

Variability of nitrogen stable isotope in suspended organic matter in waters of the western continental shelf of India and the Mandovi estuary

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First direct evidence for the addition of substantial amount of isotopically light nitrogen by *Trichodesmium* in the western continental shelf of India (WCSI), a region of global significance on account of being the largest natural seasonally-occurring coastal oxygen-deficient zone in the world with large efflux of N₂O to the atmosphere. The results for the WCSI and the Mandovi estuary are summarized in Fig. 1, which reveal significant shifts in $\delta^{15}\text{N}$ of suspended particulate organic matter (SPOM) before and after the onset of the south-west (SW) monsoon.

Discussion of results

The development of *Trichodesmium* blooms significantly lowers the $\delta^{15}\text{N}$ of SPOM during the pre-monsoon season, whereas water-column denitrification makes SPOM enriched in $\delta^{15}\text{N}$ during late SW monsoon. Another important result of this study states that the $\delta^{15}\text{N}$ of SPOM is generally lower than the mean value (7.38‰) for surficial sediments. The $\delta^{15}\text{N}$ of SPOM in the Mandovi estuary also shows significant variation during and after the cessation of SW monsoon. Depletion of $\delta^{15}\text{N}$ in SPOM during the SW monsoon could be preferential utilization of ¹⁴NO₃⁻ by phytoplankton, as has been observed in other NO₃⁻ replete areas, whereas post-monsoon season are characterized by relatively high $\delta^{15}\text{N}$ of SPOM.

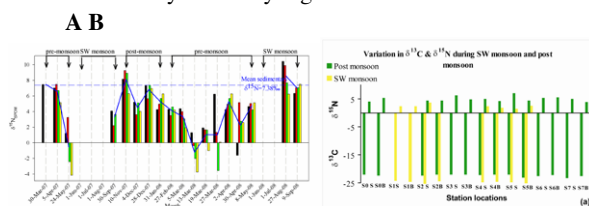


Figure 1: A) Intra-annual variations in $\delta^{15}\text{N}$ of SPOM along the WCSI. B) SW monsoon and post-monsoon changes in the Mandovi estuary.

Isotopic analysis of microarrays to link microbial identity and function

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Most microorganisms remain uncultivated, and typically their ecological roles are inferred from diversity and genomic studies. To directly measure functional roles of uncultivated microbes, we developed Chip-SIP, a high-sensitivity, high-throughput stable isotope probing (SIP [1]) method performed on a phylogenetic microarray. For this approach, we incubate microbial communities with isotopically labeled substrates, hybridize community rRNA to a microarray, and measure isotope incorporation—and therefore substrate use—by secondary ion mass spectrometer imaging (NanoSIMS).

Chip-SIP analysis of an estuarine community quantified amino acid, nucleic acid or fatty acid incorporation by 81 taxa. The resulting resource use profile (Figure 1) demonstrates that some generalist bacteria can incorporate multiple organic substrates while others specialize in 1 or 2 out of 3. We also found that bacterial functional capacity can be decoupled from phylogeny. This approach provides a means to test genomics-generated hypotheses about biogeochemical function in natural environments.

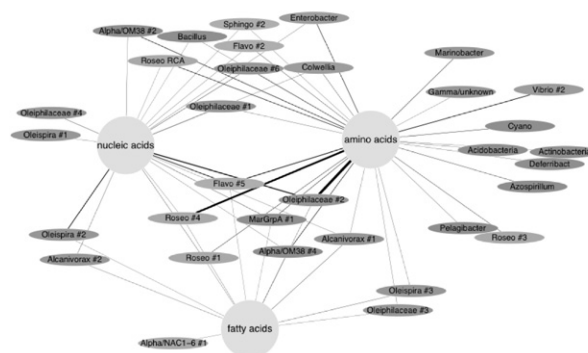


Figure 1: summary network diagram of Chip-SIP analysis of San Francisco Bay, linking substrates (circles) to microbial taxa (ovals). The thickness of the lines is proportional to the amount of substrate incorporated.

[1] Radajewski *et al.* (2000) *Nature* **403**, 646–649.