MICROBIOLOGY TODAY

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Emerging Opportunities

From the use of bacteria to redefine our life on Earth to the role of microbes in space exploration, this issue looks to the opportunities microbiology provides for all of us.

MICROBIOLOGY SOCIETY

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From the Editor

"*Microbiology Today* has been a constant throughout my Microbiology Society membership, so as I sit to write the last editorial, I thought I would look backwards as well as forward."

The Microbiology Society is not afraid to change in order to match the needs of the membership – from updating the website and moving to Open Access publishing, to a new citeable way to publish a more diverse range of monthly magazine-style articles.

Microbiology Today was first published in February 1999 with an issue focussing on the big microbiological challenges of the day: genetically modified crops, BSE and CJD, and the quarantine policy for rabies. There are some very familiar names attached to this issue, including our very own Chief Executive Peter Cotgreave with a Comment piece on the future of British science.

Not much has really changed with our last issue looking at the current microbiological landscape, specifically focussing on 'Emerging Opportunities'. Our first article looks at the opportunities on the horizon, with Matt Bawn from the University of Newcastle outlining the possibilities of bacterial genomics. Traditional approaches of bacterial genome generation and analysis have opened our eyes to new potential, and machine learning and AI seem set to revolutionize bacterial genomics all over again.

The second featured article in this issue is from Leanne Timpson from Nottingham Trent University. Leanne explores the possibilities of seaweed. In addition to the benefits to biodiversity and climate change, seaweed is proving to be a rich area for antimicrobial compounds.

Antimicrobial resistance is one of the most concerning global challenges we face, and the Microbiology Society is leading the way with the Knocking Out AMR project, an ambitious, bold and extensive scheme of work aiming to promote feasible and effective solutions to AMR. You can find out more and register interest in the project on the Society's website.

Our final featured article comes from Jack Buckley from Manchester Metropolitan University with a piece examining bark cloth as potentially a sustainable and antimicrobial fabric. With widespread interest in new and novel antimicrobial agents, and the pressing need for a sustainable future in medical practices – bark cloth wound dressings are an exciting prospect to be investigated further.

Monthly magazine-style content is planned for 2026 and will be published via *Micro Perspectives* on the Society's publishing website – get in touch if you would like to find out more. Just as when *Microbiology Today* replaced *SGM Quarterly*, and as we change again, I would like to mirror the editorial team of that first issue (Dr David Roberts, Dr Ulrich Desselberger, Professor David Rowlands, Janet Hurst, and Ian Atherton) – "The editorial team hopes that you enjoy reading it and find that the content reflects topics of current interest in microbiology."

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From the President

"This is the last issue of *Microbiology Today* and it's fitting that it comes as the last time I will write here as your President."

For many years, *Microbiology Today* has served the membership well as a place to publish our magazine content – articles on subjects of specialist study or simply of pure interest. They are not full research articles in the traditional sense, instead they share frequently insightful – and often entertaining – knowledge from across the microbiology community.

While many of us will bid a fond farewell to MT, as it has become known, we know it is time to amplify our members' voices via new and innovative channels. This means finding a way to publish your magazine content which can be easily shared and has the ability to reach and influence people not only within our community but beyond. For these reasons, the Society invites you to write for *Micro Perspectives*. These magazine-style articles are published via the journals website. 'Hot topics' and opinion pieces are welcomed, which may not be published elsewhere. Importantly, articles add to the authors publication record by providing them with a DOI. I strongly recommend you take up this opportunity, and you can read more about how to do so in Victoria's Editorial.

This transition is just one of many that I have overseen during my Presidency. The Society is facing a period of unprecedented change, and that brings opportunities and the chance to do things differently. Since I took up the role in January 2022, the Society has embraced the transition to Open Access publishing with *Microbiology*, the first journal in the portfolio to go fully OA in 2023. We have launched the Society's biggest campaign to date, 'Publishing for the community' – which emphasises how, as a not-for-profit publisher, we reinvest into the microbiology community for the benefit of all.

I have also chaired Council during a period where we have overseen a full review of Society activities resulting in the expansion of our rich and varied events programme, the launch of our ambitious and wide-ranging project 'Knocking Out AMR', and the award of the inaugural cohort of our Unlocking Potential grant – the result of the Society's first-ever fundraising activity.

Something which has been incredibly important to me has been to widen access to our community, to make the Society more inclusive as the 'home from home' we know our members value it for. This has included working hard in supporting the Society to better reflect its diverse membership across its governance structures. I am also delighted that we have introduced the Society's first Equality, Diversity and Inclusion Prize, and the first winners will present their Lectures at Annual Conference 2025.

This year Council came to an incredibly important decision – with the support of the UK's Charity Commission – to amend the Society's Articles of Association, allowing the formation of the new Board of Trustees and Advisory Council. Ratified by our membership at the AGM earlier in October, this means that in a rapidly changing environment, we will be able to bring in expertise beyond that available in the professional microbiology community and help ensure the Society continues to thrive in the modern world.

Over the course of three years I have attended numerous events including three Annual Conferences, Roadshows, scientific meetings and the AGM, Committees Day and Early Career Microbiologist of the Year competition. It has been a great pleasure to meet so many members and to talk to them about their experience of the Society. Equally, I have worked closely with the Society staff and together I believe that we have helped further the Society's principal goal to amplify our members' voices, wherever they are in the world.

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From the Chief Executive

"The world is full of threats and challenges."

But if you look them from a different perspective, each of those potential problems also offers opportunities. As we learn in this final issue of *Microbiology Today*, the challenge posed by Artificial Intelligence brings fresh chances to learn things we could never have dreamt of studying in the past, and the massive public interest in microbiological issues opens up fresh avenues for the research community.

As an organisation, perhaps the Microbiology Society's greatest opportunity comes from changes in the way that scientific publishing works. There is no doubt that in the short term, these changes represent a significant threat – our income has fallen in recent years, which is making it harder to support the community. That situation is not helped by the fact that different parts of the world are moving to Open Access at different paces. But in the medium term, there are obvious potential opportunities if we adapt to make the best of them. One of the consequences of the change in business model is that traditional rigid views about the best place to publish your research are being challenged. For many researchers in many parts of the world, new priorities are emerging. Microbiologists are realising that they have a choice – you can publish your articles with a big commercial publisher and contribute to the profits of their shareholders or you can publish with the Microbiology Society and help to generate funds that support your community. Publishing one article in one of our journals generates the funds to send four early career microbiologists to our Annual Conference to benefit from the wealth of opportunities that brings. Two articles published with us generate the revenue to fund a Harry Smith Summer Studentship, providing invaluable experience in research and supervision. All of the Microbiology Society's events, grants and training opportunities are funded by the income from publishing our journals.

Of course the reason these things are so important is because the world needs microbiology to address its greatest challenges. Last month, I had the privilege of going to New York for the United Nations High Level Meeting on Antimicrobial Resistance (AMR). The world's leaders came together to mark the huge threat posed by AMR and to recognise the need for different sectors to work together if we are to avoid a human tragedy within our lifetimes. There are very few occasions in history during which human progress and technology have gone backwards (the loss of supersonic flight when Concorde was decommissioned is the only example that springs to mind), but if we are not careful, we will lose the benefits of antibiotics that we have seen since the Microbiology Society's first President, Alexander Fleming, discovered penicillin. Every year, tens of millions of people will die unnecessarily. That UN meeting represented a colossal opportunity for the microbiology community. Of course, there was a lot of diplomatic speech-making and arbitrary ambitions that lacked specific commitments and timelines – that is how international relations works. But through the lens of AMR, there was a very genuine recognition that microbes matter, which means that microbiology matters, which means that microbiologists matter. The Microbiology Society's major and ambitious project, Knocking Out AMR, is our way of focusing on this issue.

