

IN BRIEF

SYMBIOSIS

Finding the difference

The microbial gut communities of social bees comprise only a few bacterial groups and are an emerging model system to study host-associated microbial communities. In this study, Engel and colleagues used comparative metagenomics to analyse the gut microbiota of two closely related honey bee species, *Apis mellifera* and *Apis cerana*. Although they are colonized mostly by the same 16S rRNA phylotypes, the authors found that at genomic resolution, each host species harbours a highly distinct bacterial community. Compared with *A. cerana*, *A. mellifera* displayed a much higher diversity of strains and functional gene content in the microbiota, encoding more diverse enzymes for polysaccharide degradation, which may provide more metabolic flexibility. Studies are now needed to understand the mechanisms and functional consequences of strain-level diversity among related host-associated communities.

ORIGINAL ARTICLE Ellegaard, K. M. et al. Vast differences in strain-level diversity in the gut microbiota of two closely related honey bee species. *Curr. Biol.* <https://doi.org/10.1016/j.cub.2020.04.070> (2020)

MICROBIOME

Reducing cholesterol levels

The human microbiome encodes a vast metabolic repertoire, but how microorganisms influence human metabolic health is incompletely understood. Xavier and colleagues combined bioinformatic and biochemical approaches and identified cholesterol dehydrogenases from gut microbiomes that contribute to the metabolism of cholesterol to coprostanol. The cholesterol dehydrogenases are encoded by intestinal sterol metabolism A (*ismA*) genes in uncultured members of cluster IV *Clostridium* and were shown to be prevalent across geographically diverse human cohorts. The presence of coprostanol-forming bacteria correlated with lower levels of faecal and serum cholesterol, which may suggest that these bacteria decrease host cholesterol levels in the intestine and serum. Cholesterol-metabolizing gut bacteria could be exploited as a strategy to lower serum cholesterol and thus decrease the risk of cardiovascular disease.

ORIGINAL ARTICLE Kenny, D. J. et al. Cholesterol metabolism by uncultured human gut bacteria influences host cholesterol level. *Cell Host Microbe* <https://doi.org/10.1016/j.chom.2020.05.013> (2020)

STRUCTURAL BIOLOGY

Catching the mode of action

The cell wall is a key drug target in *Mycobacterium tuberculosis*. The arabinosyltransferases EmbA, EmbB and EmbC are involved in the synthesis of the complex mycobacterial cell wall, and they are regarded as a target of the anti-tuberculosis drug ethambutol, as mutations in these proteins result in clinically resistant strains. The enzyme structures, their mechanism of action as well as the mode of action of ethambutol remained unknown. Zhang et al. determined the cryo-electron microscopy structures of heterodimeric EmbA–EmbB and homodimeric EmbC complexes, showing how the donor and acceptor substrates bind in the active site, providing insights into how arabinose is transferred. Ethambutol binds to the same site as the substrates in the EmbB and EmbC subunits, which suggests that the drug inhibits the enzymes by competing for binding. Finally, ethambutol-resistance mutations are located close to the ethambutol-binding site.

ORIGINAL ARTICLE Zhang, L. et al. Structures of cell wall arabinosyltransferases with the anti-tuberculosis drug ethambutol. *Science* **368**, 1211–1219 (2020)

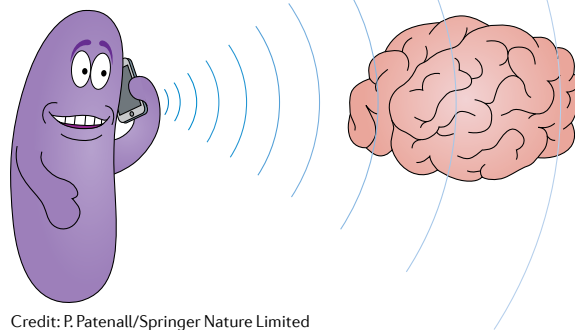
MICROBIOME

Let the gut do the guiding

Growing evidence suggests that the microbiome of animals not only affects host health but also their behaviour. However, the mechanisms involved in the gut–brain axis are not well understood. In a recent study, O'Donnell, Sengupta and colleagues report that gut-colonizing commensal bacteria produce a neurotransmitter that modulates the sensory behaviour of their host.

The authors used chemotaxis assays to test the influence of various non-pathogenic bacteria on olfactory responses of the nematode *Caenorhabditis elegans*. They found that co-culturing of the worms with multiple species of

the Gram-negative bacterium *Providencia*, particularly *Providencia alcalifaciens* strain JUb39, decreased avoidance of the volatile repellent odorant octanol, an effect that they refer to as octanol modulation. Moreover, JUb39 is ingested by *C. elegans*, colonizes the posterior intestine of the worms and, interestingly, the extent of colonization correlated with the level



Credit: P. Patenall/Springer Nature Limited

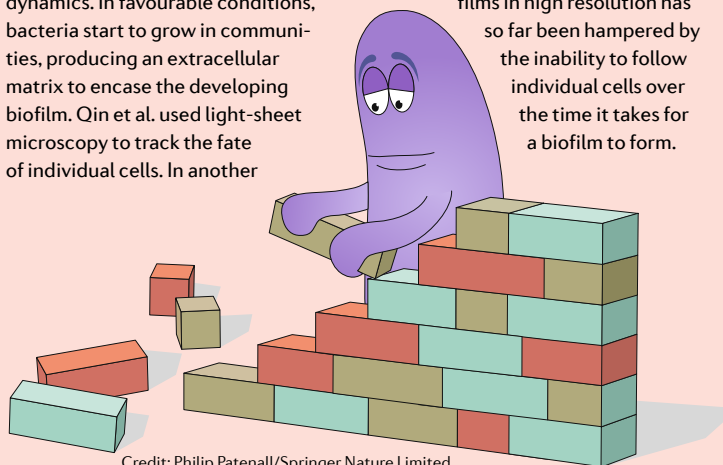
BIOFILMS

How to build a biofilm

Biofilms are complex structures, and the ever increasing capacity to image them is providing new insights into their formation and dynamics. In favourable conditions, bacteria start to grow in communities, producing an extracellular matrix to encase the developing biofilm. Qin et al. used light-sheet microscopy to track the fate of individual cells. In another

study, Rooney et al. imaged channels in mature biofilms that transport nutrients to the inside of biofilms.

Studying the development of biofilms in high resolution has so far been hampered by the inability to follow individual cells over the time it takes for a biofilm to form.



Credit: Philip Patenall/Springer Nature Limited