Our year in review

It's an exciting time to be a microbiologist and we have the honour and privilege of having front-row tickets to see the field develop and progress. As we take stock of the past year, we will count down the days until 2020 by celebrating the field and the season with a microbiology advent calendar.

As our readers may have noticed from our Table of Contents, our December issue comes with a very packed back half. We have included all of the primary research published this year that was in time to make the relevant production deadline, so that the year of publication 'in issue' would be the same as the year the studies were initially available. As an online-only journal, we can, and will from now on, include in each issue articles as they are exported to our production team, rather than compiling issues that have a specific number. Our aim to publish 10–14 articles per month will continue, but as submissions come in peaks and valleys, our issues will reflect some of that variability. This also means that given increasing submission volumes and thus pressure for space, our editorial bar will need to raise somewhat. We will nevertheless continue to consider and publish significant advances in all areas of microbiology, however big or small the specific field may be.

This December, our sled is full of microbiology goodness. Given the festive season, that we appreciate that 50 articles are a lot to digest and time is always a scarce commodity—and considering the central European influences of this editorial team—we have decided to create a microbiology advent calendar, which we hope you will enjoy. For our social media followers (you can find us @NatureMicrobiol on Twitter), we will open a virtual door every day from 1 December to reveal two of the papers in this issue under the hashtag #NMicroAdventCalendar.

As the end of the year is a time for reflection, we have selected some of the year's highlights. Discussing the whole microbiology literature would make this an impossible exercise within a short Editorial, so we have limited the scope to work published within our pages. As proud 'parents', editors find it difficult to choose among the many papers we help publish, and this selection of editor's picks has unavoidably missed important contributions and great work that we have published, for which we sincerely apologize. We began the year with an infectious disease Review focus, including pieces on tracking virus outbreaks in the twenty-first century, studying vector biology to inform infectious disease control, the role of the microbiota in infectious diseases, and developing point-of-care diagnostics. All, particularly epidemiology, vector biology and diagnostic development, were topics that we covered throughout the year in our front and back half content.

Global quantitative analyses provide important baseline data to inform policy, and we have published studies mapping lower respiratory infection morbidity and mortality in African children (2000–2017), which also identified hotspots where action is most necessary (featured on the cover this month), as well as work assessing the current and future global distribution of dengue and past and future spread of the arbovirus vectors *Aedes aegypti* and *Aedes albopictus*. Research into vector biology will helps us understand the spread of disease and highlight possible points for intervention. In this regard, other studies this year identified a role for host serum iron in Dengue virus acquisition by mosquitoes, host candidate genes that influence the ability of *Wolbachia* to reduce Dengue virus replication in the vector *A. aegypti* as well as changes in the genetic structure of *Anopheles* mosquito populations that drive *Plasmodium* dynamics.

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On the topic of antimicrobial resistance, this year saw the identification of plasmids mediating resistance to last-line antibiotics, such as tigecycline, or increased virulence in *Klebsiella pneumoniae*. The emerging role of heteroresistance in clinical practice was underscored by a study showing that its detection can afford new opportunities for combination treatment as well as more mechanistic work showing that heteroresistance is often driven by gene amplification.

Microbiology has been no stranger to the structural revolution, with cryo-electron microscopy providing in-depth insights into the functioning of ever bigger and more complex microbial nanomachines. Salient examples have been the *Salmonella* T3SS injectisome in four different states, the entire contractile injection system of the *Serratia* anti-feeding prophage in both the extended and contracted states, and an in situ structure of the intact T2SS from *Legionella pneumophila* published in this issue. Crystallization has also contributed to the structural biology bonanza, and we have published several virus–antibody complex structures; for example, the characterization of antibody neutralization mechanisms against enterovirus D68 (suspected of causing the paralysing disorder acute flaccid myelitis), as well as work defining neutralizing epitopes for human antibodies that target essential *Plasmodium vivax* invasion proteins, providing important insights for vaccine development.

An in-depth look at poxvirus structure with super-resolution microscopy showed that fusion machinery accumulates at virion tips, which is essential for effective infection. In other virology highlights, a study in this issue solves a long-standing question in the HIV-1 field by showing that cyclophilin A counteracts restriction by TRIM5α in human in primary cells. Of relevance due to the potential for spillover into humans was the identification of the Mengla filovirus in Chinese bats, and two studies highlight the relevance of interactions between influenza and respiratory bacteria for bacterial adherence and responses to influenza vaccines.

