

## IN BRIEF

**▣ VIRAL EVOLUTION****Two viruses, one capsid**

Viruses can explore the limits of genome minimalism by exploiting other viruses. For example, satellite viruses rely on the polymerase of a helper virus for replication. Zhang *et al.* describe a capsidless single-stranded RNA (ssRNA) virus, yado-kari virus 1 (YkV1), that is *trans*-encapsidated by a co-infecting double-stranded RNA (dsRNA) virus, yado-nushi virus 1 (YnV1). YkV1 has a single protein, an RNA-dependent RNA polymerase (RdRp), whereas YnV1 has both an RdRp and a capsid protein. Although the YkV1–YnV1 interaction shares similarities with helper–satellite systems and the other known example of *trans*-encapsidation, it represents a novel lifestyle in important respects: YkV1 and YnV1 have different genome types; replication occurs inside the *trans*-capsid; and the interaction is cooperative, as YkV1 boosts YnV1 production. The authors speculate that YkV1 is an evolutionary intermediate destined to become an independent dsRNA or ssRNA virus.

**ORIGINAL ARTICLE** Zhang, R. *et al.* A capsidless ssRNA virus hosted by an unrelated dsRNA virus. *Nat. Microbiol.* <http://dx.doi.org/nmicrobiol.2015.1> (2016)

**▣ STRUCTURAL BIOLOGY****A close-up of the chaperone–usher pilus**

Chaperone–usher pili are found on many bacterial pathogens; for example, in uropathogenic *Escherichia coli*, they are involved in adhesion to host tissues and biofilm formation. Hospenthal *et al.* now provide a detailed look at the composition of the pilus rod from individual subunits in a 3.8 Å resolution cryoelectron microscopy reconstruction. Each subunit interacts with five preceding and five succeeding subunits, forming the helical rod. Interestingly, almost half of the surface area of each subunit contacts other subunits and mutations in central positions of these contacting interfaces impair rod formation. Amino-terminal extensions, 10–20 residues long, provide strong hydrophobic interactions between neighbouring subunits. Furthermore, the subunits also interface through weak polar interactions, in particular between subunits not directly next to each other. This combination of strong and weak interactions enables partial uncoiling of the rod — for example, to withstand the shear forces of urinary flow — while retaining the structural integrity needed to keep the bacteria attached.

**ORIGINAL ARTICLE** Hospenthal, M. K. *et al.* Structure of a chaperone–usher pilus reveals the molecular basis of rod uncoiling. *Cell* <http://dx.doi.org/10.1016/j.cell.2015.11.049> (2015)

**▣ CELLULAR MICROBIOLOGY****A novel family of bacterial protein deacetylases**

Post-translational modifications, such as protein acetylation, are important for the regulation of protein function. Protein acetylation is widespread in *Escherichia coli*, but so far only one deacetylase, CobB, has been identified. To find new deacetylases, Tu, Guo and Chen *et al.* developed a ‘clip-chip’ assay, in which proteins with potential enzymatic activity are arrayed on a glass slide and clipped to a slide with substrate. The serine hydrolase YcgC mediated the loss of acetylation of several substrates, which were distinct from those substrates targeted by CobB. YcgC homologues have been found in other bacteria and a selection of these homologues were tested *in vivo*, confirming their deacetylase activity. Thus, YcgC and its homologues represent a new family of deacetylases in bacteria and a new type of deacetylase as none of the previously identified enzymes are serine hydrolases.

**ORIGINAL ARTICLE** Tu, S., Guo, S. J., Chen, C. S. *et al.* YcgC represents a new protein deacetylase family in prokaryotes. *eLife* **4**, e05322 (2015)