Blue Carbon in the Delta: Its History and the Prospects for Increased Carbon Storage through Wetland Restoration

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In this presentation, I will summarize an analysis we carried out on the history and future prospects for "blue carbon" storage in the Sacramento-San Joaquin Delta. Blue carbon is defined as the organic carbon stored in coastal ecosystems. Based on calculations using our data as well as the literature, we estimate that before conversion to agriculture began (~1850), the Delta contained between 150 to 210 Tg C (Tg = 1×10^{12} g, C = organic carbon) in its highly organic, peat soils. By 2005-2010, we estimate that ~100 Tg C of this blue carbon sink was lost, mainly due to microbial oxidation of the peat. The loss of this extensive wetland region contributed to the collapse of the Delta ecosystem, leading to a series of tidal wetland restoration projects beginning in the 1960s. Such efforts are continuing, yet success hinges strongly on overcoming challenges such as the shortage of suitable lands, the declining availability of sediment, invasive aquatic vegetation, and sea-level rise. The total area of wetland restoration (both managed and tidal) is slated to reach ~7600 ha by 2020. Our calculations show that the amount of carbon, which will accumulate in these restored wetlands over 100 years is ~1 Tg. This represents about 1% of the carbon lost from the Delta following conversion to agriculture. Although this amount of carbon is modest, the co-benefits that come along with wetland restoration, including retarding land-surface subsidence, expanding critical wildlife habitat, and recovering some of the historic detrital food web are highly important in and of themselves. This analysis of blue carbon shows that, although current projections for wetland restoration may not have a large carbon benefit (especially if methane emissions are considered), wetland restoration is still essential for recovering some basic ecosystem functions.

Keywords: carbon storage, wetland restoration, land-surface subsidence, Sacramento-San Joaquin Delta

Session Title: Food Web Foundations I

Compositional drivers of dissolved organic matter utilization by microbes

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Microbial assimilation is the primary means by which aquatic food webs incorporate dissolved organic matter (DOM). However, not all DOM is equally capable of assimilation, nor are all microbes equally capable of assimilating the same DOM. In an effort to better understand the relationship between microbial utilization of DOM and DOM composition, we conducted a series of incubation experiments that included source materials common to California and the Bay Delta Estuary, i.e. leachates from blue oak, loblolly pine, annual grasses from an oak savannah, and a cattail/tule mixture. Over the course of ~150 days of incubation (seven sampling time points), DOC losses ranged from 78% in the pine sample to only 45% loss in the oak sample, highlighting the impact of composition on bioavailability. These differences in bioavailability generally correspond to differences in aromaticity as indicated by carbonspecific absorbance at 254nm (SUVA254), with oak leachates containing the highest percentage of aromatic compounds. However, the strength of this study is that we measured a suite of biomarkers, including lignin, amino sugars, amino acids (totals as well as D-amino acids), carbohydrates, and utilize new data processing techniques to incorporate hundreds of compounds that are also detectable in the lignin traces. The scope of the chemical characterization is unprecedented and will lead to new insight as to timing, kinetics, and competition for various biochemicals by the microbial community. In the bigger picture, the comprehensive set of molecular tools that we are developing will enable new lines of research better equipped to capture carbon cycling dynamics in the complex and challenging Bay-Delta environment.

Keywords: Biomarkers, microbial processes, dissolved organic matter

Session Title: Food Web Foundations I

Evaluation of Delta Subregions for Nutrient Monitoring and Assessment

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Previous work has documented a large degree of spatial variability in nutrient concentrations and in seasonal and long-term trends across different geographic monitoring locations the Delta (Novick et al. 2015). Dividing the Delta into subregions for use in nutrient monitoring and assessment would fulfill two important needs: 1) allow a comparison of trends and processes across subregions to gain a better understanding of the spatial variability, and 2) improve estimates of regional long-term trends. Researchers have split the Delta up into regions for various purposes, but not yet specifically to inform the design of monitoring for nutrients, which was the objective of this study. The analysis had three key components. First, we recommended subregions in the Delta that could potentially be used for monitoring and assessing nutrients. Second, we performed time-series analyses on a 40-year dataset using non-negative matrix factorization (NMF) to assess spatial variability in dominant factors driving nutrient concentrations within and across these proposed subregions. And third, we performed power analyses for long-term trend detection to compare different sampling design options for the proposed subregions. In addition, we calculated the area of different habitat types in each of the subregions and how the existing nutrient monitoring network overlapped with each habitat type.