This is the final edition of *Microbiology Today*, marking how changes in technology have changed the ways in which we communicate. The first issue, under a different name, was published just over 50 years ago. It marks the end of one era but perhaps more importantly, the start of a new one as magazine-style content authored by members is now appearing regularly through the Society's other channels, notably as *Micro Perspectives* on the website, which receives over 3.5 million visits a year. In this world of constant change, we must seize the opportunities that are described by Seána Duggan and Justine Rudkin in this edition, both as individuals and as an organisation. If we take advantage of the new publishing models and grasp the chances that are brought about by global interest in our subject, then our community can thrive even more for the next 50 years, just as we have in the five decades since the first issue.

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Access Microbiology: Open Science for the Benefit of Our Community

In this piece, *Access Microbiology* Deputy Editor-in-Chief Seána Duggan and Editor Justine Rudkin write about the how the Society's Open Access platform is helping reduce the gap between science and society.

Traditional models of academic publishing have long been a barrier to the dissemination of knowledge, but a combination of Open Access (OA) and Society publishing is poised to democratise research and enhance scientific progress for the benefit of both scientists and the public.

OA publishing, which makes research freely available to anybody with internet access, is a necessity not only for research progress but also for reducing the gap between science and society. A compelling argument for OA is the principle of equitable access to knowledge; research funded by public money should be accessible to everyone, not just those affiliated with well-funded institutions. OA has the power to reduce marginalisation of researchers, students and institutions in developing and less-resourced areas (countries and subject fields), and helps level the playing field, allowing all researchers to read and build upon each other's work, regardless of their financial or geographical constraints.

Access Microbiology, the Society's OA publication platform, is taking things several steps further, building pre-printing, open data and open peer review into its publishing workflow. The unrestricted availability of methods and data from the point of submission allows for more rigorous peer review and validation of results, whilst open peer review itself can lead to a more constructive rather than critical process. Add in its 'sound science' policy, with submissions being assessed on their robustness rather than impact, and you have a recipe to accelerate the pace of microbiology research in our community, whilst fostering a culture of reproducibility and transparency. Indeed, *Access Microbiology* even takes replication studies and negative data, thereby reducing scientific waste and giving a home and credit to data that would usually languish unseen in lab books.

Embracing Open Access, open data and open peer review, whilst publishing science based on robustness, rather than focusing on perceived significance or novelty, will deliver us sooner to an inclusive, efficient and transparent scientific ecosystem. As traditional models of academic publishing come under increasing scrutiny and pressure, Society publishing which sees the revenue associated with publishing pumped back into the communities that produce the scientific content (for example through conference and summer studentship grants), is a win–win situation.

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MICROBIOLOGY SOCIETY

Standing on the Shoulders of Microbes: Emerging Opportunities in Bacterial Genomics

Matt Bawn

Genomics is the study of an organism's complete genome. At its heart, it comprises genome sequencing facilitated by next-generation sequencing technologies, computational analysis of individual sequences and comparison of genomes to help us understand the function and evolution of living organisms. Much as astronomers have used telescopes to look at the universe to understand the behaviour and origins of the cosmos, the genomicist uses sequencing to look at the DNA of organisms to understand the behaviour and origin of life. Genomics relies heavily on the synergy between genome sequencing and computational analysis, and advances in both have led to its widespread efficacy and application. This is particularly true in the study of bacteria. Genome sequencing is now a cornerstone of epidemiology, and the healthcare systems of many countries routinely sequence thousands of bacterial genomes associated with human and animal disease each year and make these genomes publicly available. Indeed, one of the most powerful aspects of bacterial genomics is the vast quantity of accessible data. There are now around two million bacterial genomes in online databases. The accessibility of data is mirrored by the increasing accessibility of data analysis platforms. Tools such as Galaxy, the Bacterial and Viral Bioinformatics Resource Centre and others enable researchers to interrogate genome data online, further increasing the accessibility and applicability of bacterial genomics.

A single bacterial genome can be complex. Horizontal gene transfer means that we commonly see many *selfish elements*, such as plasmids, bacteriophage, transposons, and genomic islands in genomes. Each of these mobile genetic elements (MGEs) could have their own evolutionary trajectory and confer a novel and important phenotype on the host bacteria, for example antimicrobial resistance (AMR) or increased pathogenicity. At increasing levels of genomic resolution, we are seeing what diversity within bacteria can mean. We see diversity within species, serovars and even strains, but the impact of this diversity on populations is still largely unknown. The frequency and ability of bacteria to have distinct and diverse carriage of genes amongst even closely related strains and species has led to the importance of the pangenome – the set of all genes contained within a collection of genomes. A current focus of genomics research and an emerging opportunity is to understand the factors affecting the emergence and maintenance of the pangenome as well as the function of the thousands of currently identified *hypothetical proteins*. This has important consequences for topics such as antimicrobial resistance – how do populations of bacteria maintain potentially reproductively expensive antibiotic resistance genes even in the absence of selection for them and how is this related to how we as a society use or should use current and emerging antimicrobial therapies?

Traditional approaches have relied on culturing bacterial samples to generate genomes from pooled bacterial DNA. However, in this approach we end up with an average genome; and by taking the average we often miss the interesting. Metagenomics, the sequencing of total DNA from environmental samples, has helped us realise the previously unknown depth and breadth of bacterial genomes – particularly related to unculturable bacteria – challenging our previous understanding of the relationships between the different domains of life and indeed the origin and evolution of life itself. Metagenomics techniques rely on computational *binning* methods to separate out individual genomes. This factor and others such as potential biases in sequencing can limit their resolution such that differences at the species or strain level are missed.

A potential solution to this is single-cell sequencing, in which the DNA in individual cells is generally barcoded, amplified and sequenced. This is technically more challenging, often requiring cell sorting or microfluidics approaches as well as bespoke bioinformatics analyses. Despite these challenges, the investigation of bacterial genomes at the single-cell level offers the potential to truly resolve how bacteria react and interact at the population level. Experiments have already shown the applicability of these techniques for generating thousands and tens of thousands of genomes in one experiment, and a tantalising future goal could be sequencing a million cells. With this resolution we would be able to understand the dynamics of factors such as the transfer of MGEs and AMR and ultimately the contribution of rare and minor bacterial sub-populations that are as yet unknown.

> I believe that the greatest opportunity to be offered by bacterial genomics is a refocussing of our relationship away from bacteria as sources of disease towards a greater understanding of how we can utilise bacteria to improve health and society.

Figure 1: This image was created with assistance of artificial intelligence using ChatGPT 4.0 using the DALL-E plugin. Prompt used to generate this image: astronomer using a telescope to look at a universe of microbes.

