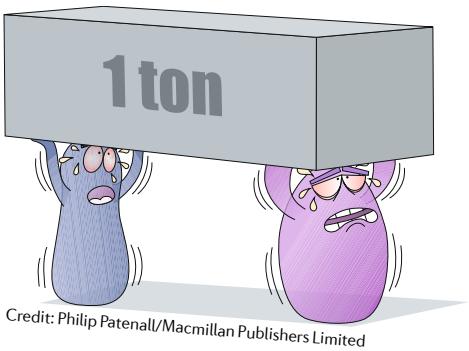

Credit: Philip Patenall/Macmillan Publishers Limited

pellicles. Specifically, bright clusters of EPS signal were observed in regions where there was reduced TasA signal, suggesting the presence of subpopulations that are specialised for EPS production. Flow cytometry of the pellicle population revealed the presence of three distinct populations of cells: ECM-OFF (EPS and TasA non-producers), ECM-ON (cells that produce both EPS and TasA) and EPS-ON (cells in which an EPS signal was detected only), confirming that wild-type *B. subtilis* can assume ECM-producing and ECM-non-producing phenotypes. However, this incomplete specialisation (that is, the absence of cells that exclusively produce TasA) does not adhere to the division of labour principle, prompting the authors to investigate whether it is beneficial or whether it can be outperformed by a genetically determined specialisation. By mixing Δ*eps* and Δ*tasA* mutants at different ratios, pellicle productivity was found to vary in response to strain frequency and a ~30% Δ*eps* frequency resulted in significantly higher pellicle growth in vitro and on the roots of *Arabidopsis thaliana* than wild-type, demonstrating that genetic division of labour between EPS and TasA producers provides a fitness benefit to biofilm communities.

Although division of labour occurs for ECM production in *B. subtilis* biofilms and genetic division of labour can outperform phenotypic division of labour, this might not be evolutionary stable in all situations and could explain why wild-type cells retain the ability to produce both ECM components.

Ashley York

ORIGINAL ARTICLE Dragoš, A. et al. Division of labor during biofilm matrix production. *Curr. Biol.* https://doi.org/10.1016/j.cub.2018.04.046 (2018)
FURTHER READING Nadell, C. D., Drescher, K. & Foster, K. R. Spatial structure, cooperation and competition in biofilms. *Nat. Rev. Microbiol.* **14**, 589–600 (2016)


Credit: Mira / Alamy Stock Photo

and dATP by adenylate kinase and nucleoside-diphosphate kinase. Whereas dAMP, dADP and dATP accumulated in control cells following exposure to dAdo, their levels were diminished in mutant cells lacking hENT1, ADK or DCK. But how does an increase in intracellular levels of dADP and dATP induce cell death in macrophages? The authors showed dAdo induces the caspase-3 pathway in control cells, a pathway that activates apoptosis. By contrast, caspase-3 activity was decreased in mutant cells lacking hENT1, ADK or DCK.

In summary, the proposed mechanism whereby *S. aureus*-generated dAdo induces macrophage apoptosis involves ENT1-mediated import of dAdo by macrophages, the conversion of dAdo to dAMP by ADK and DCK, the subsequent accumulation of dADP and dATP and caspase-3–induced apoptosis.

Andrea Du Toit

ORIGINAL ARTICLE Winstel, V., Missiakas, D. & Schneewind, O. *Staphylococcus aureus* targets the purine salvage pathway to kill phagocytes. *Proc. Natl Acad. Sci.* https://doi.org/10.1073/pnas.1805622115 (2018)

IN BRIEF

VIRAL INFECTION

Oiling the Flavivirus replication machinery

Flaviviruses modify the lipid composition at viral replication sites and induce lipophagy to drive virion production. This study found that dengue virus (DENV), Zika virus (ZIKV) and West Nile virus (WNV) rely on the host lipid droplet-associated ancient ubiquitous protein 1 (AUP1) for lipophagy. The authors used proteomics to identify differentially ubiquitylated proteins in DENV-infected cells compared to uninfected cells and found that AUP1 became unconjugated during infection. AUP1 associates with DENV non-structural protein 4A (NS4A) and relocalizes from lipid droplets to autophagosomes. Virion production was significantly reduced in AUP1-depleted cells and in cells that expressed an AUP1 acyltransferase domain mutant. AUP1-knockout cells were also resistant to DENV, WNV and ZIKV infection. Ubiquitylation disrupted the AUP1–NS4A interaction and inhibited AUP1 acyltransferase activity, which is required for phospholipid biosynthesis. The authors conclude that flaviviruses exploit the acyltransferase activity of AUP1 for lipophagy, a process that is regulated by ubiquitylation.

ORIGINAL ARTICLE Zhang, J. & Lan, Y. et al. Flaviviruses exploit the lipid droplet protein AUP1 to trigger lipophagy and drive virus production. *Cell Host Microbe* **23**, 819–831 (2018)

MICROBIOME

New drugs underfoot?

Soil-dwelling bacteria may represent a rich source of new antimicrobials and other drugs as they have already been found to produce valuable secondary metabolites, including antibiotics and antifungals. However, most of these molecules are derived from a small number of culturable taxa. This study reports draft genomes of hundreds of uncultured bacteria from a grassland soil ecosystem in northern California, United States. Using genome-resolved metagenomics, the authors analysed newly reconstructed genomes from 149 Acidobacteria, 135 Verrucomicrobia, 43 Rokubacteria and 49 Gemmatimonadetes species, which are highly abundant in soil ecosystems but had not previously been linked to secondary metabolite biosynthesis with confidence. They found 1,159 biosynthetic gene clusters that are predicted to encode various molecules, including peptides, bacteriocins and metabolites of unknown function, demonstrating that the biosynthetic potential of soil-dwelling bacteria has been underestimated.

ORIGINAL ARTICLE Crits-Christoph, A. et al. Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. *Nature* https://doi.org/10.1038/s41586-018-0207-y (2018)

VIRAL EVOLUTION

An aquatic origin of retroviruses

Relatively few retroviruses have been characterised in vertebrates other than mammals and birds, limiting our understanding of their diversity and early evolution. Now, a recent study performed a phylogenomic analysis of endogenous retroviruses (ERVs) — which provide insights into past retroviral infections — in the genomes of 72 fish, 4 amphibians and 16 reptiles. ERVs were found to be ubiquitous in the genomes of jawed vertebrates. The authors identified >8,000 ERVs and reconstructed ~450 complete or draft ERV genomes. Their analyses revealed that these ERVs clustered into five major clades that have different host distributions and that most retroviruses frequently underwent host switching and many water–land transitions. The authors posit that their analyses reveal an ancient aquatic origin of retroviruses.

ORIGINAL ARTICLE Xu, X. et al. Endogenous retroviruses of non-avian/mammalian vertebrates illuminate diversity and deep history of retroviruses. *PLOS Pathog.* **14**, e1007072 (2018)

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