IN BRIEF

ANTIMICROBIALS

Plectasin, a fungal defensin, targets the bacterial cell wall precursor lipid II

Schneider, T. *et al. Science* **328**, 1168–1172 (2010)

Host defence peptides are normally thought to act by disrupting microbial cytoplasmic membranes. Plectasin is a 40 amino acid peptide produced by the ascomycete *Pseudoplectania nigrella* and is active against several Gram-positive species. However, as Schneider *et al.* now show, despite sharing structural features with other host defence peptides, plectasin does not target the bacterial cell membrane. Kinetic analysis of the effects of plectasin on bacterial cells suggested that it had more in common with agents that disrupt the cell wall (such as vancomycin and penicillin). Plectasin treatment blocked incorporation of radiolabelled glucosamine (an essential precursor for peptidoglycan synthesis) but not isoleucine or thymidine. The authors found that plectasin disrupts cell wall biogenesis by interacting directly with the cell wall precursor lipid II.

CLINICAL MICROBIOLOGY

The human nasal microbiota and *Staphylococcus aureus* carriage

Frank, D.N. *et al. PLoS ONE* **5**, e10598 (2010)

Staphylococcus aureus colonization is a prerequisite for clinical infection and occurs persistently in approximately 50% of the healthy adult population. Frank and colleagues compared the microbial communities in the nares of healthy and hospitalized adults. In healthy adults, they found that most of the isolated ribosomal RNA sequences belonged to just two phyla, the Actinobacteria (68% of sequences) and the Firmicutes (27% of sequences). In hospitalized adults, these phyla again dominated, but their distribution was reversed, with more Firmicutes (71%) than Actinobacteria (20%). This difference was mainly due to the increased abundance of *S. aureus* and *Staphylococcus epidermidis*, although the overall number and diversity of species decreased in the nares of hospitalized adults. Interestingly, there was a negative correlation between the abundances of *S. epidermidis* and *S. aureus*, indicating competition between these species for colonization.

HIV

Structure and function of broadly reactive antibody PG16 reveal an H3 subdomain that mediates potent neutralization of HIV-1

Pejchal, R. *et al. Proc. Natl Acad. Sci. USA* 2 Jun 2010 (doi:10.1073/pnas.1004600107)

The recently discovered broadly cross-reacting neutralizing monoclonal antibodies PG9 and PG16 each have a potency against HIV-1 that is an order of magnitude greater than the potencies of previously described neutralizing antibodies. They bind to overlapping but distinct epitopes in the envelope glycoprotein on the surface of HIV-1 virions. The authors determined the 2.5 Å crystal structure of the antigen-binding fragment (Fab) of PG16 and used a 3 Å structure of the PG9 light chain to facilitate homology modelling of the PG9 Fab. The structures revealed an unusually long complementarity-determining region (CDR), H3, which extends from the surface of both antibodies. Furthermore, the H3 regions of both antibodies contained a sulphated tyrosine residue that was found to have a role in epitope binding and neutralizing activity.