gut. Similar to forensic samples containing DNA from more than one individual, the number of individuals can be determined by the number of alleles found in the most polymorphic locus (e.g., a disomic locus with five alleles in a given sample contains a minimum of three individuals). The identification of ESUs and the minimum number of individuals within each gut will be quite informative for both ecological hypothesis testing and bioenergetic model predications, and they are therefore worthy pursuits, particularly given the minimal cost and time commitment. However, the potential inability to distinguish ESUs and/or individuals will not detract from our ability to gain significant insight into predation effects for the other species or Chinook salmon in general.

Once species-, and possibly ESU-specific, assays are designed, DNA extracted from predator gut contents will serve as the template for quantitative PCR to detect the presence of DNA from each potential prey species. Specifically, the gut contents of each predator (striped bass, largemouth bass, smallmouth bass, pikeminnow) will be assayed for presence of each prey (Chinook salmon (potentially each ESU), steelhead, splittail, Delta smelt, longfin smelt, green sturgeon, white sturgeon, Wakasagi smelt, silverside). Assays will be labeled with fluorescent dyes to allow for multiplexing during the PCR process in order to detect multiple species concurrently. Positive (e.g., predator TaqMan assays) and negative (e.g., H_2O) controls will be used throughout the extraction and amplification steps to assess cross-contamination and PCR reaction success. Additionally, 6-8 no template controls will be included for each assay plate to set the limit of detection threshold above background fluorescence for each assay. Considerable replication of all samples will be conducted to ensure accurate and reproducible results.

Designing species-specific assays will not only benefit this and future predation studies but will also be of great benefit for other studies and monitoring programs that target these often-studied and/or at-risk fishes. For example, larval abundance estimates of Delta smelt may be improved if the genetic assays that distinguish between Delta and Wakasagi smelt are performed to test the accuracy of current visual assignment, given that Delta and Wakasagi smelt larvae can be difficult to distinguish (Moyle 2002). Another future application of these assays could be evaluation of water samples for the presence of key at-risk species DNA at Central Valley Project and State Water Project pumps. No matter what the application, highly sensitive and robust genetic assays should have continued utility for monitoring and understanding the factors contributing to species declines in the Delta and throughout the San Francisco Estuary.

After completion of this task, staff from CDWR, GVL, and CFS and will work collaboratively to synthesize the results from genetic assays. Specifically, we will develop regional-scale functional response curves for each predator species' likelihood of predating each prey species, given estimates for prey species' densities for the north Delta region as provided by appropriate monitoring surveys. This analysis will allow us to evaluate our hypotheses for the predator functional response curves for each species described in Table 1 (in 'Conceptual Models').

Task 3: Captive Feeding Trial

Task Leads: Brian Schreier, Louise Conrad (CDWR)
Assistance: Field technical staff (CDWR) and technical staff (CABA, UC Davis)

The purpose of this task is to assess the time interval over which salmonid DNA is detectible in the guts of striped bass post-ingestion. While this task is not contingent upon completion of any other task, it will provide background

information for the genetic assay for salmon DNA in striped bass stomach contents (Task 2) and the bioenergetics modeling effort to estimate impacts of striped bass predation on salmon for different migration routes (Task 4). Given the focus of our bioenergetics modeling on this particular predator-prey interaction, and the difficulty in obtaining many of the other predator and prey species for captive trials, only striped bass predators and Chinook salmon prey will be included in these feeding trials.

To determine the length of time over which the genetic assay will return a positive detection for salmon DNA after striped bass consume a single salmon (at field-relevant water temperatures), we will conduct a laboratory feeding trial on captive striped bass. As digestion rates may vary with age and size of predators, and our field data will provide information on the incidence of salmonid predation across a range of predator sizes, we will conduct this trial with three size ranges reflecting the sizes of striped bass we expect to commonly sample while gill netting: 400 – 500mm FL (roughly 3 years of age), 500 – 600mm FL (roughly 4 years of age), and 600 – 700mm FL (roughly 5 years of age). Striped bass will be collected from the State and Federal fish salvage facilities and various agency monitoring programs, and they will be housed at the University of California, Davis' Center for Aquatic Biology and Aquaculture (CABA) aquatic research facilities. After capture, the striped bass will be transported to CABA in an insulated fish transport tank equipped with regulators to supply oxygen.

Approximately 90 fish (30 in each size range) will be captured and transported over a two month period. Once at CABA, the fish will be divided among ten 7-foot diameter flow-through tanks (9 – 10 fish/tank) and held at 12°C (± 0.5°C). Each group of striped bass arriving to the facility will be treated for fungus and infections before being introduced into the captive population. Temperature will be continuously monitored in each tank throughout the study via a submersible water temperature data logger. Acclimation to captivity in the facility will be gauged by willingness to feed. All striped bass will be FLOY tagged (Floy Tag & Mfg, Inc.) to allow data collection on individual fish.

Striped bass will be starved for 72 hours prior to the start of the controlled feeding trial. Individual fish will then be moved to smaller holding tanks where a single Chinook smolt from the Feather River fish hatchery will be introduced. After visual verification of feeding, the time of consumption and size of smolt fed will be recorded. Striped bass will then be moved into holding tanks containing three individuals from each size range. Each holding tank will then be allowed to digest their Chinook smolts for different amounts of time: 6, 12, 24, 36, 48, 60, 72, 84, 96, or 108 hours (based upon gastric evacuation rates from Hurst and Conover 2001). Upon completion of each tank's digestion period, all fish will be euthanized with MS222 (using standard protocols) and weighed, sexed, and measured (FL in mm). Their stomachs and intestines will be immediately dissected and preserved using the same protocols used for field-caught fish. Samples from the feeding trial will then be genetically analyzed for Chinook DNA, and the results will allow for the creation of a digestion time vs. detection rate curve. These results will thus give temporal context to any patterns detected in wild striped bass samples.

Task 4: Bioenergetics Modeling.
Task Leads: Steve Zeug, Gregg, Schumer, Brad Cavallo (CFS)
Assistance: Brian Schreier, Louise Conrad (CDWR)

This task will use results from Tasks 1 and 2 to address the following questions: a) does the functional response of striped bass to salmon prey vary across habitats and/or locations?; b) how variable is the striped bass impact, or consumption rate, between habitats and/or sampling locations; and c) does the stirped bass functional response and/or impact of striped bass vary for different runs of Chinook salmon? This task will be led by fisheries biologists from CFS and is contingent upon completion of Tasks 1 and 2.

Loboschefsky et al. (in review) have developed a striped bass bioenergetics model which solves for growth, as a function of consumption, metabolism, egestion, excretion and gonad production. Several model inputs were obtained from Hartman and Brandt (1995), others were estimated by Loboschefsky et al. (in review) as indicated in Table 3.

