

Project Objectives: Please type your responses, and answer the questions in a style appropriate for laymen.

ProjectObjectives_10

Simultaneous declines of multiple pelagic organisms suggest a possible trophic linkage and that a decline in food resources is an important factor in the decline of juvenile fish (Bennett and Moyle, 1996). One hypothesis has been that in response to a decrease in primary production within the low salinity zone, a portion of the food web depends on the microbial loop, which in turn depends on the delivery of riverine organic matter (Kimmerer et al., 2006). It has been proposed that a recently introduced zooplankton species, the *Limnionthona*, can readily access this food source while the other primary species, *Pseudodiaptomus*, can not. If true, the incorporation of organic matter should differ between these two species. Further, variations to the input of riverine organic matter should impact both the source of organic matter to the Bay ecosystem and how it is incorporated.

Our research goal was to obtain a coarse "time-series" of food sources being utilized by the dominant zooplankton inhabiting the central portion of the upper SFB estuary (Suisun Bay). Based on this series of 'snapshots' delineating dominant food sources to organisms in the Bay, we hoped to further assess the impact of particular water management strategies on zooplankton community dynamics. Our efforts were focused on the upper estuary (Suisun Bay) as it is a critical habitat for the threatened Delta Smelt (Hobbs et al., 2002) [CON'T BELOW]

Summary of progress in meeting each of these goals and objectives

ProgressSummary_11

Our approach for assessing the source of food utilized by zooplankton is was to determine the stable nitrogen isotopes of individual amino acids (e.g. phenylalanine, glutamic acid) released from the acid hydrolysis of the organism's proteins. Studies have shown that the isotopic compositions of some amino acids, such as phenylalanine, are conserved as the compound is transferred from primary producer to zooplankton consumers (McClelland and Montoya, 2002). That is, this amino acid is not metabolized and re-synthesized; instead it is conservatively transferred intact. Other amino acids, such as glutamic acid, are synthesized by each organism, and during the re-synthesis, a 5-6 per mil increase in $\delta^{15}N$ relative to phenylalanine is imparted per increase in trophic step. Therefore, these two sets of amino acids (source v. trophic) provide an internally consistent tracer to observe the relative trophic position of any consumer, defined as TPglu-phe (Hannides et al., 2009). If the zooplankton rely predominantly on phytoplankton as their food source, the calculated TPglu-phe will equal 2. Alternatively, if zooplankton feed on the components of the microbial loop, the TPglu-phe will equal 3 or higher.

One way to assess the quality of the organic matter (its potential usefulness for secondary consumers) being delivered to Suisun Bay from the Sacramento and San Joaquin Rivers is to determine the concentrations of D- and L- amino acids in particulate organic matter. While most living organisms produce the L-enantiomer of amino acids, bacteria are the primary source of the D-enantiomers. Additionally, the degradation of freshly-produced, labile organic matter results in increased concentrations of diagnostic compounds such as the non-protein amino acids (NPAAs) gamma-aminobutyric acid and beta-alanine. Therefore "fresher," less degraded organic matter that would be expected to be more useful as a food source to higher organisms will have low D/L ratios and low concentrations of NPAAs. Refractory organic matter that has been significantly re-worked will have higher D/L ratios and higher concentrations of NPAAs.

A full suite of samples from winter and spring (November, 2008 and May, 2009) was collected and analyzed. Samples were collected from the two primary rivers (Sacramento and San Joaquin), the station closest to the site of X2 (where the salinity at depth is 2 PSU, a location important to juvenile fish), and at the narrow western input into Suisun Bay where salinities are higher. Complementary chemistry, temperature and salinity data are presented in Table 1. The winter sampling occurred during relatively 'low flow' river conditions and the site of X2 was very close to the Sacramento River. The spring sampling occurred during relatively 'high flow' river conditions, which is reflected in lower salinities in the Bay sampling stations.

The amino acid concentrations are variable between the two sampling periods. Interestingly, the winter 'low flow' river conditions have higher contributions of d-amino acids (attributed primarily to bacterial influence) and non-protein amino acids, reflecting a greater extent of organic matter degradation (Table 2). The San Joaquin River consistently had significantly high amino acid concentrations than the Sacramento River, and low contributions of d- and non-protein amino acids. Since chlorophyll a concentrations are also consistently higher in the SJR, we hypothesize that amino acids predominantly result from primary production in this location.

