IN BRIEF

MICROBIOME

Host–microbiome interactions lost during flight

Despite major variations in diet, host phylogeny is a major determinant of microbiome composition in mammals, but whether this trend exists in all vertebrates was unknown. Song, Sanders et al. analysed the gut microbiomes of ~900 vertebrate species, including 315 mammals and 491 birds, and assessed the contributions of diet, the relatedness of hosts and physiology to the taxonomic composition of the microbiomes. The authors found strong correlations between microbial community similarity, diet and host phylogenetic distance in nonflying mammals. By contrast, gut microbiome composition weakly correlated with diet and host phylogeny in birds, with little evidence of host specificity. Remarkably, bat gut microbiomes follow the same trend as birds, with little correlation with either diet or phylogeny. These findings suggest that host–gut microbiome phylosymbioses depend on host factors that were lost during adaptation to flight.

ORIGINAL ARTICLE Song, S. J., Sanders, J. G. et al. Comparative analyses of vertebrate gut microbiomes reveal convergence between birds and bats. *mBio* https://doi.org/10.1128/mBio.02901-19 (2020)

PARASITE DEVELOPMENT

The master of *Toxoplasma* differentiation

During initial infection, *Toxoplasma gondii* differentiates into tachyzoites that rapidly disseminate throughout the host, invading nucleated cells. A proportion of tachyzoites differentiate into slow-growing bradyzoites, which form cysts that are mainly localized within the brain and muscle tissues, but the molecular basis of this differentiation was unknown. Now, Waldman et al. identify a master regulator of chronic-stage differentiation in *T. gondii*. The authors used Cas9-mediated genetic screening and single-cell transcriptional profiling to find putative regulators of differentiation and identified the transcription factor BFD1. Δ*BFD1* parasites were unable to differentiate in cell culture or form brain cysts in mice, and *BFD1* expression was sufficient to induce differentiation in cell culture. BFD1 was found to bind to the promoters of numerous differentially regulated stage-specific genes, suggesting that BDF1 directly activates differentiation.

ORIGINAL ARTICLE Waldman, B. S. et al. Identification of a master regulator of differentiation in *Toxoplasma*. *Cell* https://doi.org/10.1016/j.cell.2019.12.013 (2020)

BACTERIAL PHYSIOLOGY

Coordinating cell growth and division in *S. aureus*

Peptidoglycan synthesis occurs at two locations in *Staphylococcus aureus* — at the cell wall during growth and mid-cell during division — but how peptidoglycan synthesis is spatially regulated throughout the cell cycle is unknown. Do et al. performed a genetic screen to find regulators of peptidoglycan synthesis and identified a membrane protein complex consisting of an amidase (LytH) that trims stem peptides from uncrosslinked peptidoglycan and its regulator to control cell growth. In the absence of LytH, peptidoglycan synthesis was spatially dysregulated, which caused cell growth and division defects. Attenuating the activity of the major peptidoglycan synthase corrected mislocalization defects and compensated for the loss of LytH. The authors propose that the amidase complex regulates the density of peptidoglycan synthase activity at the cell periphery and mid-cell to ensure that cell growth is coordinated with division.

ORIGINAL ARTICLE Do, T. et al. *Staphylococcus aureus* cell growth and division are regulated by an amidase that trims peptides from uncrosslinked peptidoglycan. *Nat. Microbiol.* https://doi.org/10.1038/s41564-019-0632-1 (2020)

BACTERIAL PATHOGENESIS

Getting carried away

Vibrio cholerae has an environmental reservoir in aquatic ecosystems and a pathogenic phase in the human intestine. To enable the transition from the environment to the host, *V. cholerae* has developed several strategies, including resistance to antimicrobial factors, which involves changes in the composition of the bacterial outer membrane. In particular, the accumulation of glycine-modified lipid A in lipopolysaccharide (LPS) increases resistance to cationic antimicrobial peptides (AMPs), and removal of the outer membrane porin OmpT confers resistance to bile salts. Most bacteria release outer membrane vesicles (OMVs) to deliver specific cargo, such as quorum-sensing signals, nucleic acids or toxins. In this study, Zingl et al. show that *V. cholerae* uses outer membrane vesiculation to exchange cell surface components following host entry, thereby promoting resistance to antimicrobial effectors.

It was previously shown that downregulation of the VacJ–Yrb ATP-binding cassette transport system under iron-limiting conditions induces phospholipid accumulation in the outer membrane, which in turn promotes the release of OMVs. During host colonization, iron limitation is a common stressor for bacteria, and thus the authors hypothesized that the genes encoding VacJ–Yrb are downregulated in *V. cholerae*, which leads to increased vesiculation. Indeed, the *yrb* gene cluster is transcriptionally silenced in *V. cholerae* during early stages of infection, and deletion of the permease of the VacJ–Yrb transport system resulted in hypervesiculation. Importantly, the hypervesiculating mutants exhibited a fitness advantage during colonization in a mouse model compared with the wildtype.

So, how is OMV release linked to this fitness advantage? The authors investigated whether differential

ARCHAEAL BIOLOGY

Asgard archaeon rises from the mud

Eukaryotes have been proposed to have originated from archaea that entered into an endosymbiotic relationship with an alphaproteobacterium, which gave rise to mitochondria. Based on metagenomic data showing the presence of eukaryotic signature proteins, Asgard archaea have been proposed as the closest living relatives of these ancestral archaea. In a 12-year feat of persistence, Imachi, Nobu et al. brought an Asgard archaeon into laboratory culture for the first time.

The team from the Japan Agency of Marine-Earth Science and Technology started their experiments in 2006, years before Asgard archaea were identified based on metagenomic sequencing. They incubated samples from a sediment core retrieved from a deep-sea methane seep off the coast of Japan for over 5 years in a continuous flow bioreactor under anaerobic conditions with methane as the main energy source. Further anaerobic in vitro enrichment cultures led to a simple community containing a

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