

IN BRIEF

BACTERIAL PATHOGENESIS

Filamentous bacteriophages affect pathogenicity of *Pseudomonas* infections in cystic fibrosis

Filamentous bacteriophages (Pf phage) — known to contribute to the virulence of *Pseudomonas aeruginosa* in animal models of acute lung infection — might have a role in the pathogenicity of *P. aeruginosa* infection in patients with cystic fibrosis. Burgener et al. investigated the prevalence of Pf phage in the sputum of 34 Danish patients with cystic fibrosis and found that samples from nine of the patients (26.5%) were consistently positive for Pf phage. Analysis of sputum samples from 76 patients with cystic fibrosis in Stanford, USA, showed the prevalence of Pf phages to be 36.2% in patients with *P. aeruginosa* infection and 27.6% in all patients. Pf phage was more prevalent in older patients in both cohorts and Pf phage correlated with both bacterial burden and chronicity of *P. aeruginosa* infection in the Stanford cohort. *P. aeruginosa* strains infected with Pf phage also had increased resistance to antibiotics. Altogether, these results suggest that Pf phages affect the pathogenicity of *P. aeruginosa* infection in cystic fibrosis.

ORIGINAL ARTICLE Burgener, E. B. et al. Filamentous bacteriophages are associated with chronic *Pseudomonas* lung infections and antibiotic resistance in cystic fibrosis. *Sci. Transl. Med.* <https://doi.org/10.1126/scitranslmed.aau9748> (2019)

SYMBIOSIS

Magnetotactic symbiosis in marine sediments

Magnetoreception has only been described in magnetotactic bacteria. Monteil et al. now report a mutualistic symbiosis between excavate protists and ectosymbiotic Deltaproteobacteria, revealing an example of eukaryotic magnetoreception acquired by symbiosis. The researchers used a magnetic enrichment protocol on anoxic marine sediments and water in a dyked area sheltered from major currents and found that north-seeking magnetotactic bacteria were the dominant magnetically responsive organisms. They observed populations of atypical south-seeking organisms that were identified to be protists. Electron microscopy of the protists revealed that they were attached to rod-shaped bacteria containing magnetite particles (magnetic ectosymbiotic bacteria). The researchers propose a number of possible mutual benefits for the bacteria and protist, and state that elaborated syntrophy, in which metabolic exchange is enabled by the positioning of the consortium in optimal redox conditions, seems to be the ultimate basis of the symbiosis.

ORIGINAL ARTICLE Monteil, C. L. et al. Ectosymbiotic bacteria at the origin of magnetoreception in a marine protist. *Nat. Microbiol.* <https://doi.org/10.1038/s41564-019-0432-7> (2019)

ENVIRONMENTAL MICROBIOLOGY

Arctic an unexpected hotspot for viral diversity

Gregory et al. performed a global survey of the ecological diversity of viruses in the oceans. They identified 195,728 viral populations, greatly exceeding the 15,280 identified in a previous ocean survey. These viral communities sorted into five distinct ecological zones — the Arctic, Antarctic, bathypelagic, temperate and tropical epipelagic, and mesopelagic. The researchers found that at the per-sample level, the patterns and drivers of viral microdiversity and macrodiversity differed and that microdiversity increased with geographic range. Although the latitudinal diversity gradient paradigm suggests that diversity of species is highest at mid-latitudes and decreases poleward, Gregory et al. found that the Arctic in fact showed high levels of marine viral diversity.

ORIGINAL ARTICLE Gregory, A. C. et al. Marine DNA viral macro- and microdiversity from pole to pole. *Cell* <https://doi.org/10.1016/j.cell.2019.03.040> (2019)

ANTIMICROBIAL RESISTANCE

***E. coli* rolls the dice**

Antibiotic resistance can arise either through the acquisition of resistance genes from other bacteria or through mutation of the bacterium's own genes. Antibiotics are known to further the development of resistance by both selecting resistant cells and by inducing mutagenesis. However, the detailed mechanisms underlying the latter phenomenon are incompletely understood. Rosenberg and colleagues now describe how the antibiotic ciprofloxacin induces a subpopulation of *Escherichia coli* cells to have high rates of mutagenesis and produce resistant mutants.

Mutation can have deleterious effects and therefore mutation rates are usually low. Ciprofloxacin is known to cause DNA double-strand breaks, leading to a DNA-damage response and the induction of error-prone DNA polymerases. When Rosenberg and colleagues treated *E. coli* cultures with subinhibitory

concentrations of ciprofloxacin, the antibiotic increased the rate of mutations that confer resistance to the unrelated antibiotics ampicillin and rifampicin compared with untreated cultures. Careful molecular characterization showed that the mutagenesis that follows DNA breaks depended on the generation of reactive oxygen species (ROS) and on the transcription factor σ^s , as well as the general stress response pathway that σ^s controls.

Interestingly, flow cytometry with fluorescent reporters for ROS or σ^s levels showed that only a subpopulation — around 20% of cells during log phase growth — activated this pathway in response to the low dose ciprofloxacin treatment. Furthermore, cell sorting confirmed that the cells that produced ROS and activated the general stress response produced 128 times as many mutants that were resistant to rifampicin than cells with a low

BACTERIAL PHYSIOLOGY

Go with the flow

Bacteria thrive in numerous environments where fluids flow, for example, rivers and streams, the blood stream and the urinary tract. Fluid flow is an important mechanical signal for bacteria and

it was assumed that bacteria sense flow by measuring the shear force of the flow. Now, Sanfilippo, Lorestani et al. report a force-independent form of flow-sensing in *Pseudomonas aeruginosa*.

To investigate how bacteria sense fluid flow, the authors developed a microfluidic-based experimental system in which *P. aeruginosa* cells are subjected to flow and their gene expression is monitored using RNA sequencing. After 20 min of flow exposure, a four-gene operon was highly induced, which the authors named *fro* (for flow-responsive operon). They then generated a fluorescent reporter strain that expresses yellow fluorescent protein (YFP) on *fro* expression and using this strain, they found that individual *P. aeruginosa* cells increased *fro* expression sixfold in response to flow. The authors called this form of environmental sensing 'rheosensing', as rheo is Greek for flow.



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