

IN BRIEF

BACTERIAL PHYSIOLOGY

Flipping the switch

The bacterial cell wall, together with the peptidoglycan layer, maintains cell shape and provides structural integrity, presenting an important antibiotic target. Peptidoglycan turnover involves the enzyme-mediated cleavage of the bonds in the peptidoglycan mesh, a process that needs to be tightly regulated to avoid detrimental effects. Dörr and colleagues investigated the regulation of the endopeptidase ShyA of *Vibrio cholerae* and found that ShyA assumes a catalytically active, open form and a closed form that is inactive. Mutations that promote the open form led to toxic effects, in line with the notion that cleavage activity needs to be controlled. The data indicated that the endopeptidase is produced as an inactive precursor, and conformational changes expose the active site. Although the signal that promotes this conformational switch is unknown, such a mechanism may enable the rapid induction of cleavage activity under rapidly changing environmental conditions.

ORIGINAL ARTICLE Shina, J.-H., Sulpizio, A. G., Kelley, A. et al. Structural basis of peptidoglycan endopeptidase regulation. *Proc. Natl Acad. Sci. USA* <https://doi.org/10.1073/pnas.2001661117> (2020)

FUNGAL BIOLOGY

Changing things up

Aspergillus fumigatus is a human opportunistic pathogen that can cause life-threatening disease in immunocompromised individuals. Treatment with antifungal drugs is often unsuccessful owing to the emergence of resistance. Cell-to-cell heterogeneity has been linked to drug susceptibility and thus might affect drug treatment. Bleichrodt et al. investigated the composition of cell walls of single fungal conidia cells and how this might affect drug susceptibility. They found that the fungal cell wall is highly heterogeneous and that the level of heterogeneity changed during germination and under different conditions. Investigating whether this heterogeneity has an effect on single cell behaviour, the authors showed that subpopulations of germinating conidia emerged that developed tolerance to a cell wall synthesis-targeting antifungal. Thus, cell wall heterogeneity provides a fitness benefit to *A. fumigatus*.

ORIGINAL ARTICLE Bleichrodt, R.-J. et al. Cell wall composition heterogeneity between single cells in *Aspergillus fumigatus* leads to heterogeneous behavior during antifungal treatment and phagocytosis. *mBio* **11**, e03015–1919 (2020)

STRUCTURAL BIOLOGY

Complex design

The de novo design of functional proteins can expand the natural protein repertoire and their application, but the computational design of de novo proteins with complex structural, functional motifs is challenging. One application for computationally designed proteins is in vaccinology — the design of immunogens that elicit targeted neutralizing antibody responses. Sesterhenn et al. developed a computational design strategy, TopoBuilder, and engineered an epitope-focused immunogen cocktail comprising three antigenic sites of the respiratory syncytial virus fusion protein, which induced robust neutralizing responses in mice and nonhuman primates. Thus, the authors provide a proof-of-principle to functionalize de novo proteins with complex functional motifs.

ORIGINAL ARTICLE Sesterhenn, F. et al. De novo protein design enables the precise induction of RSV-neutralizing antibodies. *Science* **368**, eaay5051 (2020)

MICROBIOME

The viruses and the bees

Honey bees, *Apis mellifera*, are environmentally and economically important pollinators. However, honey bees are threatened by several stressors, including pathogens. Studies on the honey bee gut microbiome have established a crucial role of bacterial community members in bee development, food digestion, homeostasis and health. By contrast, the composition and potential roles of the honey bee virome are less understood. A new study provides insights into the phage communities of honey bees, and a second study reports that a viral pathogen alters the social behaviour of its bee host.

In the first paper, Deboutte,

Matthijnsens and colleagues characterize the phage communities associated with honey bees. They found that the viral sequences displayed large inter-individual diversity, and most phage genomes remain unclassified. This diversity contrasts with the relatively simple bee bacterial microbiome observed so far. Moreover, although phage composition did not seem

to differ between healthy and weak bees, location and sampling year affected the community composition. Assigning the phage genomes to their putative hosts, the authors



ENVIRONMENTAL MICROBIOLOGY

Adapting to plastic

Millions of tonnes of plastic enter our oceans each year. Once in the ocean, plastic degrades slowly, breaking down into microplastics that are damaging to marine life. Yet, little is known about how microplastics affect marine microbial ecosystems and biogeochemical cycles. In a recent study, Seeley et al. evaluated how different microplastics influence the composition and function of sedimentary microbial communities and the implications for the microbial nitrogen cycle.

The authors prepared individual microcosms of salt marsh sediment containing either the petroleum-based plastics polyethylene (PE), polyvinyl chloride (PVC) or polyurethane foam (PUF), or the biopolymer polylactic acid (PLA) and incubated the microcosms for 16 days. After incubation, composition and diversity of the bacterial communities were determined using high-throughput sequencing of 16S rRNA genes and principal coordinate analyses (PCAs).

Overall, the authors observed that microplastic treatment resulted in substantial differences in diversity, particularly at the family level. For instance, compared with the control community (that is, in the absence of plastic), Chromatiaceae and Sedimenticolaceae families were significantly less abundant in microplastic-treated microcosms, whereas Family_XII was significantly higher. PLA-treated microcosms had the greatest α -diversity at the end of the experiment, but the community was similar to that of the control, according to β -diversity in the PCAs. PE and PUF treatments resulted in the most variation, but were similar to each other. Notably, PE and PUF treatments had markedly different communities than PVC treatment. The authors posit that these differences are due to variation in the physicochemical characteristics of the polymers.

Next, the authors investigated how microplastics may affect nitrogen cycling in sediments by monitoring dissolved