IN BRIEF

TECHNIQUES & APPLICATIONS

Shedding light on peptidoglycan growth

Our understanding of the dynamics of peptidoglycan growth has been hampered by our inability to directly image peptidoglycan synthesis *in vivo*. Given the role of D-amino acids in crosslinking the glycan strands, Kuru *et al.* investigated whether fluorescent probes attached to a D-amino acid backbone could be incorporated into peptidoglycan during its synthesis. The authors attached the small fluorophores 7-hydroxycoumarin 3-carboxylic acid (HCC-OH) and 4-chloro-7-nitrobenzofurazan (NBD-C1) to 3-amino-D-alanine (ADA) to create HADA and NADA, respectively. Strong peripheral and septal labelling of the entire population of viable bacteria was observed with both fluorophores for phylogenetically diverse bacterial species, including *Escherichia coli*, *Agrobacterium tumefaciens* and *Bacillus subtilis*. Furthermore, pulse–chase experiments allowed real-time tracking of peptidoglycan synthesis using time-lapse microscopy.

ORIGINAL RESEARCH PAPER Kuru, E. *et al.* *In situ* probing of newly synthesized peptidoglycan in live bacteria with fluorescent D-amino acids. *Angew. Chem. Int. Ed. Engl.* 10 Oct 2012 (doi:10.1002/anie.201206749)

MICROBIOME

Sequencing saliva

Previous work has shown that the oral microbial community is relatively stable compared to communities at other body sites. However, these studies involved samples taken over a period of just 15 months and did not investigate the potential role of host genotype. Stahringer *et al.* recently used 454 pyrosequencing of 16S rRNA genes to study the variability in the microbiome of 264 saliva samples derived from 107 individuals sampled over a 10-year period. This study included samples from 27 monozygotic twin pairs and 18 dizygotic twin pairs. The authors found that in contrast to the gut or the skin — sites where individuals share a core microbiome at the phylum level — the saliva contains a core microbiome at the genus level, with eight genera present in >95% of samples. The oral communities of monozygotic twins were not statistically more similar than those of dizygotic twins, and both types of twins were more similar to each other at early time points than at later time points, as the twins aged and became less likely to cohabit.

ORIGINAL RESEARCH PAPER Stahringer, S. S. *et al.* Nurture trumps nature in a longitudinal survey of salivary bacterial communities in twins from early adolescence to early adulthood. *Genome Res.* 12 Oct 2012 (doi:10.1101/gr.140608.112)

ENVIRONMENTAL MICROBIOLOGY

Ribosomal origin for polytheonamides

The marine sponge *Theonella swinhoei* and its uncultivated bacterial endosymbionts are rich sources of bioactive secondary metabolites. Two of these metabolites, polytheonamides A and B, exhibit surprising structural complexity, with 13 of the 19 amino acids that constitute the 48-residue peptides being non-proteinogenic, leading to the general assumption that these peptides were synthesized by a non-ribosomal peptide synthase. However, by mining the sponge metagenome, Freeman *et al.* identified an operon, probably from a bacterial endosymbiont, that contains an ORF corresponding to an unprocessed polytheonamide precursor, supporting a ribosomal origin for these peptides. The operon also contains six candidate enzymes that probably carry out the 48 different post-translational modifications which help create the functional polytheonamides.

ORIGINAL RESEARCH PAPER Freeman, M. F. *et al.* Metagenome mining reveals polytheonamides as posttranslationally modified ribosomal peptides. *Science* **338**, 387–390 (2012)