Springtime upwelling conditions drive thiamin-associated microbiomes in the California Current Ecosystem (CCE)

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Abstract

Seasonal upwelling makes the California Current Ecosystem (CCE) one of the most biologically productive ecosystems on Earth. Few studies have measured dissolved concentrations of thiamin (vitamin B_1; B_1), an essential metabolic coenzyme that structures marine microbial communities. To connect thiamin availability with microbial communities in the CCE, we measured both concentrations of dissolved thiamin and its biochemically related moieties (thiamin-related compounds; TRCs) and 16S rRNA gene-based microbial communities during the spring upwelling. Our data revealed significant correlations between TRC concentrations and relative abundances of bacteria, archaea, and eukaryotic algae in depths spanning the mixed layer. During our sampling dates, periods of strong upwelling were associated with lower concentrations of thiamin precursors and breakdown products, while weaker upwelling periods saw relatively high TRC concentrations. These findings suggest that upwelling-driven microbial community changes alter the dissolved pool of TRCs. TRC-associated microbial genera varied in relative abundances based on the chemical and oceanographic characteristics of individual sample stations, independent of sampling latitude. Diatoms, Proteobacteria, Bacteroidota, Verrucomicrobiota, Crenarchaeota, and other taxa of high relative abundances influenced concentrations of thiazole moieties to a larger degree than other TRCs, implicating these compounds as important metabolic currencies to CCE microbial communities. Our data show that upwelling conditions and site-specific chemical and oceanographic factors influence thiamin-related microbiomes. Eastern boundary current ecosystems are disproportionately impacted by climate change, resulting in altered food web diversity and making the study of fine-scale controls on biological productivity in these systems essential.

Background and Methods

- The California Current Ecosystem (CCE) is a biodiverse Eastern Boundary Upwelling System.

- Thiamin (vitamin B_1 or B_1) is a coenzyme required by nearly all life on Earth for anabolic and catabolic central C metabolism. B_1 is synthesized from the thiazole and pyrimidine moieties, cHET and HMP, and is abiotically degraded into HET and AmMP (Figure 7 dissolved pool).

- The TRC dissolved pool (dissolved TRCs; dTRCs) is influenced by communities of bacteria, archaea, and algae. Marine microbial communities are structured by dTRC availability.
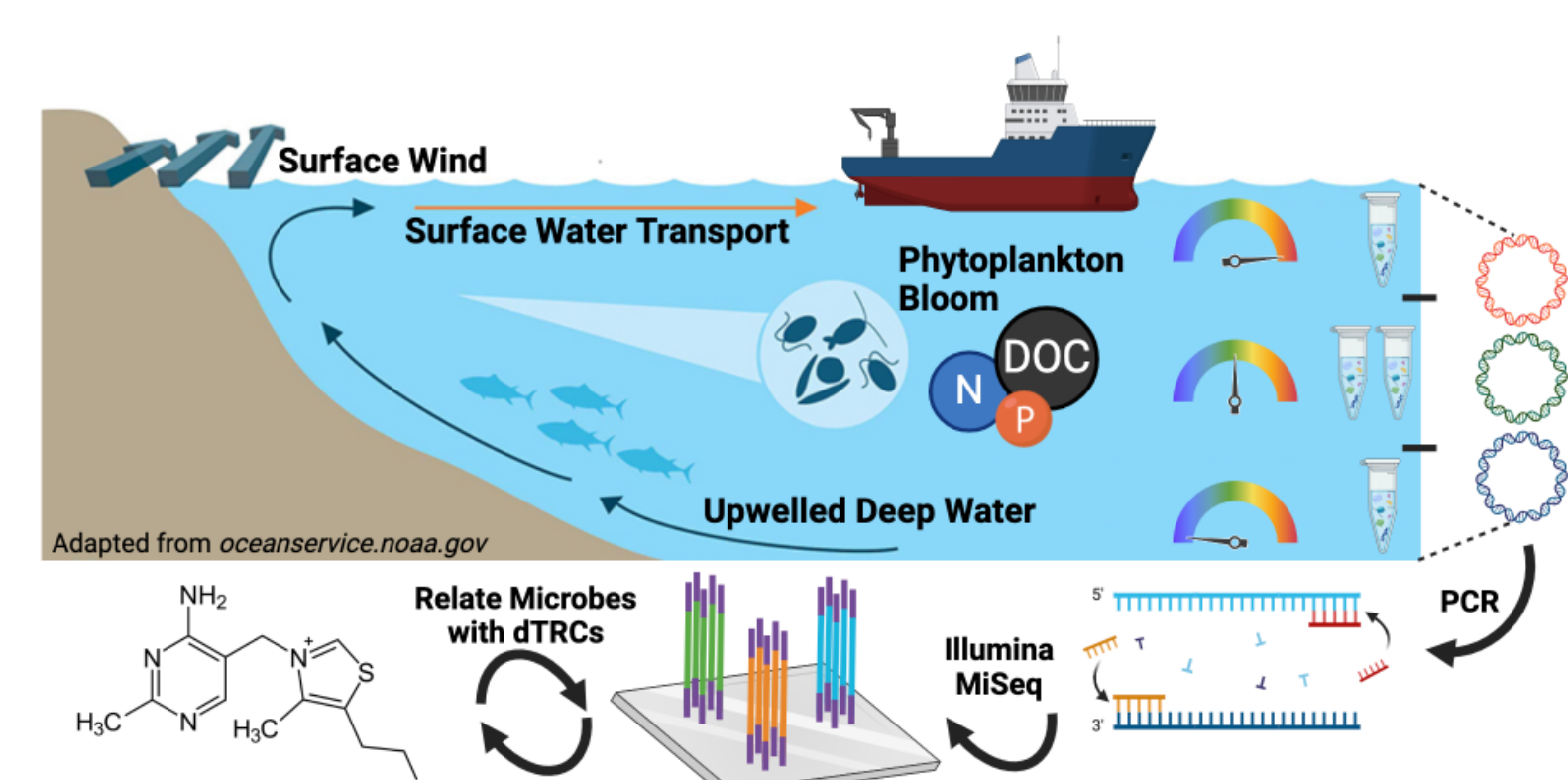

