drinking water, were dominated by cultured genera, which likely reflects sampling efforts and available culture methods. In the other environments, some of the most abundant genera often belonged to uncultured lineages, even in comparatively well-studied environments such as bioreactors or non-human hosts. Hot springs and hydrothermal vents had particularly high numbers of uncultured phyla.

Finally, the authors estimated the number of bacterial and archaeal cells on Earth based on 16S rRNA metagenome data and assuming one 16S rRNA gene copy per genome and thus per cell. They found that 7.3×10^{29} bacterial and archaeal cells belong to uncultured genera, which corresponds to 81% of all cells. To specifically address the abundance of uncultured cells in environmental samples, the authors also analysed sequences from a subset of studies that had looked at fresh water, sea water, terrestrial environments, etc. In these environmental habitats, they found that 0.5% of cells were culturable, which corresponds well with the previous estimate of 1%.

The analysis by Lloyd et al. confirms that the majority of bacteria and archaea on Earth are uncultured. Although there has been a lot of progress in culturing, not least of the human microbiota, many microorganisms and environments remain relatively unexplored. Some of this 'culture deficit' has been previously explained by the presence of viable but non-culturable cells, which assume a temporary non-growing phenotype but which can grow under the right conditions. In addition, the authors of the current study propose that some of the uncultured cells are phylogenetically divergent non-cultured cells (PDNCs), which implies that their growth requirements are drastically different from already cultured cells. The authors conclude that these PDNCs, which are widely distributed, abundant and alive, might have novel, ecologically important functions.

Ursula Hofer

ORIGINAL ARTICLE Lloyd, K. G. et al. Phylogenetically novel uncultured microbial cells dominate Earth microbiomes. *mSystems* **3**, e00055–18 (2018)

Previous studies have suggested that these membrane proteins form a complex, and using surface plasmon resonance the authors confirmed that FtsQ, FtsB and FtsL form a trimeric complex. The periplasmic domains of FtsL and FtsB do not interact on their own, but they bind to FtsQ to form a heterotrimeric complex. Moreover, the crystal structure of FtsB bound to FtsQ provided insights into the interaction surface and revealed that only residues 64 to 87 of FtsB interact with FtsQ. Mutations in the interaction interface inhibited cell division in vivo.

In summary, the insights gained from both studies into the assembly of the cell division machinery provide possible avenues for the development of cell division inhibitors.

Andrea Du Toit

Credit: Roman Milert/Alamy Stock Photo

ORIGINAL ARTICLES Eswara, P. J. et al. An essential *Staphylococcus aureus* cell division protein directly regulates FtsZ dynamics. *eLife* **7**, e38856 (2018) | Kureisaite-Ciziene, D., Varadajan, A. et al. Structural analysis of the interaction between the bacterial cell division proteins FtsQ and FtsB. *mBio* https://doi.org/10.1128/mBio.01346-18 (2018)
FURTHER READING Haeusser, D. P. & Margolin, W. Splitsville: structural and functional insights into the dynamic bacterial Z ring. *Nat. Rev. Microbiol.* **14**, 305–319 (2016)

IN BRIEF

VIRAL INFECTION

Shaping human evolution

The second interbreeding episode between modern humans and Neanderthals led to the introduction of DNA segments of Neanderthals into the genomes of modern humans, but most sequences were rapidly removed by purifying selection. However, for retained sequences it was not known whether this was due to positive selection and, if so, what selective advantage there was. Ednard and Petrov now show that long, frequent Neanderthal DNA segments in the genomes of modern humans are enriched for virus-interacting proteins (VIPs). In particular, VIPs that specifically interact with RNA viruses are enriched in modern Europeans. Thus, these segments might have been positively selected in response to viruses to provide an adaptive function. In agreement with this, many of the retained Neanderthal-derived VIPs had functions that are important for the virus life cycle. The retained Neanderthal DNA segments could provide insights into past epidemics.

ORIGINAL ARTICLE Enard, D. & Petrov, D. A. Evidence that RNA viruses drove adaptive introgression between Neanderthals and modern humans. *Cell* https://doi.org/10.1016/j.cell.2018.08.034 (2018)

ARCHAEAL PHYSIOLOGY

Profilin(g) Asgard archaea

Metagenomic studies have identified genes from Asgard archaea that are homologous to eukaryotic genes involved in membrane maintenance and function; however, whether those are functional was debated. In a recent study, Akıl and Robinson show that that primitive actin-regulating profilins are present in Asgard archaea. X-ray crystal structures of Loki profilin 1, Loki profilin 2 and Odin profilin revealed that Asgard profilins adopt the typical profilin fold. To better understand the interactions of Asgard profilins with actin, the authors determined the co-crystal structures of Loki profilin 1, Loki profilin 2 and Odin profilin bound to rabbit α-actin and found common modes of interaction. This, together with the finding that Asgard profilins modulate polymerization of mammalian actin in vitro, suggests that Asgard archaea possess functional profilin–actin systems.

ORIGINAL ARTICLE Akıl, C. & Robinson, R. C. Genomes of Asgard archaea encode profilins that regulate actin. *Nature* https://doi.org/10.1038/s41586-018-0548-6 (2018)
FURTHER READING Eme, L. et al. Archaea and the origin of eukaryotes. *Nat. Rev. Microbiol.* **15**, 711–723 (2017)

MICROBIOME

Diet and the mammary gland microbiome

Diet is one of the factors that shape the gut microbiome; however, little is known about the influence of diet on the microbiome in other tissues or organs. Shively et al. used a non-human primate model to investigate whether diet can modify the breast tissue-specific microbiota. Animals fed a Mediterranean diet had higher levels of *Lactobacillus* populations in their mammary gland tissues, whereas consumption of a Western diet led to increased levels of bacteria in the *Ruminococcus*, *Lachnospiraceae*, *Oscillospira* and *Coprococcus* genera. These results highlight both differences and similarities of the diet-mediated modulation of the microbiota in the gut and mammary gland tissues. A Mediterranean diet also led to increased levels of bile acid metabolites and bacterial-modified bioactive compounds, which may affect inflammation in the breast and modulate breast cancer risk. Thus, diet influences microbiome populations not only in the intestinal tract but also at distal sites.

ORIGINAL ARTICLE Shively, C. A. et al. Consumption of Mediterranean versus Western diet leads to distinct mammary gland microbiome populations. *Cell Rep.* **25**, 47–56 (2018)