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microbiologist

The magazine of the
Society for Applied Microbiology



> INSIDE

GEOMICROBIOLOGY

Fungal bioremediation

How microbes are solving the
pollution of the sexual revolution

Microbial response of the
Deepwater Horizon oil spill



don whitley
scientific

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Paul Sainsbury reviews the content of this issue

microbiologist

Geomicrobiology: the vast and spectacular interactions between microorganisms and the abiotic environment

Spending time with the amazing Ken Neelson, during his time in London for the *Environmental Microbiology Lecture*, opened my world to how diverse the area of geomicrobiology is. I'm not going to bore you with the details of Ken's personal achievements as you can Google these (or, of course, use your preferred search engine of choice) or better still read page 33 of the last *Microbiologist*.

Needless to say when Ken agreed to provide a brief intro to this issue I was chuffed to bits. One of the most fascinating elements of Ken's research is the solubilization of a substrate external to the bacterial cell wall – and I do urge you to investigate further how he has completely revolutionized research in this area of bacterial metabolism. Ken modestly introduces Extracellular electron transport (EET) for us during his article, but the topic and its applications could fill an entire edition of *Microbiologist*. However, in this edition we have a variety of features that highlight how microorganisms are being deployed to help solve some of society's major issues and how they are responsible for altering the very landscape of planet Earth itself.

Fungi are well known as bioremediators of natural substrates and in our first feature Geoff Gadd gives us a brief glimpse into their world – focusing on how society may soon have a new way of extracting precious and rare Earth metals from a new concept—'urban mining'. Louise Horsfall then identifies bacteria reclaiming copper from the whisky-making process and Ayuen Lual introduces us to the completely inedible sea tomatoes. You'll also read about blood falls, beer floods and how bacteria were involved in the great clean-up of the Deepwater Horizon oil spill. Lucy Eland describes how we are trying to resolve the issue of too many hormones in our sewage plants and finally answers the question 'Are fish actually changing sex?'

Did you know the Zika virus was named after the Ziika Forest in Uganda? I didn't either, but fortunately Mark Fielder for Historical Perspectives outlines what goes into naming a disease.

Some of the features in this edition may inspire you to work on microorganisms and their interactions with their subsurface environment, so you may be interested in our careers article by geomicrobiologist Megan Barnett at the British Geological Survey (BGS).

Finally, this being the edition before our Summer Conference in July, I hope those attending will use the opportunity to say 'hello' and give feedback on the magazine – it is always welcome.

Image and video competition:
Do you have an amazing microbiology picture or video? From agar art to striking SEM images why not enter SfAM's competition
<http://bit.ly/1Nvp4Lo>

NEWS IN BRIEF

Improving Science Comms

SfAM contributed to the Science and Technology Committee inquiry into Science Communication
<http://bit.ly/21GW8kw>

AMR position statement online

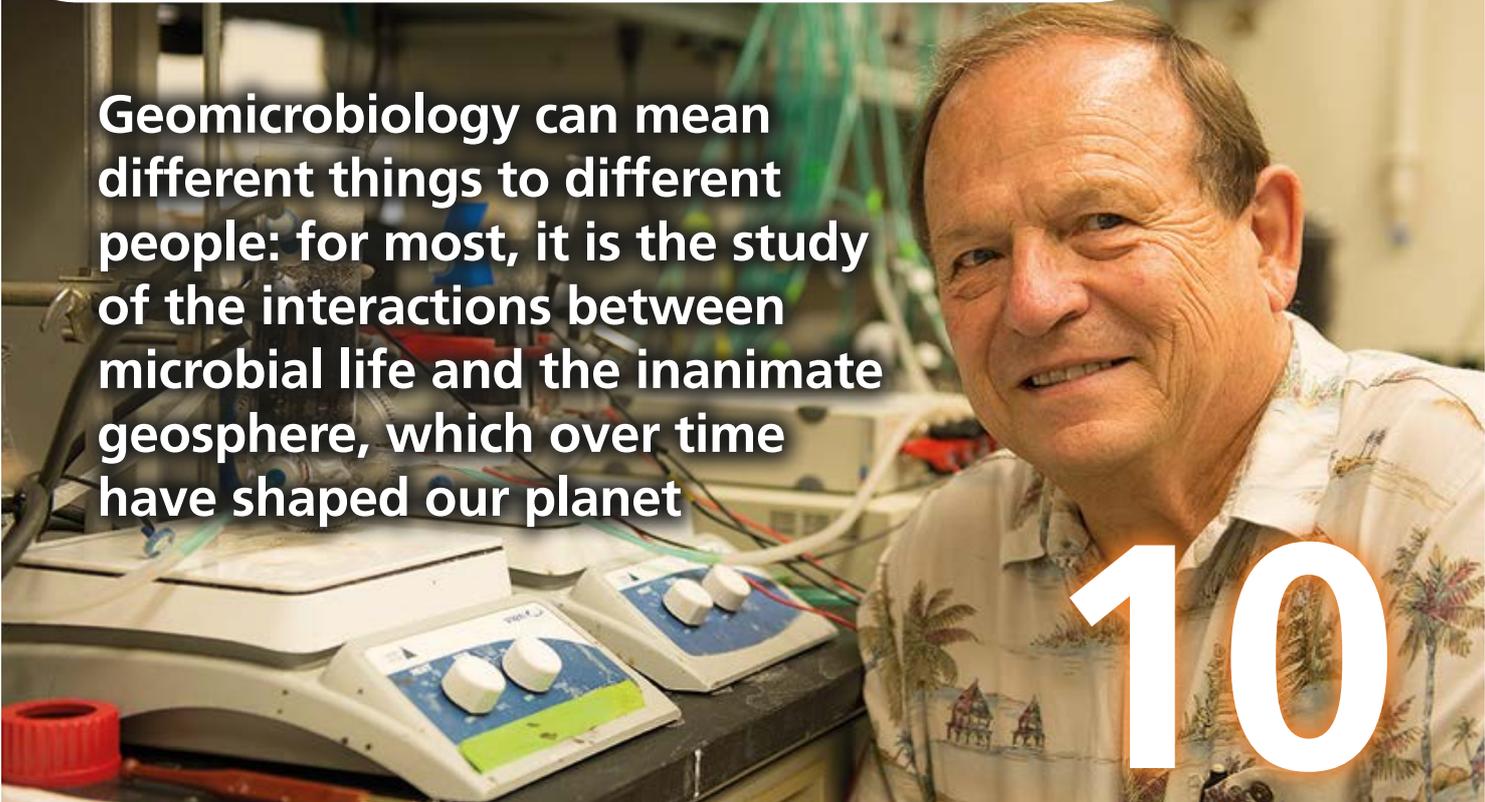
SfAM updated its position statement on antimicrobial resistance based on outcomes from the AMR Meeting in December
<http://bit.ly/1XkWRcr>

Government AMR Review

The LeSPAR group responded to the AMR Review led by government economist Jim O'Neill with a letter to the Prime Minister.
<http://amr-review.org/>



Paul Sainsbury, Editor



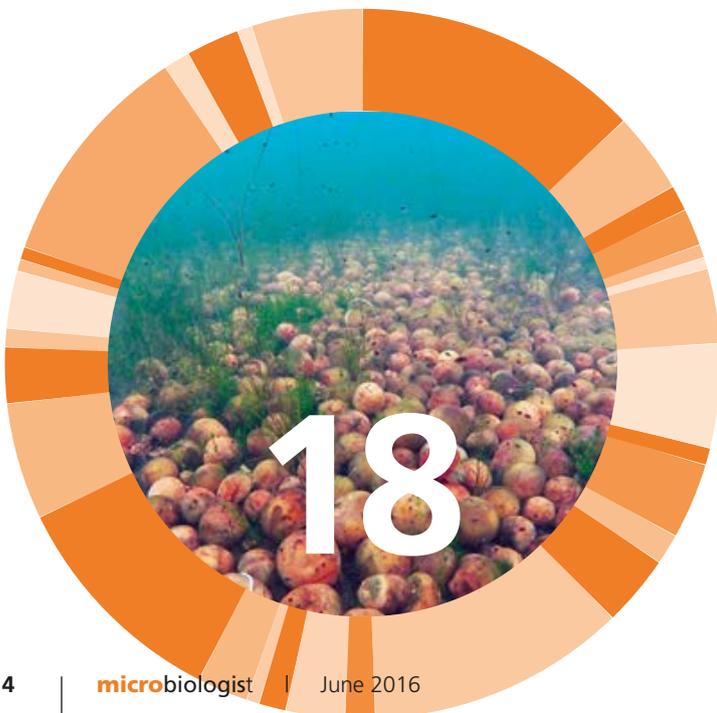
Geomicrobiology can mean different things to different people: for most, it is the study of the interactions between microbial life and the inanimate geosphere, which over time have shaped our planet

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President's column

The Society for Applied Microbiology is committed to advancing research, theory, education and practice in applied microbiology through the journals we publish. The Society publishes five journals, each of which contributes to our objectives while emphasizing a particular scholarly aspect. The *Journal of Applied Microbiology* (JAM) publishes high-quality research and review papers on novel aspects of applied microbiology, including environmental, food, agricultural, medical, pharmaceutical, veterinary, soil, systematics, water and biodeterioration. *Letters in Applied Microbiology* (LAM) provides a forum for the rapid publication of short, high-quality articles and reflects developments in biotechnology in such fields as applied microbial genetics, immunodiagnosis and fermentation science. Articles published in *Environmental Microbiology* (EMI) and *Environmental Microbiology Reports* (EMIR) are devoted to the advancement of our understanding of microbial interactions and microbial processes in the environment, and these journals publish original research reporting significant advances in this area. Our newest and open access journal *Microbial Biotechnology* (MBT) publishes papers of original research and reports significant advances in any aspect of microbial applications, including green chemistry, agriculture and functional genomics.

All of our journals are well-known globally and it is often through these journals that non-Members first recognize us when we attend international conferences. To celebrate our journals' success, we have two special lectures each year: the JAM Lecture which is given on the first evening of the Summer Conference and celebrates the *Journal of Applied Microbiology* and the *Environmental Microbiology* Lecture which is given in the autumn.

The *Environmental Microbiology* or EMI Annual Lecture was the first of these to be established and was initiated, in association with our publishers Wiley, to celebrate the success of "*Environmental Microbiology*". This lecture was established in 2008 and each year a renowned scientist has been invited to speak on their specialist area of environmental microbiology and to highlight the importance of the topic in microbiology. Over the eight years since it was established, a series of very eminent speakers have given wonderful and inspiring lectures that have opened new perspectives on just how diverse and amazing microorganisms and their

Our EMI Lecture this year is planned for the 11 October and the speaker is Professor Margaret McFall-Ngai

capabilities are. Not surprisingly this lecture has become one of the key events of the Society's calendar and places are taken up rapidly. Fortunately, the decision to video the lectures and make them available online via the Wiley YouTube channel (<https://www.youtube.com/user/johnwileysons/videos>) and more recently the SfAM blog, MicrobeBlog.org and website (<http://www.sfam.org.uk/en/events/sfam-events/emi-lecture/index.cfm>) means that many more people can view these lectures than are able to attend. It is here that the quality and increasing appeal of the lectures can really be appreciated. Over 3,000 people have now watched Ken Nealon who gave our 8th EMI Lecture in 2015. Ken has written an introductory article in this issue of the *Microbiologist* on geomicrobiology and having read it you may like to watch his lecture and see solid metal particles being solubilized by bacteria for yourself – a truly amazing piece of footage. All the other seven EMI Lectures together with the JAM Lectures are also available and provide a wonderfully accessible and relevant overview of a whole range of topics. Our EMI Lecture this year is planned for the 11 October and the speaker is Professor Margaret McFall-Ngai; it promises to be another fascinating lecture. Our Summer Conference in Edinburgh this year also reflects an environmental theme and is on *Microbial Interactions in the Environment*. I look forward to seeing many of you there.



Christine Dodd
President of the Society

Harper's Postulates

Notes from the Chief Executive

During the summer of 2016, SfAM will be moving our headquarters to Charles Darwin House, 12 Roger Street, London. This move has been prompted by many factors—the growth of the Society, a review of our strategic direction, as well as significant assessment of the operations and efficiencies in the way we work. Although we are sad to leave our existing headquarters after many years of residency in Bedford, we are certain that this move will ensure we are best placed to serve our Members in the future. It will enable the Society to continue to grow and prosper, providing real and relevant benefits to all our Members.

Members of the Society will also notice a number of changes to the way we operate over the coming months. We will be creating a dedicated membership, marketing and communications team and new online portal that will promote further engagement within our community and foster new relationships. This team will provide essential membership administration and support, ensuring that you, as Members, receive a first-class level of service.

The move will enable us to achieve many of our organizational objectives, and make our mark, ensuring we remain unique and distinct – whilst also putting us at the heart of the science policy and science communication communities. It will also facilitate further collaboration and build upon our already strong foundations with others within the Learned Society sector – many of whom already reside at Charles Darwin House. Successful examples of collaboration with visible benefits to our Members have been the creation of the Public Engagement Working Group run by the Royal Society of Biology and the LeSPAR group.

I have no doubt that, as with any large change, there will be rewards and opportunities that at the moment we haven't even considered or anticipated. We look forward to reaping those rewards and sharing them with the applied microbiology community. And of course, if any of our Members are in London, please do feel free to get in touch and pop in for a chat – we'd be very happy to welcome you.

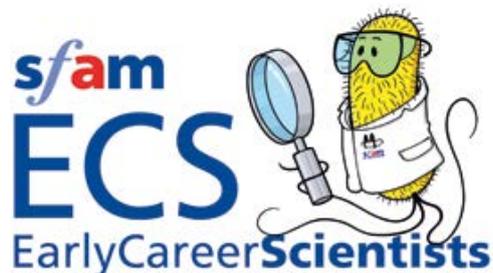


Putting us at the heart of science policy and science communication



Lucy Harper
SfAM Chief Executive

Early career scientist events at the Summer Conference



At this time of the year, the Society begins to look forward to the Summer Conference which, this year, runs from 4 – 7 of July in the Assembly Rooms in Edinburgh. As always the ECS Committee will be running a number of events throughout the conference specifically aimed at early career scientists.

Our events kick-off on Monday evening at 7:30pm, following the *Journal of Applied Microbiology* Lecture presented by Max Dow, with an icebreaker session. This is an excellent opportunity to come and meet the ECS Committee and some of the other students and early career scientists who are attending the conference in a light-hearted and friendly environment.

The centre of our events during the week is the student session taking place on Tuesday afternoon from 5:00 – 6:00pm, which this year focuses on writing skills. Those of us who are academics may be aware of the mantra "*Publish or perish*" and in a world of shrinking university funding opportunities, this has become more pertinent than ever. But writing takes many forms and

now more than ever there are so many ways to get your opinion out there. We have assembled a number of experts in diverse fields associated with scientific writing to come and provide their expertise and answer any questions you might have about writing and how to improve your own technique.

In the evening, after the student session, one of our local Committee Members will be leading a walking tour of Edinburgh. The tour will start at 7pm from the Assembly Rooms and we will begin by visiting the heart of the historic old town at the castle and walk down the Royal Mile toward Holyrood Palace. Having spent a lot of time in the city as a teenager I can thoroughly recommend attending what should be a lovely evening.

On Wednesday we have two important events, the first is at 12:45pm and is the ECS Committee Annual General Meeting. This provides our Members a chance to give feedback on the events which we have arranged and also gives you the opportunity to get involved with the Committee through our steering group. The second event is the student oral presentations which will begin at 1:30pm. Come along and support your fellow students and discover the high-quality research being carried out by your peers.

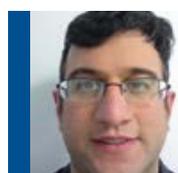
I look forward to meeting many of you at the conference in July. But before I wrap-up I wanted to mention the SfAM Autumn Meeting which is organized by ECS. This year it will take place on the 11 October at the Royal Society of Medicine. The centrepiece of the event will be a world-class panel session discussing bioethics. I encourage you to submit both oral and poster abstracts as there are a number of spots available for each and it is an excellent opportunity to gain experience of presenting your data.

Calling all student and Early Career Scientists!

We are looking for new people to join the Early Career Scientist Committee of SfAM.

We are a mix of PhD students, Postdocs and early career scientists organizing the early career scientist events at the annual Summer Conference as well as our own annual meeting. If you have an interest in organizing events and communication and are open to learn some new skills, please send us your CV and a short letter of motivation to ecs@sfam.org.uk. We meet approximately four times a year in central London and by committing to the task you will be expected to attend most of these – expenses will be paid.

If you need further information please have a look at our webpage at <http://www.sfam.org.uk/enpecs/ecs-committee/>



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Geomicrobiology can mean different things to different people: for most, it is the study of the interactions between microbial life and the inanimate geosphere (taken broadly to include the hydro- and atmospheres), which over time have shaped our planet. The Earth is like it is because of the activities (past and present) of the microbiota, and it is this relationship that constitutes the realm of geomicrobiology. The history of the planet is written in the rock record, but in order to read this history it must be viewed as a “joint authorship” – a product of geological and biological interactions. Something similar should be true of any “living” planet, and make it obvious whether active life is (or was) present.