Table 3. Summary of required datasets and anticipated locations of the dataset.

Data Requirement	Source
Striped bass weight at age	• DFG's Mark and Recapture Survey
Striped bass annual growth	• DFG's Mark and Recapture Survey
Striped bass diet proportions	• Literature [a]
Striped bass energy density	• Literature [b]
Striped bass prey energy densities	• Literature [c]

[a] e.g.: Feyrer at al. 2003; DFG *unpublished data*.
[b] Hartman and Brandt 1995; Loboschefsky et al. *in review*.
[c] e.g.: Steimle and Terranova 1985; Chipps and Bennett 2002; Vatland et al. 2008.

In order to estimate juvenile Chinook salmon consumption (i.e. grams of prey consumed per striped bass per day) we will apply an equation derived from Loboschefsky et al. (in review) which estimates daily consumption (in grams) of prey species:

(1) $C_{individual,\ daily} = [0.002103(FL) + 0.02488(T) - 0.05131] \cdot P$

Where C = $\log_{10}$-transformed grams of prey consumed in either a 1-d period; FL = striped bass FL in mm over the corresponding period; T = average water temperature in ºC over the corresponding period; P = proportion of the diet comprised of a particular prey taxon. The variable P can be viewed as a measure of prey availability; when a prey species is scarce, *P* is small for that species. However, like all piscivorous fishes, striped bass eat more fish when and where there are more fish to eat and also become more efficient piscivores as they grow larger because they gain a size advantage over more and more individual prey (Hartman 2000). Thus, *P* reflects not just the prey availability but the functional response of striped bass to changing prey density. Nobriga and Feyrer (2008) used diet composition and prey density data to estimate *P* for some Delta striped bass prey (Fig. 3). The resulting estimate of *P* for threadfin shad consumed by striped bass in the Delta was:

(2) $P = \frac{1}{1 + e^{-(-3.8136 + 0.009123FL + 0.7298CPUE)}}$

Where FL = striped bass FL in mm and CPUE = prey fish density as $\log_{10}$-transformed number of prey per 10,000 m^3 of water sampled.

To characterize the functional response of striped bass to salmon prey (Question 'a', above), we will follow the approach of Nobriga and Feyrer (2008), and use logistic regression to relate incidence of juvenile salmon in the stomachs of predators as a function of striped bass fork length and the relative abundance of juvenile salmon in the study area.

In order to apply equations (1) and (2), and to estimate juvenile Chinook consumption by striped bass, four key input parameters are required: 1) measures of water temperature, 2) measures of striped bass fork lengths, 3) estimated incidence of striped bass consumption of Chinook salmon, and 4) juvenile Chinook relative abundance. These data will be collected (or estimated) such that all four inputs are available simultaneously. Specifically, water temperatures and striped bass fork lengths will be measured directly through field sampling (Task 1). Incidence of juvenile salmon consumption will be provided by genetic analysis of stomach contents (Task 2). Relative abundance of juvenile Chinook will be estimated using the Delta Passage Model (DPM) calibrated to best available data on juvenile production resulting from natural spawning and hatchery releases. The DPM is a simulation model that predicts migration route selection, and survival probabilities up to and within the Delta based on flow conditions, opening and closing schedules of man-made barriers, and arrival timing (Cavallo et al. in prep; BDCP, 2010 Appendix E10). To parameterize the model for the specific period of interest, we will acquire escapement and juvenile emigration data for tributaries upstream of the sampling area and then use the DPM to estimate juvenile Chinook salmon abundance at specific time periods and locations in the Delta. This first stage of analysis will provide the functional response of striped bass to Chinook prey for each sampling location, in order evaluate our hypotheses regarding the relative detection rate of Chinook salmon predation compared with other potential prey, and the shape of the response with respect to striped bass length (Table 1). This analysis will be repeated for spring-, winter-, and fall-runs of Chinook salmon, provided that the effort described in Task 2 to develop run-specific assays for Chinook salmon in predator stomach contents is successful.

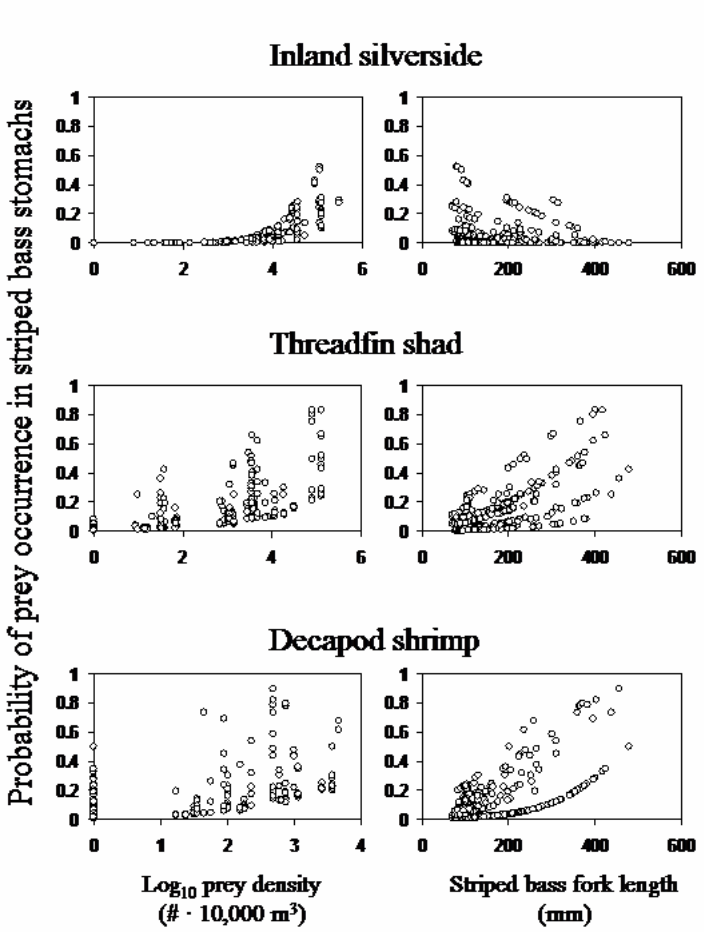

Figure 3. Predicted responses of San Francisco Estuary striped bass to three common prey taxa based on stomach contents analysis; taken from Nobriga and Feyrer (2008). Note that the scatter in each of these plots is due to the interaction of the variable plotted on the x-axis with the variable plotted on the x-axis of the panel to its right or left. In other words, striped bass size and prey density simultaneously interact to affect how frequently a prey species occurs in stomachs.