Keywords: Delta, subregions, nutrients, monitoring network, drivers

Session Title: Food Web Foundations I

Vertical Biogeochemical Variability in Sloughs Impacts Habitat Quality and Metabolic Rate Estimates

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The margins of estuaries have a disproportionately large impact on biogeochemical cycling despite their relatively small size. As direct conduits from land to the bay, sloughs and creeks exhibit variability in many parameters (e.g., dissolved oxygen, chlorophyll, suspended sediment, in/organic carbon, nutrients) that can be much larger than in other parts of the estuarine system. In order to unravel this heterogeneity—both in time at a given site and across sites at a given time—it is necessary to observe the full four-dimensional (latitude, longitude, depth, and time) system.

Preliminary results from vertical profiling of sloughs in Lower South San Francisco Bay from the Summer of 2015 suggest that the vertical variability of multiple biogeochemical parameters is greater than is often taken into account. Vertical gradients in dissolved oxygen, even when smaller than horizontal gradients, can still have first-order effects on habitat quality assessments and biogeochemical rate estimates, for example. We will provide examples from field studies completed in 2015 and 2016 as part of the San Francisco Bay Nutrient Management Strategy. Our results characterize sloughs/creeks where both habitat volume and metabolic rate estimates potentially differ depending on whether or not the observed vertical variability is taken into account. These findings will help to inform nutrient management decisions by narrowing uncertainties around habitat volume and biogeochemical rate calculations.

Keywords: deoxygenation, vertical, biogeochemistry, habitat quality, metabolic rates, slough

Session Title: Food Web Foundations I

Using Stable Isotopes to Evaluate the Effects of Seasonal and Spatial Changes in Flow and Nutrients on Biogeochemical Processes, Habitat Quality, and Ecosystem Health in the Sacramento River, northern Delta, and northern San Francisco Bay, 2006-2016

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There is increasing competition for fresh water in the San Francisco Estuary, and hence an increasing need to justify seasonal flow requirements to maintain ecosystem health in the Delta. How do we justify increased water allocations, especially during droughts? Stable isotope measurements of nutrients, particulate organic matter (POM), and water can provide unique information about the effects of flow on biogeochemical processes, nutrient and organic matter sources, and ecosystem health at different locations. Hence, isotope data can help provide managers with science-based support for models used to determine the seasonal flow and other requirements for healthy habitats for native organisms. Towards this and other long-term goals, we have piggybacked the collection of stable isotope samples onto several water quality monitoring programs in the Sacramento River, northern Delta, and northern San Francisco Bay to generate comprehensive multi-isotope datasets for most months during 10 of the 11 falls 2006-2016 and 9 of the 10 spring/summers 2007-2016. With these data, we have compared the effects of seasonal and spatial variations in flow and nutrients in wet and dry years with a wide range of flows and habitat indices, and with antecedent moisture conditions, on various habitat characteristics including organic matter quality, dominant sources of C-N-S to algal uptake, nitrification rate, locations of nitrification hotspots, etc. In specific, stable isotope measurements of nitrogen forms and bulk POM can be used to identify the dominant nitrogen sources used by primary producers over different spatial and temporal scales. The C and S isotopes of POM provide information on sources of the algae. And comparison of the downstream changes in NO3 concentrations and N/O isotopes with changes in water H/O isotopes allows quantification of seasonal and spatial changes in nitrification rate, external sources of NO3, and algal uptake.