[CON'T BELOW]

other assistance to your project since inception. Describe the nature of their collaboration.

CoopOrganiz_15

The Sacramento Regional County Sanitation District provided 3 months of critical funding support that allowed the compound specific amino acid analysis to proceed.

The USGS and Dr. James Cloern have generously provided berth space on the R/V Polaris during monthly cruises through the San Francisco Bay and immediate access to critical data such as chlorophyll concentrations and water salinity. We are also collaborating with USGS scientist Dr. Carol Kendall, who is providing 15N of nitrate and ammonia data that will assist in our interpretation of the 'source' amino acids.

AWARDS: List any special awards or honors that you, or mentor or members of the research team, have received during the duration of this project.

Awards_16

KEYWORDS: List keywords that will be useful in indexing your project.

Keywords_17

Zooplankton, organic matter, trophic levels, food webs, Suisun Bay, compound-specific isotopes

PATENTS: List any patents associated with your project.

Patents_18

number of the question you are adding to.

Additions 19

[CONT FROM PROJECT OBJECTIVES]: and is likely to be strongly affected by proposed changes to the San Joaquin River.....

Our specific objectives are: (1) To determine what sources of organic matter support the dominant zooplankton population within Suisun Bay at different time points of the year and (2) To determine if changes in water management practices modify the type and magnitude of food sources available to support zooplankton production.....

[CONT FROM PROGRESS SUMMARY]:

The sampling scheme included collecting several size fractions of zooplankton (62-200 μm , dominated by Limnoithona; 200-500 μm , dominated by Pseudodiaptomus; 500-1000 μm , dominated by copepods, primary species to be identified). Depending on location, not all fractions contained enough biomass for the ^{15}N amino acid analysis. For instance, at the highest salinity stations the vast majority of the biomass was present in the 63-200 size fraction while larger zooplankton were largely absent. During the spring sampling period, delta smelt were readily identified in the 500-1000 μm size fraction. The smelt were isolated from copepods, and the two groups were analyzed separately. The CSIA-calculated trophic levels and the average ^{15}N of the 'source' amino acids are presented in Table 3.....

There are several notable aspects of the compound specific isotope analysis (CSIA) data. First, we had predicted that the 63-200 size fraction would have a higher TL glu-phe value than that of the 200-500 size fraction due to dependence of Limnoithona on the microbial loop. Instead, the CSIA-calculated trophic levels of both size fractions were very similar to 2. This is the expected value when organisms depend predominately on primary producers. The sampling locations with the highest d-amino acids (interpreted to be have the highest bacterial influence; November Stn 657 and 6) did have slightly higher TL glu-phe than other time points/locations, but these results were not statistically significant. One explanation for these findings is that neither the Pseudodiaptomus nor the Limnoithona utilized the microbial food loop to a significant degree during the sampling periods. It is also possible that microbial processing does not impart the expected fractionation on amino acid signatures. A colleague is currently running a bacteria-zooplankton feeding experiment to explicitly determine these fractionation patterns. What is apparent, however, is that to the degree that their nitrogen sources and trophic status are reflected by the CSIA analysis, the zooplankton within these size fractions rely upon very similar food resources.....

We were serendipitously able to subject Delta Smelt from the Sacramento River to the same analysis. Their TL glu-phe of ~3 is similar to what would be expected for organisms feeding on zooplankton feeding on primary producers. What is surprising, however, is that the signature of their 'source' amino acids – which should remain largely unchanged from their food source – are distinctly different from that of co-occurring zooplankton (7.6 – 7.8 ‰ vs. 14.2 ‰). This suggests that they may rely on food sources not captured by our sampling scheme either spatially or temporally. Since Smelt have higher biomasses than zooplankton, the turnover time of nitrogen in their system will be longer. In other words, Smelt may consume co-occurring zooplankton as their primary food source, but the temporal variability in the ^{15}N of those prey may have shifted dramatically during the amount of time required for biomass replacement.....