

## IN BRIEF

## MICROBIOME

## Pick of the crop microbiome

The plant-associated microbiome is of major agricultural importance as it influences the outcome of crop infections. Chen et al. show that a member of the wheat microbiome reduces the virulence of *Fusarium graminearum*, a fungal plant pathogen that causes Fusarium head blight (FHB) — a devastating disease of small grain cereal crops. The authors cultured >12,000 bacterial isolates from the wheat head microbiome and performed a screen to determine whether any of these isolates could protect against FHB. *Pseudomonas piscium* ZJU60 was found to have a high antagonistic activity against FHB. Bioinformatic analyses of the *P. piscium* ZJU60 genome led to the identification of a biosynthetic gene cluster that produces phenazine-1-carboxamide (PCN), an antifungal molecule that is released by the bacterium. PCN was found to target a fungal histone acetyltransferase, leading to the deregulation of histone acetylation and the suppression of fungal growth and virulence.

**ORIGINAL ARTICLE** Chen, Y. et al. Wheat microbiome bacteria can reduce virulence of a plant pathogenic fungus by altering histone acetylation. *Nat. Commun.* 9, 3429 (2018)

## BACTERIAL EVOLUTION

## Next-generation bacterial taxonomy

Advances in culture-independent sequencing technologies have led to a rapid expansion in the number of bacterial genomes, necessitating a robust genome-based taxonomy for describing microbial diversity and for constructing accurate genome-based phylogenies that normalize taxonomic ranks according to evolutionary divergence, and overcome inconsistencies in historical classification schemes. Parks et al. present a standardized bacterial taxonomy inferred from the concatenation of ubiquitous single-copy proteins that covers 94,759 bacterial genomes. In this new taxonomy — referred to as the genome taxonomy database (GTDB) taxonomy — ~58% of these genomes had changes to their existing taxonomy and 99 new phyla are described, including six major monophyletic units of the Proteobacteria and the merger of the Candidate Phyla Radiation into a single phylum. The authors anticipate that the GTDB will improve the classification of uncultured bacteria.

**ORIGINAL ARTICLE** Parks, D. H. et al. A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. *Nat. Biotechnol.* <https://doi.org/10.1038/nbt.4229> (2018)

## FUNGAL PATHOGENESIS

## Slipping through the NET

*Candida auris* recently emerged as a serious fungal pathogen that can cause invasive candidiasis with mortality rates as high as 60%; however, little is known about the pathogenesis of *C. auris* and it is unclear why it is spreading rapidly in hospitals. In a recent study, Johnson et al. investigated the interaction between *C. auris* and neutrophils, which control invasive candidiasis through phagocytosis or by releasing neutrophil extracellular traps (NETs). In a co-culture in vitro system, human neutrophils were poorly recruited and killed *C. auris* at lower levels compared to *Candida albicans*. Moreover, these neutrophils failed to form NETs. When neutrophils were mixed with both *C. auris* and *C. albicans*, neutrophils preferentially interacted with and killed *C. albicans*. When these *Candida* species were injected into zebrafish larvae hindbrains, ~50% fewer neutrophils were recruited to *C. auris*, and NETs were only produced in the presence of *C. albicans*, suggesting that the evasion of neutrophils contributes to the virulence of *C. auris*.

**ORIGINAL ARTICLE** Johnson, C. J. et al. Emerging fungal pathogen *Candida auris* evades neutrophil attack. *mBio* 9, e01403 (2018)

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The authors quantified the relative amounts of free and vesicle-contained rotaviruses within the stools of rotavirus-infected piglets and mouse pups and found that vesicle-contained rotaviruses comprise 10% to 45% of the total stool rotavirus pools. Importantly, the contribution of the vesicle-contained rotavirus populations to infectivity was shown to be greater compared to that of free viruses. The authors fluorescently labelled vesicles containing rotavirus that were isolated from infected mouse pup stools and fed them to new pups. The ingested fluorescent vesicles were still intact in the harvested intestinal content, suggesting that some viruses are retained in vesicles during passage through the gastrointestinal tract.

Furthermore, animals fed vesicle-contained rotavirus had a more rapid onset of disease, more infected intestinal tissues and cleared the infection slower than animals fed equivalent numbers of free rotavirus particles. In sum, the data suggest that during faecal–oral transmission, freely dispersed rotaviruses may not reach intestinal enterocytes in high enough quantities to establish infection, and that clustering of multiple infectious viruses within extracellular vesicles increases their potency and results in greater levels of intestinal infection.

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**ORIGINAL ARTICLE** Santiana, M. & Ghosh, S. et al. Vesicle-cloaked virus clusters are optimal units for inter-organismal viral transmission. *Cell Host Microbe* 24, 208–220.e8 (2018)

Credit: Philip Patenall/Springer Nature Limited



that the oldest fossils for life originate from the stems of these lineages. The Great Oxidation Event (GOE; ~2.4 Ga), which marks the introduction of atmospheric oxygen, predates the origin of modern Cyanobacteria, indicating that photosynthesis evolved within the cyanobacterial stem lineage and not within the crown Cyanobacteria. This is compatible with a causal role of total-group Cyanobacteria in the GOE.

The last eukaryotic common ancestor (LECA) was estimated to emerge late in Earth's history (<1.84 Ga), rejecting the hypothesis that the GOE facilitated eukaryogenesis. Symbiotic mitochondria are also estimated to emerge late (2.053–1.21 Ga), reflecting a late origin of  $\alpha$ -proteobacteria, the group to which the ancestor of mitochondria belonged. A similar age estimate for both  $\alpha$ -proteobacteria and LECA suggests that mitochondrial symbiosis facilitated a rapid process of eukaryogenesis.

In summary, this study highlights that although an analysis of the fossil record is central for understanding ancient evolutionary events and the origin of eukaryotes, integration of other lines of evidence (for example, genetic and geological data) is crucial for providing an evolutionary framework to test new hypotheses that will bring us closer to understanding our origins.

Ashley York

**ORIGINAL ARTICLE** Betts, H. C. et al. Integrated genomic and fossil evidence illuminates life's early evolution and eukaryote origin. *Nat. Ecol. Evol.* <https://doi.org/10.1038/s41559-018-0644-x> (2018)