To estimate the impact of striped bass predation on migrating salmon (Questions 'b', above), it is necessary to consider the abundance of the predator: high or low incidence rates of predation may be a result of varying predator abundances, or different degrees to which predators target Chinook smolts, perhaps due to variability in habitat conditions. To examine likely impacts of predation, we will follow a quantitative approach developed by Loboschefsky (UC Davis) to create a 'consumption index' of Chinook salmon. This index will be calculated for each sampling location and Chinook run in order to compare predation effects between migration routes and sampling months.

Ideally, calculation of the consumption index would begin with the product of the fraction of Chinook in the diet of striped bass and the value of individual prey fish consumption at site *i*:

$$c_{s,t} = c_{p,t} \cdot P_{s,t}$$

Where $c_{s,i}$ is the individual consumption of Chinook (grams of Chinook per striped bass), $c_{p,i}$ is the individual consumption of prey fish (grams of prey fish per striped bass), and $P_{s,i}$ is the dietary proportion of Chinook out of the total prey fish diet (unitless). Next, to evaluate the population-level consumption on Chinook at site *i*:

$$C_{s,t} = c_{s,t} \cdot N_{sb,t}$$

Where $C_{s,i}$ is the population-level consumption of Chinook (grams of Chinook), $N_{sb,i}$ is the population of striped bass that is known to feed upon Chinook at site *i*.

However, we are unlikely to have a reliable estimate of the proportion of Chinook ($P_{s,i}$)in the striped bass diet as the genetic assay will not yield information on the number of Chinook consumed for each instance of detecting Chinook DNA in striped bass' stomachs. Moreover, we are unlikely to have an estimate of the population of striped bass at each site ($N_{sb,i}$). Thus, developing an index of predation on Chinook for relative comparisons between each sample site will require a series of assumptions, as follows:

First, we must assume that the proportion of salmon in striped bass diet approximates the prey field physically present at site *i*, then:

$$P_{s,i} \approx \frac{N_{s,i}}{\alpha_i}$$

Where $N_{s,i}$ is the number of Chinook present at site *i* (grams of Chinook), and, biologically, α_i would represent number of total possible prey species present. The number of Chinook present at each site *i* will be obtained from the Delta Passage Model. The value of α_i will not be known but a range of values will be used representing different prey field scenarios.

Next, we will assume that the number of striped bass feeding on Chinook at site *i* is approximated by the number of positive detections obtained at site *i*:

$$N_{sb,i} \approx \beta_i \cdot D_{sb,i}$$

Where $D_{sb,i}$ is the number of striped bass that were positively identified as having fed upon Chinook at site *i* (through the genetic assay) and β_i is a scaling factor that adjusts $D_{sb,i}$ to the actual number of striped bass feeding upon Chinook at site *i*. $D_{sb,i}$ will be normalized by the total number of striped bass run though the genetic assay for each site. With 100% sampling efficiency, the scaling factor (β_i) would be equal to 1. However, since the exact sampling efficiency of the gill netting effort in Task 1 will not be known, we will perform the calculations across a range of values for β_i (similar to treatment of α_i).

Finally, by combining the above assumptions, the consumption index can be calculated:

$$\overline{C_{s,i}} \approx c_{s,i} \cdot \frac{N_{s,i}}{\alpha_i} \cdot \beta_i \cdot D_{sb,i}$$

Where $\overline{C_{s,i}}$ is now an index of the population-level consumption of Chinook by striped bass at site *i*, and all other quantities are as previously defined. This consumption index will not provide a measure of the absolute number or biomass amount of Chinook salmon that are consumed by striped bass, but instead a relative measure that will allow a comparison of the predation impact across sampling locations (migration routes).This index incorporates consumption demand at each site. Thus, if a given site predicts 'higher than normal prey fish consumption' due to water temperatures or fast growth rates, this consumption index can assess what the repercussions of this area are for Chinook salmon.

The products of this bioenergetics analysis will be striped bass size class, month, and area-specific estimates of juvenile Chinook salmon consumption. The consumption index will also allow comparison of predation impacts across salmon migration routes. These results will be compared with results from acoustic telemetry studies that have documented salmon survival rates in the same areas sampled for this study (Perry et al., 2010), in order to determine if spatial variation in survival can be attributed to variability in predation risk. The analysis results will also provide baseline information on spatial and temporal variation in predation risk for salmonids that can later be used to evaluate effects of installing new water intake structures in the north Delta, which may attract heavier densities of striped bass and other predators in the future (BDCP, 2010).

4. Deliverables

- One or more presentations at the Biennial Bay-Delta Science Conference and the American Fisheries Society conference (Cal-Neva and/or international)
- Final report presenting all methods, results, and conclusions to CDFG
- GPS coordinates of all sampling locations will be collected during the course of the project. A compact disc containing these locations, along with all fish catch and environmental data, will be provided to CDFG with the final report
- Field sampling paired with genetic assay: two manuscripts in peer-reviewed scientific journals
- Impacts of striped bass on individual salmonid runs using a bioenergetics approach: one manuscript in a peer-reviewed scientific journal

5. Feasibility

The four tasks in this study (field sampling, genetic assay development and application, captive feeding trial, and bioenergetics modeling) will be carried out by individuals and organizations with the experience, expertise, and necessary equipment to perform the proposed work.

Field sampling will be led by a team of CDWR environmental scientists and field technicians with a history of successfully conducting field research that has yielded a long list of peer-reviewed scientific publications informative to resource management in the Delta over the last decade (for a complete list, visit http://www.water.ca.gov/aes/pubs/). Dr. Louise Conrad and Brian Schreier have both led extensive sampling efforts aimed at understanding the effect of predators in the Delta, and they are already working in collaboration with Drs. May and Baerwald at the Genomic Variation Laboratory at UC Davis on a parallel study using a genetic assay to detect predation of larval Delta smelt by Mississippi silversides and other small-bodied predators in the north Delta. For this study, a feeding trial using silverside predators and Delta smelt was carried out in order to determine the time interval after consumption that smelt DNA was detectable in silverside stomachs by genetic assays. Thus, this team has already established feeding trial protocols and successfully carried out a similar predation study. Additionally, this collaboration has also produced rigorous protocols for field collection of predator stomach samples under DNA sterile conditions and minimal risk of contamination. CDWR is also already in contact with the National Marine Fisheries Service to acquire federal permits to conduct the gill net sampling proposed in Task 1, and is actively working with NMFS staff to design the sampling in order to minimize take to ESA-listed species. Both Dr. Conrad and Brian Schreier have already acquired Scientific Collecting Permits from the California Department of Fish and Game. These permits will need to be amended to include permission for gill netting: this process is generally accelerated once formal permission is granted from the federal government.

