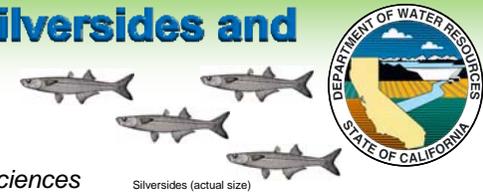


# Detecting Predation of Larval Delta Smelt by Mississippi Silversides and Other Predators Using Genetic Analysis

Brian Schreier<sup>1</sup>, Melinda Baerwald<sup>2</sup>, Gregg Schumer<sup>3</sup>, and Bernie May<sup>2</sup>

<sup>1</sup>California Department of Water Resources, <sup>2</sup>University of California – Davis, <sup>3</sup>Cramer Fish Sciences

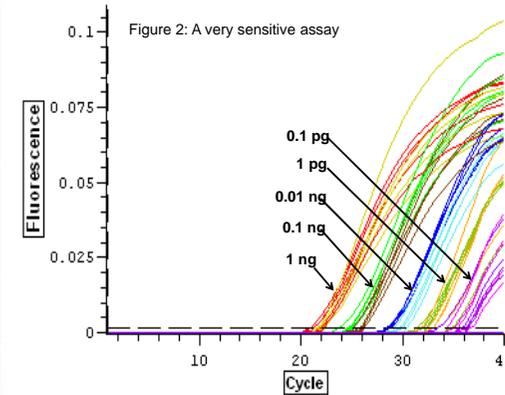
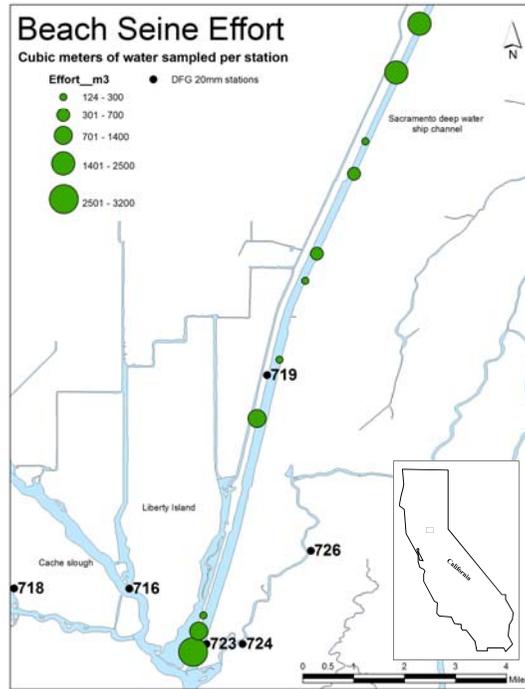
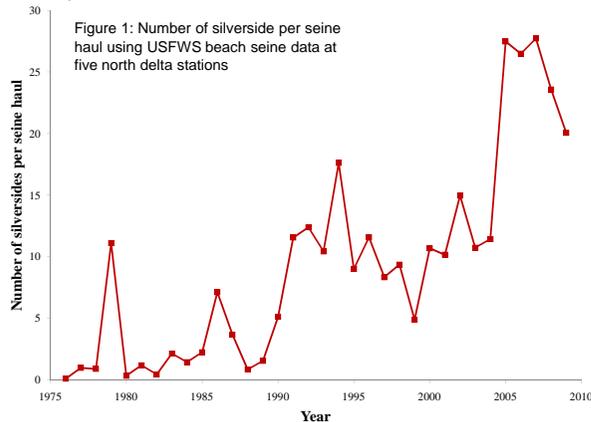


## Questions:

1. Can PCR be used to detect delta smelt DNA in the guts of predators?
2. How sensitive is the PCR method for detecting delta smelt DNA in gut contents?
3. Do silversides predate on larval delta smelt and if so, at what frequency?