Although geomicrobiology primarily concerns the geochemically relevant reactions catalyzed by prokaryotes (e.g., sulfate reduction, methane production, nitrogen fixation), we must also keep in mind that the geochemistry of the planet has also been significantly altered by eukaryotes, leaving massive mineral and hydrocarbon deposits, and a fossil record, not to mention the massive alterations of the atmosphere and hydrosphere due to human activities.

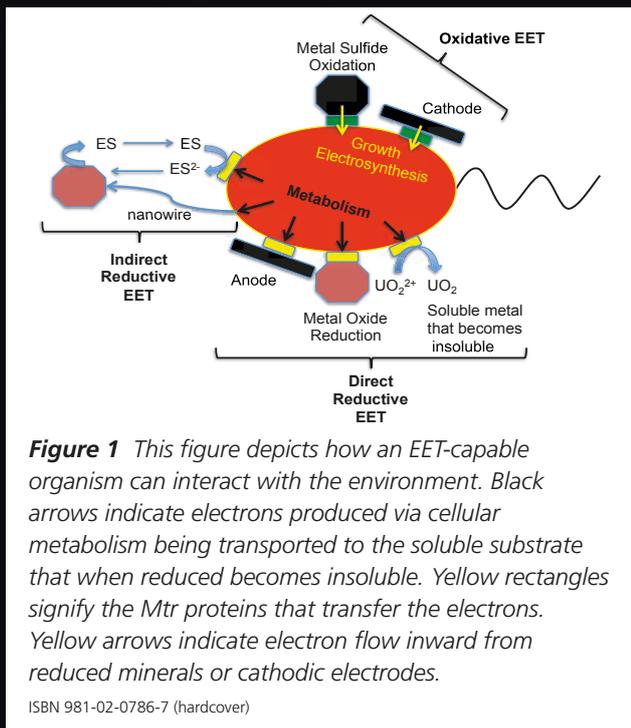
Prokaryotes are well suited for their geobiological role: their small size allows a surface to volume ratio that is far greater than eukaryotic cells, and their metabolic diversity allows interaction with a wide variety of inorganics that are not only important for life, but are also major components of many minerals. Almost all geomicrobiology involves, at some level, electron flow and redox chemistry. The key reactions of the carbon

cycle, the nitrogen cycle and the sulfur cycle, for instance, involve the movement of electrons to and from C, N and S: e.g., gaseous CO_2 is fixed through photosynthesis into organic carbon (soluble or insoluble), only to be returned to the atmosphere as CO_2 or CH_4 depending on the environmental setting. Similar reactions are seen with nitrogen and sulfur, whose redox changes allow them to cycle between chemical states and planetary reservoirs due to diverse microbial activities, often doing “jobs” that can be done only by prokaryotes (e.g., nitrogen fixation, ammonia and methane oxidation, methane formation and sulfate reduction).

So, it sounds as if geomicrobiology is really nothing new, but rather a matter of perspective. We all know about electron transport, the chemiosmotic mechanisms for coupling electron flow to ATP formation and the remarkable diversity of microbes in mediating these reactions. But wait, there is something new, or at least not well known: it is extracellular electron transport or EET. While the microbes involved with EET are not really new, what they do remains unknown to most microbiologists, being (remarkably) absent from any biology textbook and from almost all microbiology texts! EET was first reported in 1988, in two microbes (MR-1: aka *Shewanella* and GS-15: aka *Geobacter*) both capable of respiring insoluble electron acceptors (manganese and iron oxides) in the absence of oxygen. This is a forbidden pathway: cells are designed to keep electrons inside the cell and use electron flow to establish a membrane gradient. Moving the electrons out of the cell amounts to an energetic waste: electron

GEOMICROBIOLOGY

what is it, what's new and
why should we care?



Perhaps the most unexpected aspect of EET was that it could be reversible. Several laboratories have now shown that bacteria can also colonize cathodic (negatively charged) electrodes, growing on electricity (electrons) as their sole energy source. That bacteria on the cathode could efficiently transfer electrons from the cathode to other substrates such as Cr(VI) raised the possibility that electrode-based biofilms could be used for electrosynthesis of valuable products: imagine a solar-cell fed microbial system creating products and/or remediating uranium or chromium (Figure 1).

The importance of a discovery can often be judged by the new questions it raises, a few of which I add here: can microbes use electric signals to communicate? Will electrosynthesis lead to the production of valuable products by EET-capable bacteria? Is electrotrrophic metabolism an important part of symbiosis? Could these abilities be important factors for microbes in the human microbiome? Does electron exchange occur between prokaryotes and eukaryotes? All these questions (and many others) lay unanswered and waiting: questions raised by the study of geomicrobiology.

flow with no energetic advantage. But, if only insoluble electron acceptors are available, it becomes an issue of life versus death, and it is now clear that many bacterial taxa are EET-capable, and able to transport electrons to the exterior, growing via dissimilatory reduction of extracellular metal oxides.

The discovery of EET opened up a myriad of geochemically relevant metabolic “windows” thought to be off limits for microbial metabolism: namely the redox metabolism of insoluble (extracellular) compounds. It is appropriate that EET was first reported in studies attempting to resolve a geomicrobiological enigma: to explain the rate of manganese oxide reduction in sediments of Oneida Lake, NY. *Shewanella oneidensis* MR-1, an abundant inhabitant of these sediments, was isolated at Oneida Lake and after many years of study, various geochemically relevant abilities of this organism have been revealed.

To present the details would take pages, but to summarize from a geomicrobiological perspective, the EET-capable microbes can “breathe rocks” – respire insoluble extracellular electron acceptors, including properly charged electrodes. This latter capability has become a very popular area of research, dealing with microbial fuel cells and studies of electron flow. For example, measuring electron flow on an electrode during biofilm development, allows one to quantify the rate of electron transfer per cell, as well as to study the impact of surface charge on cell attachment, biofilm formation and gene expression in response to changes in surface potential. Accordingly, we now know that changes in surface charge can be sensed by bacteria on electrodes, leading to changes in expression of many genes: a kind of electrical communication, if you will.

FURTHER READING

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Professor Ken Nealson

Professor of Chemistry at the University of Southern California–Berkeley

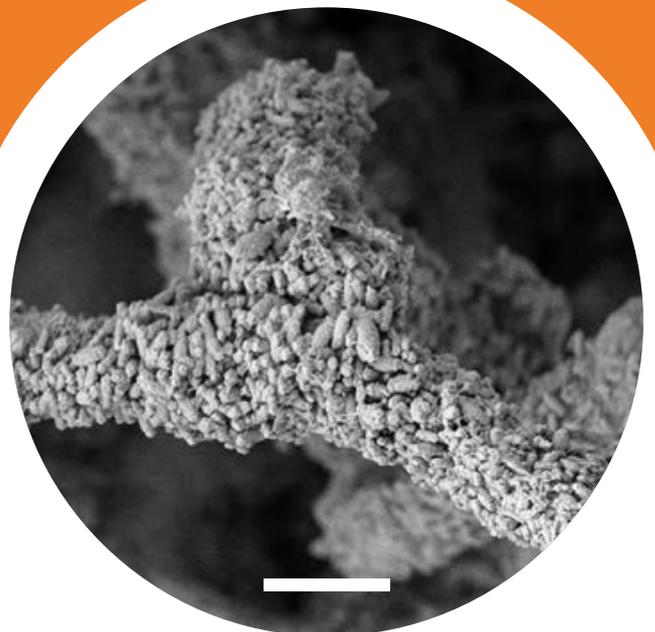
Fungal transformation and **biorecovery** of minerals, metals and metalloids

Many important metal resources are threatened by over-exploitation, inadequate recycling and reclamation, and geopolitical issues. Consumption of metals and minerals has increased steadily in recent decades and rising population growth and prosperity ensures that demand will accelerate. The rise of mega-cities has also exacerbated problems of metal recycling and reclamation and has given rise to the concept of “urban mining” which seeks to improve the recovery of important elements from urban waste. Furthermore, the increasing need for energy-efficient electronic materials such as those used in computers, mobile phones and televisions is highly dependent on a specific range of metal and mineral resources. Such “E-tech elements” include cobalt, platinum group metals and rare Earth elements, as well as metalloids like selenium and tellurium. Some of these elements are already in short supply and can be difficult to recover by conventional mining and extraction.

The EU is almost wholly dependent on imported supplies and it is, therefore, generally accepted that

there is an urgent need to improve the global security of supply of important elements. The EU is also eager to balance new mining processes with the requirements of minimizing environmental impact such as pollution and increased greenhouse gas emissions. Of the many worldwide initiatives designed to address this problem, microbial bioprocessing is seen as an essential component of the approaches that may be used to improve metal recovery.

The ability of microorganisms to change the chemical speciation of metals is well known and a variety of “bioweathering” mechanisms are involved in the microbial attack of rocks and minerals, including physical penetration and the production of acidic and/or metal complexing metabolites such as organic and inorganic acids, and siderophores. Bioreduction can also result in increased solubility, e.g., Mn(IV) to Mn(II). Such solubilization mechanisms provide a means of metal biorecovery from solid matrices. The application of bacterial bioleaching using, e.g., *Acidithiobacillus* spp., is a well-established industrial process for several



metals, for example, copper from mineral ore resources, and such mechanisms may also be applicable to the recovery of elements from other industrial and electronic wastes. Conversely, metals and metalloids can be immobilized as elemental or biomineral forms, e.g., Ag^0 , Se^0 , Te^0 and manganese oxides through redox transformations as well as by the production of metabolites such as sulfide, oxalate and CO_2 that lead to metal precipitation as sulfides, oxalates and carbonates, respectively. Biomineralization can also be mediated through the release of anionic substances that combine with metals (e.g., phosphates, carbonates and sulfates) as a consequence of mineral dissolution or from the biodegradation of organic substrates. The variety of biomineralization mechanisms used by microorganisms provides a means of recovering elements from leachates, process streams and effluents.

The growing discipline of geomicrobiology, which seeks to understand roles of microorganisms in geological processes, encompasses many aspects of microbial metal and mineral biotransformations. Species from all microbial groups can affect geochemical transformations, with the great metabolic diversity of prokaryotes ensuring that these organisms receive considerable research attention, especially regarding redox transformations in the subsurface. Fungi are less appreciated as geoactive agents, but are of profound importance in the terrestrial environment and capable of many metal and mineral transformations. Many geomycological processes are relevant to the natural cycling of elements, rock and mineral transformations, plant productivity and biodeterioration.

Fungi are ideally suited as geoactive agents and the vast majority exhibit a branching filamentous explorative lifestyle. They are chemoorganotrophic and excrete a variety of extracellular enzymes and metabolites that interact with organic and inorganic substrates. Their geoactive properties are underpinned by their metabolism and lifestyle and they can directly and indirectly mediate the formation of many kinds of minerals, including oxides, phosphates, carbonates and oxalates, as well as elemental forms of metals and metalloids such as Ag, Se and Te. Such biomineralization largely depends on the organism modifying its local microenvironment to create appropriate physico-chemical conditions for precipitation to take place and this can depend directly and indirectly on metabolism.

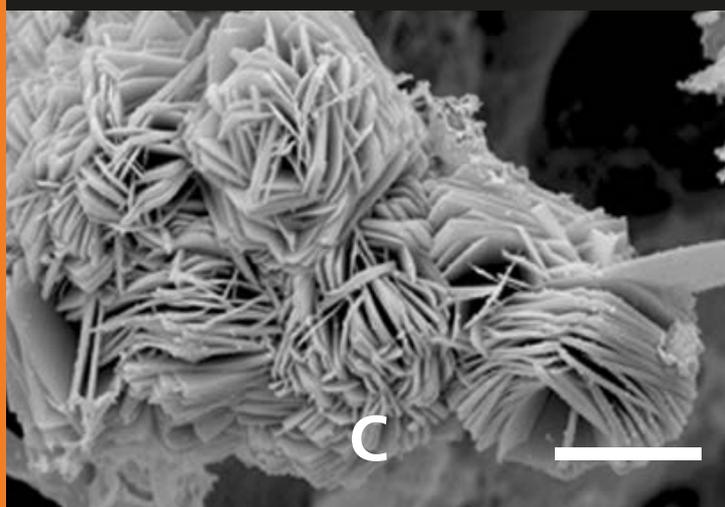
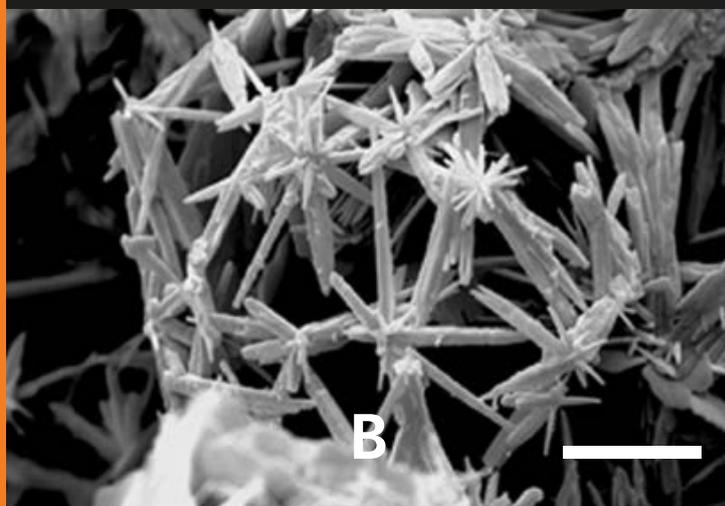
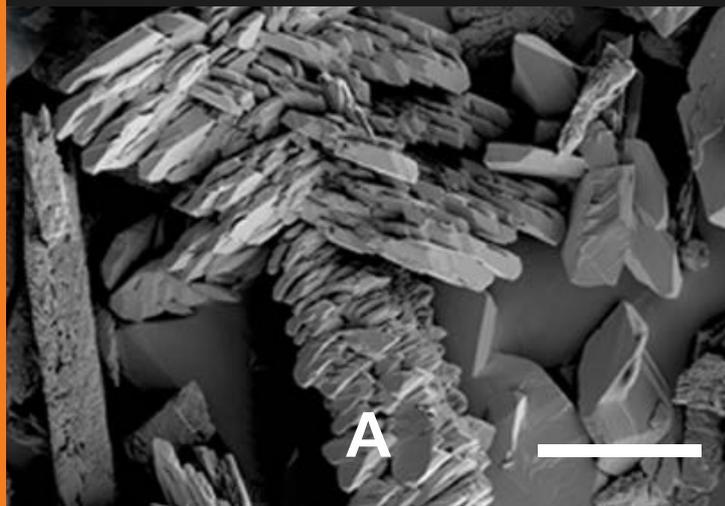


Figure 1 (left) Scanning electron microscopy images of rhodochrosite (MnCO_3) precipitation on hyphae of *Neurospora crassa* grown in urea- and MnCl_2 -amended medium (bars = 30 and 5 μm , respectively).

Figure 2 (above) Formation of lead or uranium phosphate minerals after growth of fungi on an organic phosphorus-containing substrate (glycerol 2-phosphate) in the presence of soluble $\text{Pb}(\text{NO}_3)_2$ or $\text{UO}_2(\text{NO}_3)_2$. (A) Pb minerals produced by *Aspergillus niger* (bar = 50 μm), (B) Pb minerals produced by *Paecilomyces javanicus* (bar = 5 μm) and (C) U minerals produced by *A. niger* (bar = 5 μm).

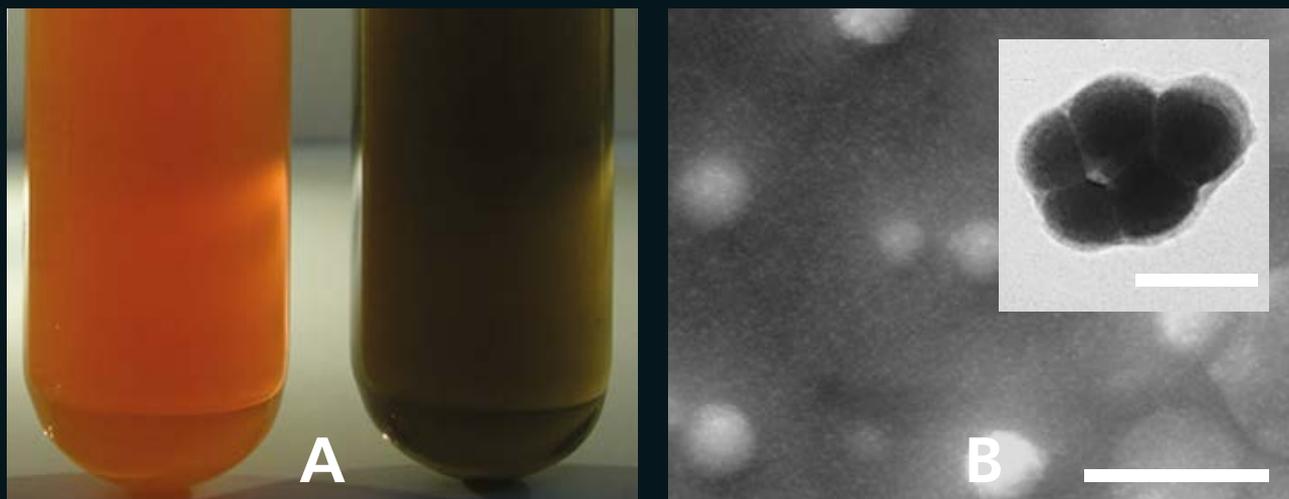


Figure 3 Fungal production of nanoscale metalloids. (A) suspensions of elemental Se (red) and elemental tellurium (black) obtained after reduction of sodium selenite or tellurite by a fungal growth supernatant and (B) scanning electron microscopy image of selenium nanoparticles (bar = 500 nm). The inset is a transmission electron microscopy image of a nanoparticle aggregate (bar = 200 nm). (C) transmission electron microscopy image of tellurium nanorods (bar = 400 nm).