With these unparalleled quantities of data, a persistent challenge remains in how we can robustly and reproducibly analyse data to generate insights from raw sequences. This is already a bottleneck in many large-scale projects, and this realisation has led to the drive to equip more researchers with computational skills and literacy. Machine learning and artificial intelligence (MLAI) have already yielded significant insights, for example estimating the invasiveness of individual strains solely from raw sequence data. With the success of tools such as AlphaFold and EVE (evolutionary model of variant effect), the efficacy and power of MLAI continues to grow and the function and role of currently *hypothetical* proteins may be readily predicted. This could open up new sources of valuable natural products. *Streptomyces* has traditionally been the source of many of our clinical antibiotics and the genus is predicted to contain thousands of biosynthetic gene clusters (BGCs). Our current analyses have identified multiple BGCs in individual *Streptomyces* genomes, but their function and activation remain elusive.

I believe that the greatest opportunity to be offered by bacterial genomics is a refocussing of our relationship away from bacteria as sources of disease towards a greater understanding of how we can utilise bacteria to improve health and society. For example, the discovery and production of new natural products, creating evolutionarily informed therapies and practices not just for bacterial infections but leveraging these towards the treatment of other diseases such as cancer.

Figure 2: This image was created with assistance of artificial intelligence using ChatGPT 4.0 using the DALL-E plugin. Prompt used to generate this image: a group of people standing on a pyramid of bacteria in the same style as the Figure 1.

Bacteria are being engineered to deliver targeted anti-cancer therapies directly to tumours. There are also significant opportunities in bioremediation – using chemical reactions mediated by bacteria to transform harmful contamination and improve the environment. Understanding the dynamics of bacterial populations through techniques such as single-cell genomics would help us create strategies to address other global challenges such as feeding an increasing population through enhancing soil bacteria, probiotics or even using bacteria as food (see further reading), or to generate cleaner and cheaper energy, for example, through the use of Microbial Fuel Cells.

At a fundamental level, bacterial genomics is redefining our view of life on Earth, and as we start to consider exploration beyond our planet, many of the applications and technologies previously described will become increasingly important. How can we grow crops on the moon or even Mars? What are the effects of spaceflight and zero gravity on the human gut microbiome? And can bacteria persist in space and even potentially contaminate other worlds through human exploration? These are all questions that can be answered through the application of bacterial genomics to astrobiology. Our increased understanding of how life emerged and evolved and generation of the essential *rules of life* gained through bacterial genomics may also offer insights into how it may have arisen elsewhere, perhaps in forms we wouldn't even have previously recognised or considered.

Further reading

Bichell R. Making food from electricity. *Smithsonian Magazine*. 2017. Available from: https://www.smithsonianmag.com/innovation/making-food-electricity-180964474/ (accessed 22 August 2024).

Rabaia MK, Abd El-Salam MM, Shaban AM, Alghamdi AS, Rezk H, Kashwani G, El-Batsh HM. Environmental impacts of solar energy systems: a review. *Renew Sustain Energy Rev* 2021;70:341–361. Available from: https://www.sciencedirect.com/science/article/pii/S1364032118306920.

Biography

Dr Matt Bawn, currently a Senior Lecturer in Microbial Genomics at Newcastle University, UK, is an interdisciplinary scientist specialising in microbial genomics with a focus on bacterial pathogens and their interactions with the environment and their hosts, and gene transfer mechanisms. His research spans computational biology, population genetics and single-cell genomics, with applications in epidemiology, microbiome studies, and method development for detecting horizontal gene transfer in bacteria.

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Seaweed: An Ancient Resource with Modern Possibilities

Leanne Timpson

Seaweed, or macroalgae, forms an integral part of marine environments. Thousands of species exist, with a wide variety of physical morphologies. Long strings of sea spaghetti, whip-like bladder wrack and sheets of kelp all provide specific functions in aquatic habitats. From providing food and shelter for marine organisms to acting as a carbon sink, seaweed has increasingly recognised roles in biodiversity, the environment and human health.

Fucus serratus (serrated wrack) and *Hilmanthalia elongata* (sea spaghetti) growing at the Irish coastline of the Atlantic Ocean. Leanne Timpson

Nothing New but What's Forgotten

Very much a traditional resource, a fossil discovered in China in 2020 suggests that the green seaweed *Proterocladus antiquus* existed on planet Earth 1 billion years ago. As well as providing oxygen to our atmosphere, seaweed also became a predominant part of the European diet during the Stone Age, when a hunter-gatherer lifestyle prevailed. With the introduction of farming and land-plant cultivation during the Neolithic Age, its use waned. Yet, in modern times, diets such as the paleo diet, centred around the consumption of naturally sourced unprocessed foods are giving rise to a resurgence in forgotten resources, such as seaweed. In Korean cuisine, wakame can be sprinkled into comforting earthenware bowls of bibimbap. Nori is used to wrap rolls of rice and meat or vegetables, known as Kimbap in Korea and as sushi in Japan, as well as in Chinese soups and seaweed salads. In addition to the emotional comfort that a bowl of ramen can provide, the seaweed addition imparts vitamins A, C and E as well as minerals iodine, copper and zinc, omega-3 fatty acids and antioxidant compounds. Although the nutritional benefits are many, it's worth noting that seaweed species can absorb heavy metals such as cadmium, which can be hazardous to health. In addition, whilst seaweed is an excellent source of iodine, overconsumption of seaweed may pose a risk to consumers in the form of thyroid gland dysfunction.

Connecting with Marine Algae

Another traditional use of seaweed is seaweed bathing, which takes us back hundreds of years. In the past, it was used by arthritis sufferers and, nowadays, it is also recommended to athletes for muscle pain or stiffness after a workout. Advocates of seaweed bathing, Kane John O'Shea and Deiric De Siun describe the experience as grounding, and it is often used by surfers as a way to warm up after bracing the waves. The most used seaweeds for bathing include alginate-rich *Fucus vesiculosus*, commonly known as bladder wrack, and *Fucus serratus*, known as serrated wrack. Harvesters work with coastal seaweed available to them, considering the time of year and harvesting cycles. Spent seaweed can be used as a soil fertiliser, imparting nutrients to the soil for farming.

Antimicrobial Resistance

Antimicrobial resistance (AMR) is one of the most relevant and concerning global challenges currently facing us. Since the discovery of Penicillin by Alexander Fleming in 1928, scientists have developed a variety of antibiotic drugs, of which there are several classes. Some antibiotics target bacteria by inhibiting their cell wall synthesis. Others prevent bacteria from synthesising DNA or proteins. But bacteria fight back. β-Lactam antibiotics, such as Penicillin, feature a heterocyclic β-lactam ring in their structure, one of the keys to inhibiting bacterial cell wall synthesis. Bacteria counter this attack by producing β-lactamase enzymes, hydrolysing the β-lactam ring and halting antibiotic activity. Other β-lactam antibiotics such as cephalosporins and carbapenems also face challenges from bacteria in terms of intrinsic or acquired resistance or from the action of carbapenemase enzymes. Bacteria target protein synthesis inhibitor antibiotics by modifying the target of action or the antibiotic structure itself. They can use efflux pumps to remove antibiotics from the cell or metabolic by-pass mechanisms to counter antibiotic action that targets their biosynthetic processes. Multidrug-resistant bacteria are of growing concern, and acquired resistance can be accelerated by human activity – through the unintentional or knowingly incorrect use of antibiotic drugs to treat or control infections. It is predicted that by the year 2050, 10 million deaths will be attributed to AMR globally, highlighting the urgent need for new and creative solutions.

