Credit: Science Photo Library/ Alamy Stock Photo

the subfamily to which *P. falciparum* belongs. The binding affinity of RH5 orthologues from six *Laverania* species for human, gorilla and chimpanzee basigin was measured using SPR and confirmed using cell-based binding assays. The promiscuous receptor-binding phenotype was observed for parasites belonging to the clade that transferred its genome segment to the ancestor of *P. falciparum*, whereas other lineages displayed host-specific receptor binding. These observations suggest that introgression led to promiscuity in RH5–basigin binding, which was crucial for transmission to humans.

Last, to explain the specificity of *P. falciparum* RH5 for human erythrocytes (that is, the loss of binding to gorilla basigin) the authors investigated the adaptive changes that occurred after the ability of introgressed RH5 to bind to both human and gorilla erythrocytes was acquired. Six amino acid differences were found between IntRH5 and a reference *P. falciparum* RH5 strain, which the authors individually mutated and then tested in binding assays. Remarkably, a single amino acid in RH5 was found to be responsible for human-specific basigin binding.

In sum, this study reveals a sequence of molecular events that led to the origin of *P. falciparum* in humans, which could inform the surveillance of future parasitic zoonoses.

Ashley York

ORIGINAL ARTICLE Galaway, F. et al. Resurrection of the ancestral RH5 invasion ligand provides a molecular explanation for the origin of *P. falciparum* malaria in humans. *PLOS Biol.* **17**, e3000490 (2019)

found that disease incidence was lower in the latter. Moreover, metagenomic sequencing and network analyses revealed that the taxonomic diversity of the endophytic microbiome became enriched and more complex in plants grown in pathogen-inoculated suppressive soils compared with soil alone. In particular, the abundance of *Chitinophaga* and *Flavobacterium* species was increased in endophytic bacterial communities from plants grown in suppressive soils in the presence of the pathogen.

In the endophytic metagenomes, the authors identified genes that exhibited increased expression following infection, such as genes encoding enzymes associated with fungal cell wall degradation, which suggests a role in protection from fungal pathogens. In addition, several previously unknown secondary metabolite biosynthetic gene clusters (BGCs) were overrepresented in the endophytic microbiomes of pathogen-inoculated suppressive soils. On the basis of metagenomics and network inference combined with de novo assembly of endophyte genomes, the authors reconstructed disease-suppressive synthetic consortia. Following colonization of the rhizosphere and root endosphere of sugar beet seedlings, disease incidence was decreased, an effect that was even observed for a 'minimal' consortium comprising one *Chitinophaga* isolate and one *Flavobacterium* isolate. Transcriptional analysis showed an increased expression of chitinase and an uncharacterized BGC in the root endosphere-colonizing consortia following pathogen challenge. Site-directed mutagenesis of this BGC in *Flavobacterium* reduced the disease-suppressive effect of the isolate alone, as well as of the minimal consortium.

Future studies uncovering microbial members and functional traits associated with different plant phenotypes will guide the targeted design of microbial consortia that promote plant health.

Andrea Du Toit

ORIGINAL ARTICLE Carrión, V. J. et al. Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. *Science* **366**, 606–612 (2019)

IN BRIEF

ENVIRONMENTAL MICROBIOLOGY

Marine microbial diversity from pole to pole

Our oceans are dominated by microbial species that are essential for marine ecosystems and have central roles in biogeochemical cycles, influencing the climate of our planet. Yet, our understanding of spatial patterns of microbial and functional diversity, and the drivers of this diversity, is limited. Now, two recent studies report ocean microbial diversity pole to pole, using data collected from the *Tara* Oceans expedition, an international and interdisciplinary project that collected 35,000 samples across the world's oceans from 2009 to 2013. Ibarbalz et al. used DNA sequencing of filtered seawater and imaging of net catches to investigate the latitudinal gradients and global predictors of diversity across bacteria, archaea, eukaryotes and major viral clades in the surface oceans. The authors observed a general decline in diversity towards the poles for most groups, mainly driven by decreases in temperature; indeed, temperature was the best predictor of diversity. To understand how global warming may affect microbial diversity, the authors modelled trends in diversity on a global scale at the beginning and the end of the 21st century and found that severe warming of the surface ocean could lead to tropicalization of diversity in temperate and polar regions. Salazar et al. used a combination of metagenomics and metatranscriptomics to survey microbial genetic composition and gene expression in the global ocean. A dataset of 370 metagenomes and 187 metatranscriptomes comprising 47 million genes was generated from 126 sites pole to pole. The authors examined gene expression changes and community turnover as the primary mechanisms shaping metatranscriptomes across latitude and depth and found that their individual contributions differ for various biogeochemical processes, including the cycling of carbon, nitrogen and sulfur, and processes involved in photosynthesis. The authors also found that the relative contribution of gene expression changes are lower in polar waters compared with non-polar regions and hypothesise that changes in community activity as a consequence of warming will be driven more by changes in composition than by gene expression.

ORIGINAL ARTICLES Ibarbalz, F. M. et al. Global trends in marine plankton diversity across kingdoms of life. *Cell* **179**, 1084–1097.e21 (2019) | Salazar, G. et al. Gene expression changes and community turnover differentially shape the global ocean metatranscriptome. *Cell* **179**, 1068–1083.e21 (2019)

RELATED ARTICLE Cavicchioli, R. et al. Scientists' warning to humanity: microorganisms and climate change. *Nat. Rev. Microbiol.* **17**, 569–586 (2019)

BACTERIAL PHYSIOLOGY

Stop and don't move

Pseudomonas aeruginosa can attach to surfaces via its polar flagellum; following irreversible attachment, changes in gene expression promote surface colonization and biofilm formation. Schniederberend et al. show that modulation of flagellar rotation is another strategy used by surface-attached bacteria to promote persistence at the surface. Wild-type *P. aeruginosa* cells stopped flagellar rotation shortly after surface attachment, whereas mutants lacking FlhF, a GTPase required for polar flagellar placement, did not. FlhF was shown to interact with the flagellar rotor component FliG, and with the polar scaffolding protein FimV, which regulates the production of cAMP. The FlhF–FimV interaction was required to stop flagellar rotation and led to an increase in intracellular cAMP levels. Cells lacking FlhF or FimV exhibited persistent flagellar rotation, an effect that could be rescued by exogenous cAMP, implicating cAMP signalling in the modulation of flagellar rotation.

ORIGINAL ARTICLE Schniederberend, M. et al. Modulation of flagellar rotation in surface-attached bacteria: a pathway for rapid surface-sensing after flagellar attachment. *PLoS Path.* https://doi.org/10.1371/journal.ppat.1008149 (2019)