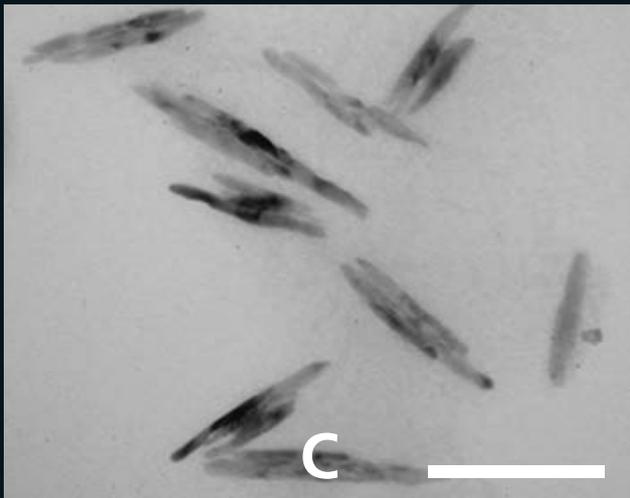
Compared with the simpler bacterial cell form, the filamentous fungal growth habitat may additionally provide more framework support and stability as a reactive network for biomineralization (Figure 1).

Fungi are very important biodegraders of organic material and can indirectly result in mineral formation where certain biodegradation products react with available metal species. For example, the action of phosphatase enzymes on P-containing organic substrates results in the release of inorganic phosphate that can then precipitate with available metals. Such fungal phosphatase-mediated metal bioprecipitation can extensively precipitate lead (Pb) or uranium (U) phosphates on hyphal surfaces during growth on a source of organic phosphorus in the presence of soluble Pb and U (Figure 2) and removal from solution of potentially toxic or radioactive elements is of great bioremedial potential. A recent discovery was the fungal-mediated formation of pyromorphite, a lead phosphate, from metallic lead. Pyromorphite is extremely insoluble and can form in Pb-polluted soil

especially when a source of inorganic phosphate is applied in abiotic soil remediation treatments. It is highly likely that soil fungi are mediating pyromorphite formation in such locations resulting in lead immobilization. Similarly, the formation of stable uranium phosphate minerals during fungal growth in the presence of uranium oxides or depleted uranium has also been demonstrated.

Microbially mediated carbonate precipitation has been used for metal and radionuclide bioremediation, soil stabilization and the reinforcement of concrete structures. Such a system may also provide a promising method for the biorecovery of toxic or valuable metals (e.g., Co, Ni and La). Many free-living fungi are capable of urea degradation resulting in alkalization of their environment due to the production of carbonate that precipitates with any susceptible metals present. Urease-positive *Neurospora crassa* can precipitate calcite (CaCO_3), as well as other metal carbonates, when incubated in urea-amended media. Biomass-free culture supernatants also have precipitative properties which facilitates metal biorecovery from solution in pure form. Pure otavite (CdCO_3) was recovered in this way, with a proportion of the particles of nanoscale dimensions (Figure 3). Fungal isolates from calcareous soil could precipitate CaCO_3 and SrCO_3 as well as olekminskite ($\text{Sr}(\text{Sr},\text{Ca})(\text{CO}_3)_2$) and Sr-containing vaterite ($(\text{Ca}_x\text{Sr}_{1-x})\text{CO}_3$), resulting in the almost complete removal of Sr from solution. Metal carbonates have several industrial applications, and are also precursors for important

Fungi are ideally suited as geoactive agents and the vast majority exhibit a branching filamentous explorative lifestyle



metal oxides. In an imaginative demonstration, the thermal decomposition of fungal biomass and precipitated MnCO_3 resulted in a carbonized biomass-manganese oxide composite material that was used as an electrode material in supercapacitors and lithium ion batteries. This was found to have some very good electrochemical properties in comparison with other Mn oxide materials prepared by abiotic means and in lithium ion batteries retained ~90% charge capacity after 200 charge-discharge cycles.

Metal-containing micro-/nanoparticles have a wide variety of applications. The use of metal-transforming microbes for the production of nanoparticles may allow some control over size, morphology and composition. This is relevant to the production of new advanced biomaterials with applications in metal and radionuclide bioremediation, metal biorecovery, antimicrobial treatments (e.g., nano-silver), solar energy, electrical batteries and microelectronics. Many fungi can precipitate nano-elemental forms of metals and metalloids through bioreduction, e.g., Ag(I) reduction to elemental silver Ag(0) ; selenate $[\text{Se(VI)}]$ and selenite $[\text{Se(IV)}]$ to elemental selenium $[\text{Se(0)}]$ and tellurite $[\text{Te(IV)}]$ to elemental tellurium $[\text{Te(0)}]$. Many of the fungal biominerals mentioned previously can be nanoscale or microscale (Figure 3), which imparts additional properties apart from metal sequestration. For example, mycogenic Mn oxides can sequester metals like Pb, Zn, Co, Ni, As and Cr and also oxidize certain organic pollutants. Many fungi produce metal oxalates upon interacting with a variety of different metals and metal-bearing minerals, e.g., Ca, Cd, Co, Cu, Mg, Mn, Sr, Zn, Ni and Pb and these have various industrial uses as well as providing another metal biorecovery mechanism.

Fungi are ubiquitous in natural environments and their roles in organic matter decomposition, element cycling and plant productivity are profound. As inhabitants of soil and rock surfaces, they are engaged in a suite of metal and mineral transformations altering metal speciation and mobility through such mechanisms as

complexation, mineral dissolution and secondary mineral formation. These are also of negative human impact with the same mechanisms being involved in the biodeterioration of rock and mineral-based materials in the built environment. On the positive side, their interactions with metals and minerals are of applied significance in land bioremediation, revegetation and detoxification of industrial effluents and wastestreams, and are an important component of the overall microbial repertoire of mechanisms that are being applied to metal biorecovery and the production of useful biomaterials. With growing concern over the management, conservation and recycling of world metal and mineral resources, it is clear that fungal capabilities may offer potentially useful solutions to an apparently insoluble problem.

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Acknowledgements

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Reclaiming copper from the whisky-making process

The making of fine single malt whisky is a skilled art that fills distillery visitors' centres throughout Scotland. Tourists and locals are both eager to learn about what goes on in the curvaceous copper stills and the source of those strangely inviting smells. The making of the lesser-worshiped blended whisky is no less impressive but a visit to a grain distillery won't be found on any sightseeing list. The processes involved are, of course, very similar; preparation and fermentation of the grain is followed by distillation in copper stills. The scale, however, is something quite different with about 275,000 litres of spirit produced a day in an intensive manufacturing process.

Of course, the larger the quantity of spirit produced, the larger the quantity of by-products that are produced too. Malt whisky distillation alone produces two very different by-products. The first distillation splits the 'wash' into 'low wines' and 'pot ale', the second distillation takes the low wines and purifies them further to the 'new make', leaving behind the 'spent lees'. Whilst the new make becomes whisky, through further processing and maturation, the pot ale

and spent lees by-products are currently used as animal feed and fertilizer, since long before the terms resource efficiency and circular economy were thought of. However, to do this, firstly the copper that dissolved from the still during the distillation must be removed. Sheep are uniquely sensitive to copper and would be poisoned by consuming such feed or even from eating grass grown on land using such a fertilizer; the same is not true for cows or pigs.

You might think that an easy solution would be to use stills made from another material, especially as this would also prolong the useful lifetime of the stills. Unfortunately things are not quite so simple. The dissolved copper is responsible for chelating sulfur-containing compounds, mainly derived from the cysteines and methionines in the grain. In doing so, it prevents them from evaporating with the alcohol as it is distilled and tainting the taste and smell of the final product – as eggy flavours to whisky would not appeal. Since this dissolved copper is actually vital to the process it must be removed from the by-products afterwards rather than the whole procedure.

The application of geomicrobiology offers real advantages over all current practices for the removal of copper from distillery by-products

Whisky makers generally use electrolysis and membrane filtration to remove the dissolved copper from the by-products but are always on the look out for greener, cleaner and cheaper methods for this removal. Some have opted to use reed beds, but perhaps biology can help in a very different way instead?

Morganella morganii is a Gram-negative, rod-shaped, single flagellated bacterium that has been shown to produce copper nanoparticles when presented with copper ions. Hypothesized to be part of its resistance mechanism, this species reduces both copper and silver ions that enter the cell, adding electrons in order to precipitate the metal and form nanoparticles. Whilst there is a lot of work still to be done to understand the mechanism used by this microorganism, its application within bioremediation is incredibly appealing. Not only does it provide an opportunity to replace electrolysis, it offers the possibility of reusing this metal in a form hundreds of times more valuable than copper usually is. Nanoparticles are more valuable than the bulk material from which they are derived. Moreover, copper nanoparticles made through chemical or

physical processing are invariably unstable, requiring additional work to provide the molecules required for their stabilization. However, during the biological synthesis of copper nanoparticles *Morganella morganii* produces a stabilization factor, one that also prevents aggregation of the nanoparticles. Therefore, the application of geomicrobiology offers real advantages over all current practices for the removal of copper from distillery by-products. The real challenge is the scale up of such a process and the isolation of the copper nanoparticles. Considering the large-scale fermentation and separation expertise that reside within the whisky industry, this is unlikely to prove an insurmountable problem.

Perhaps it will not be long before the distilling industry will be purveyors of whisky, gin, vodka and nanotech.



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Arctic lakes of Greenland

Researchers from Dartmouth University have been investigating a strange phenomenon occurring on the lake beds of the Arctic. Large gelatinous balls, known locally as sea tomatoes, have been found covering the bottom of Greenland's lakes. The sea tomatoes excrete the toxin microcystin, also known as cyanoginosin, which has been known to contaminate drinking water supplies and may pose a threat to the environment.

Sea tomatoes are in fact large glutinous colonies of cyanobacteria (genus *Nostoc*) which can reach up to 10cm in diameter; the largest of these is thought to be up to 25 years old. Cyanobacteria can be found in almost every environment worldwide. In the oceans and fresh-water they form massive green-blue or red blooms which are highly visible. These blooms can have harmful effects on aquatic ecosystems as a result of oxygen depletion and high levels of toxin excretion. They increase oxygen demand in localized areas, leading to hypoxic or anoxic conditions, killing fish. The toxin microcystin on the other hand can cause liver damage to humans and animals when consumed in a sufficiently high dose. These blooms tend to occur in eutrophic waters, in tropical or temperate regions such as China and North America. The waters are high in phosphates, nitrates and organic nutrients and promote plant life and algal growth.

Unlike the blooms however, the sea tomatoes aggregate on the floor of oligotrophic lakes, which are low in nutrients and located in areas of ice-free tundra, reaching numbers of up to hundreds of thousands in a single lake. Cyanobacteria are unusual in that unlike

the majority of bacterial species they are capable of photosynthesizing. In addition to this, a proportion can fix atmospheric nitrogen into a form which can be utilized; the combination of these features lend cyanobacteria to successful growth in otherwise inhospitable environments such as the Arctic lakes of Greenland.

Initially the levels of microcystin in the lakes of Greenland were investigated, testing the hypothesis that the low nutrient, cold lakes would contain less toxin than their temperate counterparts due to the inability of the lakes to support sufficient cyanobacterial growth. Of 19 lakes tested all contained levels of the toxin; even lakes where no sea tomatoes were positive for microcystin, suggesting that it is released by other organisms within the lake ecosystem. In addition to measuring toxin levels, the lakes have been mapped using underwater sonar and water chemistry. Data including pH, conductivity, dissolved oxygen and temperature have been recorded in order to elucidate

Home of the mysterious **SEA TOMATO**



the relationship between cyanobacteria presence and density, and the lake ecosystem including other biological life. Research in temperate areas suggests that water temperature and chemical oxygen demand are key drivers in cyanobacterial growth as well as the concentration of inorganic nitrogen.

Interestingly, several different species of sea tomato were identified in the Greenland lakes, each with a distinctive morphology. Further work is required to confirm the identity, however, initial research would suggest that the most abundant, smooth, round colonies are *Nostoc pruniforme*. The irregular, rarer form which is bumpy and contains visible nodules may well be *Nostoc zeerstedtii*. Another possible species was seen in only one lake which was very dark in colour and had not been observed previously by the researchers. In temperate areas many species of cyanobacteria may be present in a single lake. For example, in Dongping Lake

in China 25 species of cyanobacteria were recorded over a 30 month period. In this particular lake the predominant genera were *Pseudanabaena* and *Aphanizomenon*.

Work continues in Greenland to fully understand the impact of sea tomatoes on the lakes where they proliferate. It is hoped that by studying the lakes, their biological and nutrient composition, meteorological data and physical construct that a better understanding of these mysterious bacterial forms can be gained.



Ayuen Lual

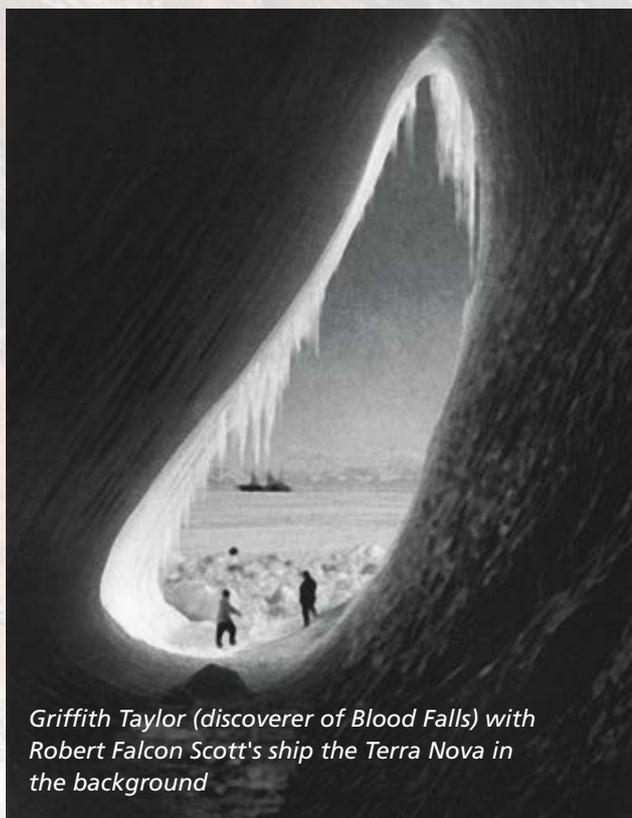
S Fails Blood B

Gateway to a microbial underworld

The monochromatic vistas of the Antarctic's Dry Valleys snowless peaks and the frigid white snout of the Taylor Glacier are vividly broken by an eerie sight; that of a five-storey, bright red outflow known as Blood Falls. Discovered in 1911, initially the red colouration was incorrectly ascribed to the presence of surface dwelling, red-pigmented algae. However, the secrets and subglacial source of the bleeding glacier's shock of colour and the undiscovered microcosm it contained remained locked beneath the ice for another century.

Blood Falls was first discovered in 1911 by geologist Thomas Griffith Taylor, during Robert Falcon Scott's *Terra Nova* Antarctic expedition (1910–1913). Scott had claimed prescriptive rights to the McMurdo Sound area of Antarctica and appointed Taylor to lead the Western Geological Party (WGP) to map the McMurdo Dry

Valleys area west of the Sound. Taylor launched into this expedition with enthusiasm, predicting “*We’ll have a ripping time I expect with no more risk than is good for us*” and compared with the challenges faced by previous expeditions, Taylor’s expedition was relatively uneventful allowing him to steadily work through the scientific questions he had set out to address, namely how land surface had been affected by glacier flow, wind, frost water and ice. During this desperately competitive period of Antarctic discovery, expedition leaders could reasonably expect the right to name the features they mapped, subject to the approval of Scott (who they referred to as ‘The Owner’). Taylor, whose name had yet to appear on any map, decided that the Dry Valley he was responsible for mapping and the glacier at its head would be worthy candidates, subsequently approved by Scott, making Taylor (in his own words) “*a cartographic entity*”. The Taylor Dry Valley and Taylor Glacier are amongst many of the features named by Taylor during an expedition into one of the world’s most extreme deserts. However, to microbiologists and astrobiologists, the feature which appears to have been of only passing interest to Taylor, Blood Falls, and the microbes populating the subglacial hypersaline lake which feed the plume, may provide important discoveries to aid our understanding of how life can prosper in the most extreme environments imaginable. This other-worldly phenomenon may yet provide clues to how life may have evolved and survived on other planets and their moons within our solar system and beyond.