Keywords: nutrients, flow, isotopes, habitat quality, drought, ecosystem health, uptake, nitrification

Session Title: Food Web Foundations I

Using Stable Isotopes to Identify Changes in Nitrogen Sources, Processes, and Uptake Over Time in the San Joaquin River and Eastern Delta

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Stable isotope measurements of nutrients and particulate organic matter (POM) can provide information about both the sources and processes controlling their concentrations and distribution. In the San Joaquin River (SJR) and parts of the San Francisco Bay-Delta region, POM is often composed almost entirely of phytoplankton and bacteria, and therefore stable isotope measurements of nitrogen forms and bulk POM can be used to identify the dominant nitrogen sources used by primary producers over different spatial and temporal scales. The USGS Isotope Tracers Project conducted multiple isotope studies in the San Joaquin River and eastern Delta from 2000 through the present, allowing us to examine how nutrient sources and biological cycling have varied over recent timescales, including during the period when significant upgrades were made to the Stockton Wastewater Treatment Plant (WWTP). Our results show that seasonal variations and flow conditions were the dominant controls on nitrate sources and concentrations to the lower SJR and Stockton Deep Water Ship Channel (SDWSC), but the upgrades to the Stockton WWTP had a significant impact on nitrogen sources used by the community of primary producers. In samples collected in 2002 and 2004 in the upper SDWSC, the δ^{15} N-POM suggested that there was a distinct spatial shift in nitrogen uptake dynamics, with uptake of nitrate dominating in the SJR above the WWTP, and nitrification of ammonium dominating in the area below the WWTP. Isotope samples collected in the years after the WWTP upgrade (2007 to present) did not show such a clear zone of nitrification, and instead indicated that both nutrient sources and nitrogen uptake were primarily controlled by physical mixing between Sacramento and San Joaquin River water, which have distinct nutrient concentrations and isotopic compositions.

Keywords: stable isotopes, nutrients, nitrate, ammonium, nutrient cycling

Session Title: Food Web Foundations II

Spatial Variability Reveals Complex Controls on Phytoplankton Abundance and Community Structure in a Shallow Tidal Freshwater System

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We used the marked spatial variability across zones in freshwater tidal wetlands in the North Sacramento-San Joaquin Delta to examine the effects of nutrients, light, contaminants, and residence time on phytoplankton abundance, size and taxonomic distribution. Phytoplankton abundance was quantified and the community structure evaluated using total chlorophyll-a concentration, chlorophyll-a size fractionation, pigment analyses, direct counts, and visual identification. Spatial variability was assessed using high-resolution mapping, discrete sampling, and enclosure experiments. While there was no evidence that light or contaminants affected the phytoplankton community, we found spatial variability across the region was characterized by strong gradients that corresponded to differences in residence time. Zones representing high and low residence time were characterized by differences in nutrient concentrations and phytoplankton communities. Zones characterized by higher residence times and lower ammonium concentrations (1 \pm 0.8 μ M) had higher chlorophyll-a concentrations (9 \pm 4 μ g L⁻¹) and the phytoplankton community was composed primarily of small cells $< 5 \mu m$ (74 \pm 8%), including picocyanobacteria. Diatom abundances, however, did not dominate the phytoplankton community even where NO₃ was available for uptake as has been observed elsewhere in in the system. Concurrently, zones characterized by lower residence time and higher ammonium concentration (13 \pm 5 μ M) coincided with lower chlorophyll-a abundance (5 \pm 1 μ g L⁻¹), but with diatoms making up a greater proportion of the phytoplankton community (27 ± 11% vs. 11 ± 5%) and showing similar percentage of small cells as the higher residence time zone but with phytoplankton nitrate uptake near zero. Our results suggest that while some tidal wetlands in the Delta support elevated phytoplankton biomass as a result of longer water residence time, the ensuing community may be composed of smaller cells that may not provide high quality food resources.

Keywords: phytoplankton abundance and community composition, freshwater tidal wetlands, residence

time

Session Title: Food Web Foundations II

Are Zooplankton and Clams Dining on Super Food or Junk Food? Application of a Phytoplankton Food Quality Index