Seaweed's Antimicrobial Compounds

Seaweed is a potential source of antimicrobial compounds. Macroalgae can be broadly classified as *Rhodophyta* (red), *Chlorophyta* (green) or *Phaeophyceae* (brown) due to the type and quantity of pigments present. Due to the adverse and challenging conditions that seaweed must contend with, including salinity, temperature, predation, resource limitation and UV radiation, they have adapted physical and chemical survival mechanisms. This includes the production of a range of secondary metabolites, the amounts of which vary depending on species, season, harvest location and developmenal stage. The secondary metabolites produced range from polyphenols to terpenes and flavonoid compounds, polysaccharides and fatty acids. Polyphenol and flavonoid compounds, most often found in the brown seaweeds, are amongst the most exciting metabolites from the point of view of antimicrobial resistance.

A study from Queen's University Belfast showed that *Fucus serratus* (serrated wrack) and *Ascophyllum nodosum* (knotted wrack) exhibit antibacterial effects against *Escherichia coli* and *Salmonella* species. The observed activity is attributed to a class of polyphenolic compounds known as phlorotannins. It has been suggested that the structure of the phlorotannins, featuring an aromatic ring and hydroxyl groups, supports hydrogen bond formation with bacterial proteins, disrupting bacterial protein function. Other polyphenolic compounds like bromophenols have been reported to elicit antimicrobial effects by damaging bacterial cell walls and membranes to increase permeability and initiate cytoplasmic leakage. A separate study demonstrated antimicrobial activity of *Fucus vesiculosis* (bladder wrack) and, to a lesser extent, *Fucus serratus* (serrated wrack) against MRSA strains. As well as polyphenolic compounds, researchers found that antibacterial peptides from *Saccharina latissima* (sugar kelp) exhibit antibacterial effects against *Staphylococcus aureus*.

Fucus serratus (serrated wrack). Kane John O'Shea and Deiric De Siun

Additionally, polysaccharides from seaweeds may elicit antimicrobial activity. Research indicates that fucoidans, a type of sulphated polysaccharide, from *Fucus vesiculosus* (bladder wrack), produce antibacterial effects against *E. coli* and *Staphylococcus aureus*. Fucoidans are suggested to bind to membrane proteins, leading to cell membrane rupture. Several studies also report on the likelihood of synergistic effects between different seaweed metabolites exerting a collective antimicrobial effect.

Future Possibilities

Commercial interest in seaweed has for a long time been mostly restricted to Asian markets, with the largest market share currently belonging to China and Indonesia. However, wider interest is increasing due to the possibilities of using seaweed for an array of applications, and the global market is predicted to increase by 11.8 billion USD by 2030. Seaweed as a source of antimicrobial compounds is also of interest, with possibilities for further exploration in this area. Differences in the concentrations and chemical structures of polyphenolic and flavonoid compounds depending on season, species and harvest location present intriguing challenges for further discovery. Synergistic effects between different types of antimicrobial compounds within species and seaweed antibiotic combinations are also gaining interest. Although not a complete solution to the problems we currently face, antimicrobial properties of seaweed species may provide interesting and complementary treatments to antibiotics.

In addition, modern biotechnological applications for seaweeds include biofuel and bioplastic production, both of which are central to climate change and the environment. Further linked to climate change, seaweeds are capable of absorbing large quantities of carbon dioxide, and therefore may be viewed as carbon sinks. It is also believed that seaweed industries can reinvigorate global coastal communities, providing a socioeconomic benefit. With an ocean of possibilities, it is an exciting time for marine algae. As with any natural resource, its cultivation and applications need to be carefully considered against the backdrop of its interconnected importance to both marine and terrestrial environments.

Further reading

Ayrapetyan ON, **Obluchinskaya ED**, **Zhurishkina EV**, **Skorik YA**, **Lebedev DV**, ***et al.*** Antibacterial properties of fucoidans from the brown algae *Fucus vesiculosus* L. of the Barents Sea. *Biology* 2021;10:67.

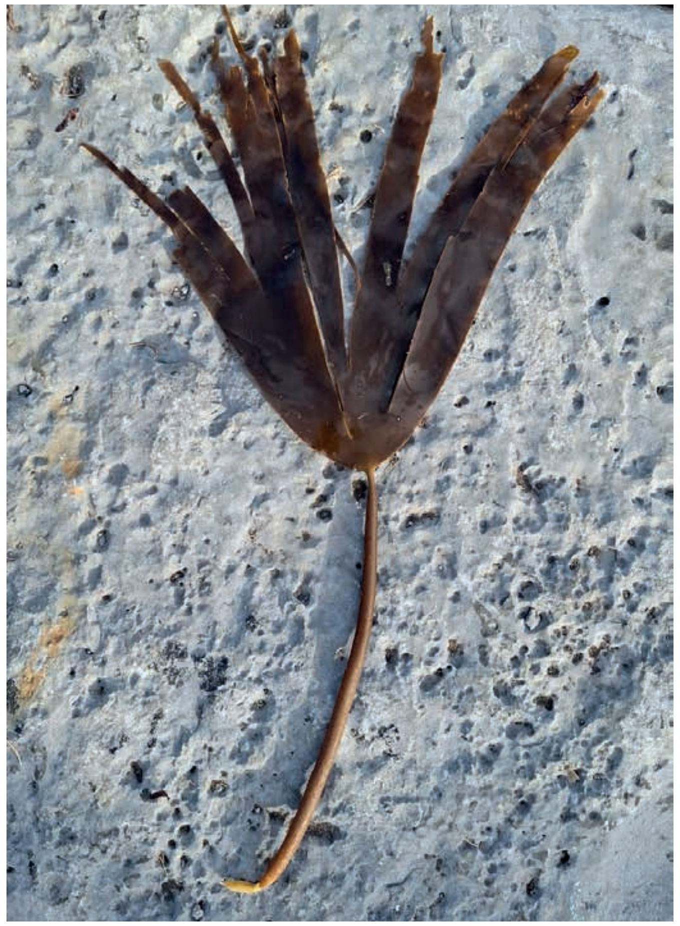
Beaulieu L, **Bondu S**, **Doiron K**, **Rioux L**, **Turgeon SL**. Characterization of antibacterial activity from protein hydrolysates of the macroalga *Saccharina longicruris* and identification of peptides implied in bioactivity. *J Funct Foods* 2015;17:685–697.

Ford L, **Stratakos A**, **Theodoridou K**, **Dick J**, **Sheldrake G**, ***et al.*** Polyphenols from brown seaweeds as a potential antimicrobial agent in animal feeds. *ACS Omega* 2020;5:9093–9103.

Higgins Hoare A, **Tan SP**, **McLoughlin P**, **Mulhare P**, **Hughes H**. The screening and evaluation of *Fucus serratus* and *Fucus vesiculosus* extracts against current strains of MRSA isolated from a clinical hospital setting. *Sci Rep* 2019;9:17911–17914.

Silva A, **Silva SA**, **Carpena M**, **Garcia-Oliveira P**, **Gullón P**, ***et al.*** Macroalgae as a source of valuable antimicrobial compounds: extraction and applications. *Antibiotics* 2020;9:642.

Singh M, **Kapoor S**, **Bagchi T**, **Paul S**, **Kar S**. Seaweed farming: an environmental and societal perspective. *Ind Microbiol Biotechnol*, Springer, Singapore.



Laminaria digitata (kelp) at Doolin, Co. Clare, Ireland. Kane John O'Shea and Deiric De Siun

Biography

Leanne is a Lecturer in Microbiology at Nottingham Trent University, UK, and Microbiology Society member. She has experience in working with enzymes from extremophile micro-organisms and worked for the Danish biotechnology company Novozymes. With a strong interest in education, she explores the antimicrobial effects of seaweed through undergraduate projects at Nottingham Trent University, UK.