Genetic assay development and application will be conducted by the GVL at UC Davis. Drs. May and Baerwald, along with Gregg Schumer, have extensive experience developing highly sensitive genetic assays necessary for detection of individual species' genetic material in predator stomach contents. They have already developed such assays for Delta smelt, Wakasagi smelt, and Mississippi silversides, along with currently creating assays for striped bass and largemouth bass. Thus, these assays will be in hand for use in the proposed project, and Drs. May and Baerwald are highly confident that development of additional assays for Chinook salmon, steelhead, Sacramento splittail, white sturgeon, green sturgeon, and longfin smelt will be possible in a timely fashion such that they can be used to analyze predator stomach contents collected for this study.

The bioenergetics modeling will be conducted by Cramer Fish Sciences. The striped bass bioenergetics model has already been fully developed and parameterized in an IEP-funded project conducted by Erik Loboschefsky (in review). This model will be available to the PIs and subcontractors for use in this study. As part of this effort, equations for predicting the proportion of the striped bass diet that is composed of a given species (e.g. Chinook salmon) have also already been developed. In addition, Cramer Fish Sciences has already developed the Delta Passage Model to be used to predict relative abundances of Chinook salmon prey across sampling reaches. Thus, virtually no model development will be necessary for completion of Task 4; rather, the work will only involve application of previously developed models. Cramer Fish Sciences staff to be subcontracted for this study (Schumer and Cavallo) are ideal choices as partners for both the genetic assay development and modeling component because they have been actively involved with the development of the genetic approach to detecting predation of rare species (for the study mentioned above investigating silverside consumption of larval Delta smelt), and have extensive experience with the use of modeling techniques to predict species abundance patterns in the Delta (e.g. Delta Passage Model) and patterns of the Delta food web.

6. Relevance to the CALFED ERP

Relevance to this PSP:
Our proposed research directly meets the needs identified in Priority 2 of the Proposal Solicitation Package, "Research that tests hypotheses identified in the DRERIP evaluation of the BDCP conservation measures and National Research Council OCAP Biological Opinion review and addresses uncertainties". Under Priority 2, our proposal addresses two of the listed needs:

- *Determine the ecological characteristics of shallow water habitat in the Delta that are beneficial for native species and less likely to support non-native species*
  We will be comparing several native and non-native predators and potential prey fish species across a range of habitat types and correlating both species-specific abundance and predation prevalence with a wide range of ecological characteristics. This analysis will allow us to determine habitat-type preferences for both native and non-native fishes as well as ecological characteristics that promote survival of native fishes via reduced predation rates.

- *Control introduced species and examines their effect on food web dynamics*
  Our study will directly address the effect that several abundant introduced species are having on the Delta's food web dynamics, with particular emphasis on several threatened fish species (e.g., Chinook salmon, steelhead, green sturgeon, Delta smelt). An increased understanding of predation impacts across ecologically and spatially diverse landscapes will allow for more targeted restoration efforts in the future (e.g., restoring particular habitat types to reduce predation effects of threatened species, location-specific predator removal). A comparison of Chinook salmon consumption by striped bass among different ecosystems will enable resource managers to determine which actions may be most successful at controlling excessive predation pressures.

The proposed research is also relevant to the needs identified in Priority 1 "Restoration projects that restore or enhance aquatic habitat in the Sacramento – San Joaquin Delta and Suisun Marsh and Bay". Specifically, results from our study will inform the following need:

- *Assessing flora and fauna response to restoration; determining changes in productivity; and monitoring hydrology and geomorphic changes in restored areas*
  By comparing abundance and predation across varying habitat types and locations, some in considerably more restored condition than others, we will be able to inform management regarding the success of existing restoration efforts to support several threatened fishes.

This is a highly collaborative proposal combining the expertise of fish ecologists and geneticists from a state agency, a university, and a fisheries and environmental consulting company. Our multidisciplinary approach will allow us to integrate habitat, spatial, and temporal variability with genetic species identification to understand predation effects on both native and non-native fishes. Moreover, the bioenergetics modeling will provide a broader synthesis of the intensity and dynamics of the predator – prey interaction between striped bass and Chinook salmon.

Relevance to CALFED issues outside this PSP:
The proposed research is relevant to wide-ranging issues outside of this Proposal Solicitation Package. It is particularly relevant to the Delta Stewardship Council's ultimate objective to develop a plan of restoration and water supply reliability for the Delta because it will contribute significant new information on several threatened fish species. Likewise, our proposed research is similarly relevant to the information needs of the Bay Delta Conservation Plan. Finally, through the application of local management issues and the information needs of the Delta Science Program and others, our research is intended to address fundamental issues about predation impacts of native and threatened species across a range of ecological conditions and habitat types.

7. Expected quantitative results (project summary):

This is a research project and will yield scientific papers and valuable tools and databases to be used for future resource management needs (see sections for 'Deliverables' and 'Other products and results'). However, the products are not quantifiable in the specific manner identified in Appendix E of the PSP (e.g. number of trees planted, diversions screened, or acres of habitat described).

8. Other products and results:

Tool Development: The development of new genetic assays for the accurate identification of six native at-risk species and one introduced fish species of the Delta. This suite of assays will build on an existing set of assays already developed for one native species (Delta smelt) and four introduced species. These tools will be useful in a broad range of scientific and monitoring studies (e.g. rapid detection of listed-species presence during time-critical monitoring activities such as salvage from state and federally-operated water pumping operations). Assay details will be publicly available.

Databases: Tasks 1 and 2 (field sampling and application of genetic assays) will yield a spatially-explicit database for the incidence rate of predation for listed and non-listed runs of Chinook salmon, steelhead, Delta smelt, longfin smelt, white sturgeon, green sturgeon, Sacramento splittail as well as Mississippi silversides and Wakasagi smelt in critical migration corridors for native fishes. This database will include information on predator abundance and habitat conditions associated with predation events, and will be publicly available.

9. Qualifications

Bernie May, PhD, received his PhD is Genetics from the Pennsylvania State University in 1980. He served for 14 years at Cornell University as Director of the Cornell Laboratory for Ecological and Evolutionary Genetics. For the past fifteen years he has been the Director of the Genomic Variation Laboratory in the Department of Animal Science at UC Davis. He currently has eight PhD students, two Project Scientists, three technicians, and two post-docs working in his laboratory who use a variety of molecular techniques (AFLPs, microsatellites, SNPs, sequencing, microarrays, etc.) to study genomic variation in natural and aquacultural populations. He has published over 175 scientific papers on questions related to genomic structure, linkage of markers to QTLs, population analysis, mixed stock analysis, genomic manipulation, effects of non-indigenous species/populations, effects of toxicants on gene pools, and isolate identification in a wide range of fish, fungi, birds, mammals, plants, and invertebrates. Current target organisms include: salmonids (golden trout, redband trout, Chinook salmon, rainbow trout, cutthroat trout), jellyfish, lion paw scallops, tui chub, fairy shrimp, delta smelt, Sacramento perch, Shasta crayfish, and sturgeon (lake, green, and white). He has managed dozens of large projects with state, federal, provincial, and tribal management agencies. He will be the overall supervisor of this project, ensuring that all tasks are accomplished and all promised deliverables are produced.

