

**Craig Carlson** reviewed progress on the Oceanic Microbial Observatory, a microbial observatory associated with the Bermuda Atlantic Time Series (BATS) station. The BATS program, on their 200<sup>th</sup> cruise this year, provides the relevant biogeochemical backdrop for this observatory. The work represents a collaborative effort between Carlson's group at UC Santa Barbara, Steve Giovannoni's group at Oregon State University and some of the research staff lead by Rachael Parsons at the Bermuda Biological Station for Research (BBSR). Objectives of this observatory were to 1) identify spatial and temporal patterns in specific bacterioplankton and prokaryotic populations and 2) to initiate experiments to investigate potential linkages between microbial processes, community structure and biogeochemical processes and events (mixing events, changes in nutrient fields, etc.) with an emphasis on discovery. Giovannoni's role has been to bring some of the uncultured bacteria into culture through low-nutrient, high-throughput extinction culturing methods. Giovannoni and Rappe recently succeeded in bringing SAR11 into culture. There are also ongoing outreach efforts geared at education in the form of summer courses at the BBSR – John Heidelberg and Steve Giovannoni offer a course in Marine Genomics and Bob Morris and Craig Carlson offer a course in Marine Microbial Ecology. BATS is located 80 km southeast of the island of Bermuda – in the Northwestern Sargasso Sea and is characterized by seasonal oligotrophy and annual patterns of temperature availability and mixing. Carlson and his colleagues are using the BATS long time series data to provide focus to questions on microbial diversity. Their carbuoy mesocosm experiments wherein deep water was inoculated into surface water media produced interesting trends of significant bacterial production and removal of DOC (3 to 5  $\mu\text{M}$ ). This suggested a physical separation of a zone of DOM production from a zone of DOM remineralization that may be related to the microbial community and the nutrient field present. They are also getting quantitative data using FISH for specific clades of bacteria – SAR11, *Cytophaga* and *Roseobacter* for example. Differences exist– SAR11 makes a major contribution and *Cytophaga* can be up to 10 to 15 % depending on the time of the year and position in the water column. Giovannoni has >2,000 strains of bacteria, many of which have been isolated from the Sargasso Sea, that won't grow on agar – 18 were selected for genomic sequencing by the Moore Foundation.