Research highlights

Viral infection

Microbial ecology

A host for redondoviruses

Parasitic control of wolf behaviour

Bioremediation

A solution for mercury pollution?

Redondoviruses are almost exclusively found in the ororespiratory tract of humans. They are highly prevalent in healthy individuals, and their abundance is increased in individuals with different conditions like periodontitis, critical and inflammatory diseases and COVID-19. These viruses are circular Rep-encoding singlestranded DNA viruses, and their cell host is currently unknown. In this new study, Keeler et al. explore which type of human cell supports redondovirus replication, and they surprisingly discover that the eukaryotic commensal amoeba Entamoeba gingivalis is their main host. The authors investigated redondovirus phylogeny and guaninecytosine content, and found that it was consistent with E. gingivalis being the host. Analysis of metagenomics datasets from individuals with oral disease and healthy individuals revealed co-occurrence of E. gingivalis and redondoviruses in both groups. In vitro, E. gingivalis grown in xenic culture in the absence of human cells was able to produce redondoviruses, and viral and protozoan DNA were co-localized. Altogether, these findings point at E. gingivalis as the host for redondovirus replication and highlight the potential contributions of eukaryotic commensal viruses to the human virome. Agustina Taglialegna

Original article: Keeler, E. L. et al. Widespread, human-associated redondoviruses infect the commensal protozoan Entamoeba gingivalis. Cell Host Microbe https://doi.org/10.1016/ j.chom.2022.11.002 (2022)

Toxoplasma gondii is a protozoan parasite that is the causative agent of toxoplasmosis, a disease associated with increased risk-taking behaviour. Although much research has been conducted on the effects of T. gondii on the behaviour of laboratory animals, little is known about its effects on host behaviour in a wild system. Meyer et al. examined T. gondii infection in wild wolves, intermediate hosts that live in close proximity to definitive hosts, cougars. It was found that wolf territory overlap with cougars was a strong predictor of T. gondii infection, consistent with wolves contracting the parasite through close interactions with infected cougars. Notably, wolves that were seropositive for T. gondii altered their behaviour to take more risks, including being more likely to disperse or become pack leaders compared with seronegative wolves. As wolves are a social species, altered behaviour of the pack leader may scale up beyond individuals to impact pack-level decision making. These findings are a rare demonstration of parasite infection altering behaviour in a wild animal population, with important implications for population biology and community ecology. **Michael Attwaters**

Original article: Meyer, C. J. et al. Parasitic infection increases risk-taking in a social, intermediate host carnivore. *Commun. Biol.* 5, 1180 (2022)

Mercury contamination in soil is a global threat to agriculture, ecosystems and public health. One possible solution is detoxification of polluted environments using mercuryresistant microorganisms, which break down mercury into less toxic forms. Using biochemical assays, Wu et al. show that the plant symbiotic fungus Metarhizium robertsii can reduce mercury accumulation in soil. Mechanistically, M. robertsii demethylates mercury via a methylmercury demethylase (MMD) and then reduces the product to Hg⁺ using a mercury ion reductase (MIR). The result is improved growth of plants under mercury stress, whereas growth is thwarted by genetic deletion of the M. robertsii genes encoding MMD and MIR. Genetic manipulation of M. robertsii to overexpress these enzymes led to further improvement in plant growth, indicating that the ability of M. robertsii to remove mercurv can be enhanced by simple genetic alterations. These findings uncover the mechanisms of mercury tolerance in fungi and may have implications for the development of cost-effective tools to clean up mercury pollution. **Michael Attwaters**

Original article: Wu, C. et al. Bioremediation of mercury-polluted soil and water by the plant symbiotic fungus *Metarhizium robertsii. Proc. Natl Acad. Sci. USA* **119**, e2214513119 (2022)

Vaccines

Broad protection from a single flu vaccine

Influenza virus is a persistent global health threat responsible for four pandemics since the turn of the twentieth century. The large diversity of influenza viruses represents a major barrier to preventing the next pandemic, with at least 18 influenza virus strains known to circulate in animal reservoirs. Several universal influenza virus vaccines are in development to target a number of conserved epitopes found across the different influenza virus strains, although these types of vaccine are difficult to manufacture and are weakly immunogenic. Now, Arevalo et al. leverage advances in nucleic acid-based vaccine technology leading to the development of a nucleosidemodified mRNA-lipid nanoparticle vaccine encoding separate haemagglutinin antigens from all known influenza virus subtypes. The vaccine induced high levels of crossreactive and subtype-specific antibodies in both mice and ferrets. When challenged with matched and mismatched viral strains, vaccinated mice and ferrets were protected from illness and death. These findings suggest that mRNA vaccines might hold the potential to protect against future pandemics by providing protection against diverse influenza virus subtypes.

Michael Attwaters

Original article: Arevalo, C. P. et al. A multivalent nucleoside-modified mRNA vaccine against all known influenza virus subtypes. *Science* **378**, 899–904 (2022)