

IN BRIEF

ARCHAEOAL GENOMICS**A new phylum for methanogens**

Previously, methanogenic organisms had only been described in the Euryarchaeota. Now, Evans *et al.* report two near-complete genomes that provide strong evidence for methanogenesis in a second archaeal phylum, the Bathyarchaeota. The genomes — obtained from an Australian methane well — contain genes indicative of methylotrophic methanogenesis using a diverse set of methylated compounds. Interestingly, one of the genomes also contains genes for complex fermentation and the other also contains genes for β -oxidation; neither of these processes have previously been seen in methanogens. By contrast, structural prediction suggested that both genomes encode a functional methyl-coenzyme M reductase complex (MCR), a universal feature of methanogens. A survey of metagenomes from geographically disparate high-methane-flux environments identified additional non-euryarchaeotal examples of genes encoding MCR components. The authors propose that methanogenesis arose in a common ancestor of the two phyla, rather than in the Euryarchaeota, and thus has a more ancient origin than has sometimes been suggested.

ORIGINAL RESEARCH PAPER Evans, P.N. *et al.* Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. *Science* **350**, 434–438 (2015)

FUNGAL BIOLOGY**To mate or tomato?**

The mechanistic basis for chemoattraction in plant–fungus interactions has long proved elusive. Turrà *et al.* found that the activity of three peroxidases — TMP1, TMP2 and CEVI-1 — in tomato plant exudate mediated a chemotropic response in the fungal crop pathogen *Fusarium oxysporum*. To determine how *F. oxysporum* processes this chemotropic signal, the authors tested deletion mutants for MAPK pathways. They found that the Mpk1 pathway was required for the fungal response to both plant peroxidase activity and α -pheromone, a fungal mating factor; this was distinct from chemoattraction to nutrients, which relied on the Fmk1 pathway. Surprisingly, the α -pheromone receptor Ste2 was also required for fungal chemoattraction towards the tomato plant, although the ligand that links peroxidase activity to this receptor remains unknown.

ORIGINAL RESEARCH PAPER Turrà, D. *et al.* Fungal pathogen uses sex pheromone receptor for chemotropic sensing of host plant signals. *Nature* <http://dx.doi.org/10.1038/nature15516> (2015)

TECHNIQUES & APPLICATIONS**Scaling up spatial imaging of the gut microbiota**

Biogeography has a fundamental role in gut–microbiota interactions; however, methods for imaging this biogeography have been lacking. Earle *et al.* took advantage of improved mucus fixation protocols to develop a pipeline for large-scale quantitative spatial imaging of gut microbiota. They developed a new computational tool, BacSpace, that stitches together a single continuous image from raw data and measures the distance coordinates of luminal fluorescence signals — separated into bacteria and host factors — to and along the epithelium. To demonstrate the utility of the pipeline, the authors eliminated microbial-accessible carbohydrates from the diet of mice colonized with microbiota from a human donor, which deprived the microbiota of its primary metabolic input. This revealed a thinner mucus layer that is in closer proximity to bacterial cells, a more homogeneous community organization, and upregulation of the inflammatory marker REG3 β .

ORIGINAL RESEARCH PAPER Earle, K.A. *et al.* Quantitative imaging of gut microbiota spatial organization. *Cell Host Microbe* **18**, 478–488 (2015)