

Quantifying the carbon export potential of the marine microbial community: coupling of biogenic rates and fluxes with genomics at the ocean surface

SCIENCE GOALS

- I. Examination of the marine microbial community composition and its influence on Net Community Productivity (NCP)
- II. Determine the extent to which members of the marine microbial community are coupled in space and time
- III. Assess the physiological status of phytoplankton and bacteria and its influence on NCP

TEAM MEMBERS

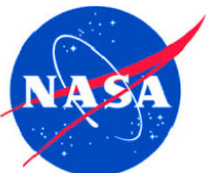
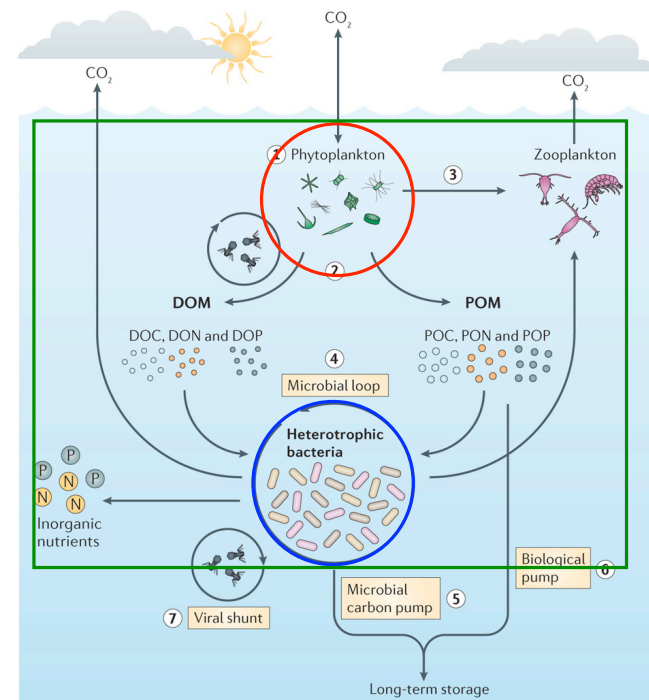
Adrian Marchetti (PI) – UNC

Scott Gifford (co-PI) – UNC

Nicolas Cassar (co-PI) – Duke

Weida Gong (Grad Student) – UNC

Laura Fisch (Grad student) - UNC



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FIELD WORK

Both Ships

- Net community production via Equilibrator Inlet Mass Spectrometry (EIMS) measurements of O_2/Ar

Process Ship

- Size-fractionated new and regenerated production via stable isotope incubations
- Community and bacterial respiration rates via O_2 drawdown
- Plankton community characterization via 18S and 16S rDNA amplicon sequencing
- Quantitative metagenomics and metatranscriptomics via high-throughput sequencing of DNA and RNA

Rates	Net Community Productivity (NCP) = Gross Primary Productivity (GPP) – Community Respiration (CR)		
Methods	1. O_2/Ar	1. ^{13}C incubations	1. O_2 incubations
	2. Calculated from GPP and CR	2. diel O_2/Ar	2. diel O_2/Ar

Table 1. Rate processes measurements and methodology. Measurements will also include $^{15}NO_3$ incubation estimates of new production.