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Barking Up the Right Tree: *Ficus natalensis* Bark Cloth as a Sustainable Antimicrobial Fabric for Use in Wound Dressing Technology

Jack Buckley

In 2008, the production of bark cloth from the Mutuba tree (*Ficus natalensis*) was dubbed an “intangible cultural heritage of humanity” by UNESCO. Bark cloth is a non-woven fibrous material that has been arduously and skilfully crafted by the Baganda people of Southern Uganda since at least the 13th century and reflects the identity of the community. Historically, the Baganda people have used it in clothing and decoration on ceremonial occasions. During the wet season, the inner tree bark of *F. natalensis* is harvested and then stretched and beaten using wooden mallets to form bark cloth. The bark cloth can be up to ten times its original size following this processing stage. This is a fully sustainable process where the trunks of the *F. natalensis* trees are wrapped in banana leaves following the harvest, which encourages the bark to re-grow, reduces infection and allows the tree to be re-harvested the following rainy season. The bark can regenerate for up to 100 years and, compared with the production of conventional cloth, the process requires relatively few resources and moderate amounts of labour.

However, the introduction of fabrics, such as cotton, has resulted in the production of bark cloth becoming an endangered process for the people of the Baganda community. Recently, interest in bark cloth has been revived due to its properties and sustainable nature, with applications as far-reaching as luxury fashion and water filtration systems. Due to its unique properties (natural variations in thickness, texture, good porosity and antimicrobial activity), bark cloth has also received interest in medical applications, namely, being utilised in wound dressings.

By 2050 antimicrobial-resistant infections are estimated to exceed a mortality rate of 10 million per annum. Meticillin-resistant *Staphylococcus aureus* (MRSA) is one of the leading causes of skin and soft tissue, surgical site, and wound infections. These infections are usually manageable, but they can lead to life-threatening complications. MRSA is associated with a higher mortality rate, longer hospital stays and ultimately higher healthcare costs. In 2017, it was estimated that multidrug-resistant infections, both in the community and in hospitals in the USA alone cost $4.6 billion. With the ever-increasing threat of antimicrobial resistance, the evaluation and development of novel treatment methods are imperative. Current commonly used antimicrobial wound dressings are impregnated with antimicrobial products (examples include metals or naturally occurring products, such as honey). Research into the use of natural products with medicinally relevant properties has intensified as we strive for more sustainable alternatives. Our recent research has evaluated and confirmed the antimicrobial activity of the *F. natalensis* bark cloth against MRSA.

Kirsten Scott & Lesli Robertson

F. natalensis bark cloth was shown to exhibit excellent antimicrobial activity against *S. aureus* strain USA300 (an MRSA strain). After 24 hours of constant exposure, the bark cloth resulted in a seven-log reduction in MRSA viability when compared with the untreated control. This result demonstrated that the bark cloth was able to kill MRSA over an extended period of time, thus giving weight to its viability for use as a medical textile, and represents highly beneficial properties for use in wound care. Scanning electron microscopy (SEM) was performed to provide further details regarding the antimicrobial mechanism of activity of the bark cloth. The imaging revealed bacterial attachment and biofilm formation on the fibrous structure of the bark cloth. Apparent morphological aberrations to the cell ultrastructure such as invaginations and perforations were observed. Such phenotypic alterations highlight a bactericidal, contact-kill effect against MRSA.

Thus far, the *F. natalensis* bark cloth has demonstrated long-lasting antimicrobial activity against MRSA *in vitro*. Further characterisation has revealed good gaseous transmission and good porosity, parameters that make this material an ideal candidate for use in wound dressings. Furthermore, the bark cloth is 100% bio-degradable, completing the compositing process in just a few weeks. Other beneficial properties of wound dressings, such as wettability and moisture regulation, are currently under investigation.

To date, the active antimicrobial agent(s) are yet to be identified. However, the elemental composition of the bark cloth has been reported, with metals such as magnesium, calcium and chlorine present on the surface of the bark cloth, which could provide insight into the observed antimicrobial activity. Future research will look to elucidate the antimicrobial activity of the bark cloth using a metabolomic approach using mass-spectroscopy and/or nuclear magnetic resonance (NMR) to characterise and quantify compounds of interest. We will also aim to evaluate bark cloth cytotoxicity against human cell lines, and use molecular techniques such as RNA-seq to examine bacterial responses to the bark cloth. *In vitro* wound modelling would also further provide invaluable data relating to the viability of this material for use in wound care management.

> **The use of natural sustainable products in healthcare, particularly wound care management, is an exciting avenue to explore.**

The use of natural sustainable products in healthcare, particularly wound care management, is an exciting avenue to explore. *F. natalensis* bark cloth provides a unique opportunity as it can be utilised as a whole natural product. Investigations are underway to determine the feasibility of using *F. natalensis* bark cloth as a wound dressing; however, this preliminary study could pave the way for other sustainable products to be utilised throughout healthcare.

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Further reading

Butler JA, Slate AJ, Todd DB, Airton D, Hardman M, *et al.* A traditional Ugandan *Ficus natalensis* bark cloth exhibits antimicrobial activity against methicillin-resistant *Staphylococcus aureus*. *J Appl Microbiol* 2021;131:2–10.

Jones A. Investigating the unique properties of Ugandan barkcloth as a potential filtration material for cleaning contaminated waters. *UWE Bristol - Healthy Waters Blog* [Internet]. 2022. Available from: https://blogs.uwe.ac.uk/healthy-waters/investigating-the-unique-properties-of-ugandan-barkcloth-as-a-potential-filtration-material-for-cleaning-contaminated-waters/ (accessed 9 November 2024).

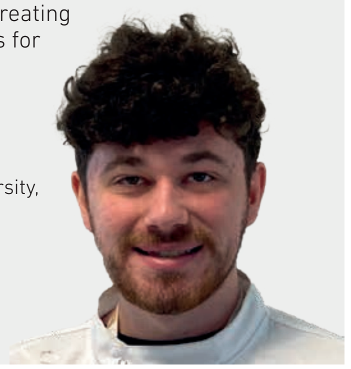
Rwawiire S, Tomkova B. Thermo-physiological and comfort properties of Ugandan barkcloth from *Ficus natalensis*. *J Text Inst* 2013;105:648–653.

Scott K, Butler JA, Spurgin K, Venkatraman PD. Restorative fashion: collaborative research, benign design and the healing powers of the mutuba tree. *J Appl Arts Health* 2023;13:357–372.

Venkatraman PD, Scott K, Liauw CM. Environmentally friendly and sustainable bark cloth for garment applications: evaluation of fabric properties and apparel development. *Sustain Mater Technol* 2020;23.

Biography

Jack is a Microbiology Society member and MSc by research student at the Manchester Metropolitan University, UK. Passionate about sustainability in medicine and with hopes to show the viability of whole natural products in combatting AMR, Jack's research is currently aimed at investigating and creating natural antimicrobial textiles for wound care.