Figure 1: Graphical methods. Simplified depiction of the coastal sampling locations, sample collection, and lab workflow.

Results and Discussion
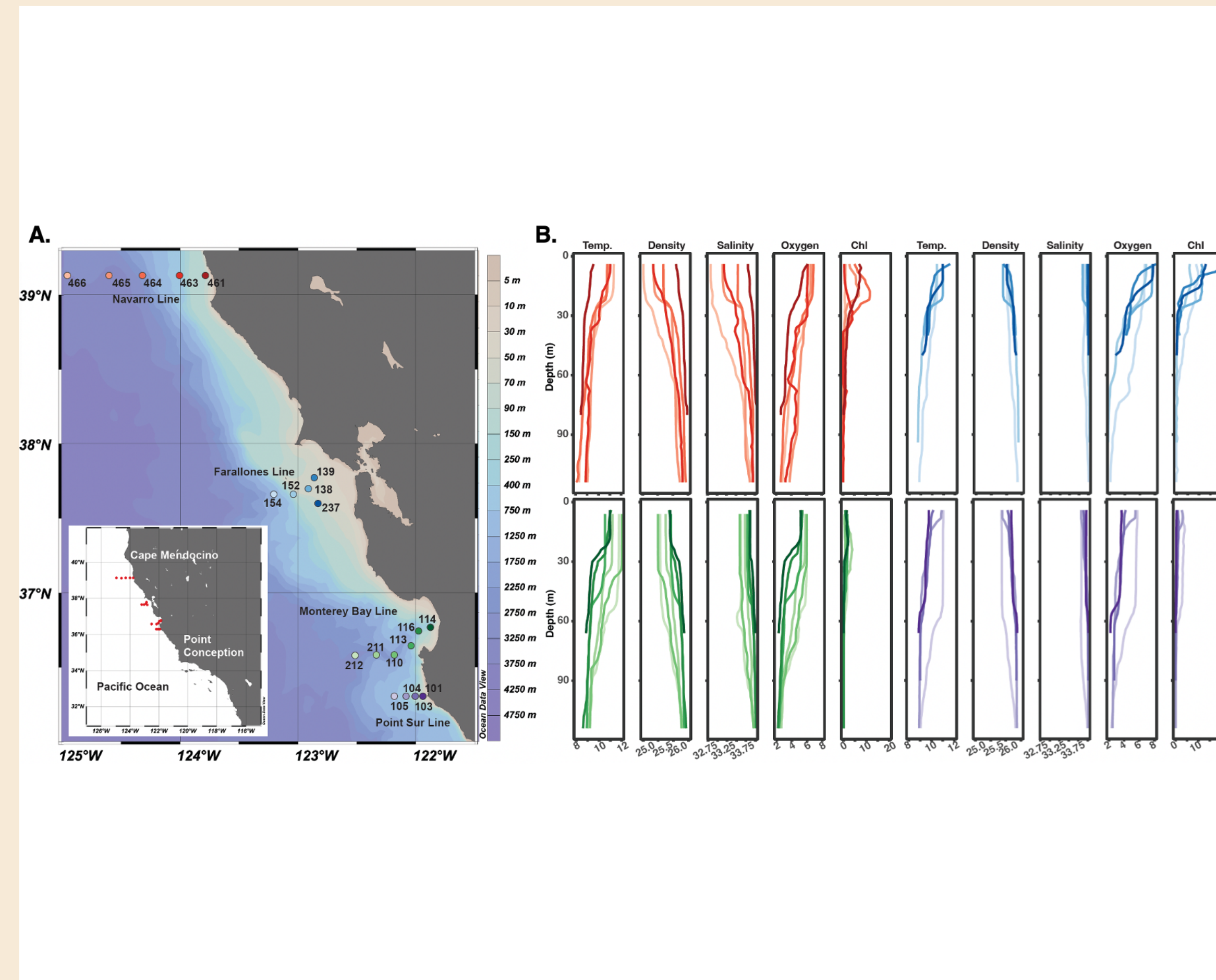
Figure 2: Study region and oceanographic conditions. A. Central CCE sampling locations. Sampling line (horizontal