Griffith Taylor (discoverer of Blood Falls) with Robert Falcon Scott's ship the Terra Nova in the background

Antarctica’s Dry Valleys are almost entirely free from ice and snow, with the exception of the few isolated glaciers which exist there, and conditions of low humidity and high winds make them amongst the most arid places on Earth. Despite this, Blood Falls provides both a clue and a portal to the thriving microbial community which exists buried in one of the most extreme environments on earth. Blood Falls is the surface manifestation of a subglacial discharge emanating from a pristine, ancient hypersaline groundwater system trapped beneath the Taylor Glacier’s 400 metres of ice. Geochemical analysis of Blood Falls and microbial diversity analysis using 16S rRNA gene clone library construction from DNA isolated from the site indicate that the source of Blood Falls is not the glacier itself but rather that the brine plume and the bacteria contained within are of marine origin. The subglacial brine, marine waters trapped during the Pliocene Epoch (c. 5 million years ago) in the McMurdo Valley networks when the Dry Valleys were deep fjords, have been cryo-concentrated giving rise to a hypersaline basin isolated for at least 1.5 million years. The enormous weight of the Taylor Glacier pressurizes the subglacial materials leading to the expulsion of a plume of hypersaline brine from the subglacial basin beneath, through the glacier front where it flows into the ice-covered Lake Bonney, which also increases the salinity of this system. The Taylor Glacier is completely frozen to its bed, preventing surface-derived water from penetrating to the base, therefore maintaining the pristine conditions in the subglacial hypersaline basin. Sunlight is also entirely absent from this ecosystem.

Contrary to the view of Griffith Taylor, the crimson hue of Blood Falls is not the product of pigmented algae but rather is due to high iron concentrations which oxidize (alongside other dissolved salts) upon contact with air and give the Falls their distinctive blood red colour. The discharge, in addition to being rich in iron (total iron concentration c. 3.45–3.8 mM) is also anoxic, and high in both chloride (Cl⁻, 1,375–1,440 mM) and sulfate (SO₄²⁻, 50 mM), markedly distinct in composition from the Taylor Glacier outflow. However, the cryo-concentrated subglacial brine feeding the falls is not red in colour, since oxygen is largely absent. Interestingly, bacterial numbers in the surrounding Taylor Glacier outflow are lower than those of the subglacial outflow of Blood Falls. All this indicates that a thriving population of microorganisms exists within this subglacial hypersaline lake. The metabolically active microbiome of the Blood Falls system has a relatively low diversity, nearly all of which are related to the genus *Desulfocapsa*. The majority (46%) of clones from the samples taken at Blood Falls belong to the genus *Thiomicrospira* and related to the species *Thiomicrospira arctica*, an obligate chemoautotroph. In addition, a bacterium closely related to the iron-reducing autotroph *Shewanella frigidimarina* was isolated. Finally, members of the

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sulfur- and iron-reducing *Geobacteraceae* and organotrophs belonging to the Bacteroidetes were also discovered. Taken together, a picture emerges of the lifestyle of the microorganisms populating this extreme habitat.

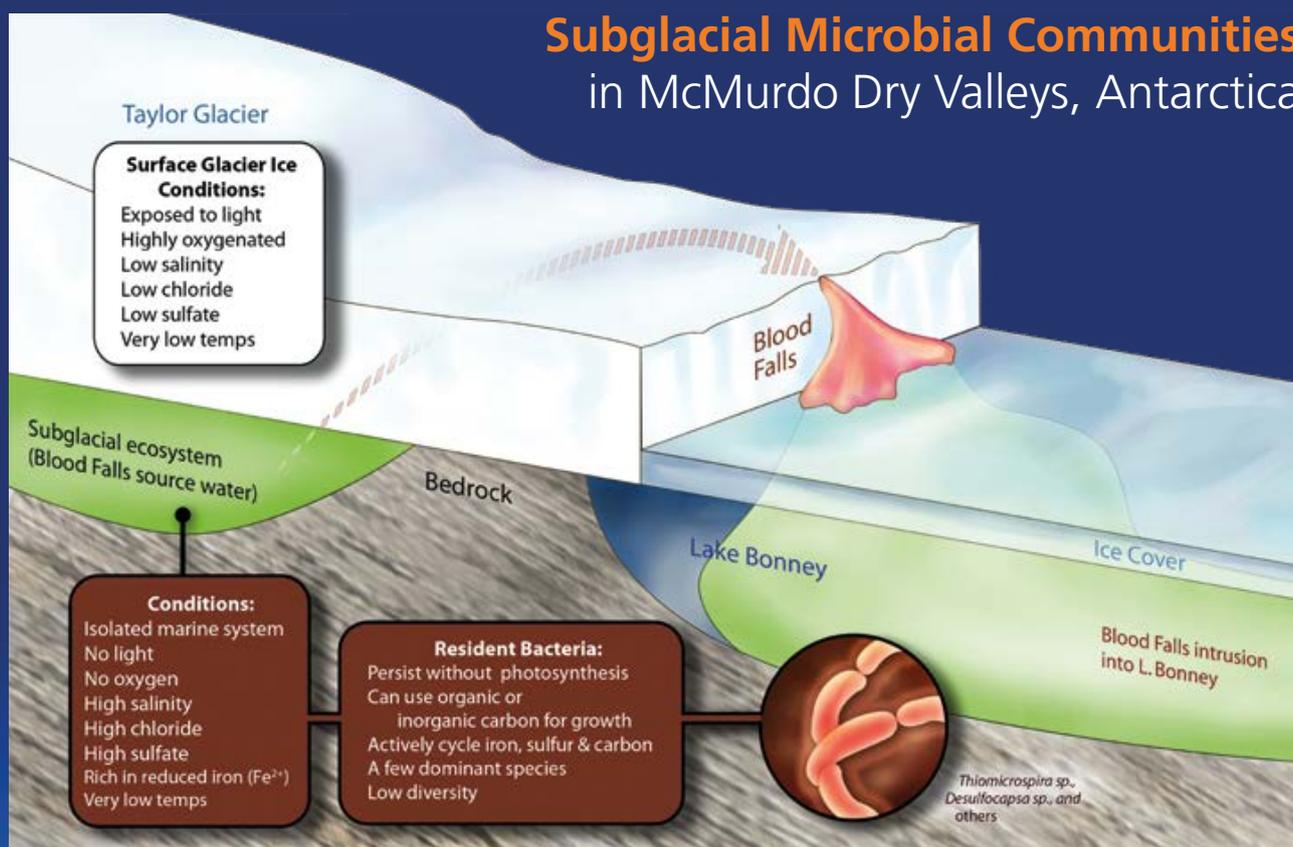
Microbial growth here must occur in the absence of light, under cold and anoxic conditions. In addition, organisms beneath the glacial surface experience high salinity and high concentrations of iron. The bacterial microbiome beneath the Taylor Glacier appear to be capable of growth chemoautotrophically or chemoorganotrophically and are capable of harvesting energy from either bedrock minerals or ancient marine organics by respiring Fe(III) and SO_4^{2-} . In 2015, a group led by Dr Jill Mikucki, University of Tennessee, used an ice-melting probe, IceMole1, to extract the first ever samples directly from the subglacial source waters of Blood Falls. The data obtained from these studies will enhance our current understanding of one of the least explored environments on Earth.

This unique microbial ecosystem offers microbiologists an opportunity to examine the evolution and adaptation of life in extreme hypersaline environments, which astrobiologists believe mimic closely those which may be found on planets and their moons within our solar systems. The microbiome buried alive beneath the ice of the Taylor Glacier may provide a model for how life survives and prospers under ice in harsh conditions (no light, no oxygen, hypersaline brines (with low water activity) and in sub-zero temperatures). From studies of the solar system, the moons of Jupiter, Ganymede and Europa, are thought to contain massive salt oceans beneath their ice-covered surfaces. If life does exist there, it may share more characteristics with that in Blood Falls and the hypersaline subglacial basin which feeds it, than anywhere else on Earth. The examination of life within this harsh environment may provide insights into how life persists during prolonged periods of depressed global temperatures, the so-called 'Snowball Earth' theory. This may also have implications for the search for life in the Martian subsurface permafrost.

Life within this harsh environment may provide insights into how life persists during prolonged periods of depressed global temperatures



Subglacial Microbial Communities in McMurdo Dry Valleys, Antarctica



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How **MICROBES** are solving the pollution of the sexual revolution

Synthetic hormones have been at the heart of revolutionizing contraception for millions of women throughout the world since they first became available in the 1960s. Mimicking the natural sex hormones, synthetic oestrogens are used to control the reproductive cycle and also to replace natural hormones at the onset of the menopause, through hormone replacement therapy (HRT). 17 α -ethinyl oestradiol (EE2) is the most widely used synthetic oestrogen compound and has a much higher potency than the natural 17 β -oestradiol (E2).

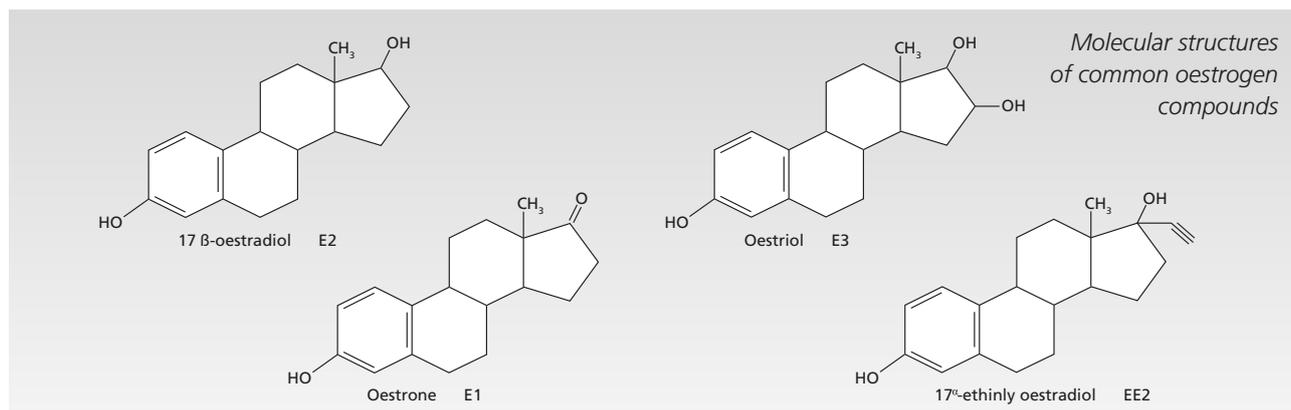
The therapeutic benefits of hormone treatments are well known, however, the fate of these compounds once they have left the human body are a cause for concern. Since the publication of the book *Silent Spring* in 1962, awareness of the future effects of chemicals on the environment has been raised. The presence of an ethinyl group stabilizes EE2 resulting in a higher potency than E2. This is important for its therapeutic use allowing the drug to have a longer shelf life and to be taken orally. It is thought that the ethinyl group hinders enzyme binding and metabolism of EE2 by bacteria. Therefore, the effect of EE2 on aquatic life will be greater as its chance of degradation is reduced compared with E2.

Many studies on aquatic life downstream of wastewater treatment plants have shown feminization of fish and other amphibians as well as reduced fertility rates. This was found to be due to oestrogen compounds present at as low as 1 ng/l concentrations in the water. Bioaccumulation of oestrogens has also been seen in

the tissues of freshwater worms and a number of other aquatic organisms. Although there is no conclusive evidence, there is concern that oestrogens at low concentrations in the drinking water supply could have similar effects in humans. A lowering of the average sperm count in humans may be a result of oestrogen contamination, though this has yet to be proven conclusively.

So what happens after these synthetic and natural oestrogens have played their role in the human body? The compounds are excreted in urine in a conjugated form or in an unconjugated form in faeces. Conjugation renders the compounds inactive; however, it is a reversible process, with the majority of the oestrogen reaching the wastewater treatment plants in the unconjugated, active form.

Biological wastewater treatment systems have been developed to use the natural ability of bacterial communities to break down and remove polluting compounds from wastewater. They are designed for the removal of oxidizable organic carbon (known as biochemical oxygen demand), oxidizable chemicals (known as chemical oxygen demand) and nutrients, especially nitrogen and phosphorus, which can cause eutrophication in waterways downstream of the treatment plant. The ability of bacterial communities in wastewater treatment plants to remove micropollutants, including synthetic oestrogen compounds has only recently become a priority. In 2013, both E2 and EE2 were placed on a watch list for the EU water framework directive by the EU commission in



Fluorescence-in-situ-hybridization microscopy to show a complex microbial floc of activated sludge. Ammonia oxidizing bacteria (AOBs) thought to be involved in the breakdown of EE2 are stained in blue. All other bacteria present are stained green

order for further data to be gathered with which to determine appropriate control measures. This directive governs the standards to be achieved by European waterways, rather than being a direct measure of the outputs from sewage treatment plants. Treatment plants that have outputs into small streams will have to achieve a better rate of removal due to the lack of dilution, compared with a large river or ocean discharge.

Expected future regulations are likely to be based on predicted-no-effect-concentrations (PNEC). This is the concentration at which the compound no longer has an effect on the organisms most sensitive to it. PNECs have been measured and predicted for all of the forms of oestrogen, being just 0.1 ng/l for EE2, and 2 ng/l for E2, concentrations that are difficult to measure using current laboratory methods.

How can such a low concentration of such common compounds be achieved in UK waters?

The biological wastewater treatment systems currently used in the UK are already able to reduce the concentration of oestrogen compounds down to between 1–30 ng/l. The removal achieved, however, is variable across treatment plants and over time. Removal of oestrogens is achieved by a range of processes linked to the hugely complex microbial community that is maintained in a wastewater treatment plant, either in the flocs of an aerated activated sludge plant or on the stones of a trickling filter. These communities are hugely diverse, with an estimated 10^9 cells/ml and over 1,000 species in an average activated sludge plant.

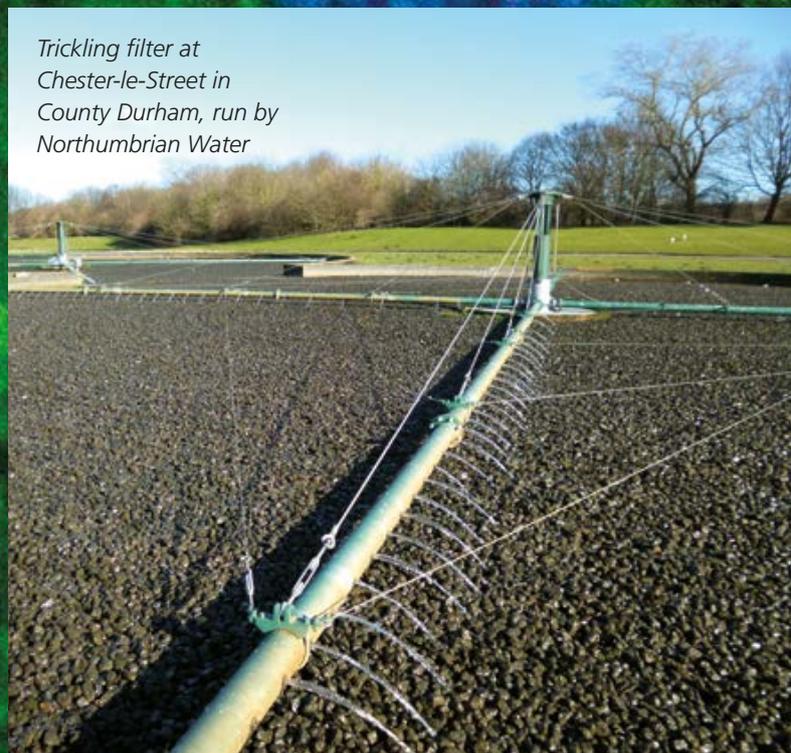
Chemical and physical removal

Volatilization of oestrogen compounds is thought to be negligible. Their hydrophobic nature high octanol-water partition coefficients mean that they are readily adsorbed onto solids, including on to cell surfaces and the extracellular material that make up biofilms or flocs in the treatment plants. Sorption is a rapidly occurring process, and to some extent a reversible one, that has been reported to account for between 10–30% of oestrogen removal in a treatment plant.

Degradation by microbes

Biodegradation of hormones by bacteria in the wastewater treatment plant is the dominant removal mechanism for oestrogen compounds. Longer retention times of both the bacterial biomass and the water in a sewage treatment plant result in greater degradation of oestrogen compounds. This is thought to be related to the increase in bacterial species diversity that is seen when retention times are longer. Slow-growing organisms, with more diverse metabolisms proliferate when retention times are longer and are believed to contribute to degradation.

We know that biodegradation accounts for most of the oestrogen removal, but the exact mechanisms are not well understood. A number of heterotrophic bacteria common in wastewater treatment plants have been isolated that are able to use E2 and EE2 as a substrate



Trickling filter at Chester-le-Street in County Durham, run by Northumbrian Water

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for growth. These include *Rhodococcus zopfii*, *R. equi* and *Sphingobacterium* sp. JCR5. The conversion of E2 into E1 and a number of other products has been observed, however, the enzymes that catalyse this have not yet been identified.