The following were all CALFED contracts on which Dr. May was a co-PI or PI

Contract #	Title	PI	Outcome
unavailable	Biological assessment of green sturgeon in the Sacramento-San Joaquin watershed	J. Cech	*completed as contracted*
P014004	San Joaquin River basin Fall-run chinook salmon genetic baseline and discrimination	B. May	*completed as contracted*
1132321G005	Biological assessment of green sturgeon in the Sacramento-San Joaquin watershed	A. Klimley	*completed as contracted*
02P34	Restoration of Sacramento perch to San Francisco Estuary	P. Moyle	*completed as contracted*
113322J006	Sex-reversal in Central Valley Chinook salmon: occurrence and population genetic consequences	B. May	*completed as contracted*
4600002763	Population genetics of splittail	B. May	*completed as contracted*
02DP57	Biological assessment of green sturgeon in the Sacramento-San Joaquin watershed	A. Klimley	*completed as contracted*
05WRGR0012	Are apparent sex-reversed Chinook salmon a symptom of genotoxicity?	B. May	*completed as contracted*
1036	Predicting the effects of invasive hydrozoa (jellyfish) on pelagic organisms under changing saline and temperature regimes	B. May	*partially completed*
E078004	Population biology, life history, distribution, and environmental optima of green sturgeon	A. Klimley	*partially completed*

Melinda Baerwald, PhD, is a project scientist at the University of California, Davis. Baerwald's expertise in

conservation genetics and genomics spans the specific areas of predation, hybridization, infectious disease resistance, and local adaptation. Currently, Dr. Baerwald is a PI or co-PI of four funded projects, three of which study fish species inhabiting the San Francisco Estuary (Chinook salmon and Delta smelt). She is also a co-PI of a project recently recommended for funding by the Delta Science Program entitled "Understanding the Scale and Mechanisms of Connectivity between Splittail Populations and the Implications for Management". She is the lead author of a Genetic Management Plan for restoring spring-run Chinook to the San Joaquin and coordinates the genetic aspects of an IEP-funded project to examine silverside predation on larval Delta smelt. Baerwald has authored or coauthored 13 peer-reviewed scientific journal articles and has been an invited speaker at many universities and international conferences.

Louise Conrad, PhD, received her PhD in Animal Behavior from the University of California, Davis in 2008. Her post-doctoral work was an IEP-funded project investigating the distribution, abundance, and impact of introduced largemouth bass in the Sacramento-San Joaquin Delta. For this project, she led a 2-year, regional-scale sampling effort to for largemouth bass to understand their habitat associations and their diet composition. This work is currently in preparation for publication in peer-reviewed journals and has already been presented at local scientific conferences. Dr. Conrad is now the senior environmental scientist for the Aquatic Ecology research team at CDWR. In this role, she oversees applied research projects of four Masters and PhD-level environmental scientists and three field technicians. Current research conducted by this group includes floodplain ecology of the Yolo Bypass, continuing research on diet and abundance patterns of largemouth bass in the Delta, and habitat conditions associated with larval Delta smelt predation. In addition to this research, Conrad is a member of the IEP Management Team, a body that identifies research priorities to guide management of natural aquatic resources in the Delta.

Brian Schreier, MS, is an environmental scientist with the California Department of Water Resources in Sacramento, CA. Currently, he is serving as a fisheries ecologist for the Department working on delta smelt and native/non-native fishery issues. He is a co-PI on an Interagency Ecological Program-funded project examining predation on larval delta smelt by Mississippi silversides using genetic techniques.

Bradley Cavallo, MS, is a Senior Scientist and President of Cramer Fish Sciences. Cavallo is a recognized expert in the ecology and management of Central Valley salmonids. He holds degrees from the University of California at Davis (B.S. 1994) and University of Montana (M.S. 1997). Cavallo has more than 13 years working to understand and resolve ecosystem problems of the Central Valley. Brad is the lead developer of the Delta Passage Model and has authored numerous technical and peer-reviewed fishery studies, and regularly presents results of his scientific endeavors at public policy forums and professional society conferences. Brad worked closely with Matt Nobriga in the application of the striped bass bioenergetics model to assess salmonid predation for the BDCP effects analysis.

Gregg Schumer is an experienced Molecular Biologist with Cramer Fish Sciences. Schumer earned his B.S. from UC Santa Cruz and has since acquired more than nine years of intensive working at the Canadian National Microbiology Institute Special Pathogens Level 4 containment unit in Winnipeg, Manitoba. Previously Gregg had started and operated an Influenza PR8/34 and Human Rhinovirus Type 14 production facility in Montreal, Canada for a private firm. Prior to this Gregg studied Gene Therapy and Molecular Virology at the University of Pennsylvania from 2001- 2004. His studies in molecular virology, gene therapy and most recently vaccine production for level 4 pathogens gives him a unique perspective on the field of fisheries biology. Since January 2010, Gregg has been working collaboratively with the GVL at UC Davis develop molecular based techniques for the detection and identification Delta smelt, Wakasagi smelt, and longfin smelt and other aquatic species.

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Section 7: Project Budget

Budget Summary - All Tasks						
	Task 1a	Task 1b	Task 2	Task 3	Task 4	Total
	DWR	Cramer	UCD	DWR	Cramer	
PERSONAL SERVICES						
Total Personal Services	$ 102,451.54	$ 8,580.00	$ 203,972.82	$ 7,604.22	$ 115,259.73	$ 437,868.30
OPERATING EXPENSES						
Materials	$ 12,690.00	$ 1,800.00	$ 98,700.00	$ 12,380.00	$ 1,780.00	$ 127,350.00
Equipment						
Operating Expenses/Equipment	$ 12,690.00	$ 1,800.00	$ 98,700.00	$ 12,380.00	$ 1,780.00	$ 127,350.00
						$ -
SUBTOTAL	$ 115,141.54	$ 10,380.00	$ 302,672.82	$ 19,984.22	$ 117,039.73	$ 565,218.30
						$ -
ADMINISTRATIVE OVERHEAD	$ 77,459.32	$ -	$ 75,668.21	$ 5,711.27	$ 6,250.00	$ 165,088.79
GRAND TOTAL	$ 192,600.85	$ 10,380.00	$ 378,341.03	$ 25,695.48	$ 123,289.73	$ 730,307.09