transects) color: red for Navarro (NAV), blue for Farallones (FAR), green for Monterey (MON), and purple for Point Sur (SUR). B. Station profiles of temperature (°C), density (kg•m^{-3}), salinity (PSU), oxygen (ml•L^{-1}), and chlorophyll-*a* (mg•L^{-1}).
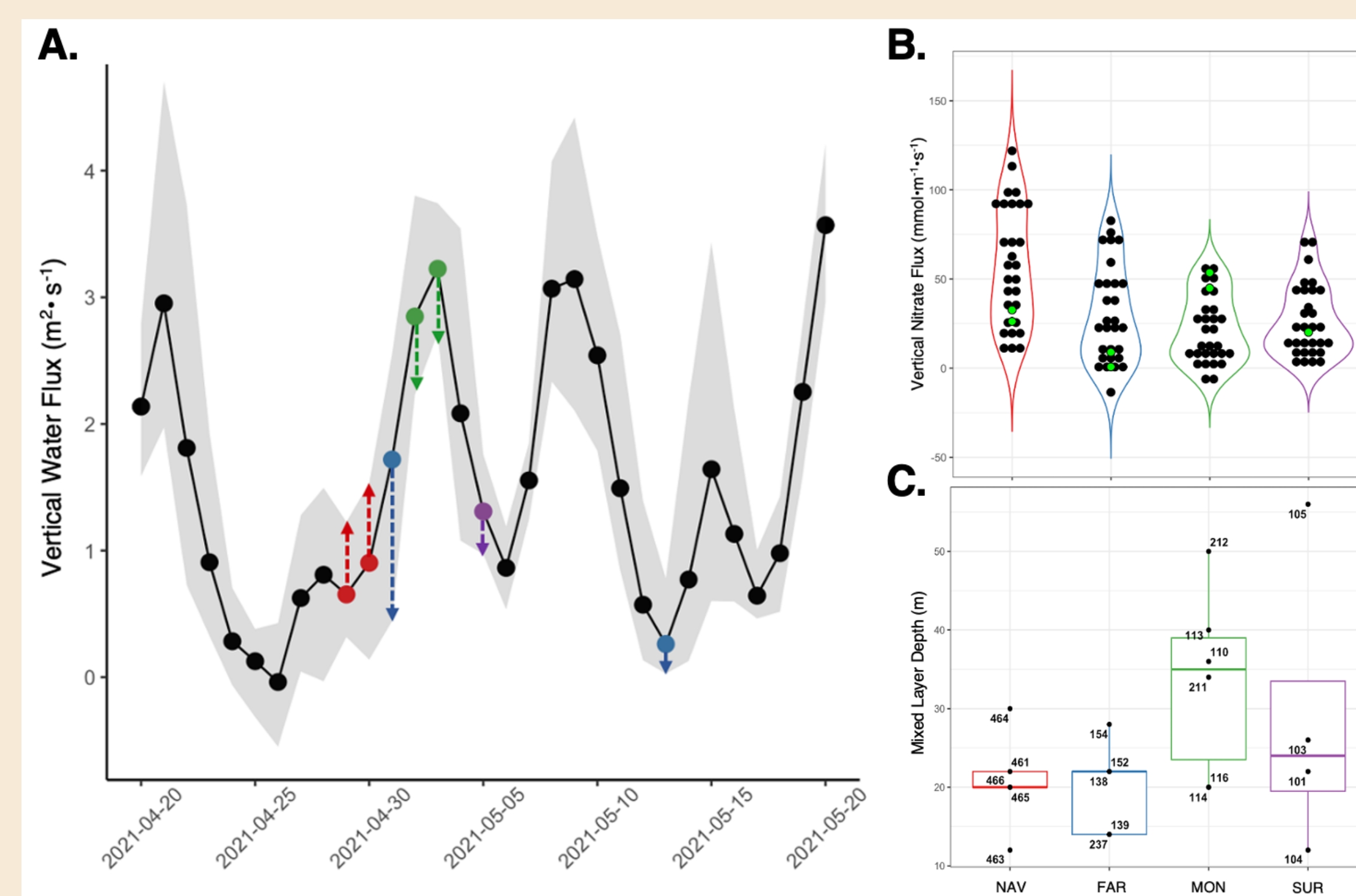