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Phytoplankton are the largest living component of biomass in San Francisco Bay and the primary food source upon which the Bay's consumers (e.g., zooplankton, clams, crabs, flatfish, shrimp) ultimately depend. The patterns and processes of phytoplankton biomass variability in this estuary are relatively well understood, but what about the quality of this food resource for consumers? Food quality varies with phytoplankton attributes such as cell size, palatability, and biochemical composition. We address one biochemical component, the phytoplankton derived long-chain fatty acids (LCEFA) that cannot be synthesized by animals and are essential dietary components and indicators of food quality for consumers. We used results of a new meta-analysis that indexes phytoplankton food quality based on differences in LCEFA content and omega-3:omega-6 fatty acid ratios among algal groups. This index reflects the greater nutritional value of diatoms, dinoflagellates, and cryptophytes than of chlorophytes and cyanobacteria, due to their higher LCEFA content and larger fatty acid ratios. We applied the index to a San Francisco Bay-Delta dataset of phytoplankton community composition determined by microscopy (1992-present) and HPLC pigment analysis (2011-2014) to explore patterns of phytoplankton food quality along the salinity gradient of this large nutrient-enriched estuary.

Keywords: phytoplankton; fatty acids; EFA; LCEFA; community composition; taxonomy; pigment

Session Title: Food Web Foundations II

High-Throughput Genetic Sequencing Provides Novel Insight into the Cache Slough Complex Food Web

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The Delta's Cache Slough Complex (CSC) is considered key habitat for delta smelt and other native fish. Delta smelt are found year-round in the CSC despite high water temperature, low salinity, and contaminants. These stressors may be offset by a relatively abundant food supply, yet CSC plankton food web interactions are poorly understood compared with other areas of the estuary. In this study, we describe planktonic copepod (Pseudodiaptomus forbesi) feeding patterns using high-throughput genetic sequencing (HTS). This method identifies prey items with high taxonomic specificity, including rare or fragile prey. HTS does not require expertise in plankton taxonomy. The most common phytoplankton prey detected were cyanobacteria (Dolichospermum (=Anabaena) sp. and Synechococcus sp.) and green algae similar to Spirogyra sp. These results indicate that nutritionally deficient cyanobacteria may be an important energy source for copepods. Ciliate protists were the most commonly detected nonphotosynthetic eukaryotic prey. Cryptophytes, diatoms and eustigmatophytes were detected frequently in water samples, but less frequently in copepod guts. Inherent biases of HTS in food web studies (primer bias, gene copy number bias, and overamplification of predator DNA) mean that HTS prey results may not be quantitative in terms of biomass. However, a quantitative analysis (qPCR) could be applied to samples after HTS has been used to identify prey items. The decreasing cost and increasing accessibility of this technology make HTS a valuable tool for food web studies in the Bay-Delta.

Relevance: Food abundance is a key bottom-up control of fish populations. A better understanding of food web interactions in the CSC may guide restoration efforts for delta smelt and other fish.

Keywords: food web; Cache Slough; delta smelt; copepods; genetics

Session Title: Food Web Foundations II

Long-Term Seasonal Trends in the Prey Community of Delta Smelt (*Hypomesus transpacificus*) Within the Sacramento-San Joaquin Delta, California

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Abiotic factors and species introductions can alter food web timing, disrupt life cycles, and change life history expressions and the temporal scale of population dynamics in zooplankton communities. We examined physical, trophic, and zooplankton community dynamics in the San Francisco Estuary, California, a highly altered Mediterranean climate waterway, across a 43-year dataset (1972–2014). Before invasion by the suspension-feeding overbite clam (Potamocorbula amurensis) in the mid-1980s, the estuary demonstrated monomictic thermal mixing in which winter turbidity and cool temperatures contributed to seasonally low productivity, followed by a late-spring-summer clearing phase with warm water and peak phytoplankton blooms that continued into early winter. Following the clam invasion, we observed a shift in peak phytoplankton bloom timing, with peak productivity now occurring in May compared to June prior to the invasion. Peak abundance of several zooplankton taxa (Eurytemora affinis, Pseudodiaptomus, other calanoids, and non-copepods) also shifted to earlier in the season. We present the first evidence of a shift in the timing of peak abundance for zooplankton species that are key prey items of delta smelt (Hypomesus transpacificus), a federally threatened pelagic fish species. These timing shifts may have exacerbated well-documented food limitations of delta smelt due to declines in primary productivity since the invasion of the overbite clam. Future conservation efforts in the estuary should consider measures designed to restore the timing and magnitude of pre-invasion phytoplankton blooms.

Keywords: Primary productivity, Ecological succession, Pelagic Food web, Seasonality

Session Title: Food Web Foundations II