IN BRIEF

STRUCTURAL BIOLOGY

T6SS cases its own tail

The bacterial type VI secretion system (T6SS) is a nanomachine that punctures the membranes of competing bacteria and, during pathogenesis, those of host cells. In addition to the tail, which is composed of a contractile sheath and a tipped arrow that punctures the membrane of the prey cell, T6SS function relies on the TssJ–TssL–TssM membrane complex, which is an assembly point and anchor for the tail. Now, Durand *et al.* describe the structure of the TssJ–TssL–TssM complex from *Escherichia coli* at 11.6 Å resolution. 10 copies of each protein are arranged with fivefold symmetry: in the periplasm, 10 pillars (TssJ and TssM) surround a 15–20 Å channel and are connected to 10 arches (TssM); these arches extend to a base (TssM and TssL) located in the inner membrane and the cytoplasm. The authors propose a mechanism of action in which the inner TssM pillars are pushed outwards to create a larger ring that accomodates the tail during secretion; this would protect the membrane of the attacking cell, which might otherwise be punctured by the contraction of the tail.

ORIGINAL RESEARCH PAPER Durand, E. *et al.* Biogenesis and structure of a type VI secretion membrane core complex. *Nature* http://dx.doi.org/10.1038/nature14667 (2015)

MICROBIOME

An encrypted growth signature

Most metagenomic analysis methods are based on the relative abundance of a marker gene or of sets of genes in functional pathways. However, these methods offer a static view of microbial composition and provide no information on growth dynamics. Korem *et al.* devised a new approach that measures the number of copies of a sequence at each genomic site for each species in a metagenome. For most bacterial species, a single peak and a single trough are produced, corresponding to the replication fork and replication terminus; the ratio of the two is a proxy for growth rate, as confirmed by a wide range of *in vitro* and *in vivo* measurements. Remarkably, application of the method to human faecal datasets revealed new links between bacterial growth rates, rather than composition, and type 2 diabetes, Crohn disease and ulcerative colitis.

ORIGINAL RESEARCH PAPER Korem, T. *et al.* Growth dynamics of gut microbiota in health and disease inferred from single metagenomic samples. *Science* http://dx.doi.org/10.1126/science.aac4812 (2015)

BACTERIAL GENOMICS

Evolution of hypervirulence in *Klebsiella*

Hypervirulent *Klebsiella pneumoniae* is a globally emerging pathogen that causes pyogenic liver abscesses. Hypervirulent strains are restricted to capsular serotypes K1 and K2 and are particularly associated with the clonal complex K1 CC23. To understand the evolution of hypervirulence, Struve *et al.* sequenced the genomes of 30 hypervirulent isolates and 35 non-hypervirulent isolates. A phylogenomic analysis indicated that CC23 isolates had undergone clonal expansion from a recent ancestor. Furthermore, several elements that may be associated with hypervirulence were identified, including a large virulence plasmid only present in hypervirulent strains. The virulence factors encoded by the plasmid include RmpA, a regulator of capsule production, and the siderophores aerobactin and salmochelin. Unique to the CC23 isolates was a recently acquired genomic island encoding the toxins microcin E492 and colibactin and the siderophore yersiniabactin.

ORIGINAL RESEARCH PAPER Struve, C. *et al.* Mapping the evolution of hypervirulent *Klebsiella pneumoniae*. *mBio* **6**, e00630-15 (2015)