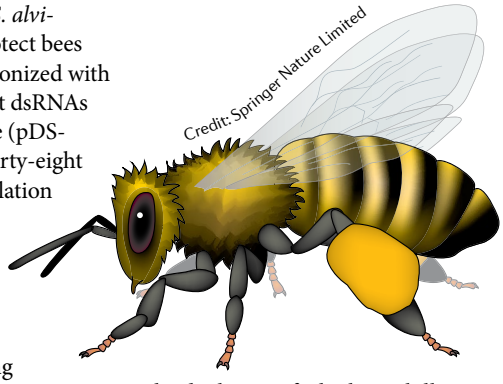
Next, to determine if *S. alvi*-generated dsRNA can protect bees from DWV, bees were colonized with *S. alvi* expressing different dsRNAs against the DWV genome (pDS-DWV1–pDS-DWV3). Forty-eight hours after the oral inoculation of bees with DWV, DWV levels in bee haemolymph were lower in all bees colonized with a dsRNA-producing *S. alvi*, including *S. alvi* producing pDS-GFP; *dicer* was also upregulated in most of these bees. Thus, the immune system might be non-specifically induced by dsRNAs in *S. alvi*-colonized bees. Furthermore, *S. alvi* expressing pDS-DWV2, but not control plasmids, increased the survival of bees injected with DWV (a delivery mechanism mirroring how *V. destructor* transmits DWV to bees), suggesting that *S. alvi*-delivered RNAi might protect honey bees from DWV.

Finally, as feeding *V. destructor* mites ingest dsRNA from bee fat bodies, the authors inoculated bees with *S. alvi* producing dsRNA against 14 mite genes (pDS-VAR), the depletion of which can kill *V. destructor*, and exposed bees to *V. destructor* after 5 days. Mites feeding on bees colonized with *S. alvi* expressing pDS-VAR died sooner than those feeding on bees colonized with *S. alvi* producing pNR or pDS-GFP. Thus, engineered *S. alvi* can protect honey bees from pathogens. It will be interesting to determine if this approach can also improve bee hive health.



Katharine H. Wrighton

ORIGINAL ARTICLE Leonard, S. P. et al. Engineered symbionts activate honey bee immunity and limit pathogens. *Science* **367**, 573–576 (2020)

Secondary-structure predictions revealed that the effector has an amphipathic α-helix in its N-terminal region, referred to as an amphipathic helix (APH). The effector was shown to localize to the plasma membrane, where it induces membrane tubulation. Depletion of the APH led to a loss of membrane localization and reduced the tubulation phenotype. This, together with the finding that the APH can bind to specific phospholipids in a synthetic membrane system, suggests that this domain directs the effector to the cytosolic leaflet of the plasma membrane, and this leads to membrane perturbations.

Next, the authors noticed that endogenous SemC co-localized with EGFR at elementary body contact sites on the plasma membrane, which suggests that the effector is recruited to sites of EGFR-mediated endocytosis. But what role does SemC have during the entry process? Co-expression studies revealed that SemC co-localizes with sorting nexin 9 (SNX9; a host endocytic scaffold protein that contains a membrane-curvature-sensing Bin/Amphiphysin/Rvs (BAR) domain) at the plasma membrane. Pull down experiments suggested an interaction between those proteins, and using deletion mutants, the authors were able to establish that an interaction is mediated by the Src homology 3 (SH3) domain of SNX9 and C-terminal proline-rich repeats (PRRs) in SemC. Recruitment of SNX9 to the membrane was also dependent on the APH domain of the effector, which led the authors to hypothesize that SemC locally deforms the membrane, and membrane curvature is then sensed by SNX9.

In sum, the findings suggest a model whereby secreted SemC binds and bends the cytoplasmic leaflet of the plasma membrane and recruits SNX9 to the deformed plasma membrane at chlamydial entry sites, where they facilitate EGFR-mediated endocytosis of *C. pneumoniae* elementary bodies.

Andrea Du Toit

ORIGINAL ARTICLE Hänsch, S., Spona, D. et al. *Chlamydia*-induced curvature of the host-cell plasma membrane is required for infection. *Proc. Natl Acad. Sci. USA* **117**, 2634–2644 (2020)

IN BRIEF

MICROBIOME

Skin deep

The skin is composed of two layers, the epidermis and dermis, and is colonized by a diverse microbiota. Skin microbiota studies have mostly analysed samples from the outermost layers of the epidermis, and few studies have investigated the microbiota using invasive sampling techniques. To better understand the spatial distribution of microorganisms in the skin, Bjarnsholt and colleagues used high-throughput sequencing to analyse full-thickness skin biopsy specimens and found divergent bacterial communities between the epidermal and dermal compartments. Dermal communities were less complex and less rich but more conserved compared with epidermal communities. Moreover, the dermal communities are functionally distinct and less affected by external factors. The findings suggest that all skin compartments should be considered in future studies.

ORIGINAL ARTICLE Bay, L. et al. Universal dermal microbiome in human skin. *mBio* https://doi.org/10.1128/mBio.02945-19 (2020)

BACTERIAL EVOLUTION

Ancient history

The Neolithic transition marks the shift in human cultural practices from hunting and gathering to agriculture, and this transition is thought to have facilitated the emergence of human-adapted pathogens. Key et al. reconstructed eight *Salmonella enterica* subsp. *enterica* genomes from human teeth of transitional foragers, pastoralists and agropastoralists and provide insights into the evolutionary history of *S. enterica*. subsp. *enterica*. Ancient genomes from prehistoric pastoralists and agropastoralists clustered in a single previously uncharacterized phylogenetic branch (Ancient Eurasian Super Branch), which contains the human-adapted serovar Paratyphi C. *S. enterica* strains older than 3,000 years were possibly host generalists and not specifically adapted to humans, and an increase in pseudogenization might have promoted host adaptation. In sum, the findings provide evidence that cultural transitions are linked to the emergence of human-adapted *S. enterica*.

ORIGINAL ARTICLE Key, F. M. et al. Emergence of human-adapted *Salmonella enterica* is linked to the Neolithization process. *Nat. Ecol. Evol.* https://doi.org/10.1038/s41559-020-1106-9 (2020)

CLINICAL MICROBIOLOGY

Catching a breath

Current efforts to control tuberculosis include effective treatment as well as early detection. Williams et al. assessed the potential of face-mask sampling as a diagnostic method. They collected face-mask samples from patients with confirmed pulmonary tuberculosis over 24 hours and identified exhaled *Mycobacterium tuberculosis* using PCR. *M. tuberculosis* was detected at least four times more frequently in face-mask samples than in sputum samples. Exhaled *M. tuberculosis* output showed no diurnal pattern, with mostly consistent levels, although high-variable and low-variable outputs were also detected. In a prospective active case-finding pilot study, individuals with symptoms of tuberculosis provided sputum and face-mask samples. Infection was detected in mask samples from individuals who were sputum-negative, but became sputum-positive at 6 weeks. Thus, the approach shows potential for diagnosis and screening.

ORIGINAL ARTICLE Williams, C. M. et al. Exhaled *Mycobacterium tuberculosis* output and detection of subclinical disease by face-mask sampling: prospective observational studies. *Lancet Infect. Dis.* https://doi.org/10.1016/S1473-3099(19)30707-8 (2020)