BIOS-SCOPE - A collaborative program for the study of microbial oceanography in the North Atlantic Subtropical Gyre.

The collective metabolism of remarkably diverse marine microbes governs massive biogeochemical cycles in the global ocean. Integrated scientific approaches that combine genomic data with field measurements of dynamic processes have been a powerful platform for exploring microbial plankton functions and advancing knowledge about oceanic cycling of nutrients, energy and carbon. Driven by a rapid pace of genomic discovery, the scientific community is now honing approaches to assemble a trans-disciplinary knowledge base about complex ocean systems. The greatest progress may lie ahead with new discoveries that surprise us, or alter our vision of how these vast living networks are organized.

At a few sites in the global ocean, resources and opportunity have converged to enable physical, chemical, and biological oceanographers to collect time-series data that are effective for resolving repeating patterns in dynamic processes. Of these sites, the Bermuda Atlantic Time-series Study (BATS) in the northwestern Sargasso Sea has been one of the most important. This station in the subtropical gyre has distinctive characteristics: it rhythmically transitions between cool, productive periods of deep winter mixing, and warm, highly-stratified periods in the summer and autumn when nutrients and productivity decline to extreme lows. The result is that regular annual patterns of spring phytoplankton blooms and photosynthetic production occur (*1, 2*), followed by a transition to a different and highly stratified system of microbial communities that are adapted to ultra-low nutrients surface conditions (*3, 4*). In this dynamic system, dissolved organic matter (DOM) biogeochemistry (*5-7*) and its interactions with microbial processes (Carlson et al. 1996, 2002, 2004), bacterioplankton genomic diversity (*4, 8-11*) and vertically migrating zooplankton dynamics that contribute to redistribution of DOM (*12-14*) have been studied more intensively and for a longer period (> two decades), than at any other ocean site. At BATS, it was first recognized that this annual cycle drives seasonal patterns of semi-labile DOM accumulation (i.e. DOM that turns over on time scales of months to years), redistribution of DOM via mixing (*5, 7*) and DOM removal that fuels microbial production. These DOM dynamics correspond with spatiotemporal patterns in microbial community structure in the euphotic (0-140) and upper mesopelagic zones (140 – 300m) (*4, 10, 15*).

Metabolite release into the environment is a key part of the global carbon cycle. Through photosynthesis and the subsequent release of fixed carbon by exudation, zooplankton grazing or viral lysis, the DOM pool in the world's surface oceans can double in one season. DOM freshly released from cells is quickly altered by heterotrophic metabolism and abiotic chemical reactions until only semi-labile DOM or refractory DOM remains. The rapidly changing fraction is called labile DOM. This fraction includes many metabolic intermediates - such as aldoses, osmolytes and amino acids - that transit through the DOM reservoir as they move between cells. In the field, these molecules often turn over on short time scales - less than a day - and thus their ambient concentrations can be low. Nevertheless, labile compounds can move through the system at high rates and are likely to be important to the various processes that can change within a day (e.g., the diurnal shift between photosynthesis, respiration and grazing rates associated with vertically migrating zooplankton). Although the chemical details of labile DOM turnover remain largely unexplored, enough is known to predict that traffic in these compounds is important to microbial networks, and could play a major role in determining microbial niches and diversity.

Indeed, metabolite production (or modification) could be the basis for synergistic or antagonistic relationships among species within complex metabolic networks in all regions and strata of the ocean. Since all heterotrophs (and most autotrophs) require exogenous carbon substrates for growth or metabolism, identification of the molecules that serve as the currency for microbial interspecies interactions is a critical first step towards unraveling the chemical underpinnings of microbial networks.

The suite of compounds produced or exuded by a given microbe or zooplankton is a function of both its metabolic state and its interactions with other organisms. 'Metabolomics' - the study of the full suite of compounds found in or around a cell - is intimately linked to other 'omics' fields, such as genomics, transcriptomics and proteomics. The detection and quantification of individual metabolites plays a particularly important role in validating cellular functions that have been predicted from genomes, and in discovering new functions that are beyond the range of current gene annotation science. For metabolomics, metabolites are extracted from either inside or outside cells and characterized with a variety of techniques, including mass spectrometry or NMR spectroscopy. The goal of 'untargeted' metabolomics studies is the resolution and identification of new metabolites as indicators of novel metabolic pathways. In contrast, studies that seek to quantify the dynamics of specific metabolites, or 'targeted' metabolomics, use authentic standards and are optimized for the physico-chemical properties of the target compounds. Targeted metabolomics studies are often limited to the few 100s of metabolites associated with core metabolism due to the need for a priori knowledge of metabolites and their structures.