Degradation by direct metabolism seems unlikely given the extremely low concentrations of oestrogens in the wastewater. More probable is a situation where enzymes that would usually degrade other steroidal and aromatic molecules may act non-specifically on oestrogens if they happen to collide. Enzymes such as monooxygenases and dioxygenases are thought to fit the bill. These enzymes have been linked with the bioremediation of polyaromatic hydrocarbons (PAHs) from the oil industry and are the subject of ongoing research as they are produced by a broad range of bacteria and use many aromatic pollutants as substrates.

The pathways involved in the breakdown of EE2 are more controversial, with little agreement about the mechanisms. One suggestion is that there is a link between biomass that has the ability to remove ammonia and EE2 degradation. In a treatment plant, ammonia oxidizing bacteria (AOBs), such as *Nitrosomonas* sp. and *Nitrospira* sp., oxidize ammonia to nitrite, with hydroxylamine as an intermediate. Nitrite oxidizing bacteria (NOBs) then convert this nitrite to nitrate. The enzyme ammonia monooxygenase (AMO), which catalyses the conversion of ammonia into hydroxylamine, is able to convert oestrogens into hydrophilic products that have no oestrogenic activity. This process is thought to be the first step in the degradation of EE2, with heterotrophic organisms carrying out further degradation. It has also been suggested that there is competition between ammonia and oestrogens for the removal by AMO. The lack of a consensus on the exact mechanisms involved means that this is very much an active topic of research.

More to be done

The need to reduce the effect of hormones on the environment is pressing, regardless of their source or if they are synthetic or natural. Further work is required to elucidate the pathways, genetically characterize the organisms and enzymes involved, and potentially synthetically engineer or evolve organisms with enhanced oestrogen degradation capability. With a better understanding of the way bacteria carry out this vital function, the wastewater treatment plants of the future can be designed with micropollutants in mind. And in the short term, so that additional treatment mechanisms could be put in place to meet the soon to be applied regulations.

It is vital that wastewater from both humans and agriculture is treated to ever more stringent standards, as ultimately this will determine how much oestrogen enters the environment and therefore the quality of our drinking water sources.



Activated sludge lane at Tudhoe Mill wastewater treatment plant in County Durham, run by Northumbrian Water

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Lucy E. Eland

Interdisciplinary Computing and Complex BioSystems Group, Newcastle University



The need to reduce the effect of hormones on the environment is pressing, regardless if they are synthetic or natural

Spreading the word in public and in Parliament

Spring was full of events engaging young scientists in policy, and activities engaging the public in science. At 'SET for Britain', a poster competition in the House of Commons, 200 early career researchers, across bioscience, chemistry, physics, engineering and maths, shared their work with dozens of politicians and expert judges. RSB helps to organize 'SET for Britain' as a rare opportunity for politicians to meet some of our most promising early career scientists and understand their work.

During our 'Voice of the Future' event, early career researchers descended on the House of Commons to grill MPs and Ministers on their science policies. The RSB, SfAM and many other scientific organizations sent representatives and the Q&A panel sessions were broadcast live on Parliament TV. We were thrilled that Major Tim Peake recorded a video message for the event from the ISS. He replied to a question from Jo Johnson MP, describing how his experiments in space often focus on finding ways to counter the negative effects of growing old on the body. Peake also praised the UK's commitment to helping to lead Europe in collaborative research and technological development through the European Space Agency.

These events in Parliament ensure MPs not only have an awareness of the great research going on in their constituencies, but also gain a greater understanding of the international collaborative nature of science. It is important that MPs make policy decisions informed by evidence, and a greater mutual understanding between MPs and scientists will improve this. The Government needs to ensure the UK continues to lead the world in biological research where we have enormous strength.

The links between science, knowledge and democracy were also highlighted by Sir Paul Nurse Hon FRSB, who wrote a brilliant commentary to celebrate the 50th anniversary of our Journal of Biological Education. He argued that a good science education is vital in order

for people to participate effectively in democracy; as it gives an understanding of how reliable knowledge is produced.

Increased participation in our national biology competitions is an important part of our biological education work. Joining the Biology Challenge and the British Biology Olympiad, we have now launched the Intermediate Biology Olympiad for Y12 students in England and Wales, Y13 in Northern Ireland and S5 in Scotland. We wish the best of luck to our four winners of this year's British Biology Olympiad (age 16–18) who will represent the UK at the International Biology Olympiad in Vietnam in July. Schools are also encouraged to take part in our Nancy Rothwell prize for specimen drawing, open until September; and our amateur photography competition, closing in August.

Our public engagement work continues to educate and enthuse budding biologists and their families at festivals all over the country. We challenged visitors to reduce their food waste and improve their knowledge of nutrition in 'The Hungry Games'; activities developed with the Biochemical Society and the Nutrition Society; at the Northern Ireland and Brighton Science Festivals.

Food security for our growing global population is one of the biggest challenges of the 21st century. However, in the UK we still throw away a fifth of the food we buy and don't always think about getting the best nutrition from our diets. Activities included card games, quizzes and expert explanations of how changing our food habits could have a positive effect on the environment as well as our health: we even cooked up a selection of tasty nutritious and sustainable dishes for the public to try.

You can also take part in our new citizen science project #BritainBreathing, a free app to track seasonal allergies which has now launched on android. Developed with The University of Manchester and the British Society for Immunology, it can allow people in the UK to track their symptoms, such as those associated with hay fever or asthma, while contributing to scientific research. Data will be anonymously shared with researchers who will map against time, location, pollution, weather and pollen, in order to study when and why allergies are occurring and increasing.



Dr Mark Downs CSci FRSB
*Chief Executive of the
Royal Society of Biology*

Readers of the *Microbiologist* will be interested to know that MICROBE 2016 is being hosted at the Hilton Hotel, Sheffield, later this year.

Following the success of previous MICROBE meetings, the conference will include the usual elements, including an original and refreshing lecture programme, an extensive trade exhibition dedicated to medical microbiology, a poster exhibition and at the end of both days, there will be ample time to relax and socialize. Delegates will be accommodated in the Hilton Hotel and in the adjacent Hotel Metropolitan, so no road transport is required during the conference.

The lecture programme is almost complete and will include the following diverse range of speakers and topics:



Final conference details will be announced in the quarterly newsletters (microbeconference@gmail.com to obtain a copy) or on the web site:

www.microbe.org.uk

Delegate places are still available at £199 per person. This fee includes accommodation, all meals and access to all elements of the conference. There are a few twin-bedded rooms available and delegates can share at the reduced fee of £149 per person. There is no formal closing date for applications; bookings will be taken until the conference is full.

Professor Jonathan Cohen

Diagnosing sepsis: does the microbiology matter?

Dr Paul Dark

Surviving sepsis: delivering precision medicine with rapid diagnostics.

Mr Saurabh Sinha

Neurological clinical case.

Dr Laura Prtak

Bacterial meningitis case study.

Dr Simon Johnston

Host-parasite interactions.

Dr Alison Cope

Mosquitos and viral infections – a never ending fight!

Dr Trevor Winstanley

EUCAST: life after BSAC.

Dr Sheena Cruickshank

Parasites – the master manipulators.

Mark Prescott

CPA to UKAS.

Professor Mark Pallen

Clinical application of microbial genomics and metagenomics: the future is here.

Shila Seaton

UK laboratories NEQAS performance.

Neil Bentley

Ebola testing home and away.

Professor Mark Fielder

Antimicrobial resistance in veterinary and human medicine – are we at breakpoint?

Dr John White

Sexually transmitted infections – why the laboratory is more important than ever.

Dr Andy Borman

Dimorphic fungi – new pathogens from the Old World. The impact of molecular approaches to fungal identification.

Group Captain Andrew Green

Emerging and persistent infectious diseases: when politics, security and society collide.

MICROBE 2016

23 – 25 September 2016

The Deepwater Horizon (DWH) disaster of April 2010 is marked as one of the largest maritime oil spills on record resulting in the deaths of 11 platform workers and injuring many others. An estimated 4.1 million barrels (700,000 tonnes) of crude oil gushed from the leaky Macondo-252 well and entered the Gulf of Mexico over a period of 84 days. Several distinctive features set the DWH spill apart from other oil spills at sea, one of which was the duration of the spill and depth at which it occurred – 1,500 m below the sea surface. Another was the unprecedented formation of a hydrocarbon-enriched plume that formed at 1,000 – 1,300 m depth within the water column, spanning an impressive 35 km on a horizontal transect within the water column.

The fate of oil in the environment is largely dictated by the presence and activities of natural communities of oil-degrading bacteria, most of which belong to the Order *Oceanospirillales*, and include *Alcanivorax*, *Cycloclasticus*, *Oleispira*, *Oleiphilus* and *Thalassolituus*. These organisms are almost always found to be enriched following an oil spill. They lie at the heart of natural and anthropogenic oil-spill remediation and are, therefore, critical to restoring oil-impacted ecosystems to their natural state. During the DWH oil spill, the formation of the massive deepwater oil plume triggered dramatic microbial shifts, notably of bacterial taxa belonging to the *Oceanospirillales* (termed DWH *Oceanospirillales*), *Cycloclasticus* and *Colwellia* that were found significantly enriched within the plume. This succession from aliphatic hydrocarbon-degrading bacteria (*Oceanospirillales*) to obligate degraders of

aromatic hydrocarbons (*Cycloclasticus*) and psychrophilic hydrocarbon-degrading generalists (*Colwellia*) closely resembles the microbial dynamics that is typically observed in seawater following oil contamination.

Oil from the leaky Macondo well also reached the sea surface in the Gulf of Mexico, forming expansive oil slicks that also triggered dramatic microbial community shifts, notably an enrichment of *Cycloclasticus* and, to a lesser extent, *Halomonas*, *Alteromonas* and *Pseudoalteromonas*. These microbes are recognized for producing exopolymeric substances – i.e., biopolymers released extracellularly into the seawater that can behave as dispersants to facilitate the dispersal of the oil and increase its bioavailability for biodegradation.

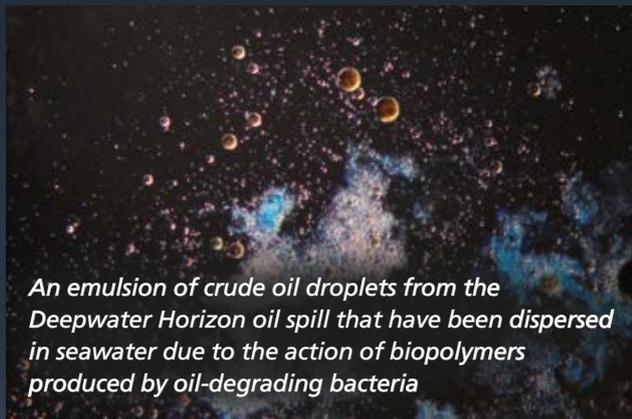
Cultivation and cultivation-independent techniques, including single-cell genomics, revealed that these bacteria possessed the metabolic capacity to degrade oil hydrocarbons. Their enrichment and dominance in surface oil slicks and deepwater plume waters during the spill reflected their important role in the biodegradation of the oil. Recently, the reconstruction of draft genomes for some of these hydrocarbon degraders allowed the identification of hydrocarbon-degradation pathways, which revealed that the combined capabilities of the microbial community in degrading the oil exceeded those of its individual components (unpublished results).

During the DWH oil spill, more than 7 million litres of the synthetic dispersant Corexit-9500 were applied on sea surface oil slicks and at the leaky well head to promote the formation of small, slow-rising droplets, and help increase the bioavailability of the oil for



Unprecedented nature and microbial response of the

DEEPWATER HORIZON OIL SPILL



An emulsion of crude oil droplets from the Deepwater Horizon oil spill that have been dispersed in seawater due to the action of biopolymers produced by oil-degrading bacteria

microbial degradation. Hitherto, little was known of its influence on the microbial community response and degradation of the oil. Recent work has shown that the presence of the dispersant significantly altered the microbial community in plume waters through selection of dispersant-degrading bacteria, such as *Colwellia*, that bloomed in the deep waters of the Gulf during the spill. The application of dispersant during the spill had thus significantly altered the otherwise natural microbial response. Whilst the environmental impact and fate of dispersant usage continues to be a topic of debate, these findings highlighted the importance of having prior knowledge of their effects upon oil-degrading bacteria – information that would guide decisions on their application for oil-spill contingency – considering these microorganisms are a key factor to the natural attenuation process.

Whilst the water column microbial community response to the DWH spill was intensively studied and is well documented, the formation of marine oil snow (MOS; aka oil aggregates) was another distinctive feature of this spill. MOS was observed during the first research cruise on *R/V Pelican* to the DWH site in early May 2010 and was frequently encountered around the vicinity of surface oil slicks. MOS can be described as a mucilaginous floating organic matter with a “fluffy” or gelatinous off-white appearance and containing oil droplets embedded within its amorphous matrix. By June 2010, a little over a month after the onset of the spill, MOS was no longer visible at DWH and it is now known that it had sedimented to the seafloor in what is described as the “Dirty Blizzard”. Although conjecture still surrounds its genesis at DWH, MOS formation appears to have been directly associated with the influx of crude oil during the spill and its interaction with bacterial and phytoplankton cells, and with mucilaginous polymers (e.g., transparent exopolymer

particles, TEP) that are ubiquitous in the water column. MOS has been proposed to act as “hot spots” where microorganisms are concentrated, including oil-degrading bacteria, and where oil biodegradation was occurring in a heightened state of activity within the water column on these suspended particles.

The unique nature of the DWH oil spill provided the means for the evolution of a complex microbial community response that varied within water column depths and had triggered the formation of unprecedented quantities of MOS. With oil exploration moving further into more challenging environments, such as deepwater provinces, the DWH spill can be seen as a template to learn from as a reference to future major oil spill events at sea. One important aspect to take into careful consideration are methods, such as dispersant applications, as part of contingency plans to combat oil spills at sea, especially in challenging environments where less is likely to be known of their effects on the indigenous microbial communities and other organisms.

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Infection leads to insult: WHAT'S IN A NAME?

For many years the way we have named new diseases has often been associated with places or locations or perhaps eponymously. There are a great number of examples, such as Guillain Barré syndrome, Chagas Disease, Addison's Disease, listeriosis and Cock's peculiar tumour, to name a few. In fact, a quick search of the Internet revealed a list of some 517 diseases that have been given eponymous titles.

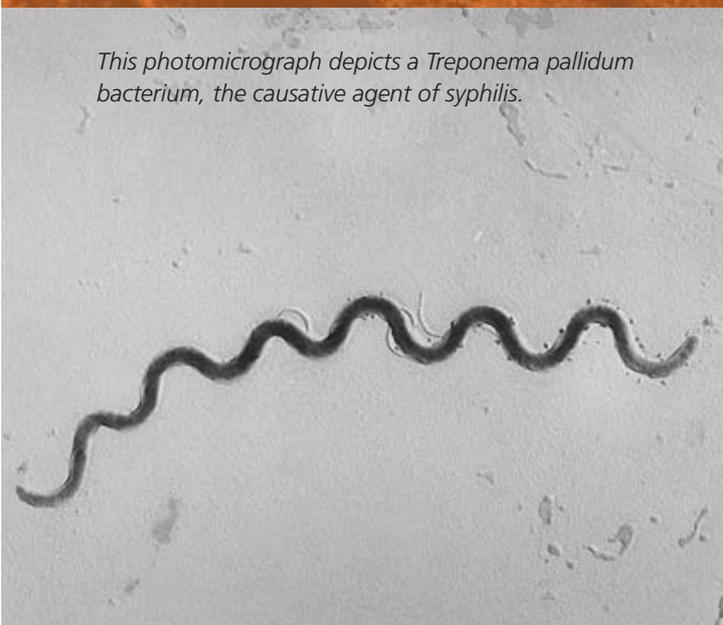
In recent times we have seen outbreaks or the reporting of several different infectious diseases or disease types including Ebola virus disease, West Nile virus, Lyme disease, Zika virus and antibiotic resistance problems caused by organisms carrying New Delhi Metalloproteinase (NDM) enzymes. All these diseases have been named as a result of the locations in which they were discovered or identified. These names are not

given with any form of malice or ill-feeling; they are solely based on identification and geography. However, this has not always been the case.

The spread of syphilis throughout Europe in the 1500s sheds some interesting light on the naming of a disease. Syphilis was widely known as the 'French disease' to the Italians, Polish and Germans and lovingly called the 'Italian disease' by the French. Indeed, the Italian physician and poet Girolamo Fracastoro wrote a pastoral poem entitled '*Syphilis sive morbus gallicus*' which translates from Latin as 'Syphilis or the French disease'. The insults carried on, with the Dutch who referred to the infection as the 'Spanish disease', the Russians who called it the 'Polish disease' and the Turks who referred to it as the 'Christian or Frank (Western Europe) disease'. The *Entente Cordiale* between Britain and France was not yet in place so we also traded insults with our neighbours, syphilis being termed as the 'French' or 'British' disease respectively. It is clear that in this context the naming of the disease had far more to do with insults, xenophobia and political posturing than anything else.