Figure 3: Patterns of upwelling intensity and mixed layer depth in the central CCE during April and May 2021. Daily average A. cumulative upwelling transport index (CUTI) and B. biologically effective upwelling transport index (BEUTI) values. C. Mixed layer depths.
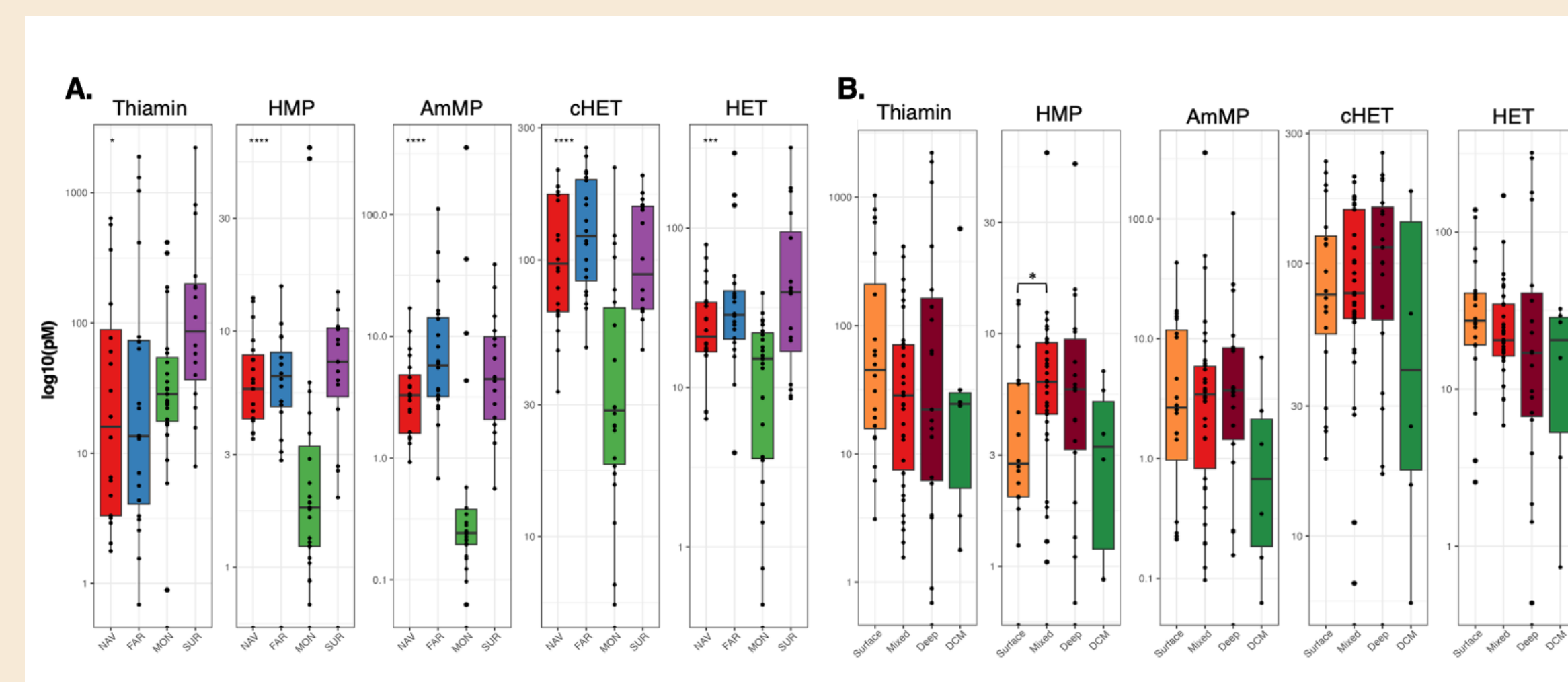

