IN BRIEF

ARCHAEAL GENETICS

Increasing diversity

Diversity-generating retroelements (DGRs) facilitate the rapid diversification of DNA sequences through a process involving reverse transcription and retrohoming, which generates multiple variants of a target gene. To date, DGRs have only been identified in bacteria and bacteriophages, but Paul *et al.* now report the discovery of archaeal DGRs. Analysis of viral metagenomes obtained from methane seep sediments revealed a putative archaeal virus that encodes a complete and active DGR, the target gene of which shared structural homology with a tail fibre protein, suggesting that the DGR might have a role in generating alternative tail fibres to possibly expand host tropism. The authors also identified multiple DGRs in the genomes of two uncultivated subterranean Nanoarchaeota, which suggests that DGRs might be prevalent in archaea and might confer selective advantages in subsurface environments.

ORIGINAL RESEARCH PAPER Paul, B. G. *et al.* Targeted diversity generation by intraterrestrial archaea and archaeal viruses. *Nature Commun.* http://dx.doi.org/10.1038/ncomms7585 (2015)

STRUCTURAL BIOLOGY

Where to make the cut

The CRISPR–Cas system is an archaeal and bacterial adaptive immune system that provides sequence-specific defence against foreign nucleic acids. Whereas type I and type II systems recognize and cleave double-stranded DNA, the type III complex (known as Cmr) targets single-stranded RNA (ssRNA), and comprises six proteins and a CRISPR RNA (crRNA) that is complementary to target ssRNAs. Taylor *et al.* used cryo-electron microscopy to solve the structure of the intact Cmr complex of *Thermus thermophilus* in both the absence and presence of a target ssRNA. The structures showed that the Cmr–crRNA complex adopts a capsule-like structure with a double-helical core comprising Cmr4 and Cmr5 subunits capped by Cmr2–Cmr3 and Cmr1–Cmr6 heterodimers. Following binding to ssRNA, the complex undergoes conformational changes to accommodate the crRNA–target ssRNA duplex, and the thumb-like β-hairpin domains of Cmr4 intercalate between segments of the duplex, which facilitates target cleavage at six nucleotide intervals.

ORIGINAL RESEARCH PAPER Taylor, D. W. *et al.* Structures of the CRISPR–Cmr complex reveal mode of RNA target positioning. *Science* http://dx.doi.org/10.1126/science.aaa4535 (2015)

BACTERIAL GENETICS

Pneumococci switch it up

Streptococcus pneumoniae isolates express one of more than 90 polysaccharide capsule variants (known as serotypes, which can be further classified into serogroups) that are the target of current vaccines. However, bacteria can change their serotype through recombination to evade vaccine-induced immunity. Croucher *et al.* assessed whether patterns in serotype switching occur by examining a collection of 616 whole-genome pneumococcal sequences that were collected following routine vaccination. They found an increased rate of within-serogroup switching than that expected by chance, which could not be fully explained by more frequent recombination, genetic epistasis or bacterial metabolism. These data provide novel insight into vaccine-induced bacterial evolution, but further studies are required to identify the determinants of within-serogroup switching.

ORIGINAL RESEARCH PAPER Croucher, N. J. *et al.* Selective and genetic constraints on Pneumococcal serotype switching. *PLoS Genet.* http://dx.doi.org/10.1371/journal.pgen.1005095 (2015)