Thankfully, we are no longer in a world where the naming of a disease or malady to cause insult is acceptable. Scientists now align names purely with locations of origin or identification. However, this too has become problematic with the naming (or emergence) of diseases with place causing offence to nations; it is felt this approach is, or could be, construed as stigmatization associated with the name. Recently the Indian Government had issues with the naming of NDM, some of the Arabic States took exception to Middle Eastern Respiratory Syndrome (MERS) and some African states perceived very negative connotations with diseases such as Zika virus, Rift Valley fever, Congo haemorrhagic fever and, of course, Ebola.

This photomicrograph depicts a Treponema pallidum bacterium, the causative agent of syphilis.



HISTORICAL PERSPECTIVES



So it is clear we need to adopt a prudent approach, as a scientific community, to ensure as best we can we do no harm in the way we name new disease discoveries. The WHO recently issued guidelines for naming new human infectious diseases. This guidance would now discourage names such as Ebola, swine flu, West Nile virus, Zika and so on in favour of names that are more neutral and describe the disease in more general terms. The briefing paper suggests that more generic terms should be used such as respiratory disease, hepatitis, neurologic syndromes and so on. It also suggests that specific progressive terms should be incorporated where needed, such as progressive or juvenile. The WHO paper also states that, if it is known, the causative pathogen should be used as part of the disease name; for instance, a novel coronavirus respiratory syndrome. Finally, names also need to be short! So, in short we have to rethink our naming processes to some extent but additionally, as a global community, we need to also keep some perspective.

It was also noted by the WHO that disease naming can and does have negative connotations with implications for trade and travel. We are currently seeing a number of questions being asked about the safety of people intending to go to Brazil (both spectators and athletes) for the upcoming Olympic Games. In 2009, some countries limited the sale of pork and pork products from countries affected by the swine flu outbreak – although in reality swine played a minimal role and slaughtered pigs would not spread the infection.

The WHO have spent time trying to establish a useful and meaningful alternative to the current methodology of naming. They have considered the potential of naming infections after the Greek gods, in a similar fashion to that employed for naming comets. The WHO have also considered the alternate naming of infections with male and female names, as is undertaken when naming hurricanes. It was assumed here that no one would complain about their name being associated with a weather event. However, it was also noted that a weather event is transient whereas the emergence of

an infection or disease might well be more permanent! Consequently, both ideas were discarded.

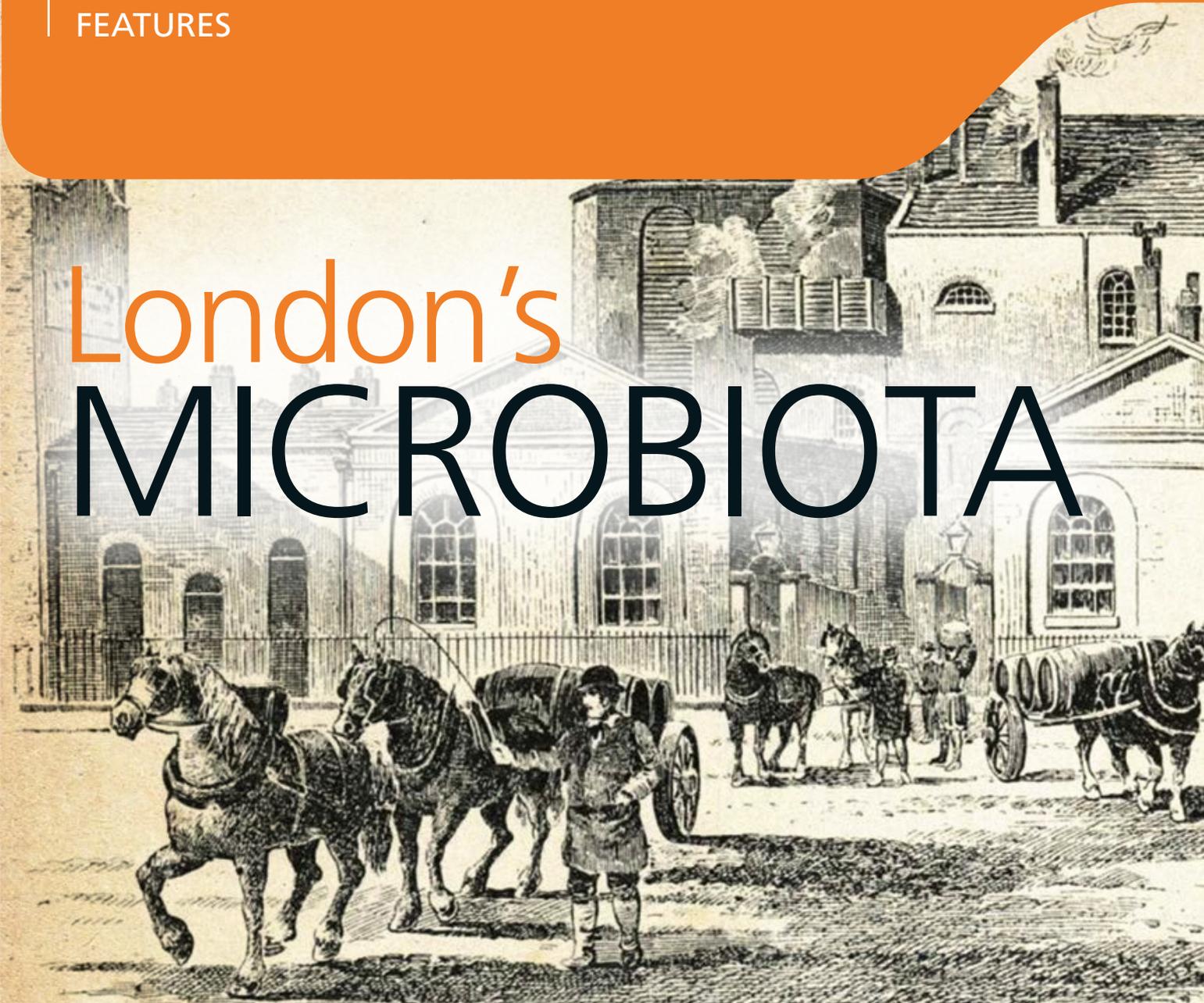
So we are left with the new system laid out in the paper by the WHO (http://apps.who.int/iris/bitstream/10665/163636/1/WHO_HSE_FOS_15.1_engpdf?ua=1) to advise us on future naming events. It is, however, conceded that this makes the naming of new diseases more difficult. Whichever way is chosen, the process is fraught with problems and the solution provided by one individual may well provide irritation for a second individual. A new henipavirus isolated in the Cedar Grove neighbourhood in Australia was simply named as Cedar Virus – adhering to the WHO's mandate on short names – but what does this tell you about the virus? Does it affect Cedar trees? There are still complaints that the name hurts property prices in the area. The Norwalk virus is the only virus in the *Norovirus* genus and has been commonly referred to as Noro. Noro is a common Japanese name so it was suggested that the virus should be called by the name Norwalk virus – but will this cause offence elsewhere? SARS was used as an acronym to describe severe acute respiratory syndrome so as to avoid the common name of Chinese flu. Consequently, this caused offence in Hong Kong which is officially known as Hong Kong SAR (specialist administration region). No one said this would be easy!

Whatever the final solution transpires to be, we need to be sure that the name does accurately and proportionately reflect the disease being described and never deliberately causes offence by being used pejoratively.



Mark Fielder
Kingston University

London's MICROBIOTA

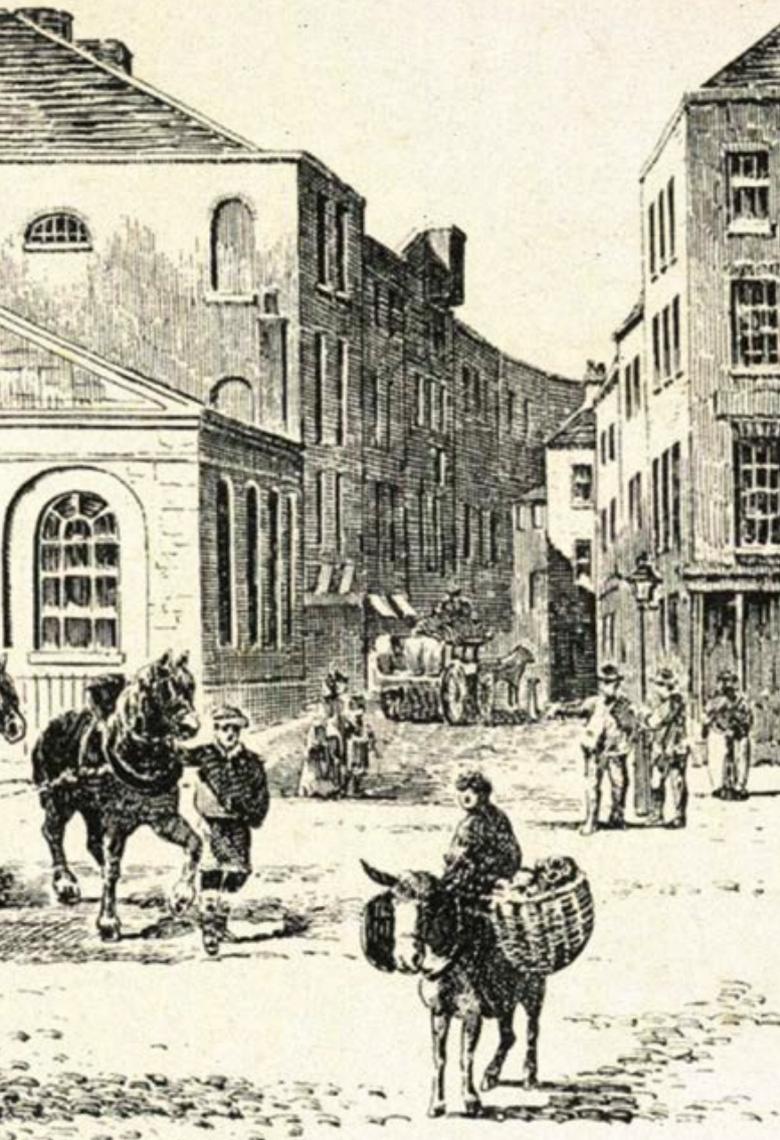


An occasional series on applied microbiology themes in the capital

The Dominion Theatre stands at the southern end of Tottenham Court Road where it meets Oxford Street and Charing Cross Road. The Grade II listed theatre opened in 1929 and has contributed untold delight to lovers of musical theatre ever since. One notable recent offering, based on the music of Queen, ran for 12 years during which time the theatre's frontage was graced by a massive statue of the group's lead singer, Freddie Mercury, apparently having some form of seizure. Sadly though, I am not concerned here with the glittering achievements of British musical theatre but with another unfortunate event which occurred on the site more than 200 years ago – the Great Beer Flood of 1814.

In the 18th century, a new beer, strong, dark, aged and bitter, became increasingly popular in London, eventually dominating the market. Called by the brewers 'entire' or 'entire butt', the precise origin of the





name is obscure but may have derived from the practice of combining the wort obtained from several mashings of a single charge of malt to brew one beer: hence entire. Its popularity among porters – at the time a large section of the working class population employed in carrying loads around London and unloading ships in the Thames – led to it being more commonly known as ‘porter’.

Porter brewers used what was known as ‘high blown malt’, a malt that had been rapidly dried at high temperature so that it had popped like popcorn, had acquired a dark colour through extensive Maillard reactions and possessed relatively low amylase activity. It was the first beer suited to very large-scale production. It could be brewed at higher temperatures than other beers and, in the absence of artificial cooling, this meant that the brewing season could be extended into the warmer months and that larger

fermentation vessels could be used because heat retention was less of a problem. Porter production also required higher capital investment since the product had to mature for about 12 months before consumption to clarify and develop its characteristic taste. The latter is thought to have been due in part to the activity of *Brettanomyces* species, nowadays generally regarded as beer spoilage organisms.

As production and demand grew, conventional butts (108 gallon casks) were replaced by increasingly large vats for maturation, setting up a competition between brewers over who had the demonstrably larger vat. A visitor to Thrale’s brewery in Southwark in 1775 described a dinner for 100 people held in an empty vat with a capacity of 54,000 gallons. In 1790, 200 people dined in a new 60 ft diameter vat at a Clerkenwell brewery. But scant regard was given to safety aspects and this *hubris* had its inevitable consequence.

Where the Dominion Theatre now stands was previously occupied by the Horseshoe Brewery, acquired by Henry Meux in 1809, and largely devoted to the production of porter. On 17 October 1814 one of the iron retaining hoops on a 22 foot high maturation vat fell off. A little later the vat burst launching a flood of 570 tons of porter in a wave of beer and debris which damaged other vessels, demolished the wall of the storehouse and flooded out into the surrounding area. There it destroyed the back wall of a nearby pub and flooded cellars in the overcrowded and insanitary slums of the St Giles ‘rookery’. Eight people died of drowning – all women and children. It was said that the death toll would have been much higher if the vat had burst later in the day when more people had been at home.

In the aftermath, the tragedy was ruled to have been ‘an act of God’ with no one responsible and the fortunate brewery was even able to reclaim the duty it had paid on the lost beer. Rather smaller amounts were collected for the families of those who had died. One story told was that of an enterprising soul who exhibited the body of a drowned relative to view for a small fee. This proved so popular that the weight of the crowd gathered in the room proved too much for the floor which collapsed, precipitating them and the body into the cellar which was still knee-deep in porter.

The brewery continued in operation for another 100 years but was closed in 1922 and demolished the following year to make way for the theatre. Aesthetically it appears not to have been much of a loss since it was described in the press at the time as ‘frankly hideous’.



Martin Adams

SfAM President 2011–2014



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SfAM Winter Meeting

2016

19 January 2016

One Great George Street, London, UK

PSYCHROPHILES AND EXTREMOPHILES

Within the magnificent Grade II listed, four-domed, Edwardian setting of One Great George Street, London, on 19 January 2016 the Society for Applied Microbiology hosted its Winter Meeting on Psychrophiles and Extremophiles.

Guest speakers explored the reservoirs of undiscovered biodiversity represented by psychrophilic bacteria and how these organisms have evolved to live in the presence of extremely cold and harsh conditions.

Starting the meeting, SfAM President Christine Dodd introduced the 2016 Denver Russell Memorial Lecture given by Professor Charles Cockell (University of Edinburgh). Professor Cockell's talk on Astrobiology revealed the many ways in which researchers are trying to answer the question of whether or not there is life on Mars (or in fact anywhere else in the universe).

After describing the six principle factors which are traditionally thought to limit microbial life, Charles explained the difference between the predominant salts on Earth and on Mars. Martian salts are dominated by magnesium and iron sulfates from the acidic weathering of basaltic rock. The presence of multivalent ions (Fe^{2+} ; Mg^{2+} ; SO_4^{2-}) results in a higher ionic strength for Martian brines compared with brine on Earth which is dominated by monovalent ions (Na^+ ; Cl^-). It was proposed that this may be the limiting factor for microbial life on Mars, rather than the water activity.

Rosa Margesin (University of Innsbruck, Austria) followed, outlining how the successful colonization of cold environments by psychrophilic organisms is due to a complex range of structural and functional adaptations of the cellular constituents of these organisms. Rosa took the examples of cryoconite and permafrost to illustrate the different populations existing in these two extreme environments.

Cryoconite (ice dust) holes form when collections of airborne rock particles, soot and microorganisms cause localized melting of ice. It has been found that cryoconite communities display geographical variation. For example, clusters of bacteria in Arctic cryoconite holes differ from those in Antarctica and from those in Alpine regions. In most locations bacteria are found to dominate but viruses outnumber bacteria in Svalbard and Greenland glaciers. *Janthinobacterium* species which dominate Arctic glacier surfaces therefore require antiviral defences for their survival.

Viable bacteria from 70–85 genera can be found in permafrost, with greater viable recovery observed in the Arctic compared with the Antarctic. Permafrost communities demonstrate a high abundance of Gram-positives (Actinobacteria), as well as methanogenic and halophilic Archaea and fungi (Ascomycota). This contrasts with the low abundance of Gram-positive bacteria found in cryoconite holes.

Delving deeper into the constituents of the psychrophilic cell, Tony Collins (University of Minho, Portugal) explained how the production of the cold-adapted enzymes that these organisms need to survive indicates a vast array of adaptive features, notably at the level of the membranes, transcription and translation processes, protein folding and enzyme activities. Drawing on his work in Antarctica, Tony described how psychrophiles manage to function in this harsh environment by having proteins with more flexible, open structures than those of mesophiles or thermophiles. Tony also discussed how aspects of these flexible enzymes have applications in diverse industries and examples of such applications were given: cold-adapted enzymes in washing detergents to facilitate the use of lower temperatures for washing clothes; cold-adapted β -galactosidase for the removal of lactose

from milk at low temperatures to avoid the effects of heat on taste; cold-adapted xylanase in baking to increase dough volume, improve crumb structure and lengthen shelf life.