Detailed Budget for Each Task

Task 1a - Field Sampling-DWR										
	Year 1			**Year 2**			**Year 3**			**Total**
PERSONAL SERVICES										
	Number of Hours	*Hourly Rate*	*Total*	*Number of Hours*	*Hourly Rate*	*Total*	*Number of Hours*	*Hourly Rate*	*Total*	
Staff Level										
Conrad, Senior ES, Base level (5% time)	80	$34.06	$ 2,724.80	80	$34.06	$ 2,724.80	80	$34.06	$ 2,724.80	$ 8,174.40
Schreier, ES Range C, Step 2	520	$29.37	$15,272.40	520	$29.37	$ 15,272.40	200	$29.37	$ 5,874.00	$ 36,418.80
Frantzich, ES Range C, Step 2	208	$29.37	$ 6,108.96	208	$29.37	$ 6,108.96	200	$29.37	$ 5,874.00	$ 18,091.92
Loya, F&W Tech, Base + 5%	208	$20.23	$ 4,207.84	208	$20.23	$ 4,207.84	0	$20.52	$ -	$ 8,415.68
Nelson, Scientific Aide	208	$12.46	$ 2,591.68	208	$12.46	$ 2,591.68	0	$11.58	$ -	$ 5,183.36
Vella, Scientific Aide	208	$12.46	$ 2,591.68	208	$12.46	$ 2,591.68	0	$11.58	$ -	$ 5,183.36
Staff Benefits		@ %			@ %			@ %		
Conrad, Senior ES, Base level		28.16%	$ 767.30		28.16%	$ 767.30		28.16%	$ 767.30	$ 2,301.91
Schreier, ES Range C, Step 2		28.16%	$ 4,300.71		28.16%	$ 4,300.71		28.16%	$ 1,654.12	$ 10,255.53
Frantzich, ES Range C, Step 2		28.16%	$ 1,720.28		28.16%	$ 1,720.28		28.16%	$ 1,654.12	$ 5,094.68
Loya, F&W Tech, Base + 5%		28.16%	$ 1,184.93		28.16%	$ 1,184.93		28.16%	$ -	$ 2,369.86
Nelson, Scientific Aide		9.28%	$ 240.51		9.28%	$ 240.51		9.28%	$ -	$ 481.02
Vella, Scientific Aide		9.28%	$ 240.51		9.28%	$ 240.51		9.28%	$ -	$ 481.02
Total Personal Services			$41,951.60			$ 41,951.60			$18,548.34	$102,451.54

ERP Proposal: Native Fish Predation

Task 1a - Field Sampling-DWR Cont.										
	Year 1			**Year 2**			**Year 3**			**Total**
OPERATING EXPENSES										
Materials										
	Cost/item	*# of items*	*Total*	*Cost/item*	*# of items*	*Total*	*Cost/item*	*# of items*	*Total*	
Field Sampling Expenses										
Sterilization materials (bleach/ethanol)	$300.00	1	$ 300.00	$300.00	1	$ 300.00	$300.00	0	$ -	$ 600.00
MS222	$170.00	8	$ 1,360.00	$170.00	8	$ 1,360.00	$170.00	0	$ -	$ 2,720.00
Fuel for boat (cost/day)	$100.00	30	$ 3,000.00	$100.00	30	$ 3,000.00	$100.00	0	$ -	$ 6,000.00
Dissecting supplies	$1,000.00	1	$ 1,000.00	$1,000.00	1	$ 1,000.00	$1,000.00	0	$ -	$ 2,000.00
Gill nets	$350.00	2	$ 700.00	$350.00	1	$ 350.00	$350.00	0	$ -	$ 1,050.00
Buoys/anchors/lines	$40.00	8	$ 320.00	$40.00	0	$ -	$40.00	0	$ -	$ 320.00
Total Operating Expenses/Equipment			$ 6,680.00			$ 6,010.00			$ -	$ 12,690.00
SUBTOTAL			$48,631.60			$ 47,961.60			$18,548.34	$115,141.54
ADMINISTRATIVE OVERHEAD (@ 95.08%, not including benefits and equipment)			$31,849.29			$ 31,849.29			$13,760.74	$ 77,459.32
GRAND TOTAL			$80,480.89			$ 79,810.89			$32,309.08	$192,600.85

ERP Proposal: Native Fish Predation

Task 1b - Field Sampling-Cramer										
	Year 1			**Year 2**			**Year 3**			**Total**
PERSONAL SERVICES										
	Number of Hours	*Hourly Rate*	*Total*	*Number of Hours*	*Hourly Rate*	*Total*	*Number of Hours*	*Hourly Rate*	*Total*	
Staff Level										
TBD, Biologist II	20	$89.00	$1,780.00	20	$89.00	$ 1,780.00	20	$89.00	$ 1,780.00	$ 5,340.00
TBD, Bio-Technician II	20	$54.00	$1,080.00	20	$54.00	$ 1,080.00	20	$54.00	$ 1,080.00	$ 3,240.00
Staff Benefits		@ %			@ %			@ %		
NA										
Total Personal Services			$2,860.00			$ 2,860.00			$ 2,860.00	$ 8,580.00
OPERATING EXPENSES										
Materials										
	Cost/item	*# of items*	*Total*	*Cost/item*	*# of items*	*Total*	*Cost/item*	*# of items*	*Total*	
Travel (per trip)	$50.00	2	$ 100.00	$50.00	2	$ 100.00	$50.00	2	$ 100.00	$ 300.00
Boat Use (per trip)	$250.00	2	$ 500.00	$250.00	2	$ 500.00	$250.00	2	$ 500.00	$ 1,500.00
Total Operating Expenses/Equipment			$ 600.00			$ 600.00			$ 600.00	$ 1,800.00
SUBTOTAL			$3,460.00			$ 3,460.00			$ 3,460.00	$ 10,380.00
ADMINISTRATIVE OVERHEAD 25%*			$ -			$ -			$ -	$ -
GRAND TOTAL			$3,460.00			$ 3,460.00			$ 3,460.00	$ 10,380.00

* Task 1b and 4 will be part of a subcontract to Cramer Fish Sciences from UCD. Overhead will be 25% of first $25,000 in Task 4

ERP Proposal: Native Fish Predation

Task 2 - Genetics - UCD										
	Year 1			Year 2			Year 3			Total
PERSONAL SERVICES										
	Number of Hours	*Hourly Rate*	*Total*	*Number of Hours*	*Hourly Rate*	*Total*	*Number of Hours*	*Hourly Rate*	*Total*	
Staff Level										
Melinda Baerwald, Project Scientist	560	$ 25.00	$ 14,000.00	560	$ 26.25	$ 14,700.00	350	$27.56	$ 9,646.88	$ 38,346.88
TBD, Research Technician	2080	$ 17.50	$ 36,400.00	2080	$ 18.38	$ 38,220.00				$ 74,620.00
Bernie May, Adjunct Professor	173	$ 67.50	$ 11,677.50	173	$ 70.88	$ 12,261.38	120	$74.42	$ 8,930.25	$ 32,869.13
Staff Benefits		@ %			@ %			@ %		
Melinda Baerwald, Project Scientist		40.9%	$ 5,721.33		44.4%	$ 6,524.35		45.4%	$ 4,376.47	$ 16,622.15
TBD, Research Technician		40.9%	$ 14,875.47		44.4%	$ 16,963.31				$ 31,838.78
Bernie May, Adjunct Professor		27.5%	$ 3,215.21		30.3%	$ 3,713.15		30.8%	$ 2,747.54	$ 9,675.90
Total Personal Services			$ 85,889.51			$ 92,382.19			$ 25,701.13	$ 203,972.82

