IN BRIEF

ENVIRONMENTAL MICROBIOLOGY

Ammonia oxidation kinetics determine niche separation of nitrifying Archaea and Bacteria

Martens-Habbena, W. *et al. Nature* 30 Sep 2009 (doi:10.1038/nature08465)

The aerobic oxidation of ammonia was initially thought to be restricted to ammonia-oxidizing bacteria (AOB). However, over the past 5 years it has become clear that ammonia-oxidizing archaea (AOA) can also oxidize ammonia under aerobic conditions. As AOA are widespread in marine environments, they could potentially make a major contribution to the global nitrogen cycle, but the extent to which AOA can compete with AOB, bacterioplankton and phytoplankton for ammonia was unclear. Martens-Habbena *et al.* report the detailed characterization of the ammonia oxidation kinetics of the mesophilic crenarchaeon *Candidatus* Nitrosopumilus maritimus str. SCM1. The authors conclude that their results provide "unequivocal evidence for the existence of oligotrophic ammonia oxidizers among the Crenarchaeota and their ability to compete for ammonium as [an] energy source in nutrient-deprived oligotrophic oceans."

TECHNIQUES & APPLICATIONS

Tn-seq: high-throughput parallel sequencing for fitness and genetic interaction studies in microorganisms

van Opijnen, T., Bodi, K. L. & Camilli, A. *Nature Methods* **6**, 767–772 (2009)

Tim van Opijnen, Kip Bodi and Andrew Camilli describe a new high-throughput method to determine quantitative genetic interactions in bacteria. The method, which the authors call Tn-seq, is based on the assembly of a saturated, genome-wide *mariner* transposon insertion library. Once the library has been selected under specific test conditions, the change in frequency of each transposon mutant can be determined by massively parallel sequencing of the transposon-flanking regions, giving a measure of the effect of each transposon insertion on fitness. As a proof of concept, the authors defined the network of interactions for five genes in *Streptococcus pneumoniae*, three transcriptional regulators and two ATP-binding cassette transporters. A total of 97 high-confidence interactions were observed, and catabolite control protein A (CcpA) was identified as a master regulator. This method can be used in many different environments and in a wide range of bacteria.

STRUCTURAL BIOLOGY

Universal architecture of bacterial chemoreceptor arrays

Briegel, A. *et al. Proc. Natl Acad. Sci. USA* 23 Sep 2009 (doi:10.1073.pnas.0905181106)

Bacterial chemotaxis is controlled by a sensory transduction system involving transmembrane methyl-accepting chemoreceptors (MCPs), which cluster in large arrays with other chemotaxis proteins at the cell poles. Previous work suggested that the basic functional unit for MCPs is a trimer of dimers, but there were conflicting data on the precise arrangement of MCPs in the arrays. Briegel *et al.* used whole-cell cryo-electron tomography to examine the arrangement of chemoreceptors in 13 species, including *Magnetospirillum magneticum*, *Thermotoga maritima* and *Listeria monocytogenes*. Almost 700 tomograms were examined and it was found that all of the MCPs adopted a highly conserved 12 nm hexagonal array, which is consistent with the functional unit being a trimer of dimers and the evolutionary conservation of this arrangement across diverse bacterial taxa.