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Promoting Antimicrobial Resistance Awareness for Healthcare Providers and the Public

Katelyn Mroczek and Thiru Vanniasinkam

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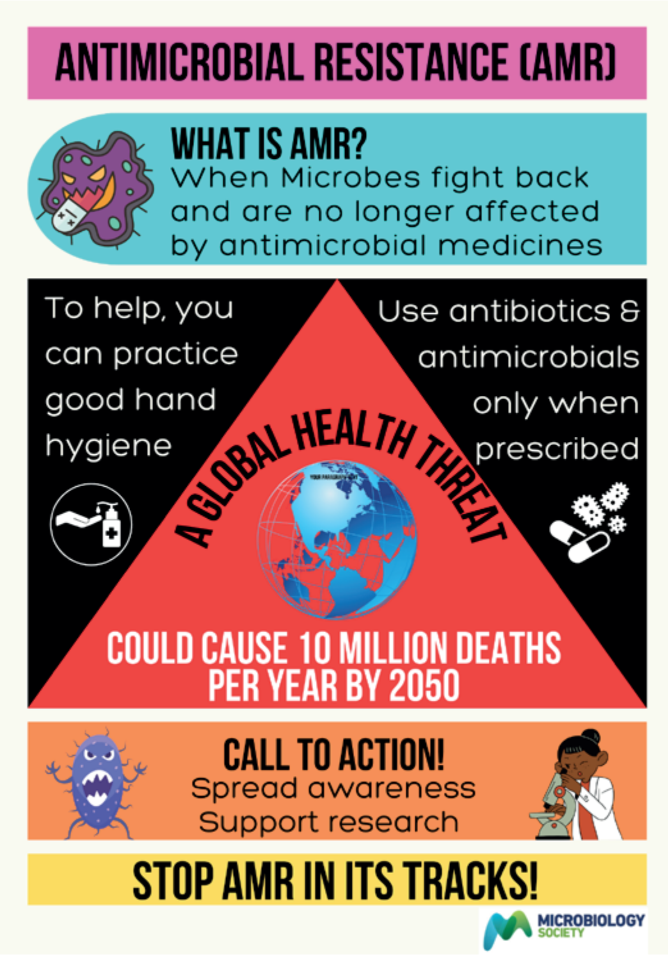
Antimicrobial resistance (AMR) continues to be a significant public health concern globally. Education is a critical part of any strategy to combat AMR. Despite decades of work by scientists and healthcare providers in developing and implementing materials to educate the lay public and healthcare workers on the dangers of AMR, there are still significant issues in getting the message across to the public on this topic. For example, what AMR is and what each and every individual can do to stop its spread. In the meantime, cases of AMR continue to increase worldwide, putting the health of humans, animals, plants and the broader environment at risk [1,2].

The important question to ask at this time is, what are some issues to consider if we want to get better outcomes when we conduct campaigns on AMR awareness? Based on an article published last year, it appears that while certain initiatives, such as World Antimicrobial Resistance Awareness Week (WAAW), can make a difference in the short term, there may need to be more longer term interventions conducted to ensure better AMR awareness and action to address the spread of AMR [1]. The biggest issue with any long-term plan is the lack of resources, which impacts the ability of many countries to conduct AMR education events/training throughout the year.

Healthcare providers may receive AMR education as part of their continuing professional development/education in many countries. However, there is a bigger challenge when considering approaches aimed at educating the public on AMR. Strategies that have been used to enhance awareness of public health issues include storytelling [3], using social media and text messaging. However all of these have had variable success. Key obstacles to enhancing public awareness of AMR may include an overall lack of health literacy in the community and difficulty in accessing AMR-specific information outside of a healthcare setting.



ANTIMICROBIAL RESISTANCE (AMR)

WHAT IS AMR?
When Microbes fight back and are no longer affected by antimicrobial medicines

To help, you can practice good hand hygiene

A GLOBAL HEALTH THREAT

Use antibiotics & antimicrobials only when prescribed

COULD CAUSE 10 MILLION DEATHS PER YEAR BY 2050

CALL TO ACTION!
Spread awareness
Support research

STOP AMR IN ITS TRACKS!

Figure 1: AMR poster.

What we are proposing for this year's WAAW is to develop visually appealing posters with focused, simple slogans and messages to educate the public and healthcare providers on AMR. We will also be considering previous research when designing the posters, and ensuring they are strategically displayed in locations such as healthcare facilities and public buildings and spaces, e.g. local libraries [4]. The messaging will need to be carefully considered for each target group, as there is research that shows the importance of positive vs negative messaging depending on the audience [5]. The message will be aligned to the World Health Organization's theme of 'Educate. Advocate. Act now', and the aim will be to enhance awareness of AMR by visual communication, which has been shown to be highly effective [6]. Another consideration is ensuring that following WAAW there is a plan to continue AMR messaging within the community. This will require further planning to evaluate other approaches to promote health literacy more widely in the community, including in schools. Strategies such as competitions to design AMR posters or public lectures on AMR are other approaches worth considering as we start developing material for WAAW 2024.

References

1. **Fuller W**, **Kapona O**, **Aboderin AO**, **Adeyemo AT**, **Olatunbosun OI**, ***et al.*** Education and awareness on antimicrobial resistance in the WHO African Region: a systematic review. *Antibiotics* 2023;12:1613.
2. **Walker S**. Effective antimicrobial resistance communication: the role of information design. *Palgrave Commun* 2019;5:24.
3. **Appiah B**, **Anum-Hagin D**, **Gyansa-Luterrodt M**, **Samman E**, **Agyeman FKA**, ***et al.*** Children against antibiotics misuse and antimicrobial resistance: assessing effectiveness of storytelling and picture drawing as public engagement approaches. *Wellcome Open Res* 2021;6:202.
4. **Hasanica N**, **Ramic-Catak A**, **Mujezinovic A**, **Begagic S**, **Galijasevic K**, ***et al.*** The effectiveness of leaflets and posters as a health education method. *Mater Sociomed* 2020;32:135–139.
5. **Wansink B**, **Smith LE**, **Pope L**. Which health messages work best? Experts prefer fear- or loss-related messages, but the public follows positive, gain-related messages. *J Nutr Educ Behav* 2015;47(Suppl.)
6. **Woloshin S**, **Yang Y**, **Fischhoff B**. Communicating health information with visual displays. *Nat Med* 2023;29:1085–1091.

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MICROBIOLOGY SOCIETY

Champions Q&A: Joshua Kurucz

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This is a regular column to introduce our Champions and the work they do to promote microbiology and the Society. In this issue, we're pleased to introduce Joshua Kurucz.

Where are you currently based and what is your role?

I am a Master's student at the University of Northern British Columbia, Canada. My supervisor is Dr Chow Lee.

What area of microbiology do you specialise in and what's exciting you about it at the moment?

My current area of specialisation is natural product discovery from fungi. My research is analysing the genes present in a biosynthetic gene cluster derived from Indian paint fungi. My goal is to be able to extract a complex metabolite or metabolites with some form of anticancer potential. This area of research is fascinating as it poses a way to bring natural therapies to the forefront of advanced medicinal research. Opposed to some wonder pill with undefined benefits from some plant extract, this research allows us to identify the key beneficial compounds from natural sources and use them as alternative and hopefully safer treatments for a range of conditions.

You recently joined the Champions Scheme, why did you decide to become a Society Champion?

I thought it would be an excellent start to my journey into higher academia. Once I completed my undergraduate degree, I was unsure of exactly how to meet other professionals and how to network my research ideas properly. By joining the Champions Scheme, and Society in general, I have been given access to a wealth of opportunities, information and potential colleagues. On a less selfish note, I also joined to increase awareness in the field. The importance of microbiology cannot be overstated, yet it seems deprioritised in many cases.