ERP Proposal: Native Fish Predation

Task 2 - Genetics - UCD Cont.												
OPERATING EXPENSES												
	Year 1				Year 2				Year 3			Total
Materials												
Molecular supplies			$ 46,000.00				$ 34,000.00				$ 3,000.00	$ 83,000.00
Office supplies			$ 400.00				$ 400.00				$ 400.00	
Publication			$ 500.00				$ 1,000.00				$ 1,000.00	
Equipment lease and maintenance			$ 3,000.00				$ 3,000.00				$ 2,000.00	$ 8,000.00
Travel			$ 1,000.00				$ 1,500.00				$ 1,500.00	$ 4,000.00
Total Operating Expenses/Equipment			$ 50,900.00				$ 39,900.00				$ 7,900.00	$ 98,700.00
SUBTOTAL			$ 136,789.51				$ 132,282.19				$ 33,601.13	$ 302,672.82
ADMINISTRATIVE OVERHEAD (@ 25%, not including benefits and equipment)			$ 34,197.38				$ 33,070.55				$ 8,400.28	$ 75,668.21
GRAND TOTAL			$ 170,986.88				$ 165,352.74				$ 42,001.41	$ 378,341.03

ERP Proposal: Native Fish Predation

Task 3 - Feeding - DWR												
	Year 1				**Year 2**				**Year 3**			**Total**
PERSONAL SERVICES												
	Number of Hours	*Hourly Rate*	*Total*		*Number of Hours*	*Hourly Rate*	*Total*		*Number of Hours*	*Hourly Rate*	*Total*	
Staff Level												
Conrad, Senior ES, Base level (5% time)	0	$34.06	$ -									$ -
Schreier, ES Range C, Step 2	120	$29.37	$ 3,524.40									$ 3,524.40
Frantzich, ES Range C, Step 2	40	$29.37	$ 1,174.80									$ 1,174.80
Loya, F&W Tech, Base + 5%	40	$20.23	$ 809.20									$ 809.20
Nelson, Scientific Aide	40	$12.46	$ 498.40									$ 498.40
Staff Benefits		@ %										
Conrad, Senior ES, Base level		28.16%	$ -									$ -
Schreier, ES Range C, Step 2		28.16%	$ 992.47									$ 992.47
Frantzich, ES Range C, Step 2		28.16%	$ 330.82									$ 330.82
Loya, F&W Tech, Base + 5%		28.16%	$ 227.87									$ 227.87
Nelson, Scientific Aide		9.28%	$ 46.25									$ 46.25
Total Personal Services			$ 7,604.22									$ 7,604.22

Task 3 - Feeding - DWR Cont.												
OPERATING EXPENSES												
	Year 1				**Year 2**				**Year 3**				**Total**
Materials												
	Cost/item	*# of items*	*Total*									
Feeding Trial Facilities												
12' diameter holding tanks (for 3 months)	$825.00	2	$ 1,650.00									$ 1,650.00
7' diameter holding tanks (for 1 month)	$131.00	10	$ 1,310.00									$ 1,310.00
5' diameter feeding tanks (for 3 months)	$135.00	2	$ 270.00									$ 270.00
4' diameter feeding tanks (for 1 month)	$26.00	10	$ 260.00									$ 260.00
Feeding Trial Expenses												
Feeder fish	$0.10	15000	$ 1,500.00									$ 1,500.00
Bulk fish food (5 lb)	$35.00	10	$ 350.00									$ 350.00
MS222	$170.00	3	$ 510.00									$ 510.00
Medicated treatments/effluent tests (for fungus)	$500.00	8	$ 4,000.00									$ 4,000.00
Sterilization materials (bleach/ethanol)	$300.00	1	$ 300.00									$ 300.00
Dissecting supplies	$500.00	1	$ 500.00									$ 500.00
Husbandry supplies	$500.00	1	$ 500.00									$ 500.00
HOBO water temperature data logger	$123.00	10	$ 1,230.00									$ 1,230.00
Total Operating Expenses/Equipment			$ 12,380.00									$ 12,380.00
SUBTOTAL			$ 19,984.22									$ 19,984.22
ADMINISTRATIVE OVERHEAD (@ 95.08%, not including benefits and equipment)			$ 5,711.27									$ 5,711.27
GRAND TOTAL			$ 25,695.48									$ 25,695.48

ERP Proposal: Native Fish Predation

Task 4 - Bioenergetics - Cramer										
	Year 1			**Year 2**			**Year 3**			**Total**
PERSONAL SERVICES										
	Number of Hours	*Hourly Rate*	*Total*	*Number of Hours*	*Hourly Rate*	*Total*	*Number of Hours*	*Hourly Rate*	*Total*	
Staff Level										
Cavallo, Senior Scientist III	8	$157.00	$ 1,256.00	8	$164.85	$ 1,318.80	112	$173.09	$ 19,386.36	$ 21,961.16
Zeug, Biologist III	8	$100.00	$ 800.00	8	$105.00	$ 840.00	320	$110.25	$ 35,280.00	$ 36,920.00
Schumer, Biologist IV	180	$111.00	$ 19,980.00	180	$116.55	$ 20,979.00	126	$122.38	$ 15,419.57	$ 56,378.57
Staff Benefits		@ %			@ %			@ %		
NA										
Total Personal Services			$ 22,036.00			$ 23,137.80			$ 70,085.93	$ 115,259.73
OPERATING EXPENSES										
Materials										
	Cost/item	*# of items*	*Total*	*Cost/item*	*# of items*	*Total*	*Cost/item*	*# of items*	*Total*	
Travel (per 100 mile trip)	$50.00	2	$ 100.00	$50.00	2	$ 100.00	$50.00	2	$ 100.00	$ 300.00
Phone	$40.00	1	$ 40.00	$40.00	1	$ 40.00	$40.00	1	$ 40.00	$ 120.00
Goldsim Software Licensing Use (per month)							$200.00	2	$ 400.00	$ 400.00
Primer Select Software (license acquisition)	$1,500.00	1	$ 1,500.00							
										$ 1,500.00
Total Operating Expenses/Equipment			$ 1,640.00			$ 140.00				$ 1,780.00
SUBTOTAL			$ 23,676.00			$ 23,277.80			$ 70,085.93	$ 117,039.73
ADMINISTRATIVE OVERHEAD 25%*			$ 5,919.00			$ 331.00			$ -	$ 6,250.00
GRAND TOTAL			$ 29,595.00			$ 23,608.80			$ 70,085.93	$ 123,289.73

* Task 1b and 4 will be part of a subcontract to Cramer Fish Sciences from UCD. Overhead will be 25% of first $25,000 in Task 4

Budget Justification

Task 1 – Predator Sampling

Task 1a: Staff time is reflective of the actual field time to be spent sampling (8 hours per day, 15 days per sampling period, 4 sampling periods over two years = 480 hours). For each sampling day, 3-4 people will be required to operate the sampling vessel, tend the nets, and dissect predators. Additional time is added to account for study preparation, permitting, and organizing. During year three, staff time will be used to analyze data collected and write reports.

