identified bacterial genera that are typical in the bee gut, such as *Lactobacillus*, *Bifidobacterium* and *Gilliomella* species. Finally, the authors reported a large metabolic overlap between bacterial and phage proteins, which suggests that phages may affect metabolic pathways and thus perhaps the health of their bee hosts.

To prevent pathogen spread within and between bee colonies, social bees exhibit adaptive behaviours as well as nestmate recognition systems. Pathogen-induced behavioural changes have been implicated in affecting pathogen transmission. In the second paper, Dolezal and colleagues investigated whether infection of honey bees by Israeli acute paralysis virus (IAPV) affects social interactions among colony members. They reported that inoculation reduced social contacts between members of the honey bee colony compared with control groups, which suggests an adaptive social immunity mechanism to reduce pathogen transmission via physical contact within colonies. Moreover, inoculated bees exhibited less aggression towards bees from other colonies, and this effect was associated with changes in the abundance of cuticular hydrocarbons, which are present on the surface of all insects and used by bees to discriminate colony members from invading bees. Indeed, IAPV-inoculated bees were more likely to be accepted into a new colony, which increases the probability of spreading infection between colonies. These responses were specific to IAPV infection, suggesting that the virus has evolved to manipulate host behaviour to enhance its transmission to new nests.

Andrea Du Toit

ORIGINAL ARTICLES Deboutte, W. et al. Honey-bee–associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. *Proc. Natl Acad. Sci. USA* https://doi.org/10.1073/pnas.1921859117 (2020) | Geffre, A. C. et al. Honey bee virus causes context-dependent changes in host social behaviour. *Proc. Natl Acad. Sci. USA* https://doi.org/10.1073/pnas.2002268117 (2020)

Credit: Anton Petrus/Alamy Stock Photo

inorganic nitrogen concentrations in the overlying water, by measuring denitrification rates and quantifying relative abundances of nitrification and denitrification genes. Compared with the control, they found that PUF and PLA treatments promoted nitrification and denitrification, whereas PVC inhibited both processes. PUF and PLA treatments increased NO_3^- and NO_2^- concentrations and decreased the concentration of NH_4^+ and the expression level of a gene required for ammonia oxidation. By contrast, in the PVC-treated microcosm, NO_3^- and NO_2^- concentrations, the rate of denitrification and nitrite reductase gene expression were all reduced compared with the control.

In sum, this study suggests that microplastic pollution could have profound effects on microbial communities and nitrogen cycling.

Ashley York

ORIGINAL ARTICLE Seeley, M. E. et al. Microplastics affect sedimentary microbial communities and nitrogen cycling. *Nat. Commun.* **11**, 2372 (2020)
RELATED ARTICLE Amaral-Zettler, L. A., Zettler, E. R. & Mincer, T. J. Ecology of the plastisphere. *Nat. Rev. Microbiol.* **18**, 139–151 (2020)

IN BRIEF

BIOFILMS

When an immune response backfires

Biofilm formation by *Pseudomonas aeruginosa* facilitates chronic infection by avoiding immune clearance and reducing the efficacy of antimicrobial therapy. Now, Riquelme et al. find that *P. aeruginosa* utilizes itaconate, an abundant immunometabolite produced by myeloid cells in response to infection, to promote biofilm formation. Itaconate induces bacterial membrane stress, resulting in increases in anti-stress extracellular polysaccharide (EPS) expression and a decrease in lipopolysaccharide (LPS) expression. Itaconate-adapted *P. aeruginosa* accumulate mutations in the *lptD* gene, encoding a membrane protein that translocates LPS to the bacterial surface, leading to further substantial increases in EPS synthesis. In turn, EPS production stimulated even greater itaconate production by myeloid cells in mice. This metabolic adaptation in both pathogen and host skews infection towards chronic infection.

ORIGINAL ARTICLE Riquelme, S. A. et al. *Pseudomonas aeruginosa* utilizes host-derived itaconate to redirect its metabolism to promote biofilm formation. *Cell Metab.* https://doi.org/10.1016/j.cmet.2020.04.017 (2020)

ANTIMICROBIALS

Finding a good combination

Antibiotic adjuvants have no or little antibiotic activity themselves but can enhance the activity of co-administered antibiotics, or reverse antibiotic resistance mechanisms. Now, Song, Liu et al. report a broad-spectrum antibiotic adjuvant that reverses resistance in multi-drug resistant (MDR) Gram-negative pathogens. The short linear antibacterial peptide known as SLAP-S25 carries four non-natural amino acids of 2,4-diaminobutanoic acid and was found to increase the efficacy of antibiotics in all major classes. SLAP-S25 potentiated the efficacy of antibiotics against diverse Gram-negative bacteria, including carbapenem-resistant and colistin-resistant *Escherichia coli*, and reversed resistance to MDR *E. coli* in animal models. SLAP-S25 binds to lipopolysaccharide and phosphatidylglycerol to induce membrane damage, which is required for synergy with antibiotics.

ORIGINAL ARTICLE Song, M. & Liu, Y. et al. A broad-spectrum antibiotic adjuvant reverses multidrug-resistant Gram-negative pathogens. *Nat. Microbiol.* https://doi.org/10.1038/s41564-020-0723-z (2020)

VIRAL INFECTION

Opening the stargate

Giant viruses are enormous in size and complexity, hampering our understanding of their life cycles. Scrad et al. developed an in vitro model of Mimivirus infection to understand the initial stages of the life cycle and viral genome release. By subjecting virions to different environmental conditions, including low pH, high temperature and high salt concentrations, they were able to generate four infection intermediates that represent different stages of genome release through the starfish-shaped delivery portal known as stargate. The authors visualized the different intermediates by electron microscopy and identified proteins that are released during the initial stages of infection using mass spectrometry, allowing them to propose a model of genome release. In their model, the stargate portal slowly 'unzips' rather than releasing the genome en masse.

ORIGINAL ARTICLE Schrad, J. R. et al. Structural and proteomic characterization of the initiation of giant virus infection. *Cell* https://doi.org/10.1016/j.cell.2020.04.032 (2020)