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IN BRIEF

MICROBIOTA

Leishmaniasis breaks the equilibrium

The skin microbiota affects wound healing, inflammatory and immune responses to infections, and chronic skin diseases. Gimblet *et al.* investigated the role of the skin microbiota in cutaneous leishmaniasis and found that infection with *Leishmania* spp. parasites caused a decrease in bacterial diversity in the skin of both humans and mice; in particular, this dysbiosis was characterized by a greater abundance of *Staphylococcus* spp. and *Streptococcus* spp. in infected individuals than in healthy individuals. This dysbiosis seemed to be transmissible to uninfected distant skin sites, as well as to co-housed naive mice. *Staphylococcus* spp. were found to be dominant in moderate lesions, whereas *Streptococcus* spp. were more abundant in severe lesions in infected mice, which suggests that disease severity contributes to dysbiosis. Moreover, the transfer of the dysbiotic microbiota to naive mice prior to infection exacerbated skin inflammation and increased disease severity compared with control mice.

ORIGINAL ARTICLE Gimblet, C. *et al.* Cutaneous leishmaniasis induces a transmissible dysbiotic skin microbiota that promotes skin inflammation. *Cell Host Microbe* http://dx.doi.org/10.1016/j.chom.2017.06.006 (2017)

VIRAL EVOLUTION

Every flu evolves in the same way

Influenza viruses, similarly to other viruses, rapidly acquire *de novo* mutations when they replicate within their host cells. However, how the emergence of viral variants in the host is reflected at a global scale is still poorly understood. In a new study, Xue *et al.* used a deep-sequencing approach to analyse longitudinal samples from immunocompromised patients who had long-term influenza infections. The authors found that the same set of mutations had emerged independently in several patients, most commonly in the genes that encode haemagglutinin (HA) and neuraminidase. Furthermore, many of the mutations in HA had also reached high global frequency in the decade following patient infections. This study shows that viral evolution and variation in the host parallel evolution at a global scale. Understanding these dynamics will help to predict the evolution of influenza viruses and the design of more effective vaccines.

ORIGINAL ARTICLE Xue, K. S. *et al.* Parallel evolution of influenza across multiple spatiotemporal scales. *eLife* **6**, e26875 (2017)

STRUCTURAL BIOLOGY

Insights into bacterial microcompartments

Many bacteria have primitive proteinaceous organelles that are known as bacterial microcompartments (BMCs). All BMCs share a common architecture, with a selectively permeable protein shell that encapsulates different metabolic enzymes. Although detailed structural information is available for the single components of the shell, how the shell assembles was unknown. In a new study, Sutter *et al.* determined the crystal structure of an intact shell from *Haliangium ochraceum*, thereby revealing the basic principles of its assembly. In particular, by using a recombinant system that contained selected components of the shell, the authors generated a complete 40 nm shell with a molecular mass of 6.5 MDa and determined its structure to a resolution of 3.5 Å. Considering that these structures are widely conserved in bacteria, these findings probably apply to various functionally distinct bacterial organelles.

ORIGINAL ARTICLE Sutter, M. *et al.* Assembly principles and structure of a 6.5-MDa bacterial microcompartment shell. *Science* **356**, 1293–1297 (2017)