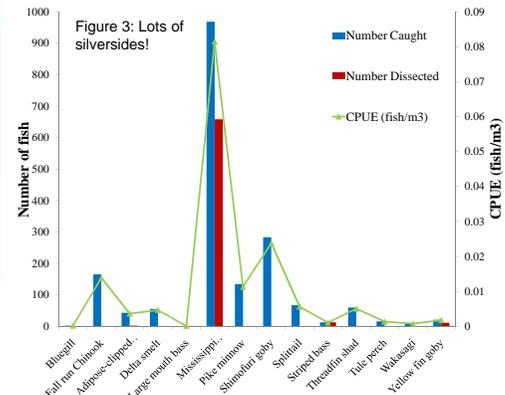
## Background:

- Morphological identification of larval fish in gut contents is notoriously difficult, and this new tool will provide a quick and cost effective method for detecting and quantifying predation.
- Polymerase chain reaction (PCR) assays have been used in multiple taxa (insects, fish, mammals, etc) to detect predation and to map out food webs (King et al. 2008). Our assay utilizes mitochondrial DNA (mtDNA) to maximize the number of copies of target DNA (and thus maximize our ability to detect target species) in a sample.
- Silversides are increasing in the north delta (Figure 1) where they co-occur with larval delta smelt, and silversides have been shown to readily predate larval delta smelt in the lab (Bennett 2005).
- Our initial goal in developing this assay was to investigate the potential top down effects of Mississippi silverside (*Menidia audens*) predation on larval delta smelt (*Hypomesus transpacificus*) in the northern Sacramento-San Joaquin delta.



## Sensitivity Assay

Delta smelt quantitative PCR TaqMan<sup>®</sup> assay is capable of detecting as little as 0.1 picograms of template Delta smelt DNA in 100 nanograms of silverside DNA.



## Beach Seine Catch

A total of 658 silversides, one bluegill, one largemouth bass, 13 striped bass, one threadfin shad, and 11 yellow fin gobies were collected for dissection and genetic analysis.

## Methods:

### PCR assay development:

Several mtDNA regions from three smelt species (delta, longfin, and Wakasagi) along with 13 other fish species found in the delta were sequenced and compared. Species-specific regions of the CytB1 gene capable of amplifying smelt DNA were identified.

### Assay characterization:

Tissue samples from delta smelt and Mississippi silverside were used to determine the sensitivity of the assay (Figure 2). Additional samples of other delta fishes and zooplankton were also tested to verify that no other species would cross-amplify and give false positive results. A feeding study will be conducted to model smelt DNA degradation in the guts of predators.

### Predator sampling:

Beach seines were conducted in the Sacramento deep water ship channel from April 14-30, 2010 (Figure 3). Silversides and other putative predators were stored overnight in 95% ETOH on dry ice, and were dissected the next day. Guts were removed using sterile techniques and further preserved in 80% ETOH on dry ice for transport to UC-Davis Genomic Variation Laboratory.



## Preliminary Results:

1. **Yes; initial results show that all 3 smelt species' DNA are independently detectable in the guts of predators. Future feeding trials will model the degradation of smelt DNA in the guts of predators.**
2. **Very; the assay can detect 0.1 pg of smelt DNA in 100 ng of predator DNA. Typical analyses aim for detections at 500-1000 pg of target DNA.**
3. **Unsure; so far we have analyzed 270 wild silverside guts with one positive. However, 388 silversides remain to be analyzed and all guts will be run through three times to ensure accuracy.**

## Next Steps:

Funding will be sought for additional sampling to occur in spring 2011 for larval delta smelt predators. The PCR assay will have multiple applications, which include studying predation effects on juvenile and adult smelt species.

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## References

- Bennett, W. A. 2005. Critical assessment of the delta smelt population in the San Francisco Estuary, California. San Francisco Estuary and Watershed Science 3:2. <http://repositories.cdlib.org/jmie/sfews/vol3/iss2/art1>.
- King, R. A., D. S. Read, M. Traugott, and W. O. C. Symondson. 2008. Molecular analysis of predation: a review of best practice for DNA-based approaches. *Molecular Ecology* 17:947-963.