

IN BRIEF

BACTERIAL PHYSIOLOGY**Alternative ways to flip out**

Previous work in *Escherichia coli* has provided evidence that MurJ is the flippase responsible for transport of the cell wall precursor lipid II across the cytoplasmic membrane. However, deletion of MurJ paralogues in *Bacillus subtilis* does not affect cell viability, which suggests that the bacterium has an alternative flippase. Meeske *et al.* performed a synthetic lethal screen and identified *ytgP* (a known MurJ paralogue, which was renamed *murJ*) and *ydaH* (which is not a MurJ paralogue) as a synthetic lethal pair; this suggested that YdaH is an alternative flippase in *B. subtilis* and it was therefore renamed Amj (alternate to MurJ). Notably, both Amj and MurJ from *B. subtilis* supported lipid II flipping in *E. coli* and rescued a lethal mutant *E. coli* strain lacking MurJ. As depletion of MurJ in *B. subtilis* leads to increased expression of Amj, the authors propose that Amj is an alternative flippase that supports *B. subtilis* growth when MurJ is inhibited.

ORIGINAL RESEARCH PAPER Meeske, A. J. *et al.* MurJ and a novel lipid II flippase are required for cell wall biogenesis in *Bacillus subtilis*. *Proc. Natl Acad. Sci. USA* <http://dx.doi.org/10.1073/pnas.1504967112> (2015)

ARCHAEOLOGICAL EVOLUTION**Bridging the gap**

Eukaryotes are thought to have arisen via the engulfment of a proto-mitochondrion by an archaeon, suggesting that many features of the eukaryotic cell were present in the archaeal ancestor. However, known archaea lack certain eukaryotic hallmarks of cellular complexity, such as an endomembrane system and the means to phagocytose a proto-mitochondrion. In this study, Spang *et al.* sequenced uncultivated metagenomes from a deep sea vent and discovered one complete and two partial novel archaeal genomes that constitute the new candidate phylum 'Lokiarchaeota'. The predicted proteome of these novel archaea contains homologues of many eukaryotic proteins that function in the endomembrane system and in phagocytosis, including actin and related proteins, and Ras superfamily GTPases, suggesting that this phylum provides the missing link in eukaryogenesis.

ORIGINAL RESEARCH PAPER Spang, A. *et al.* Complex archaea that bridge the gap between prokaryotes and eukaryotes. *Nature* <http://dx.doi.org/10.1038/nature14447> (2015)

MICROBIAL ECOLOGY**Sharing is caring**

Zelezniak *et al.* developed a modelling approach termed 'species metabolic interaction analysis' (SMETANA) that maps all possible interspecies metabolic exchanges according to the genomic potential encoded by all species present in microbial communities. They analysed more than 800 communities in soil, water and human gut samples, and identified co-occurring subcommunities, which are groups of species found together within different samples. Their analysis revealed that the species present in the communities display increased resource competition compared with random microbial assemblies, suggesting that resource availability in different habitats shapes the overall composition of the community. By contrast, the species present in the smaller subcommunities have a high degree of dependency on exchanged metabolites, particularly amino acids and sugars. These data highlight how the interplay between competitive and cooperative strategies shapes the composition of complex microbial communities.

ORIGINAL RESEARCH PAPER Zelezniak, A. *et al.* Metabolic dependencies drive species co-occurrence in diverse microbial communities. *Proc. Natl Acad. Sci. USA* <http://dx.doi.org/10.1073/pnas.1421834112> (2015)