What opportunities are you hoping to take advantage of as a Society Champion?

I first hope to take advantage of the many funding opportunities and produce my own activity. Using the resources at hand, I can better communicate the importance of my research and microbiology as a whole. I also hope to take advantage of the networking opportunities. The Society provides a way to link individuals with a common goal and common passion. Together, we are able to share our unique expertise, experience and interests to better ourselves and, in turn, further the field. Lastly, I want to utilise the Society's learning materials. The Society provides an array of learning materials and online resources to allow us to grow and progress in our positions and our academic journey.

What advice would you give to other microbiologists looking to get involved with the Society?

My only advice is to take the step and reach out. As daunting as it may seem, this programme is full of helpful and excited people who only want to see you prosper. Take the leap and get involved with the Society. You have absolutely nothing to lose and truly so much to gain.

What do you hope to achieve in your career in the future?

As I am still very early in my career, a lot remains uncertain, but my aspirations are deadset. After completing my Master's, I want to continue to medical school and acquire a PhD in immunology. Using my education, I intend to research natural microbial sources and search for potential therapeutic compounds. Later, I'd like to open a clinical practice, treating a variety of autoimmune conditions, likely focusing on Myalgic encephalomyelitis/Chronic fatigue syndrome, as it is a condition that affects someone extremely close to me. By combining my research and clinical work, I can hopefully give patients a safe, natural and effective treatment, where currently very limited options are available.

GET INVOLVED

If you would like to find out more about the Champions Scheme, please get in touch via getinvolved@microbiologysociety.org.

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Comment:
Space Microbiology – Growing our Reach Towards the Stars

Katherine Baxter


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Since the emergence of commercial spaceflight in the early 2010s, the graph of annual number of objects launched into space resembles that of a microbial growth curve [1], and we are currently in the exponential phase. Our reach towards the stars is set to continue on this trajectory for the foreseeable future, with a long list of space exploration planned, including the development of several commercial low Earth orbit space stations, the return to the Moon's surface planned for 2026, and the launch of the first components of Gateway – humanity's first Lunar space station and staging post – to Mars scheduled for 2028. As microbiologists, we may not currently see the relevance of our work in space exploration; however, this is set to change.

The Space Revolution Will be Microbial

All life on Earth is underpinned by microbial processes. From biogeochemical cycles driving nutrient recycling and oxygen production, to the health-supporting microbiomes of individual organisms. If we are to become a space-faring species it is crucial that we harness and utilise these microbially based systems in order to support our expansion beyond Earth, literally taking 'a little piece of home' with us as we take our first steps beyond the relative safety of low Earth orbit.

The overwhelming potential of microbially derived technology in space exploration is recognised in the 2021 'Biology in Space and Analogue Environments' roadmap from the European Space Agency [2] and the 2023 'Thriving in Space' Decadal Survey from the National Academies of Science, Engineering and Medicine [3]. These two publications – which advise the scientific activities of ESA and NASA, respectively – acknowledge the need for greater understanding of space environment on both beneficial and pathogenic micro-organism interactions in order to maintain crew health, safeguard food production and maintain the material safety of the spacecraft environment. In addition, space biotechnology applications could synthesise pharmacologically active products in line with crew requirements, allowing a precision-medicine approach to address changes in drug metabolism and product stability which occur in spaceflight [4,5].

Beyond the health and safety of the craft and crew, these publications are also cognisant of the fact that micro-organisms have the promise to provide mission-critical functions, such as bioregenerative life support and waste-processing systems, *in situ* resource utilisation (where micro-organisms are used to process and extract useful components from Lunar and Martian rock and soil), and fuel production. Currently, life support and environment control are provided by artificial means and require replenishing from Earth, which is both expensive and impracticable for long-term deep space exploration such as a mission to Mars, a 2–3 year round trip across 4 billion kilometres of space depending on the interplanetary trajectory [6]. Taking a biobank of organisms specifically engineered and selected for these roles that can be revived as and when needed is more practicable and cost-efficient than resupply from Earth and gives us greater scope for exploration of deep space.

Translating Technology Towards Earth

Using micro-organisms to support space exploration also has profound implications for multiple aspects of terrestrial microbiology. Firstly, the spaceflight environment is severely detrimental to organism health and we need to be able to develop countermeasures in order to ensure crew health and mission success. In humans, all major body systems are affected [7], plants display notable differences in physiological processes [8], and micro-organisms exhibit changes to metabolism, growth, virulence, biofilm formation and antimicrobial resistance [9]. These physiological changes mimic terrestrial conditions including aging, gut microbiome dysbiosis and immune system dysfunction, meaning any countermeasures developed to protect against infection and microbiome disruption in space can be directly applied to these conditions in terrestrial healthcare. In terms of plant health, microbiome augmentation could promote health and improve nutritional content and yield, which could be used for terrestrial crop management and mitigation of climate-related impacts in agriculture. With regards to micro-organism physiology specifically, the study of spaceflight-induced changes to micro-organisms allows opportunity for novel insight into the processes underpinning the emergence of virulence and antimicrobial resistance in response to stress, with the potential to reveal new targetable systems and pathways for drug development and antimicrobial surface technology.

Moving from healthcare towards environmental applications, the potential for space-developed microbial technology to improve sustainability, tackle climate change and aid progression towards a circular economy is significant. Technologies derived from bioregenerative life support and waste systems could return damaged ecosystems to health, effectively 'terraforming' them from inhospitable environments to those capable of supporting biodiverse life. Microbial *in situ* resource utilisation could reduce the environmental impact of mining by replacing traditional extraction methods, and we are already making headway with fuel production from micro-organisms in the form of biofuels and microbial fuel cells to reduce carbon release and replace our reliance on fossil fuels.

Beyond the Horizon

The past 60 years of crewed spaceflight has brought us many technological advances we benefit from every day, from the cameras in mobile phones to virtual reality systems, memory foam mattresses and medical imaging systems. Equally, the evolution of microbial technologies to support our return to the Moon and onward travel to Mars has similar potential for societal advancement. Microbes have been hitching a lift into space with us since the very beginning – it's time for them to actively participate. *Ad Astra*.

References

1. **Our World in Data.** Yearly number of objects launched into outer space. Available from: https://ourworldindata.org/grapher/yearly-number-of-objects-launched-into-outer-space (accessed 25 August 2024).
2. **Antunes A, *et al.*** ROADMAP #9: biology in space and analogue environments. In: ESA SciSpacE white papers – final version. 2021. pp. 1–49. Available from: https://esamultimedia.esa.int/docs/HRE/09_Biology_Biology_in_Space_Analogue_Environments.pdf (accessed 25 August 2024).
3. **National Academies of Sciences, Engineering, and Medicine.** Thriving in space: ensuring the future of biological and physical sciences research: a decadal survey for 2023–2032. 2023 Sep 12. Available from: https://nap.nationalacademies.org/catalog/26750/thriving-in-space-ensuring-the-future-of-biological-and-physical (accessed 25 August 2024).
4. **Dello Russo C, *et al.*** Physiological adaptations affecting drug pharmacokinetics in space: what do we really know? A critical review of the literature. *Br J Pharmacol*. 2022;179:2538–2557.
5. **Daniels VR, Williams ES.** Exploring the complexities of drug formulation selection, storage, and shelf-life for exploration spaceflight. *Br J Clin Pharmacol*. 2023 Nov 8.
6. **NASA.gov.** Humans to Mars [Internet]. Available from: https://www3.nasa.gov/sites/default/files/atoms/files/acr22-wp-mars-transportation.pdf (accessed 25 August 2024).
7. **Krittanawong C, *et al.*** Human health during space travel: state-of-the-art review. Cells. 2022;12:40.
8. **Sathasivam M, Hosamani R, Swamy BK.** Plant responses to real and simulated microgravity. *Life Sci Space Res*. 2021;28:74–86.
9. **Senatore G, Mastroleo F, Leys N, Mauriello G.** Effect of microgravity and space radiation on microbes. *Future Microbiol.* 2018;13:831–847.

