IN BRIEF

BACTERIAL EVOLUTION

An intriguing new bacterial phylum

Metagenomic surveys have identified uncultivated microbial species whose genomes are predicted to correspond to ultra-small cell sizes. In a new study, Brown *et al.* describe the genomes of 797 ultra-small bacteria obtained by metagenomic sequencing of 0.2 µm filtrates from aquifier samples. The genomes coalesced into ~35 candidate phyla, which the authors propose represent a 'candidate phyla radiation (CPR)' of common origin that may comprise more than 15% of the bacterial domain. CPR genomes have several unusual features, including in ribosomal genes: all genomes lack the gene for ribosome protein L30 (rpL30); one-third of the genomes have a self-splicing intron and/or open reading frame insertion in the 16S rRNA gene; and some of the genomes do not encode rpL1 or rpL9, which were thought to be universal in bacteria.

ORIGINAL RESEARCH PAPER Brown, C. T. *et al.* Unusual biology across a group comprising more than 15% of domain Bacteria. *Nature* http://dx.doi.org/10.1038/nature14486 (2015)

STRUCTURAL BIOLOGY

CRISPR preorders for Cas

In type II CRISPR–Cas adaptive immunity systems, a CRISPR RNA (crRNA) forms a hybrid structure with a *trans*-activating crRNA (tracrRNA) that, together with recognition of a protospacer adjacent motif (PAM), guides the Cas9 endonuclease protein to foreign DNA. Jiang *et al.* solved a 2.9 Å crystal structure of *Streptococcus pyogenes* Cas9 in complex with a synthetic guide RNA (sgRNA; a crRNA–tracrRNA fusion). sgRNA binding induced several conformational changes in Cas9; notably, the PAM-interacting domain, which is disordered in the apo form of Cas9, adopted a structured conformation that allowed recognition of PAM. Within the sgRNA itself, the 'seed' sequence, which initiates target binding, had an A-form conformation that favours hybridization with DNA. Together, these findings show how the type II CRISPR–Cas complex is preorganized prior to making contact with target DNA.

ORIGINAL RESEARCH PAPER Jiang, F. *et al.* A Cas9–guide RNA complex preorganized for target DNA recognition. *Science* **348**, 1477–1481 (2015)

TECHNIQUES & APPLICATIONS

A first genome assembly for nanopore sequencing

The 'MinION' nanopore sequencer works by applying an ionic current across an electrically resistant membrane permeabilized by protein nanopores. The sequence of DNA molecules passing through each nanopore is determined by measuring changes to this current. Nanopore sequencers can vastly increase the permissible length of input DNA and remove the need for DNA amplification; however, MinION has an error rate of ~20% that calls for the development of error correction methods. Using DNA from *Escherichia coli* K-12 MG1655, Loman *et al.* now report the first genome assembly to be based solely on MinION data using a bioinformatics pipeline that reduced the error rate to ~0.5%. First, errors were corrected using the consensus from iterative multiple alignments of overlapping sequence reads; next, the corrected reads were assembled into a genome; finally, the sequence was further corrected by comparison with raw electric current data from MinION using Nanopolish software. The resulting complete *E. coli* genome assembly is a milestone for nanopore sequencing.

ORIGINAL RESEARCH PAPER Loman, N. J., Quick J. & Simpson J. T. A complete bacterial genome assembled *de novo* using only nanopore sequencing data. *Nat. Methods* http://dx.doi.org/10.1038/nmeth.3444 (2015)