The importance of understanding population-level dynamics in host–pathogen interactions was highlighted by work showing that, by silencing quorum sensing, *Staphylococcus aureus* builds tightly packed biofilms that can withstand attack by phagocytes, and that biofilm morphology of the filamentous fungus *Aspergillus fumigatus* is associated with response to oxygen tension and impacts disease progression in vivo. As examples of more classical immune evasion strategies, a *Legionella* effector deubiquitinase was shown to specifically hydrolyse linear ubiquitin chains to inhibit host inflammatory signalling, and the *Rickettsia* effector OmpB to generate a capsule-like shield that prevents xenophagy.

Exploring the connections between our gut microbiota and brain function contiues to be an important focus of research, and work in our pages has contributed, for example, evidence for microbiome links to

human mental health and depression on a population-wide level, identifying and characterizing GABA-modulating bacteria in the human gut and showing that microbiota-induced serotonin production in the intestine modulates bacterial colonization. Beyond the gut–brain axis, research has shown that cooking shapes the structure of the gut microbiome, and results from the integrative human microbiome project (iHMP) in large human cohorts shed light into gut microbiome structure and metabolic activity in inflammatory bowel disease.

Environmental microbiomes were also represented in our pages, for example, by an integrated genomic characterization of coral and its microbial partners, which demonstrated the critical and diverse roles that microorganisms have within the coral holobiont, emphasizing they should be taken into account to effectively inform reef conservation strategies. Another study analysed data from near-ground and high-altitude air above Antarctica, which are hard-to-analyse, understudied, low-biomass environments, providing insights into the role of airborne transport limitation in determining microbial biogeographic patterns. Diatom viruses, shown to respond to silicon limitation, were found to be important players in diatom blooms, triggering bloom collapse and thus contributing to diatom-mediated biogeochemical cycling. With increased sequencing power and decreasing costs, virus discovery efforts have evidenced that the sheer diversity poses limitations for assembly and classification. This year has seen continued efforts in virus discovery, such as the demonstration that inoviruses are virtually everywhere and that giant *Prevotella* phages are abundant in the gut, as well as method development for viral classification.

The archaea field is buzzing with activity, and we have published several articles that provide insight into archaeal metabolism, suggesting that the Archaea are likely more important for biogeochemical cycles than previously thought. Among them, analyses of Asgard archaea metabolic capabilities have put forth new scenarios for eukaryogenesis; for example, the suggestion that the archaeal protoeukaryote ancestor was capable of mixotrophy and aerobic respiration, or a 'reverse flow model' that involves electron or hydrogen flow from an archaeal host to a bacterial symbiont. Some of these issues were discussed in a thought-provoking News & Views piece. The recently described and long-awaited culture of a Lokiarchaeota-related Asgard archaeon, which some have compared to the moon landing of microbial ecology, warrants a mention here despite not being published in our pages[1].

> "we [...] thank the authors of all submitted papers, our reviewers and our readers for your support, without which *Nature Microbiology* would not be possible."

We have published some great applied microbiology, some of which has caught the public's attention, as did the paper identifying enzymes in the gut microbiota that can efficiently convert A and B type blood cells to 'universal' donor O. Other highlights are the development and clinical validation of a DNA-based diagnostic to assess the presence of 1,250 bacteria, DNA viruses, fungi and eukaryotic parasites, and the engineering of avirulent mutants of *Burkholderia* that retain their biocontrol properties, reinvigorating its potential as a biopesticide. Tools enable fields to move forward, which we hope will be the case for approaches to make non-model microorganisms tractable or speed up research, such as Mobile-CRISPRi for gene knock-down in unculturable bacteria; chassis-independent recombinase-assisted genome engineering (CRAGE) to activate biosynthetic gene clusters in undomesticated bacteria; a characterization of minimal genomes and metabolic pathways enabling rapid replication in *Vibrio natriegens*, a promising model bacterium; or the generation of genetically engineered strains of *Cryptosporidium* to make life cycle progression and parasite sex tractable.

Last but not least, the winner of our weird and wonderful category was a swimming eukaryotic doughnut that uses its flagellum like a prokaryote would.

Looking back at the microbiology in our pages and beyond in 2019, the Editorial in our first issue remains just as timely. As we said then, microbiologists live in interesting times, and we are honoured that you have allowed us to help the field develop and grow. As the year comes to a close, we would like to thank the authors of all submitted papers, our reviewers and our readers for your support, without which *Nature Microbiology* would not be possible. We look forward to another exciting year of microbiology. ❐

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References

1. Imachi, H. et al. Isolation of an archaeon at the prokaryote-eukaryote interface. Preprint at https://www.biorxiv.org/content/10.1101/726976v1 (2019).