Biography

Katherine is a Research Associate in the School of Molecular Biosciences at the University of Glasgow, UK, and is interested in biofilm formation, interkingdom microbial community dynamics and space microbiology. She is a NASA STAR program alumnus, Coordinator of the UK Space Life and Biomedical Sciences Association (UK Space LABS), and Biofilm Subgroup Co-Chair for the GeneLab Microbes Analysis Working Group (AWG).

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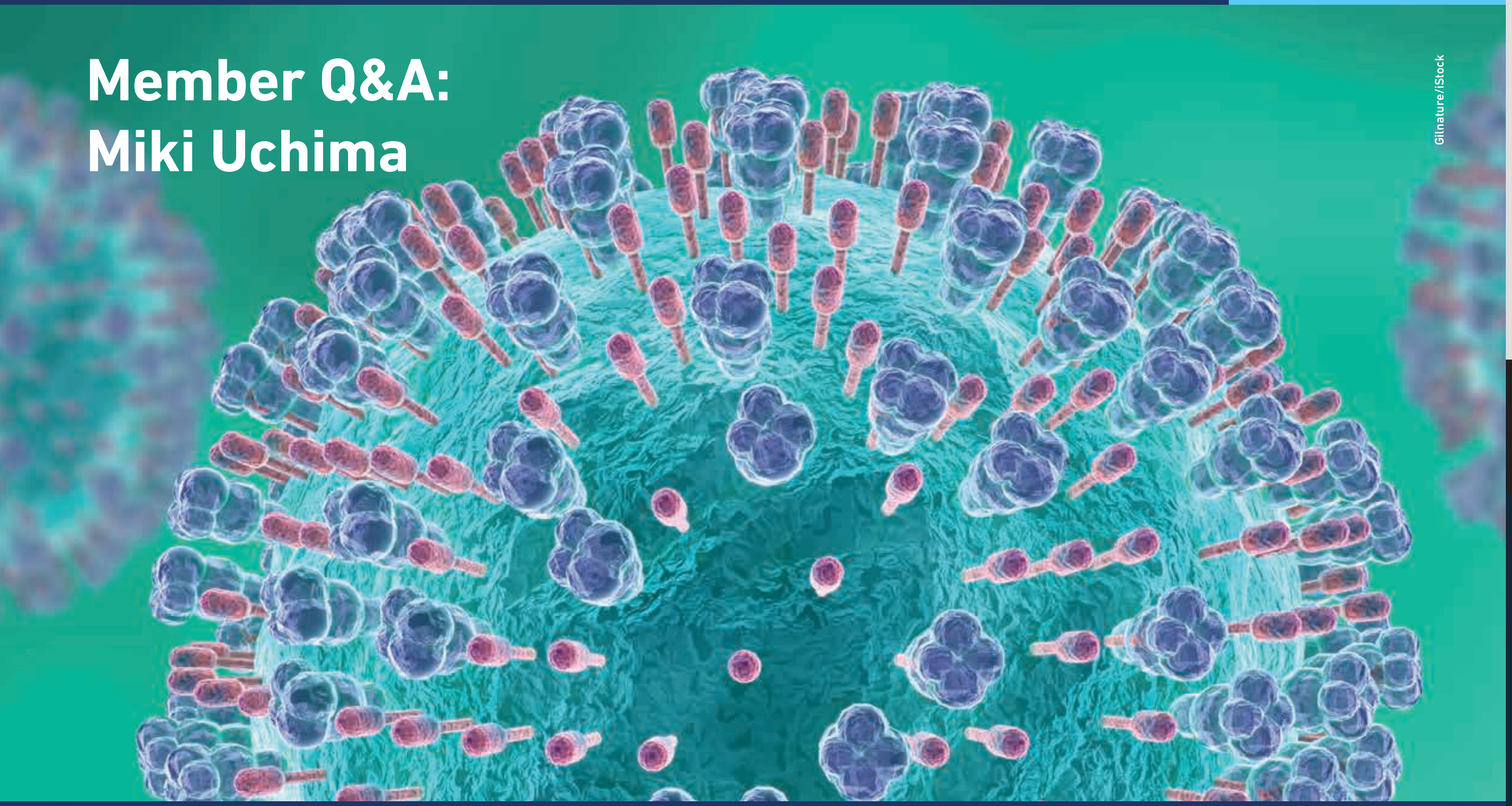
Member Q&A: Miki Uchima



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This is a regular column to introduce our members. In this issue, we're pleased to introduce Miki Uchima.

Where are you currently based and what is your role?

I am a third-year PhD student based in London, UK. As a joint PhD student, I have two home institutes: the Francis Crick Institute, UK, and the Department of Infectious Diseases within King's College London, UK.

What area of microbiology do you specialise in?

Virology. I am interested in understanding the interplay between hosts and pathogens. Currently, I am focusing on how influenza A virus adapts to different hosts and how this might trigger different immune responses.

When and why did you first become interested in microbiology?

I think it is difficult to pick a specific time point; instead it was a natural progression. My parents have been a big influence in making me interested in nature and they were always encouraging me to follow my curiosity.

During my studies, I became particularly fascinated by the immune system. I think it is incredible how smoothly it seems to work for most of us despite all of the micro-organisms we are surrounded by, and that live inside of us. That then lead to my next interests in bacteria and viruses. Given the complexity of the immune system, I think the strategies that micro-organisms have obtained to evade the immune system and hijack the host cell machinery are astonishing.

As an early career microbiologist, what are some of the professional challenges you face and how do you overcome these?

A PhD project is typically the first long-term project that one has to manage, and there are many aspects that you will only learn as you progress and inevitably encounter failure. For me, the most pertinent anxiety is whether or not my project will be successful. This has forced me to adjust my expectations regarding the reality of scientific discovery. Additionally, I have learnt that working on a question that no one has the answer to is inevitably an uncertain adventure. However, one is gifted the opportunity to add a tiny drop in the pool of human knowledge.

You are an incoming member of the Impact and Influence and Early Career Forum Executive Committees. What made you want to join these?

The Society is doing excellent work to support the development of early career researchers and gives them a platform to expand their network. Additionally, the Society is encouraging scientific collaboration and knowledge-sharing and raising public awareness of science-related topics. I believe that the scientific community can tackle major global health challenges, but to do so, we need to increase public trust in science. By joining the Impact and Influence Committee, I hope to represent early career researchers and contribute to the work of the Microbiology Society.

What do you hope to achieve in your career in the future?

I hope I can look back on my career and be proud of myself in the sense that I had done the best I could have and made a positive impact, however small it may be.

GET INVOLVED

If you would like to find out more about the opportunities available for early career members, please get in touch via getinvolved@microbiologysociety.org.

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