Following a short break the topic of high-rate, low-temperature, anaerobic digestion wastewater treatment was covered. This area is of particular interest for many who study psychrophilic organisms and Tom Curtis (Newcastle University, UK) reminded the audience that wastewater treatment is one of the most successful and important applications of applied microbiology today. Tom described a process in which wastewater reactors were seeded with bacteria found in high arctic areas and deep alpine lakes in an attempt to make an arguably intrinsically unsustainable technology more energy efficient. Further work is needed to understand more about the psychrophilic bacteria being employed, an important consideration in the UK being that it is important for the system to work for biomass at 4°C (winter) but also at 10–15°C (summer).

Vincent O'Flaherty (National University of Ireland, Galway) was able to elaborate further on the subject of anaerobic digestion at psychrophilic temperatures using process data from several years of laboratory and pilot-scale research experiments. Most notably Vincent was able to share with us the unexpected phenotypic changes that had been observed in the persistent methanogenic consortia of these systems. The main problem at lower temperatures is that methane

becomes more soluble and reactor liquor viscosity increases. Much is now known about the methanogens involved but knowledge of the bacteria is still lacking.

To end a fascinating day, Alan Dobson (University College Cork, Ireland) reported on his mining of our oceans for novel bioactive molecules with biotechnological and pharmaceutical applications. Specifically probing the microbiota of deep-sea sponges, Alan has identified a number of bacterial genera as producers of bioactive compounds with antibacterial activity against methicillin-resistant *Staphylococcus aureus* (MRSA), *Salmonella enterica* serotype Typhimurium and *Clostridium difficile*.

Interestingly, bacteria account for 40% of the net weight of a sponge. Many of the molecules found in these bacteria are already known but a novel lantibiotic, subtilomycin, has been identified from the MMA7 strain of *Bacillus subtilis*. Similarly, a novel thiopeptide antibiotic cluster has been identified by sequencing *Streptomyces sp.* strain SM2. Although encouraging, Tony stressed that issues such as bioavailability, toxicity and penetration need to be addressed before the clinical relevance of such discoveries can be understood.

The appropriately themed Winter Meeting gave the audience an insight into the world of psychrophilic and psychrotolerant microorganisms, showing us many of the wide-ranging applications that the study of these chilly bugs can, and will, contribute.

Antimicrobial Resistance 2016

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24 November 2016**

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DENVER RUSSELL MEMORIAL LECTURE 2016

Professor Charles Cockell

The 2016 Denver Russell Memorial Lecture was given by Charles Cockell, Professor of Astrobiology at the University of Edinburgh, and Director of the UK Centre for Astrobiology. Professor Cockell began by exploring some of the themes and questions that underpin astrobiology, including the one that I bet most of us have wondered about at some point, "Is there life elsewhere in the Universe?" While astrobiology may sound extra-terrestrial, the roots of the subject are firmly grounded on Earth and Cockell explained how exploring the limits of microbial life on Earth could help us to advance our understanding of life in extreme environments beyond Earth.

Professor Cockell discussed some of the evidence that tells us that there was liquid water elsewhere in the Universe. For example, on Mars, the Curiosity Rover identified pebbles that have been shaped by water, as well as sediments from ancient lakes. The surface of Europa, a moon in the Jupiter system, is covered with ice, with evidence of a liquid ocean under the ice, which is a current priority for the European Space Agency and NASA to explore. Furthermore, images of geysers erupting on the surface of the icy Saturn moon Enceladus have been captured by NASA's Cassini spacecraft.

Of course key questions remain – are any of these places habitable or did they ever host life? In order to begin to answer any of these questions, we look to extremophile microbiology to examine life at the limits. Professor Cockell presented data from his research group including examination of whether extremophiles exhibit more than one extreme. So far, none have been observed and it remains to be seen whether this is an inability to adapt to multiple extremes or whether it is simply biochemically impossible. Another fascinating question that Cockell's group are exploring is: are Martian brines habitable? 'Typical' Martian brines (salts in water) are



Professor Charles Cockell

dominated by iron and magnesium ions and it turns out that ionic strength is a more appropriate predictor of growth than water activity. Data collected by Cockell's group will not only help us to predict limits to life, but they will also aid our understanding of the geochemical history of Earth (& Mars).

Charles Cockell is Professor of Astrobiology in the School of Physics and Astronomy at the University of Edinburgh and Director of the UK Centre for Astrobiology. He was previously the Professor of Geomicrobiology with the Open University and a microbiologist with the British Antarctic Survey, Cambridge, UK.

His scientific interests have focused on astrobiology, geomicrobiology and life in extreme environments including studies on volcanic and impact crater environments. He has also contributed to plans for the human exploration of Mars and led the design study Project Boreas, which planned and designed a research station for the Martian North Pole. He was also the first Chair of the Astrobiology Society of Britain and is the author of *Astrobiology: Understanding Life in the Universe*.

This was a really fascinating and inspirational presentation, and a stunning example of applied microbiology in action. You can watch a recording of the presentation on the SfAM website by following the link: <http://microbeblog.org/2016/01/27/is-there-life-beyond-the-earth/>

SfAM Environmental Microbiology Lecture 2016

Margaret McFall-Ngai is a pioneer and international leader in the field of animal–microbe interactions and her research into the relationship between a host and its microbiome continues to challenge traditional microbiological notions.

The Society for Applied Microbiology is delighted to announce that Margaret McFall-Ngai, Professor of Medical Microbiology and Immunology at the University of Wisconsin-Madison, has agreed to present the annual SfAM *Environmental Microbiology Lecture*.

The lecture entitled “***Waging peace: establishment and maintenance of stable alliances between animals and their microbial partners***” will be held on the 11 October 2016 at the Royal Society of Medicine, One Wimpole Street, London.

McFall-Ngai also holds the title of Affiliate Professor at the University of Hawaii and is one of the foremost life scientists encompassing the fields of immunology, symbiosis and marine biology. She is an undisputed expert in the biological study of interactions between microbes and their animal hosts and her widely published and reported work on the ability of squid to acquire and activate bioluminescent bacteria cuts across the disciplines of physiology, ecology, immunology and evolutionary biology.

Her major research interests focus on the associations between animals and their specific symbiotic prokaryote partners – in particular, how are environmentally rare bacteria harvested from the host’s habitat during the onset of a horizontally transmitted symbiosis, the establishment and maintenance of the specific symbiotic microbiome, the influence of bacteria on the developmental of the host tissues with which they associate, the similarities and differences between



pathogenic and beneficial animal–bacterial interactions and how the symbiont population is maintained over the host’s lifetime.

Her work is the subject of regular media coverage and she has produced a prolific and outstanding portfolio of research publications in *Science*, *Proceedings of the National Academy of Sciences of the United States of America* (PNAS), *Environmental Microbiology*, *Environmental Microbiology Reports* and other top journals.

Professor McFall-Ngai received her PhD in Biology from UCLA in 1983 and is the recipient of numerous awards and honours and most recently was appointed to the Advisory Board of the Global Health Initiative at the École Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland, and Gordon and Betty Moore Endowed Sabbatical Professorship at the California Institute of Technology.

All Members of SfAM will have received an invitation to the lecture with this issue of *Microbiologist* and for those who are unable to attend, the lecture will be available online, soon after the event.



SfAM Summer Conference 2016

4 – 7 July 2016

The Assembly Rooms, Edinburgh, UK

MICROBIAL INTERACTIONS IN THE ENVIRONMENT

This meeting aims to promote the latest scientific research on the role of microorganisms in soil and plant ecosystems. The Society for Applied Microbiology is pleased to announce the Summer Conference on **Microbial Interactions in the Environment**, to be held on 4 – 7 July 2016 in Edinburgh, UK. This will be a vibrant international conference with lectures and workshops detailing the current state of knowledge and recent advancements in the science of plant and soil microbiology.

The conference will enable delegates a chance to meet with leaders in the field and converse about the soil microbial communities that confer critical benefits or pathogenic disadvantages to our ecosystem.

The meeting will also provide a unique platform to share the latest news on the microbiota of plants that may be beneficial or detrimental to the organisms they colonize.

DAY 1

Workshop & JAM Lecture

Workshop: Science policy

Journal of Applied Microbiology Lecture
The Diffusible Signal Factor (DSF) family of bacterial cell-cell signals

Max Dow, *University College Cork, Ireland*

Drinks reception and buffet

Students and Early Career Scientists' 'beach ball' icebreaker, with canapés and wine

Quiz night

DAY 2

Soil microbiology – gaseous nitrogen emissions

N_2O reducing microbes and their importance as N_2O sinks
Sara Hallin, *Swedish University of Agricultural Sciences, Sweden*

Regulation of denitrification at the cellular level
Lars Bakken, *Norwegian University of Life Sciences, Norway*

Soil nitrogen emissions to the atmosphere – an agricultural perspective
Tom Misselbrook, *Rothamsted Research, North Wyke, UK*

Copper control of bacterial nitrous oxide emission
David Richardson, *University of East Anglia, UK*

New single cell tools for functional analyses of microbes in their ecosystems
David Berry, *University of Vienna, Austria*

Determination of N_2O processes in soil using stable isotope approaches
Reinhard Well, *Johann Heinrich von Thünen Institute, Germany*

Bridging microbial community ecology and N-cycling
Laurent Philippot, *INRA, Dijon, France*

The protein network of the denitrification respirasome of *Pseudomonas aeruginosa*
Dieter Jahn, *Technische Universität Braunschweig, Germany*

Students and Early Career Scientists' session: Writing skills

Exhibition with wine, canapés and a competition

Students and Early Career Scientists' social event: Edinburgh walking tour



DAY 3

Plant – microbe interactions

Cyclic-di-GMP signalling and virulence in the plant pathogen *Xanthomonas campestris*
Robert Ryan, *University of Dundee, UK*

Evolution of plant bacteria to overcome stress
Robert Jackson, *University of Reading, UK*

Investigating the biology of plant infection by the rice blast fungus *Magnaportha oryzae*
Nick Talbot, *University of Exeter, UK*

Subversion of autophagy by the Irish potato famine pathogen *Phytophthora infestans*
Yasin Dagdas, *The Sainsbury Laboratory, Norwich, UK*

Endophytes and their biotechnological uses
Gabriele Berg, *Graz University of Technology, Austria*

Early Career Scientists Committee AGM

Student Member oral presentations

SfAM Award Lectures

SfAM New Lecturer Research Grant Lecture:
Following my gut feelings – from pathogens to probiotics and back
Roy Sleator, *Cork Institute of Technology, Ireland*

New insights into oil biodegradation processes of deep water provinces
Tony Gutierrez, *Heriot-Watt University, Edinburgh, UK*

Glycoprotein N-linked glycans as targets for antibody-based detection of *Campylobacters*
Danielle Weaver, *The University of Manchester, UK*

W H Pierce Prize Lecture

SfAM Annual General Meeting

Drinks reception and conference dinner

DAY 4

Plant – microbe interactions

Plants as alternate hosts for human and animal pathogens
Nicola Holden, *The James Hutton Institute, UK*

Rhizosphere microbiology and plant health
Andrzej Tkacz, *University of Oxford, UK*

Decoding the plant – microbiome language: new opportunities for pathogen control and biodiscovery
Peer Schenk, *University of Queensland, Australia*

Rhizobium interactions with plants
Allan Downie, *John Innes Centre, UK*

Closing date for registration:

Monday 20 June 2016

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www.sfam.org.uk/summer

SfAM AGM AGENDA

85th Annual General Meeting of the Society for Applied Microbiology
6 July 2016, 5.15 pm, The Assembly Rooms, Edinburgh, UK

- 1 Apologies for absence.**
- 2 Approval of minutes** published in September 2015 *Microbiologist* of the 84th Annual General Meeting held in Dublin, 2015.
- 3 Matters arising from the previous minutes.**
- 4 Report of the Trustees of the Society 2015:**
 - (i) Report of the President.
 - (ii) Report of the General Secretary.
 - (iii) Report of the Meetings Secretary.
 - (iv) Report of the Treasurer.
- 5 Adoption of the 2015 Annual Report.**
- 6 Election of new Members (including Honorary Members), deaths and resignations.**
- 7 Nomination and election of Trustees:**
 - (i) Vice President.
 - (ii) Meetings Secretary.
 - (iii) Treasurer.
- 8 Nomination and election of new Committee Members.**
- 9 Any other business*.**

**To ensure the meeting keeps to time items of any other business must be raised with the General Secretary at least 24 hours before the start of the meeting.*

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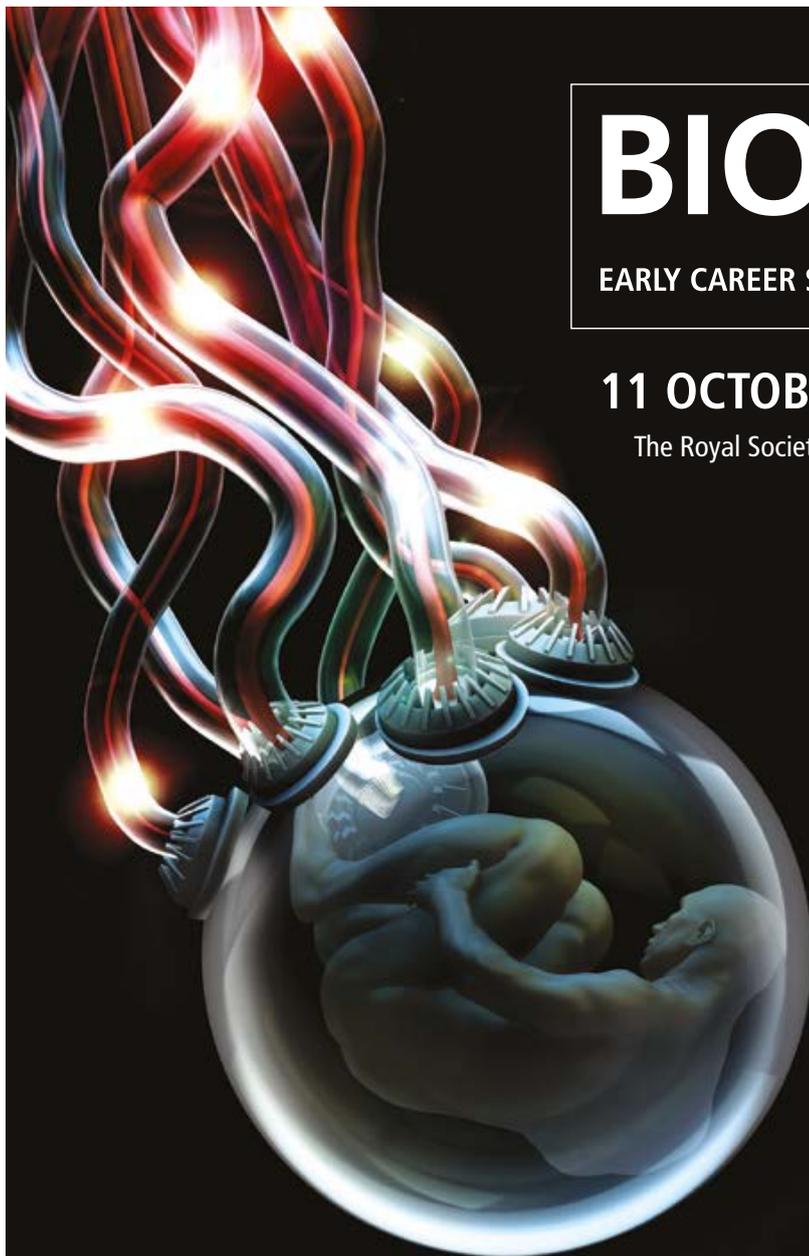
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BIOETHICS

EARLY CAREER SCIENTISTS RESEARCH CONFERENCE

11 OCTOBER 2016 | 11:00 – 17:00

The Royal Society of Medicine, 1 Wimpole Street, London UK

SPEAKERS INCLUDE:

Anne Glover, Professor and Vice-Principal External Affairs & Dean for Europe, Aberdeen

Bobbie Farsides, Professor of Clinical and Biomedical Ethics and Law, Brighton

David Jones, Director of the Anscombe Bioethics Centre, Oxford

John Bryant, Head of HEA Committee on Bioethics, Exeter

£50 non Member £30 Member

(£5 early bird discount before 9 September 2016)

VISIT WEBSITE TO BOOK OR CONTACT US FOR FURTHER DETAILS

Sfam and the ECS committee are proud to invite undergraduate, postgraduate and early career scientists to attend and participate in the fourth ECS Research Conference on 11 October 2016 at The Royal Society of Medicine, London.

Bioethics is an emerging topic in the media and will be a familiar subject to those working with animal models and gene editing, however, in the context of microbiology it is rarely discussed.

This year's conference is specifically aimed at highlighting how bioethics is relevant in microbiology and will feature a panel discussion with leaders in the field. As always, the conference is a chance for early career scientists to present their data and network with other early career microbiologists.

This year's event will be followed in the evening by the SfAM's annual *Environmental Microbiology Lecture* on animal-microbe interactions given by Professor Margaret McFall-Ngai.