Figure 4: dTRC concentrations by sampling line and depth in the central CCE. dTRC concentrations (pM, log scale) by A. sampling line and B. depth. Thiamin's biosynthetic precursor compounds are cHET and HMP, and its abiotic degradation products are AmMP and HET.

- Microbial communities influence dTRC concentrations in response to (modeled) upwelling, particularly with thiazole compounds.

- Both the compositions and diversity of microbial communities and concentrations of dTRCs differ by upwelling intensity and sampling lines. Microbial communities are influenced by upwelling-related oceanographic properties (Figure 6C).

- The mixing of deep water into the surface layer could place selective pressure on bacteria, archaea, and algae, thereby influencing the thiamin dissolved pool (Figure 7). In a future of intensified upwelling in the CCE with climate change, thiamin-associated microbiomes could increasingly alter dTRC availability to higher trophic levels.

Results and Discussion
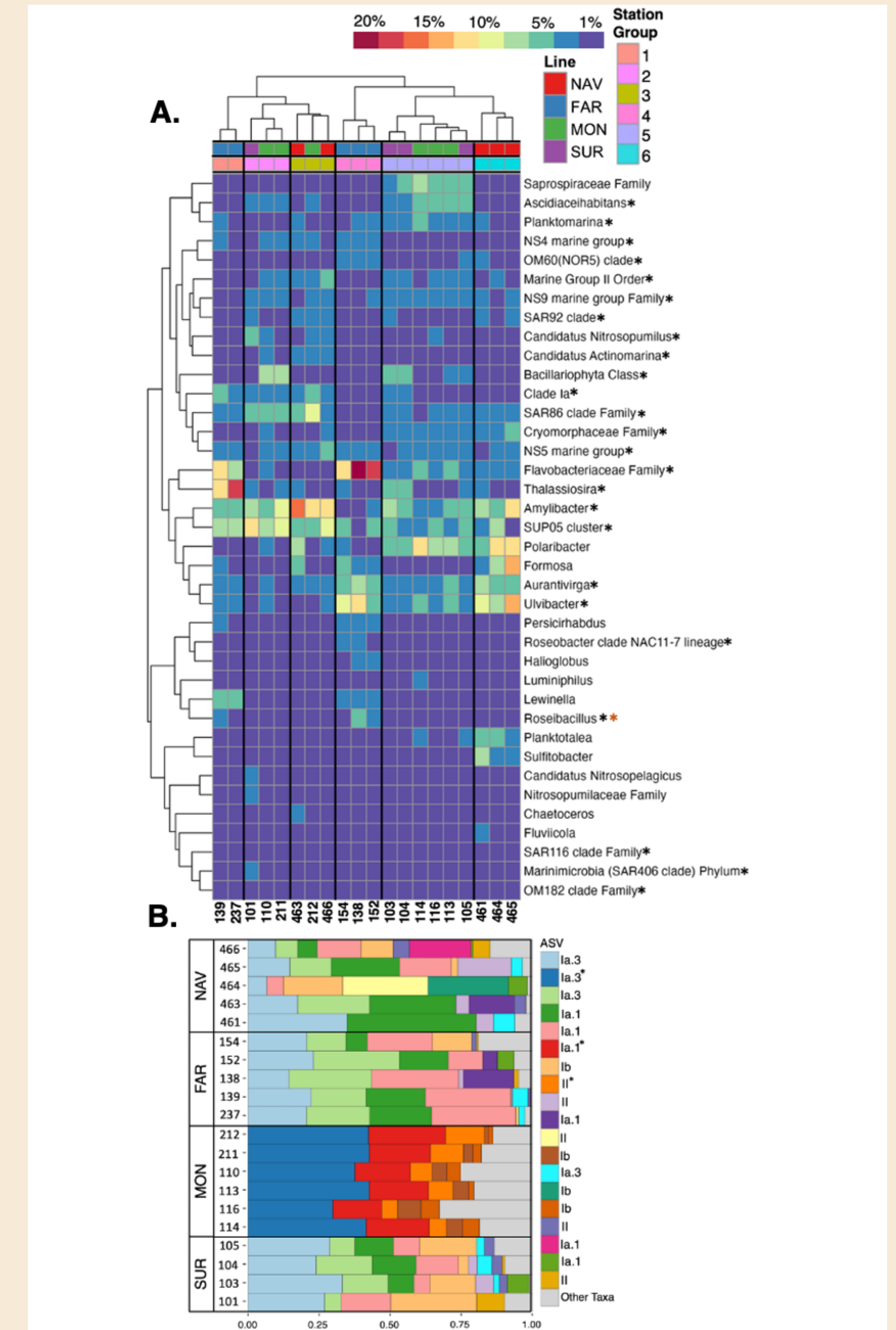
Figure 5: Station relative abundances of taxa. A. Prevalent genera per station. B. SAR11 ASVs and ecotypes (clade Ia). *Differentially abundant with cHET (black) and HET (orange).
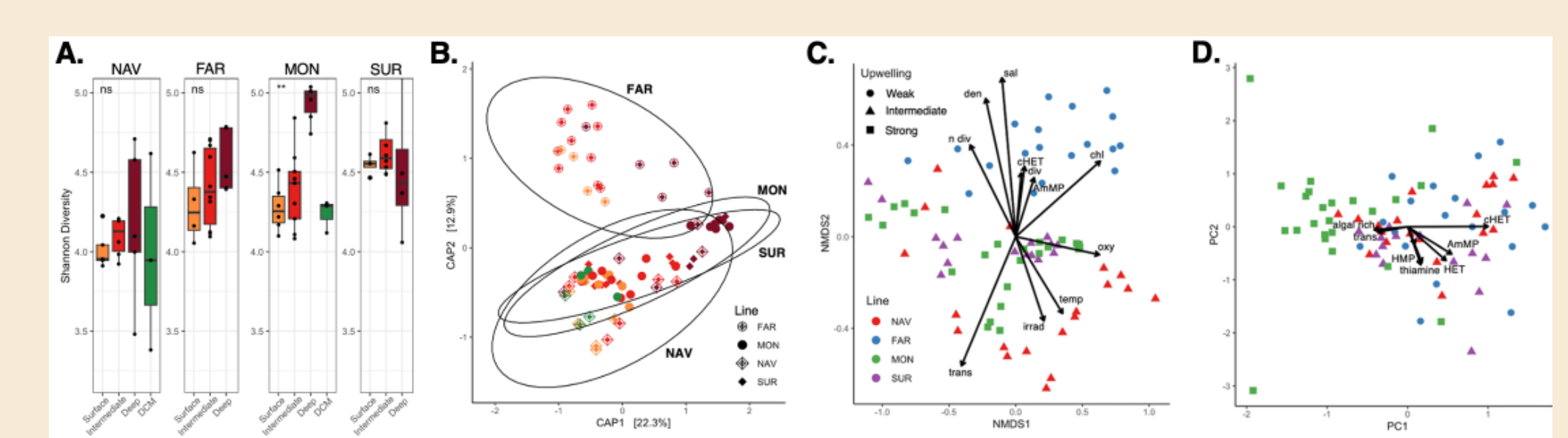
