

Quantification and modeling of DOC and DON release in marine systems: a study of increasing trophic complexity

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Abstract

The enormous size and reactivity of the pool of dissolved organic matter (DOM) in the oceans makes it a critical component of the global C cycle. The primary source of DOM, encompassing both dissolved organic carbon (DOC) and nitrogen (DON), in marine environments is phytoplankton production. Direct release by metabolically active phytoplankton can be substantial depending on the cells' physiological state. Viruses have been shown to release DOM during viral lysis, but the quantitative significance of this DOM source is unknown. DOM release by micro- and mesozooplankton ingestion and excretion is also a major source of DOM. This proposal seeks to provide a *conceptual and mechanistic* understanding of DOC and DON production via the three processes of direct release, viral lysis, and zooplankton grazing.

We propose to work in three systems, each of which reliably undergoes large changes in phytoplankton biomass: batch cultures of four phytoplankton species; Chesapeake Bay, with cruises comparing spring and summer; and in parcels of recently upwelled water off Monterey Bay as they are transported offshore. The proposed research consists of a culture, field, modeling, and education component.

In culture, we will quantify DOM release directly from phytoplankton in monospecific cultures by measuring DOC and DON production rates in parallel during exponential, stationary, and senescent growth (as regulated by N availability). Viruses and grazers will then be added sequentially to quantitatively determine their effect on production rates and the chemical composition and lability of the DOC and DON produced. Initially, a thorough examination of the effect of filtration on measured production rates will be completed using custom-designed diffuser cells. The culture component will address the following questions:

- *How are the magnitudes of DOC and DON production related during different physiological growth stages?*
- *What is the relative quantitative importance of direct release, viral lysis, and micro- and mesozooplankton grazing to rates of DOC and DON production at different growth stages?*
- *Does the chemical composition of the released DOC and DON change with respect to the growth phase and operative release mechanisms and does the composition relate to the lability?*

In the field, we will measure *in situ* rates of DOC and DON production in parallel experiments and then quantify the effect of grazing on these rates using classic grazer release and dilution studies. We propose a modification of the multiplicity of infection technique combined with a dilution approach to tease apart release that results directly from phytoplankton with that mediated by viral lysis. The following questions will be addressed:

- *What processes are quantitatively most important in the release of DOC and DON in situ – direct release, release via viral lysis, and/or release via grazing?*
- *Does the relative importance of the three mechanisms change under high nutrient conditions (spring and in recently upwelled water) relative to a low nutrient condition (summer and aged upwelled water)?*
- *How is the qualitative composition of in situ DOC and DON modulated by taxonomic composition, growth rates of phytoplankton, viral lysis, and grazing?*

In our modeling effort we will formulate a mechanistic model to simulate the observed variability and fractionation of DOC and DON between LMW and HMW fractions and refractory and labile forms in the batch culture and field experiments. Focusing on systems with large biomass accumulations is ideal for the modeling because the factors that give rise to phytoplankton blooms and the consumer responses that follow are tractable problems. The culture and field components have been designed to provide data on all the relevant processes.

The educational component will consist of two parts. First, we will develop a marine science mini-school to be offered annually to the general public. Second, we will create an interactive computer model of the C cycle that can be used by mini-school lecturers and in public displays at a number of venues. The highly interdisciplinary nature of the proposed research, its use of sophisticated analytical techniques, and its relevance to important societal concerns combine to make it an ideal project for widespread dissemination to the general public.

Understanding the sources, composition and mechanisms that drive DOM formation is critical, because DOM is the largest organic matter pool in the ocean, and small changes in marine DOM can potentially effect a large change in other pools (such as atmospheric CO₂). In the past three decades tremendous advances have been made in our understanding of the cycling of organic matter in the surface ocean. We now have much more accurate estimates of primary productivity, vertical particle flux, and the role(s) of bacteria and viruses within the plankton. However, despite our knowledge of the abundance of viral particles, we have no quantitative appreciation of their role in DOM cycling. Similarly, we still lack a simultaneous assessment of the effects of grazers, bacteria, viruses and phytoplankton on the pools of DOC and DON, as well as of the environmental factors that influence the biological components. The research proposed herein will provide the first simultaneous determination of three biological constraints on DOM production - direct release, viral lysis, and zooplankton grazing. This information will greatly improve our understanding of the controls of this pathway in the C cycle – an understanding essential to generating predictive models that rigorously include the role of DOM in elemental cycling in the ocean.