IN BRIEF

MICROBIAL ECOLOGY

Layers of complexity in the ground

The soil microbiome is highly diverse and microbial community members have key roles in nutrient cycling and carbon storage. Bahram, Hildebrand et al. used metagenomics and metabarcoding of topsoil samples to analyse the global distribution patterns and functional gene repertoires of soil microorganisms. They found opposing biogeographic trends for bacteria and fungi based on contrasting diversity patterns and functions across the latitudinal gradient. Environmental variables and niche differentiation determined soil microbial composition, and the global distributions of soil bacteria and fungi strongly associated with soil pH and precipitation, respectively. Moreover, bacterial antibiotic-resistance genes associated with the relative abundance of fungi, which suggests that in addition to environmental factors, inter-kingdom interactions between bacteria and fungi also shape microbial soil communities.

ORIGINAL ARTICLE Bahram, M., Hildebrand, F. et al. Structure and function of the global topsoil microbiome. *Nature* https://doi.org/10.1038/s41586-018-0386-6 (2018)
FURTHER READING Fierer, N. Embracing the unknown: disentangling the complexities of the soil microbiome. *Nat. Rev. Microbiol.* **15**, 579–590 (2017)

MICROBIOME

Defending the niche

Intestinal commensal microorganisms mediate colonization resistance against bacterial pathogens through various mechanisms, including activation of the host immune system and production of antagonistic molecules. Microbial-derived short-chain fatty acids (SCFAs) were reported to inhibit pathogen growth, an effect that was not well understood. Jacobson et al. used a mouse model of oral *Salmonella enterica* subsp. *enterica* serovar Typhimurium infection in which mice were not pre-treated with an antibiotic to study colonization resistance. They showed that commensal *Bacteroides* spp. produce the SCFA propionate, which disrupts intracellular pH homeostasis in *S.* Typhimurium, leading to slow and reduced pathogen growth. In sum, this study uncovers how the unperturbed, resident microbiota directly protects the host from enteric infection.

ORIGINAL ARTICLE Jacobson, A. et al. A gut commensal-produced metabolite mediates colonization resistance to *Salmonella* infection. *Cell Host Microbe* https://doi.org/10.1016/j.chom.2018.07.002 (2018)

FUNGAL PATHOGENESIS

Taking control over the host

The pathogenic fungus *Entomophthora muscae* induces behavioural changes in infected flies: infected hosts climb to a high location, extend their proboscis, become affixed and lift their wings up and away from their dorsal abdomen, thus assuming a 'pose' that enables the fungal spores to be ejected into the surrounding environment. How the fungus gains control over its host remained elusive, owing to the lack of experimental tools in existing model systems. Elya et al. isolated an *E. muscae* strain from wild *Drosophila melanogaster*, thus providing a new system to study fungal-induced behaviour in the laboratory. They examined the progression of the infection process, the host immune response and transcriptional changes in both the flies and fungus during the course of infection. They showed that the fungus invades the nervous system of its host, which might be a means to achieve behavioural changes in the host.

ORIGINAL ARTICLE Elya,C. et al. Robust manipulation of the behavior of *Drosophila melanogaster* by a fungal pathogen in the laboratory. *eLife* https://doi.org/10.7554/eLife.34414 (2018)
FURTHER READING Johnson, K. V.-A. & Foster, K. R. Why does the microbiome affect behaviour? *Nat. Rev. Microbiol.* https://doi.org/10.1038/s41579-018-0014-3 (2018)

VIRAL INFECTION

Maximizing delivery

Norovirus or rotavirus infections are a major cause of gastroenteritis. Viral transmission occurs through the faecal–oral route, and it was the long-standing notion that infection of new hosts is mediated by individual virus particles. Recent studies are challenging this view, including the finding that enteroviruses are transmitted as viral clusters inside extracellular vesicles in vitro. In this study, Santiana, Ghosh et al. showed that rotaviruses and noroviruses are transmitted in stool as clusters of viruses within vesicles, and that this mode of transmission provides a replication advantage.

They first investigated transmission of rotavirus, and they found that in vitro, rotavirus was able to non-lytically exit cells inside extracellular vesicles that originated from the plasma membrane. The authors confirmed these findings in vivo, showing that vesicles that contain infectious viruses were shed into stool from infected piglets and mouse pups. Based on vesicle size and lipid composition, they suggest that these vesicles are derived from microvilli plasma membranes of enterocytes.

Next, the authors asked whether other enteric viruses are also shed into stool inside extracellular vesicles. They collected stool samples from individuals infected with norovirus and found that the virus is shed into stools inside exosomes that are derived from the tissues of infected hosts. When human intestinal enteroid cell cultures were inoculated with norovirus-containing exosomes isolated from stools, the authors observed an increase in norovirus genome copy number, suggesting that the virus-containing exosomes are infectious. Thus, both rotaviruses and noroviruses could be shed into stool within extracellular vesicles.

ARCHAEAL EVOLUTION

A new timeline of life's early evolution

Studies of ancient evolutionary events that led to the emergence of cellular life on Earth rely on the fossil record, but interpreting this record is problematic because of a paucity of fossil evidence and challenges in confirming relationships within the deepest branches of the tree of life. In a recent study, Betts et al. integrate genomic and fossil evidence to derive a timeline of life's early evolution and the origin of eukaryotes.

The authors first derived a number of calibrations for their timeline of key events in the history of life using multiple lines of evidence, including fossils, biomarkers and isotope geochemistry. They used microfossils from the ~3.4 billion years ago (Ga) Strelley Pool Formation, Australia, as the earliest record of life; the oldest confirmed fossils of crown Eukaryota (~1.1 Ga *Bangiomorpha pubescens*); the oldest known fossils of total-group Eukaryota from the >1.6191 Ga Changcheng Formation, North China; and the timing of the last formative stage of Earth's formation (the Moon-forming impact event which melted and sterilized the Earth) to estimate the emergence of the last universal common ancestor (LUCA), the origin of the two primary lineages of life (Archaebacteria and Eubacteria), and the divergence of the eukaryotes from within Archaebacteria. The authors used these key time constraints combined with nine others to calibrate the timescale of life that was estimated from 29 conserved and universally distributed proteins using Bayesian molecular clock dating.

In their timeline, LUCA predates the end of the late heavy bombardment >3.9 Ga (a period of intense comet and asteroid bombardment). The crown groups of the two primary domains of life emerged later (<3.4 Ga), implying