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Deciphering The Role of Plankton Taxa in Particle Flux

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The sinking of phytoplankton derived particulate organic matter to the deep ocean constitutes an important removal process of atmospheric CO_2 and is termed the biological carbon pump. Understanding the taxon specific connection between phytoplankton communities in the euphotic zone and their contribution to particle flux is a high priority in current oceanographic research and provides a basis to evaluate how carbon export might change in a future ocean. Here we present results from DNA-based molecular studies that investigate the taxonomic composition of cyanobacterial and protist communities retrieved from shallow particle traps in comparison to those living in the euphotic zone. This research has been mainly carried out in the Sargasso Sea at the Bermuda Atlantic Time-series Study site (BATS). Trap material collected at this oligotrophic ocean site reveals a surprisingly high diversity of small, non-mineral ballasted taxa, some of which are over-represented compared to the euphotic zone communities. But the majority of clones in the traps belong to mostly heterotrophic protist taxa. By analyzing the fingerprints of prey DNA in guts and fecal pellets of dominant zooplankton grazers we find that there is a close link between prey utilization and the recovery of those taxa in the traps, showing the importance of fecal pellets in packaging and mediating their flux out of the euphotic zone.