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IN BRIEF

ANTIMICROBIALS

Pump it out

The tripartite efflux pump CmeABC is the most important efflux system in *Campylobacter* spp. that confers multidrug resistance. Yao, Shen *et al.* report the identification of a CmeABC variant that exhibits enhanced efflux function. This variant, termed resistance-enhancing CmeABC (RE-CmeABC), was more potent in excreting several antibiotics, including florfenicol and fluoroquinolones, which is probably because of the overexpression and sequence variation of RE-CmeABC. Structural modelling suggested that altered antibiotic-binding kinetics enhance the function of the inner membrane transporter CmeB. Moreover, genotyping analysis implied that clonal expansion and horizontal transmission were involved in the spread of this variant. Thus, the acquisition of a functionally enhanced efflux pump provides an efficient means for bacterial adaptation to selective pressure by antibiotics.

ORIGINAL ARTICLE Yao, H., Shen, Z. *et al.* Emergence of a potent multidrug efflux pump variant that enhances *Campylobacter* resistance to multiple antibiotics. *mBio* **7**, e01543-16 (2016)

BACTERIAL PATHOGENESIS

Spirochete spreading

The ability of *Treponema pallidum* to disseminate throughout the host and exit from the vasculature is crucial to its pathogenesis. This process is governed by *T. pallidum* proteins, including TP0751 (also known as pallilysin), that mediate attachment to the host extracellular matrix (ECM). However, the molecular mechanisms that underlie TP0751–ECM interactions are incompletely understood. Parker, Houston *et al.* solved the crystal structure of TP0751 to a resolution of 2.15 Å and reported that TP0751 adopts an eight-stranded β-barrel-containing lipocalin structure. Using a peptide library that represents the full TP0751 sequence they showed that binding to host ECM components was mediated by the lipocalin domain. The TP0751 ECM-binding peptides could inhibit the adhesion of a TP0751-expressing *Borrelia burgdorferi* strain to host cells. Thus, targeting defined regions of TP0751 could control the dissemination of *T. pallidum*.

ORIGINAL ARTICLE Parker, M. L., Houston, S. *et al.* The structure of *Treponema pallidum* Tp0751 (pallilysin) reveals a non-canonical lipocalin fold that mediates adhesion to extracellular matrix components and interactions with host cells. *PLoS Pathog.* **12**, e1005919 (2016)

ARCHAEAL GENOMICS

Divergent methanogenic archaea

Methanogenic anaerobic archaea produce the largest amount of methane on Earth. Methane metabolism was thought to originate early in the evolution of the phylum Euryarchaeota, a notion that was challenged following the discovery of putative methane metabolism in the archaeal phylum Bathyarchaeota. Vanwonterghem *et al.* now report five near-complete genomes from population genomes that were recovered from anoxic environments with high methane flux. These genomes encode methyl-coenzyme M reductase genes that are divergent from known sequences, and the authors suggest that these archaea belong to a new phylum, which they term Verstraetearchaeota. Metabolic reconstruction revealed the presence of key genes that are associated with methylotrophic methanogenesis and fermentation processes.

ORIGINAL ARTICLE Vanwonterghem, I. *et al.* Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. *Nat. Microbiol.* http://dx.doi.org/10.1038/NMICROBIOL.2016.170 (2016)