The BATS site perfectly enhances the BIOS-SCOPE vision of understanding carbon cycle transitions by applying time-series statistical methods to biological and chemical data, and applying insights gained from metagenomics and plankton cell biology to discover new carbon cycle transformations.

The BIOS-SCOPE team mission is to achieve a better understanding of ocean food web sources, sinks and transformations of DOM. Advances in knowledge and technology now poise us to investigate the specific mechanisms of DOM incorporation, oxidation and transformation by zooplankton and the distinct microbial plankton communities that have been discovered at BATS.

Importance for the Field: The result of complex processes that produce and consume DOM can be long-term storage of organic matter, or efficient recycling, depending on the chemistry of the DOM molecules, their physical location in the oceans, and the capacity of the microbial community to harvest them as resources (*16*). At BATS, these processes fluctuate seasonally, leading to predictable patterns in the quantity and quality of DOM that accumulates in the water column. Because of its seasonality, and the accumulated background of knowledge from the time-series study, BATS has become a natural laboratory for studying the biological machinery that leads to long-term DOM storage. Today our field is populated with ideas about DOM, many of which need to be tested with experiments and data, and accepted, modified, or discarded to reach a more accurate understanding of complex DOM dynamics. The BIOS-SCOPE team and science plan are focused on achieving a better theoretical grasp of the biological factors controlling DOM transformations in the Western Sargasso Sea.

What causes the balance between DOM production and consumption to shift, leading to DOM accumulation in some environmental circumstances, but its consumption elsewhere? Theories have emerged to explain patterns of DOM oxidation. Rapidly expanding genomic data have shown that planktonic ecosystems are intensely competitive, and that that generalist DOM oxidizers (heterotrophic bacterioplankton) don't fare well in this competition (*11*). Theory supported by sparse examples explains patterns in DOM distributions as a consequence of the costs and benefits of specialized metabolism for the harvesting of DOM resources by oxidative cells. DOM may accumulate not because it is intrinsically resistant to biological uptake and oxidation, but because the "economics" of oxidizing a compound vary depending on the depth, season, and the availability of growth factors. If this theory is correct, then DOM quantity as well as its source, distribution and composition are intricately tied to the seasonality and stratification of heterotrophic microbial plankton communities. To validate these ideas, more information is needed about patterns of variation in DOM composition across the seasons, and the depths spanning the euphotic and aphotic zones. More knowledge is also needed about specialized DOM oxidation activities of very abundant, but as of yet poorly understood, microbial plankton. To test these ideas we need specific examples where DOM chemistry, metagenomic data, and cell biology all support a unified interpretation of a broadly observed environmental process.

Oceanographers recognize the challenge of connecting DOM dynamics to complex cellular processes. This challenge follows a remarkable series of advances in biological oceanography that were enabled by new technologies for genome sequencing and culturing cells. We are now in a period when genomes and cultured cells are available for many of the most abundant microbial plankton lineages. New DOM characterization approaches that utilize advances in mass spectrometry are making it possible to reconstruct a global view of the carbon production and oxidation activities of plankton cells. The convergence of these approaches and technologies is analogous to the development of high throughput gene chip microarrays, which changed biology by providing a perspective of cells as complex systems of interacting nodes. Implementing new technologies for functional genomics at the environmental level is a challenging but a logical path forward links the passing era of expansive genome sequencing to the future, where reconstructing and modeling environmental processes, and extrapolating them to global scales, are important goals.

Goals: The theories presented above are being tested on a technically challenging scientific frontier that merges advances in measuring DOM chemistry and genome analysis with cell biology and field campaigns. The aim of BIOS-SCOPE is to expand knowledge about the BATS ecosystem and gather the new forms of data that are needed to test these ideas. The overarching goal of the BIOS-SCOPE is to form and foster collaborations of cross disciplinary science that utilize a broad suite of genomic, chemical, ecological, and biogeochemical approaches to evaluate microbial process, structure and function on various scales. These scales will range from organism-compound and organism-organism interactions to large biogeochemical patterns on the ecosystem scale. For this purpose we have assembled a cross-disciplinary team including microbial oceanographers (Carlson and Giovannoni), a chemical oceanographer (Kujawinski), biological oceanographer / zooplankton ecologists (Maas and Blanco-Bercial) and microbial bioinformatician (Temperton) with the expertise and technical acuity that are needed to study complex interactions between food web processes, microbes and DOM quantity and quality in the oligotrophic ocean. This scientific team has a vision of harnessing this potential to

produce new discoveries that provide a mechanistic understanding of the carbon cycle and explain the many emergent phenomenon that have yet to be understood.

