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## Letter

# Taking metagenomic studies in context

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Today we are witnessing an explosion in interest in marine microbial communities, including Bacteria, Archaea, protists and viruses. Recent advances in genomic science have helped scientists to study microorganisms with much greater precision than ever before and provided new ways to evaluate ecosystem diversity and functional potential. In their article 'Metagenomic marine nitrogen fixation – feast or famine?', published in this issue of *TIM*, Johnston *et al.* have focused on one specific area – the nitrogen cycle – and have attempted to draw conclusions from the lack of particular N<sub>2</sub>-fixing genes in the Sargasso Sea metagenomic data described by us (1). We wish to clarify that a key piece of context from our study [1] is unaccounted for by Johnston *et al.*, and cannot be neglected if accurate conclusions are to be drawn.

The failure of their effort to detect key elements of biological nitrogen fixation in the Sargasso Sea database (SSDB) cannot be taken to infer, as the authors do, the 'patchiness' of the *nif* genes in marine samples. The Sargasso study was not designed to fully elucidate the nitrogen cycle from the Sargasso Sea ecosystem, but

rather to describe the gene complement found within a particular biological size fraction extracted from the filtered samples. Owing to their size, many nitrogen fixing cyanobacteria potentially present in the samples collected would not be represented in the size fraction examined in the Sargasso study, which focused on microbes captured on a 0.1 µm filter after passing through a 0.8 µm prefilter (Table S1 in Ref. [1]). Clearly, many nitrogen-fixing cyanobacteria could well be found on the larger size fractions, which have yet to be analyzed.

Johnston *et al.* rightly point out that metagenomic databases are rich resources leading to intriguing questions, not only of the genes and pathway components identified as being present in particular samples, but also which genes are conspicuously absent. It is crucial, however, to take great care to consider the full context of the samples being analyzed before any conclusions are drawn.

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