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IN BRIEF

MICROBIOME

Phage community in the gut

The gut microbiome has an important role in human health, but the role of phages in maintaining the structure and function of the gut microbial community is unclear. Manrique *et al.* analysed phages that are associated with the gut microbiome of healthy individuals and identified 23 phages that were common in more than half of the individuals. This set of gut microbiome phages was less prevalent in individuals with gastrointestinal disease, which suggests that they have a role in human health. Next, the authors investigated the structure of the phage community using a network analysis tool. They identified 44 phage groups, of which nine were shared across more than 50% of healthy individuals. On the basis of their results, the authors propose the existence of a healthy gut phageome (HGP) that comprises a core, a common and a low overlap group. Future studies are required to elucidate the role of the phageome in health and disease.

ORIGINAL ARTICLE Manrique, P. *et al.* Healthy human gut phageome. *Proc. Natl Acad. Sci. USA* http://dx.doi.org/10.1073/pnas.1601060113 (2016)

VIRAL INFECTION

HCMV and host interplay

The interferon-induced ubiquitin-like modifier ISG15 can be conjugated to proteins (ISGylation) to modify their function. ISGylation is markedly induced following viral infection as part of the immune response, but the viral substrates and strategies that are used to counteract the antiviral response are not well defined. Kim *et al.* show that ISG15 expression and protein ISGylation are induced following infection with human cytomegalovirus (HCMV). Increased ISGylation inhibited viral growth as well as virion release at low multiplicity of infection. The levels of ISG15 and ISG15 conjugates decreased later during the course of infection, which was dependent on the viral protein IE1. Furthermore, the viral protein pUL26 interacted with ISG15 and was ISGylated, which decreased its stability and inhibited its ability to downregulate nuclear factor-κB (NF-κB) signalling. Interestingly, pUL26 had an inhibitory effect on ISGylation during the late phase of infection and thus, in addition to IE1, also combats the ISG15-mediated antiviral response.

ORIGINAL ARTICLE Kim, Y. J. *et al.* Consecutive inhibition of ISG15 expression and ISGylation by cytomegalovirus regulators. *PLoS Pathog.* http://dx.doi.org/10.1371/journal.ppat.1005850 (2016)

PARASITE GENOMICS

Scrutinizing apicomplexans

Sidik *et al.* report the first genome-wide CRISPR–Cas9 screen in an apicomplexan, *Toxoplasma gondii*. They targeted all annotated protein-coding genes and screened for genes that are needed during infection of human fibroblasts. The authors identified ~200 previously uncharacterized fitness-conferring genes that were only present in apicomplexans, which they called indispensable conserved apicomplexan proteins (ICAPs). Using functional assays, they found that ICAP12 was crucially important for the invasion of host cells. They renamed this protein claudin-like apicomplexan microneme protein (CLAMP) to reflect its subcellular localization and structural similarity to mammalian tight junction proteins. Finally, the CLAMP orthologue in *Plasmodium falciparum* was shown to be essential for growth during the asexual stages of its life cycle. This work provides a framework for future studies investigating apicomplexan biology.

ORIGINAL ARTICLE Sidik, S. M. *et al.* A genome-wide CRISPR screen in *Toxoplasma* identifies essential apicomplexan genes. *Cell* http://dx.doi.org/10.1016/j.cell.2016.08.0193 (2016)