We posit that with new developments in 'omic' approaches and high resolution mass spectrometry that the time is right to integrate state of the art measurements of DOM chemical composition with microbial and zooplankton community ecology. Linking these data will allow microbial oceanographers to understand pathways of DOM transformation that drive the emergence of distinct bacterioplankton communities in the oceanic water column. Our multi-pronged approach will combine time-series surveys of microbial and zooplankton community, DOM character, structure and targeted proteomics with ship-based and shore-based experiments that test the linkages between specific DOM molecules, their source and microbial community structure and function. We will:

1. Resolve ecosystem and community structure dynamics of microbial (prokaryotic and protistan) and zooplankton populations in the upper 1000 m at BATS.
2. Resolve monthly to seasonal variability of DOM composition using ultrahigh resolution mass spectrometry and high-pressure liquid chromatography (HPLC) approaches.
3. Identify compounds that are important in DOM cycling by integrating measurements of chemical diversity with the study of bacterioplankton genomes.
4. Directly track the flux of ^{13}C-labeled substrates into bacterioplankton biomass using stable isotopic probing (SIP) in experiments with natural communities growing in whole seawater and in experiments with pure cultures growing in sterilized seawater.
5. Track the transformation of the labeled "extracellular compartment" (i.e. DOM) in short-term (SIP) incubations via ultrahigh resolution mass spectrometry and nuclear magnetic resonance spectroscopy
6. Apply mass spectrometry to high throughput metabolic "footprinting" experiments with natural plankton suspensions and microbial cultures isolated from BATS, to measure the DOM "signatures" of cells – both oxidation by heterotrophs, and production (exudation) by phototrophs and zooplankton. These data will be linked to genome features to understand how oxidative specialization evolved, and how it creates links in plankton networks.
7. Combine bioinformatic analyses of existing and new 'omics' datasets with the rich metadata provided by BIOS-SCOPE collaborators in a systems-biology approach to understand carbon flow within this system.

Proposed work Plan

I. Ecosystem Dynamics – The proposed time-series work will be largely conducted in conjunction with the monthly cruises hosted by the BATS program aboard the R/V *Atlantic Explorer* and BIOS-SCOPE annual collaborative cruises.

1. Ecosystem Dynamics and Network Analyses (EDNA): Assimilation of new technologies and discoveries into the BATS data collection will refocus the program on finer scales of community structure and food web dynamics, such as zooplankton activity, that impact the vertical restructuring of DOM pools. Expanding the coverage of diversity estimates from DNA to include protists and mesozooplankton will extend the BATS time-series exploration to microbial interactions and ecosystem dynamics that transcend phylogenetic boundaries.

Time-series depth profiles of microbial and zooplankton community structure will be collected on monthly BATS cruises and with greater resolution on BIOS-SCOPE process cruises. Prokaryotic and protistan DNA (2-4 L) will be collected via Niskin Bottles over ten targeted depths in the euphotic (0-140 m) and the mesopelagic (140 – 1000 m) and concentrated onto 0.2 µm filters. The extraction of prokaryotic DNA and plastids will follow methods established for the BATS site as outlined in (*4, 10*). Illumina sequencing (HiSeq) from the 5' region of archaeal, bacterial, and plastid 16S rRNA genes will be prepared with the general primers (27Fb, 515F and 519R and 926R) (*10, 17-19*). To economize, amplicon sequencing will be multiplexed with barcode sequences, and sequenced to a depth of ~5000 sequences per sample.

Mesozooplankton sampling will be carried out seasonally via a Multiple Opening/Closing Net and Environmental Sensing System (MOCNESS) equipped with 200 µm nets during the mid-day and mid-evening. This sampling pattern will provide a relatively high-resolution description of the deep vertical migrating (DVM) zooplankton community as it allows for vertically stratified sampling of eight depths within the upper 1000 m. Upon retrieval, the catch from each net will be divided into three splits; ½ preserved in ethanol for molecular analysis, ¼th preserved in formalin for morphological counts, and ¼th dried on filter paper for biomass analysis. This effort will be complementary to the monthly analysis of the epipelagic (0 – 200 m) zooplankton community at the BATS site, and in parallel to the classic BATS specific sampling. Amplicon-based metabarcoding will be used for micro and mesozooplankton and will be performed based on the hypervariable V9 region (*20, 21*). The procedure will follow established protocols, and amplicon sequencing will be done on an Illumina™ HiSeq Sequencer. Computational analyses of the micro and macro zooplankton community will be carried out at the BIOS Bioinformatics Cluster.