Equipment needed for Task 1a includes materials to maintain a DNA sterile work environment critical for preventing contamination of stomach samples, as well as supplies for humanely euthanizing collected predators and proper equipment for dissecting them on the boat. Sampling gear, consisting of gill nets and buoys/anchors, will need to be purchased initially, but we also estimate needing to replace one of the nets after the first year of sampling due to damage from debris. Boat fuel costs are estimated based on fuel consumption rates for the proposed CDFG vessel (*R/V Mudsucker*), the aforementioned number of sampling hours, and a fuel price of $5.00/gallon at Antioch marina.

Task 1B: Staff time is reflective of the actual field time to be spent sampling and including travel (10 hours per day, 2 staff per day, 2 days per year over three years = 120 hours). Our staff will be used to supplement sampling crews provided by DWR. Though no intensive field sampling is planned for Year 3, we have allocated some hours for post-survey data collection.

Materials needed for Task 1b include travel costs ($0.50 per mile) and boat use ($250 per day includes fuel and maintenance). These amounts are standard rates charged by CFS for field projects.

Task 2 – Genetic Assay Development and Application

Personal Services

Dr. May will devote 120 - 173 hours per year for project coordination and oversight. Dr. Baerwald will devote 350 – 560 hours per year for daily supervision of laboratory research, data analysis, and preparation of reports/manuscripts. A research technician (to be determined) will devote 2080 hours per year for the first two years to conduct laboratory experiments for the genetic assay development and genetic screening of predators outlined in the proposal. Fringe benefits are 27.5 – 30.8%/year (Dr. May), 40.9 – 45.4 %/year (Dr. Baerwald), and 40.9 – 44.4%/year (research technician) as dictated by UC Davis policy.

Operating Expenses

Funds of $46,000 in year 1 (assay development, processing of predator samples), $34,000 in year 2 (continued processing of predator samples), and $3,000 in year 3 (completion of predator sample processing) to cover the molecular studies in this project. Additional expenses include office supplies ($400/year), publication costs ($500 - $1,000/year), equipment maintenance and lease ($3,000 per year), and travel for conferences ($1,000 - $1,500/year).

Task 3 – Captive Feeding Trial

Staff time for the feeding trial reflects hours for 4 staff to assist with the actual feeding trial and dissections (covering a one week period). Additional time is included for one staff person to organize logistics and collect/transport wild stripers to captivity. The feeding trial will only occur once, so no hours or equipment will be necessary for years 2 and 3 of the project.

Facility costs for this task are based on quoted rates from the UC-Davis Center for Aquatic Biology and Aquaculture (CABA). The 12’ diameter tanks will be utilized for holding striped bass during the collection and acclimation period. During the same period, 5’ diameter tanks will be used to house feeder fish for the striped bass. During the actual feeding trial, 7’ diameter tanks will be used to house fish for each time step, with 4’ diameter tanks being used to conduct the actual feeding of smolts to striped bass. CABA bills tank usage by the whole month.

Materials for the care of captive striped bass include feeder fish for the striped bass (with food for the feeder fish) and general fish husbandry supplies (nets, buckets, etc). CABA also requests funds be set aside to treat all new fish for fungus and infections, and their operating permit requires all facility effluent be tested for these medications whenever they are used.

Additional equipment costs include materials for creating a DNA sterile work environment for the dissections, as well as supplies for humanely euthanizing fish and conducting the dissections. Temperature loggers will be necessary for each trial tank so that we can account for water temperature when analyzing the digestion rates of striped bass.

Task 4 – Bioenergetics Modeling
Staff time for task includes hours for one staff person (Gregg Schumer) to work with UC Davis in the genetic analysis of stomach contents and to assist with subsequent bioenergetic analysis. Hours for other staff (Brad Cavallo and Steve Zeug) are required to conduct bioenergetic analysis and to operate the Delta Passage Model to estimate juvenile Chinook salmon abundance. Hours for all three staff also include time necessary to coordinate the project with UCD and DWR staff and to help prepare and review project reports and manuscripts.

Materials needed for Task 4 include travel costs ($0.50 per mile) assuming two 100 mile trips and $40 for long distance phone charges. Travel and phone charges will be incurred as a result of coordination and meetings with UCD and DWR project collaborators. Additional material costs include software licensing required for operation of the Delta Passage Model (Goldsim) and Primer Select Software which is specialized software required to design genetic primer-probes sets required for develop prey species genetic barcodes and detection assays. The monthly Goldsim software license fee is standard monthly fee charged by CFS. The Primer Select software for one time purchase of two-year license. While Goldsim is used for other CFS projects, the Primer Select software is not expected to be used for other or future projects.

Administrative Overhead

UC Davis Administrative Overhead
The current administrative overhead rate is 25%, as shown in the example below. For this task, the total indirect cost rate is $75,668.21.

The current indirect cost rate for VM:APC is 25% with all California State Agencies (Waiver # 03R-135).

· Class Waiver	No.: **03R-135**	Date Approved: **5/9/2003**	Sponsor Code:
Campus: **OP**	Reason: **C** [A=vital interest; C=sponsor policy]		
Sponsor Name: *CALIFORNIA STATE AGENCIES*			
Project Title: **CALIFORNIA STATE AGENCY AGREEMENTS****			
Waiver Rate: **25.00% MTDC***			
Notes: *UNLESS OTHERWISE SET FORTH IN STATUTE, REGULATION, OR PUBLISH POLICY THAT APPLIES TO ALL RECIPIENTS. C&G MEMO 03-02. SEE OTHER STATE CLASS WAIVERS FOR SPECIFIC PROGRAMS.			

CA Dept of Water Resources Administrative Overhead
For CDWR, the administrative overhead rate is 95.08%. These funds are devoted to salaries, healthcare benefits, and retirement costs for all managerial-level staff at CDWR.