IN BRIEF

ENVIRONMENTAL MICROBIOLOGY

Prospecting the rare biosphere

The rare biosphere, which consists of operational taxonomic units (OTUs) that exhibit low relative abundance, has been illuminated in recent years by the application of next-generation sequencing technologies to environmental samples. However, errors introduced in sequencing and PCR steps have hampered exploration of the unknown phylogenetic diversity that is thought to exist in the rare biosphere. To address this, the authors developed a combined bioinformatic and molecular pipeline to interrogate an existing data set of ~6.5 million assembled paired-end Illumina reads of 16S rRNA from an Arctic tundra soil sample. They used targeted bioinformatics followed by PCR amplification and DNA sequencing to retrieve low-abundance OTUs with weak similarity to known organisms. The authors recovered seven lineages, three of which were found to represent extremely divergent taxonomic entities, validating this targeted approach for use in exploring the rare biosphere.

ORIGINAL RESEARCH PAPER Lynch, M. D. J. *et al.* Targeted recovery of novel phylogenetic diversity from next-generation sequence data. *ISME J.* 12 Jul 2012 (doi:10.1038/ismej.2012.50)

BACTERIAL PHYSIOLOGY

There were never such devoted sisters

In eukaryotic cells, sister chromatid cohesion (SCC) keeps newly replicated chromosomes tightly associated until the onset of mitosis, ensuring high-fidelity chromosome segregation and repair of DNA damage. In bacteria, molecular evidence for physical SCC had been lacking, although fluorescence imaging had demonstrated a short period of colocalization for newly duplicated loci. Lesterlin *et al.* set up a recombination-based system that probed the ability of *Escherichia coli* sister chromatids to interact physically. They found that, following their replication, sister loci were consistently involved in a cohesion step that lasted 10–32 minutes. Importantly, factors that are known to reduce the colocalization of sister loci in fluorescence assays had no effect on cohesion, suggesting that the two phenomena are distinct. The authors propose that cohesion ensures the availability of the sister chromatid for repair of damage to newly synthesized DNA and may also help to control the timing of chromosome segregation.

ORIGINAL RESEARCH PAPER Lesterlin, C. *et al.* Sister chromatid interactions in bacteria revealed by a site-specific recombination assay. *EMBO J.* 20 Jul 2012 (doi:10.1038/emboj.2012.194)

BACTERIAL GENOMICS

Connecting genotypes and phenotypes

Given the large fraction of genes of unknown function that is found in most sequenced genomes, developing high-throughput approaches to assign genotypes to a particular phenotype is a priority. One approach involves determining the effect of a defined environmental condition on growth rate and fitness for single-gene-knockout libraries; however, such genome-wide libraries are available for only a handful of organisms. These authors instead used their recently developed Tn-seq method to generate a detailed genotype–phenotype map of the pathogen *Streptococcus pneumoniae*. They measured the fitness of mutant libraries in 17 different *in vitro* conditions and two *in vivo* environments in mice. Using this approach, they uncovered leads for gene function and antibiotic action, and correlated *in vitro* stress conditions with *in vivo* colonization and disease states.

ORIGINAL RESEARCH PAPER van Opijnen, T. *et al.* A fine scale phenotype-genotype virulence map of a bacterial pathogen. *Genome Res.* 23 Jul 2012 (doi:10.1101/gr.137430.112)