During the winter and the summer cruises a Reeve net (1 m mouth, 150 µm mesh) will be towed obliquely from 150 m to the surface at the start of each evening when the echo-sounder indicates that the DVM zooplankton have returned to the surface, and late evening (~ 4 am) prior to the descent of the DVM layer. Undamaged live individuals of zooplankton groups of interest will the individually picked and fixed in RNAlater for transcriptomic analyses of the metazoan and associated microbiome.

2. Characterize the molecular composition of marine DOM over depth and time at BATS at various scales of lability and time. Molecular-level variation in DOM composition is virtually unknown, a question that is just now becoming tractable with the application of ultrahigh-resolution FT-MS, and quantitative HPLC. Vertical sampling through the euphotic and upper mesopelagic zones will occur on various time scales; a) diel surveys to address high flux / highly labile compounds; b) monthly to seasonal surveys to address annual variability in labile and semi-labile compounds; and c) interannual surveys to address long-term trends in the accumulation and/or removal of semi-labile DOM. Variability on the different time scales will be used to rank organic molecules by their susceptibility to oxidation by natural microbial plankton communities. Time-series depth profiles of metagenomes and DOM composition will be collected and determined at the BATS site. We will a) characterize DOM composition by LC/FT-MS and LC/TSQ-MS (*22*) and PAD-HPLC (*6*); b) identify semi-labile DOM m/z markers that correlate with community structure of prokaryotes and zooplankton by multivariate statistics; c) determine sources and sinks for these markers by metabolic reconstruction and testing of

cell cultures and natural assemblages for production and consumption; d) document natural patterns of DOM variation associated with hydrographic processes at BATS.

II. Experimental Work: The experimental work described below will be the focus of the BIOS-SCOPE collaborative experiment and process cruises and will be conducted at sea, or in laboratories at BIOS, UCSB, WHOI and OSU.

3. Stable Isotopic Probing (SIP) experiments will be designed to track the sources, chemical transformations, and fates of DOM compounds as they pass through natural microbial communities and pure cultures from OSU's culture collection. These experiments will follow ^{13}C and ^{15}N labeled DOM as it is incorporated into microbial DNA, RNA or phospholipids. The incorporation of the stable isotope macromolecules can be measured by buoyant density centrifugation and/or mass spectrometry, and resolved at fine scales of microbial diversity (*23-26*). Multiplexed Illumina sequencing of the 16S ribosomal RNA gene amplicons from the heavy and light fractions of CsCl density gradients, and the identification of labeled peptides by mass spectrometry (*25*) can identify specific microbial lineages that are assimilating labeled compounds into biomass. These methods don't require a priori selection of specific phylotypes for study, a key advantage over phylogenetically-targeted methods such as autoradiography. We propose to use a combination of SIP, DOM characterization and DOM remineralization experiments to evaluate the metabolic capabilities of the microbial population in the photic and mesopelagic zones at BATS.

Our previous research has shown that "sole carbon source" model, common in microbiology, underestimates the variety of mechanisms at work in complex microbial communities. In the proposed experiments, we will use both simple substrates such as individual model compounds, and complex substrates, such as fresh or "aged" (diagenetically altered) photosynthate, zooplankton exudates and viral lysates. Isotopically-labeled complex substrates will be made by growing and uniformly labeling the organic matter in an automated mass culturing system of relevant phytoplankton species with stable isotopes (*23*). Labeled zooplankton exudate will be generated by feeding them with stable isotopically labeled algal cultures. Initially harvested DOM will be considered "fresh" material of which a portion will be highly labile. We will also generate additional lability fractions of the labeled DOM by molecular size fractionation (semi-labile DOM), solid-phase extraction (recalcitrant/ "humic" material) and with biological "aging" (both semi-labile and recalcitrant). The DOM derived from the various treatments described above will be fully characterized by LC/FT-MS, NMR and PAD-HPLC analysis in order to determine the initial conditions of the labeled DOM to be used in SIP experiments.

