

IN BRIEF

➔ ANTIMICROBIALS

The central role of lipids in daptomycin action

Daptomycin is a last-resort antibiotic that is used against resistant bacteria, such as methicillin-resistant *Staphylococcus aureus* (MRSA). Although it is a membrane-targeting antibiotic, its exact mechanism of action was unknown. Müller et al. used *Bacillus subtilis* to determine the effects of daptomycin. They observed that fluorescently labelled daptomycin colocalized with a lipid-mimicking dye that specifically stains membrane regions that contain many fluid lipids. This interaction decreased membrane fluidity, which led to the detachment of enzymes that are responsible for cell wall and lipid synthesis. In contrast to the role of lipid binding in the activity of daptomycin, Pader et al. showed that bacteria can also take advantage of this mechanism for resistance. The authors found that *S. aureus* sheds phospholipids that absorb daptomycin before it can target the bacterial membrane. However, this resistance mechanism can be inactivated either by co-treatment with oxacillin or in strains that also secrete phenol-soluble modulins (PSMs), which have surfactant properties and disrupt lipid binding.

ORIGINAL ARTICLES Müller, A. et al. Daptomycin inhibits cell envelope synthesis by interfering with fluid membrane microdomains. *Proc. Natl Acad. Sci. USA* <http://dx.doi.org/10.1073/pnas.1611173113> (2016) | Pader, V. et al. *Staphylococcus aureus* inactivates daptomycin by releasing membrane phospholipids. *Nat. Microbiol.* 2, 16194 (2016)

➔ TECHNIQUES AND APPLICATIONS

Shining a light on persisters

Persister cells can survive antibiotic treatment despite being genetically identical to sensitive cells. Persistence is a particular problem for the treatment of *Mycobacterium tuberculosis*; however, so far there was no straightforward way to identify and quantify persisters of this bacterium. Jain et al. developed a dual-reporter mycobacteriophage that enables the fluorescent detection of persisters. The authors induced persistence in an in vitro model and identified a set of consistently upregulated genes in these cells. They then constructed a reporter bacteriophage that constitutively expressed GFP to verify infection and a red fluorescent protein, tdTomato, under the control of the *dnaK* promoter, which was specifically activated in persisters. They showed that a small number of *M. tuberculosis* cells from the sputum of patients were tdTomato positive and thus primed for persistence and two weeks after the start of antibiotic treatment the number of persister cells increased.

ORIGINAL ARTICLE Jain, P. et al. Dual-reporter mycobacteriophages (Φ^2 DRMs) reveal preexisting *Mycobacterium tuberculosis* persistent cells in human sputum. *mBio* 7, e01023-16 (2016)

➔ ENVIRONMENTAL MICROBIOLOGY

A small soil bacterium dominates

Verrucomicrobia is one of the most abundant, although least characterized, phyla in soil. Brewer et al. identified a new verrucomicrobial lineage, which they termed 'Candidatus *Udaeobacter copiosus*'. In the >1000 soil samples examined, this lineage was frequently one of the most abundant. In grassland soils in particular, 'Ca. *Udaeobacter copiosus*' accounted for up to 30% of the recovered taxa. The authors assembled a draft genome from one such soil sample and estimated the full genome to be approximately 2.81 Mb, which is substantially smaller than the average genome size of other soil bacteria. This genomic reduction and putative genome streamlining is reflected by a loss of versatility in metabolic pathways; however, this successful soil bacterium encodes many amino acid and vitamin transporters.

ORIGINAL ARTICLE Brewer, T. E. et al. Genome reduction in an abundant and ubiquitous soil bacterium 'Candidatus *Udaeobacter copiosus*'. *Nat. Microbiol.* 2, 16198 (2016)