

Impact of lower salinity waters on bacterial heterotrophic production and community structure in the offshore NW Mediterranean Sea.

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We investigated the impact of water masses originating from freshwater input on bacterial heterotrophic metabolism and community structure at an offshore site in the oligotrophic NW Mediterranean Sea in 2007 and 2008. By combining 16S rRNA gene clone libraries and MICRO-CARD-FISH we determined the dominant operational taxonomic units (OTU) and their contribution to bulk abundance and activity in the presence of buoyant water masses characterized by lower salinity (LSW, < 37.9) and compared these with the winter and spring phytoplankton blooms. We demonstrate that organic matter associated with LSW markedly stimulated bacterial heterotrophic production as determined by [³H]-leucine incorporation. The OTUs SAR11-IA, SAR11-IIB, SAR86-I and SAR86-III were dominant in all clone libraries, while the *Roseobacter* clade and the *Bacteroidetes* OTU NorSea72 were more specific to the spring phytoplankton bloom. The relative contribution of these OTUs to leucine incorporation varied between 23% and 69% for SAR11, 2% and 17% for *Roseobacter* and was up to 4% for NorSea72. Together, they accounted for roughly 50% of bulk abundance and leucine incorporation during the four situations investigated. Our results suggest that a few cosmopolitan OTUs respond to different DOM sources in the NW Mediterranean Sea.