4. Identify labeled intermediates in DOM and proteins that are produced and released by microbial processes acting on ^{13}C- and ^{15}N-labeled substrates in the SIP experiments. The theoretical model that guides our experimental designs was changed by the realization that some heterotrophic cells may process organic matter to extract energy and then release the processed DOM at the cell surface. Unbalanced carbon budgets are a major vexation to marine geochemists, who seek to understand oxygen declines that exceed predictions based on measurements of particulate organic carbon (POC) transport and DOC export (*27*). Partial or complete oxidation without assimilation can be studied by merging experiments that track isotopes as they move through the microbial community with methods that also track their movement through the DOM pool.

SIP will be coupled to mass spectrometry to further examine the transformation of isotopically-labeled substrates into protein or DOM fractions on a molecular level. When incubations are conducted with non-labeled controls, proteins or DOM molecules with enriched isotopic values can be easily discerned from their non-labeled counterparts. This information can give important insights into the specific transport proteins used for our different substrates. For DOM, LC/FT-MS provides sufficient resolution to track the isotope-label into individual molecules. These data are coupled to tandem mass spectrometry to identify common structural elements within produced (or consumed) DOM compound classes. These controlled seawater culture experiments will be performed with isolates from OSU culture collection and with ambient bacterioplankton assemblages from surface Sargasso seawater.

6. Identify sources of DOM that are specific to mesozooplankton and determine how microbes respond to these organic compounds using bottle experiments, transcriptomic analysis of bacterial response and metabolomic analyses of zooplankton exudates. For example, experimental data and metabolic reconstruction from genomes support the conclusion that SAR11, the most abundant class of microbial plankton found at BATS, has unique biochemical machinery for oxidizing taurine, an animal metabolite. Concentrations, fluxes, and spatiotemporal patterning of taurine cycling in the oceans have not been studied. How much taurine do mesozooplankton produce? Is taurine just one of a suite of compounds that comprise a mesozooplankton chemical signature? Did specific microbial taxa evolve to use these compounds, and, if so, do zooplankton distributions control this sector of food webs? Which zooplankton compounds aren't oxidized, leading to DOM accumulation?

7. Plankton Cell System Biology: We moved to functional genomics to experimentally study BATS microbial plankton at sea and in controlled laboratory settings. This has been an effective platform for mining discoveries of new phenomena from plankton genomes. Working within an interdisciplinary setting we keep a focus on issues germane to ocean ecosystems, for example our recent discovery of lipid modifications that change phosphorus-to-carbon ratios. Under the auspices of BIOS-SCOPE, DOM oxidation will be studied with metabolic footprinting technology. This technology has the throughput that is needed to broadly characterize the carbon oxidation activity of cells and provide the scale of information appropriate for environmental research. By analogy, there was a time when transcription was studied one gene at a time, but a more comprehensive understanding of cell biology arose when microarray approaches were used to provide global view of gene expression. Our vision is to develop a global perspective on DOM metabolism that is tightly tied to genomes and spatiotemporal patterns in dominant populations of microbial plankton.

8. Bioinformatic integration- High resolution characterization of DOM mechanisms and rates of carbon processing and bacterioplankton-zooplankton interactions will be analyzed in conjunction with legacy and contemporary metagenomic datasets from the BATS site to identify underlying molecular mechanisms, co-occurrence of taxa and functional enrichment that underpin carbon flux. Assembly and annotation of metagenomic datasets by cutting-edge bioinformatic techniques will be used to explore the diversity, seasonality and functional capacity of the uncultured microbial majority, focusing on transportation and metabolism of carbon moieties. Viral sequence space within these metagenomes will be explored to identify correlations between infection events and carbon exchange. Network analyses will characterize metabolic and taxonomic hubs correlated with shifting DOM signatures. This work will provide a two-way intellectual bridge between reductionist science and holistic approaches to understanding complex community interactions. Hypotheses generated through

bioinformatic methods can be tested in model organisms and any experimental findings will be framed within a broad ecosystem context.