Figure 6: Microbial alpha and beta diversity and dTRC distributions. A. Shannon diversity by sampling line. B. Constrained analysis of principal coordinates (CAP; constrained by sampling depth and line) and C. non-metric multidimensional scaling (NMDS; stress = 0.113) microbial ordinations. D. dTRC principal component analysis.
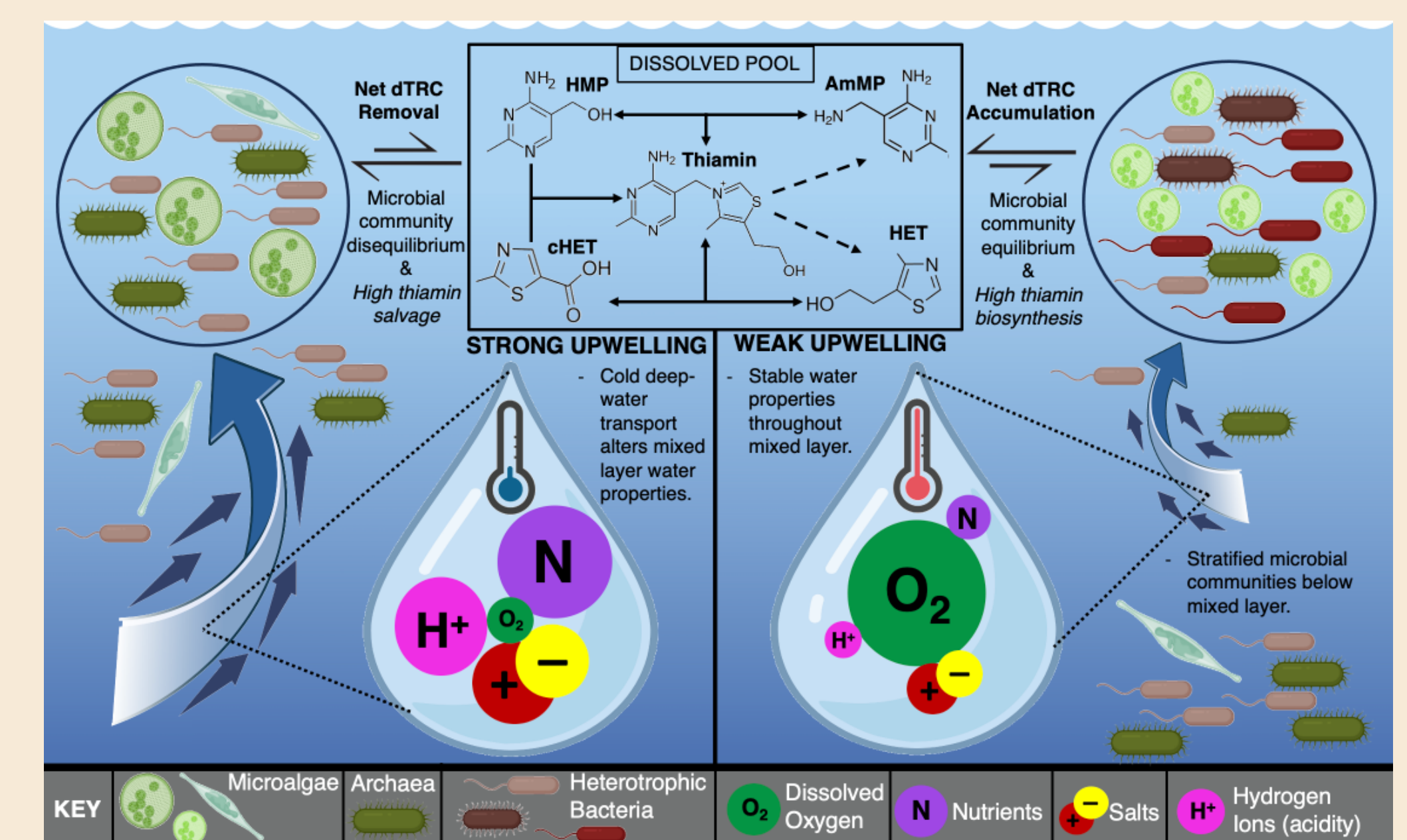
Figure 7: Upwelling conceptual diagram. The influence of microbial communities on surface layer dTRCs. In the dissolved pool, dashed arrows indicate abiotic degradation and solid arrows indicate microbial TRC cycling.

Acknowledgements