9. Synergistic activities with SCOPE-ALOHA. Another important ocean time-series site, Station ALOHA, is located in the subtropical Pacific Ocean near Hawaii and is the home of the Simon's SCOPE program. These two ocean time-series stations, while both located in subtropical oceanic gyres, are uniquely different. As described above, the higher latitude of BATS, and its location at the northern edge of the North Atlantic subtropical gyre, result in deep winter mixing that triggers a seasonal pattern of biogeochemical and biological succession that is distinct from Station ALOHA. In addition, because of the elevated atmospheric deposition of iron in the tropical and subtropical North Atlantic, microbial metabolism drives inorganic phosphorous to ultra-low concentrations compared to Station ALOHA. BATS microbial communities have evolved remarkable adaptations to low phosphorous, for example lipid modifications that lower phosphorous requirements for cell replication. The fundamental physical and chemical differences between BATS and ALOHA are also manifested in the pronounced seasonality of microbial community structure in the northwestern Sargasso Sea. The development of the BIOS-SCOPE program at BATS will provide synergism and a rare opportunity for two research groups to compare and contrast the microbial community structure and function in the context of the differing biogeochemistry and physical processes of the two systems.

BIOS-SCOPE collaborative Team

Blanco-Bercial (BIOS) is a biological oceanographer with expertise in assessing temporal and spatial patterns of marine metazoan using genetic barcoding approaches. He will co-lead the component focused on the variability of vertically migrating zooplankton and will use metagenomics and metatranscriptomic approaches to analyze metabolic potential of migrating metazoan and their associated microbiome.

Carlson (UCSB) is a microbial oceanographer with extensive expertise in the functioning of microbial communities, DOM cycling in marine systems and biogeochemistry of the BATS site. While all PIs will share in the commitments to the success and oversight of the project, Carlson will serve as director of the overall BIOS-SCOPE project. He will oversee overall science plan of the multi-institution project and will coordinate with Drs. Curry, Maas, Blanco-Bercial (BIOS), Giovannoni (OSU), BIOS-SCOPE Investigator Kujawinski (WHOI) and BIOS-SCOPE Fellows (i.e. Temperton yrs 1-2 then TBD) on cross cutting and integrative research, reporting activities and paper writing. He will also directly oversee the UCSB subcontract focused on microbial processing and response to dissolved organic matter variability, SIP experiments and DOM diagenetic characterization. He will participate on cruises and collaborative field experiments. Carlson will also develop synergistic activities with the PI's of the SCOPE project in HI.

Curry (BIOS) is the president and CEO of the Bermuda Institute of Ocean Sciences. He will serve as lead PI and will provide administrative oversight of the project.

Giovannoni (OSU) is a microbial oceanographer with expertise in microbial diversity, bioinformatics, biochemistry, systems biology and cell culture. He will directly oversee the OSU subcontract that is focused on identifying new and significant mechanisms of DOM oxidation in microbial plankton, both in

controlled laboratory experiments and experiments in the field. Giovannoni will coordinate Illumina HiSeq Sequencing efforts for the collaborators. He will collaborate with other BIOS-SCOPE and SCOPE PIs to develop bioinformatics databases and analytical tools for omics data, including amplicon and metagenomic sequence data.

Kujawinski (WHOI) is a chemical oceanographer who applies metabolomics tools to characterize dissolved and cell-associated organic matter. In particular, she integrates chemical data with systems biology tools to understand the underpinnings of microbial consortia and their functions. She will directly oversee the WHOI subcontract focused on the ESI FT MS characterization of DOM and the microbial processing and response to DOM variability and will participate on cruises and collaborative field experiments. She will lead the development of the informatics pipeline and database used to analyzed DOM mass spectral data.

Maas (BIOS) is a biological oceanographer with expertise in physiology of zooplankton and how factors of oxygen, pH, and temperature can affect animal function. She will co-lead the time series collection of migrating zooplankton and the phylogenetic characterization of the micro and macrozooplankton community. She will coordinate experiments with BIOS-SCOPE PIs to determine the ecological interaction between the zooplankton and the prokaryotic community by examining the release of metabolites at various depths and under varying nutrient states and the subsequent response by the microbial community.

Parsons (BIOS) is an associate specialist with expertise in molecular microbial ecology, microscopy and biogeochemistry. In addition to scientific contribution to the BIOS-SCOPE program, Parsons will assist with the logistics of overseeing initial processing and reposition of BIOS-SCOPE samples streams coming from BATS cruises of BIOS-SCOPE collaborator visits. She will assist with experimental set-up and sampling during and after visits. Parsons will help with pre and post cruise and experimental logistics associated with BIOS-SCOPE cruises.

Temperton (Exeter Univ) is a bioinformatician with extensive knowledge of the functional and taxonomic diversity associated with marine microbial communities observed at the BATS site. His research will focus on integrative computational analyses of existing and new multi-'omic datasets (including single-cell genomics) to better understand the interactions of microbial communities and their associated viruses with dissolved organic matter.

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