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JournalWATCH

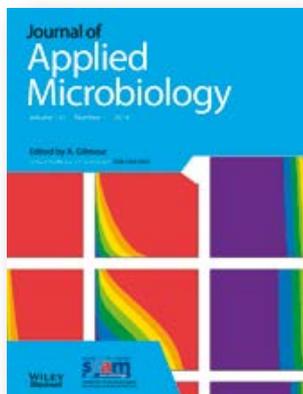
Highlights and featured articles from the SfAM journals

Journal of Applied Microbiology

www.journalappliedmicro.com

Nanotechnology based anti-infectives to fight microbial intrusions

M. Rai *et al.*



With the rise in human population across the globe especially in developing countries, the incidence of microbial infections are increasing with greater pace. On the other hand, available medication and therapies are found to be insufficient for the complete cure of such microbial infections due to the development of resistance against various antibiotics. Therefore, to cope with the menace of microbial

infections and drug resistance, there is demand for new and compelling technology, which has the ability to impede these problems. Many research groups worldwide are finding a ray of hope in nanomaterials owing to their unique properties. In the present review we have discussed the reasons behind the development of new materials based on nanotechnology. It is mainly focused on pioneering studies on the application of nanomaterials like carbon nanotube, fullerene, dendrimers, nanocomposite and metal nanoparticles in combating dreadful pathogens. Moreover, the concerns about their toxicity have also been discussed.

<http://onlinelibrary.wiley.com/doi/10.1111/jam.13010/full>

The challenge of using experimental infectivity data in risk assessment for Ebola virus: why ecology may be important

P. Gale *et al.*

Analysis of published data shows that experimental passaging of *Zaire ebolavirus* (EBOV) in guinea pigs changes the risk of infection per plaque-forming unit (PFU), increasing infectivity to some species while decreasing infectivity to others. Thus, a PFU of monkey-adapted EBOV is 10⁷-fold more lethal to mice than a PFU adapted to guinea pigs. The first conclusion is that the infectivity of EBOV to humans may depend on the identity of the donor species itself and, on the basis of limited epidemiological data, the question is raised as to whether bat-adapted EBOV is less infectious to humans than nonhuman primate (NHP)-adapted EBOV. Wildlife species such as bats, duikers and NHPs are naturally infected by EBOV through different species giving rise to EBOV with different wildlife species-

passage histories (heritages). Based on the ecology of these wildlife species, three broad 'types' of EBOV-infected bushmeat are postulated reflecting differences in the number of passages within a given species, and hence the degree of adaptation of the EBOV present. The second conclusion is that the prior species-transmission chain may affect the infectivity to humans per PFU for EBOV from individuals of the same species. This is supported by the finding that the related *Marburg virus* requires 10 passages in mice to fully adapt. It is even possible that the evolutionary trajectory of EBOV could vary in individuals of the same species giving rise to variants which are more or less virulent to humans and that the probability of a given trajectory is related to the heritage. Overall the ecology of the donor species (e.g., dog or bushmeat species) at the level of the individual animal itself may determine the risk of infection per PFU to humans reflecting the heritage of the virus and may contribute to the sporadic nature of EBOV outbreaks.

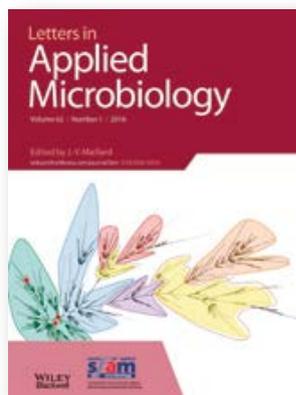
<http://onlinelibrary.wiley.com/doi/10.1111/jam.12973/full>

Letters in Applied Microbiology

www.lettersappliedmicro.com

Advantage of MALDI-TOF-MS over biochemical-based phenotyping for microbial identification illustrated on industrial applications

S.K. Urwyler and J. Glaubit



MALDI-TOF-MS has revolutionized the speed and precision of microbial identification for clinical isolates outperforming conventional methods. In contrast, few performance studies have been published so far focusing on suitability for particularly industrial applications, geomicrobiology and environmental analytics. This study evaluates the performance of this proteomic phenotyping on

such industrial isolates in comparison with biochemical-based phenotyping and genotyping. Further, the study exemplifies the power of MALDI-TOF-MS to trace cost-efficiently the dominating cultivable bacterial species throughout an industrial paint production process. Vital information can be retrieved to identify the most crucial contaminating source for the final product.

<http://onlinelibrary.wiley.com/doi/10.1111/lam.12526/full>

Antifungal properties of organic extracts of eight *Cistus* L. species against postharvest citrus sour rot

H. Karim *et al.*

The effectiveness of methanol and chloroform extracts of eight Cistaceae species to control citrus sour rot decay, caused by *Geotrichum citri-aurantii*, was investigated in both *in vitro* and *in vivo* conditions. Methanol extracts of these plant species exhibited more interesting activity against *G. citri-aurantii*, in both *in vitro* and *in vivo* conditions, compared with chloroform extracts. Under *in vitro* trials, obtained results showed that methanol extracts of all tested plants revealed a highest significant antifungal activity with inhibition zones that ranged between 12.33 and 16.33 mm in diameter. All tested methanol extracts totally inhibited spore germination when tested at 10 mg ml⁻¹. Incidence of sour rot was significantly lowered to 11.11% when fruits were treated with *Cistus populifolius* and *Cistus ladanifer* methanol extracts compared with 100% in the control. The disease severity was lowered to 5.19% and 6.04% when fruits were treated with the same methanol extracts respectively.

<http://onlinelibrary.wiley.com/doi/10.1111/lam.12507/full>

Microbial Biotechnology

www.microbialbiotech.com

Estimating the success of enzyme bioprospecting through metagenomics: current status and future trends

Manuel Ferrer *et al.*



Recent reports have suggested that the establishment of industrially relevant enzyme collections from environmental genomes has become a routine procedure. Across the studies assessed, a mean number of approximately 44 active clones were obtained in an average size of approximately 53,000 clones tested using naïve screening protocols. This number could be significantly increased in

shorter times when novel metagenome enzyme sequences obtained by direct sequencing are selected and subjected to high-throughput expression for subsequent production and characterization. The pre-screening of clone libraries by naïve screens followed by the pyrosequencing of the inserts allowed for a 106-fold increase in the success rate of identifying genes encoding enzymes of interest. However, a much longer time, usually in the order of years, is needed from the time of enzyme identification to the establishment of an industrial process. If the hit frequency for the identification of enzymes performing at high turnover rates under real application conditions could be increased while still covering a high natural diversity, the very expensive and time-consuming enzyme optimization phase would likely be significantly shortened. At this point, it is important to review the current knowledge about the success of fine-tuned naïve- and sequence-based screening protocols for enzyme selection and to describe the environments worldwide that have already been subjected

to enzyme screening programmes through metagenomic tools. Here, we provide such estimations and suggest the current challenges and future actions needed before environmental enzymes can be successfully introduced into the market.

<http://onlinelibrary.wiley.com/doi/10.1111/1751-7915.12309/full>

Succession of lignocellulolytic bacterial consortia bred anaerobically from lake sediment

Elisa Korenblum, Diego Javier Jiménez and Jan Dirk van Elsas

Anaerobic bacteria degrade lignocellulose in various anoxic and organically rich environments, often in a syntrophic process. Anaerobic enrichments of bacterial communities on a recalcitrant lignocellulose source were studied combining polymerase chain reaction–denaturing gradient gel electrophoresis, amplicon sequencing of the 16S rRNA gene and culturing. Three consortia were constructed using the microbiota of lake sediment as the starting inoculum and untreated switchgrass (*Panicum virgatum*) (acid or heat) or treated (with either acid or heat) as the sole source of carbonaceous compounds. Additionally, nitrate was used in order to limit sulfate reduction and methanogenesis. Bacterial growth took place, as evidenced from 3 to 4 log unit increases in the 16S rRNA gene copy numbers as well as direct cell counts through three transfers on cleaned and reused substrate placed in fresh mineral medium. After 2 days, *Aeromonas bestiarum*-like organisms dominated the enrichments, irrespective of the substrate type. One month later, each substrate revealed major enrichments of organisms affiliated with different species of *Clostridium*. Moreover, only the heat-treated substrate selected *Dysgonomonas capnocytophagoides*-affiliated bacteria (Bacteroidetes). Towards the end of the experiment, members of the Proteobacteria (*Aeromonas*, *Rhizobium* and/or *Serratia*) became dominant in all three types of substrates. A total of 160 strains was isolated from the enrichments. Most of the strains tested (78%) were able to grow anaerobically on carboxymethyl cellulose and xylan. The final consortia yield attractive biological tools for the depolymerization of recalcitrant lignocellulosic materials and are proposed for the production of precursors of biofuels.

<http://onlinelibrary.wiley.com/doi/10.1111/1751-7915.12338/full>

Environmental Microbiology

www.env-micro.com

Microbial activity in forest soil reflects the changes in ecosystem properties between summer and winter

Lucia Žifčáková *et al.*

Understanding the ecology of coniferous forests is very important because these environments represent the globally largest carbon sinks. Metatranscriptomics, microbial community and enzyme analyses were combined to describe the detailed role of microbial taxa in the functioning of the *Picea abies*-dominated coniferous forest soil in two contrasting seasons. These seasons were the summer, representing the peak of plant photosynthetic activity, and late winter, after an extended period with no photosynthate input. The results show that microbial



communities were characterized by a high activity of fungi especially in litter where their contribution to microbial transcription was over 50%. Differences in abundance between summer and winter were recorded for 26–33% of bacterial genera and <15% of fungal genera, but the transcript profiles of fungi, archaea and most bacterial phyla were significantly different among seasons. Further,

the seasonal differences were larger in soil than in litter. Most importantly, fungal contribution to total microbial transcription in soil decreased from 33% in summer to 16% in winter. In particular, the activity of the abundant ectomycorrhizal fungi was reduced in winter, which indicates that plant photosynthetic production was likely one of the major drivers of changes in the functioning of microbial communities in this coniferous forest.

<http://onlinelibrary.wiley.com/doi/10.1111/1462-2920.13026/full>

Even therapeutic antimicrobial use in animal husbandry may generate environmental hazards to human health

Felipe C. Cabello and Henry P. Godfrey

The potential negative impact for human health of veterinary use of antimicrobials in prophylaxis, metaphylaxis and growth promotion in animal husbandry was first established in the 1960s and 1970s. Determination of the molecular structure of antimicrobial resistance plasmids at that time explained the ability of antimicrobial resistance genes to disseminate among bacterial populations and elucidated the reasons for the negative effects of antimicrobials used in food animals for human health. In this issue of *Environmental Microbiology*, Liu *et al.* (2016) show that even therapeutic use of antimicrobials in dairy calves has an appreciable environmental microbiological footprint. We discuss the negative implications of this footprint for human health and the possibility they may lead to calls for increased regulation of veterinary antimicrobial use in terrestrial and aquatic environments.

<http://onlinelibrary.wiley.com/doi/10.1111/1462-2920.13247/full>



Melissa McCulloch
Wiley-Blackwell

Environmental Microbiology Reports

www.env-micro-reports.com

Advances in genomics, transcriptomics and proteomics of toxin-producing cyanobacteria

Paul M. D'Agostino *et al.*



A common misconception persists that the genomes of toxic and non-toxic cyanobacterial strains are largely conserved with the exception of the presence or absence of the genes responsible for toxin production. Implementation of -omics era technologies has challenged this paradigm, with comparative analyses providing increased insight into the differences between strains of the same species. The implementation

of genomic, transcriptomic and proteomic approaches has revealed distinct profiles between toxin-producing and non-toxic strains. Further, metagenomics and metaproteomics highlight the genomic potential and functional state of toxic bloom events over time. In this review, we highlight how these technologies have shaped our understanding of the complex relationship between these molecules, their producers and the environment at large within which they persist.

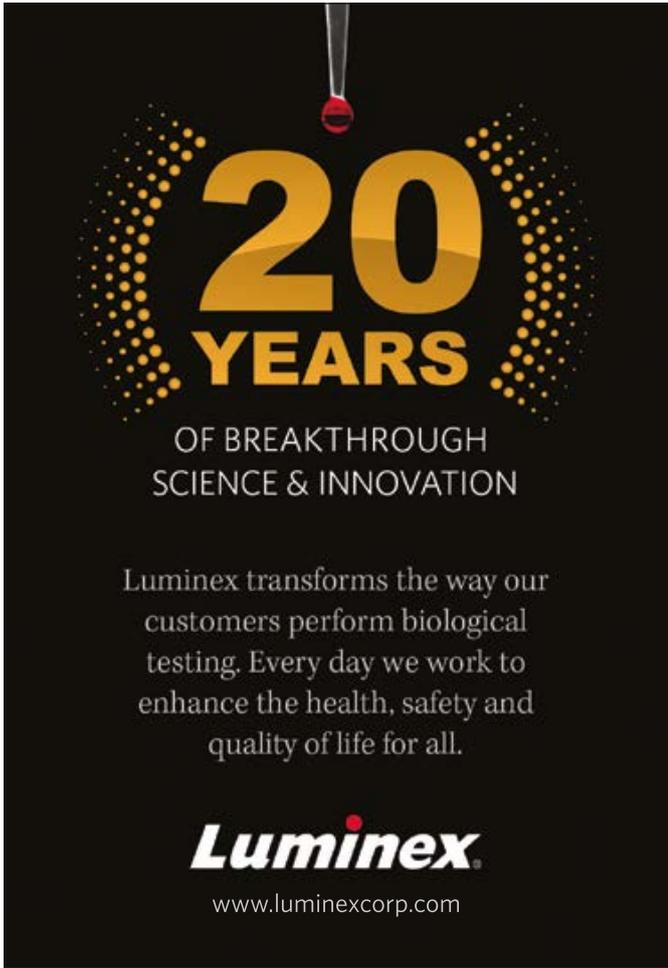
<http://onlinelibrary.wiley.com/doi/10.1111/1758-2229.12366/full>

Deep microbial life in high-quality granitic groundwater from geochemically and geographically distinct underground boreholes

Kohei Ino *et al.*

Deep granitic aquifer is one of the largest, but least understood, microbial habitats. To avoid contamination from the surface biosphere, underground drilling was conducted for 300 m deep granitic rocks at the Mizunami underground research laboratory (URL), Japan. Slightly alkaline groundwater was characterized by low concentrations of dissolved organic matter and sulfate and the presence of >100 nM H₂. The initial biomass was the highest (~10⁵ cells ml⁻¹) with the dominance of *Hydrogenophaga* spp., whereas the phylum Nitrospirae became predominant after 3 years with decreasing biomass (~10⁴ cells ml⁻¹). One week incubation of groundwater microbes after 3 years with ¹³C-labelled bicarbonate and 1% H₂ and subsequent single-cell imaging with nanometer-scale secondary ion mass spectrometry demonstrated that microbial cells were metabolically active. Pyrosequencing of microbial communities in groundwater retrieved at 3–4 years after drilling at the Mizunami URL and at 14 and 25 years after the drilling at the Grimsel Test Site, Switzerland, revealed the occurrence of common Nitrospirae lineages at the geographically distinct sites. As the close relatives of the Nitrospirae lineages were exclusively detected from deep groundwaters and terrestrial hot springs, it suggests that these bacteria are indigenous and potentially adapted to the deep terrestrial subsurface.

<http://onlinelibrary.wiley.com/doi/10.1111/1758-2229.12379/full>



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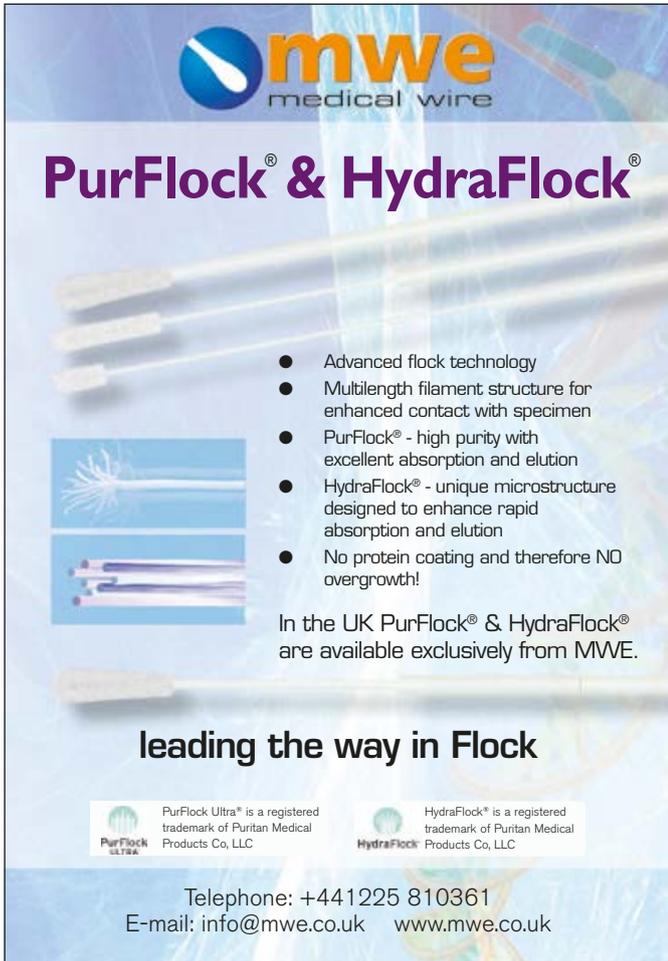
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MEMBERSHIP Benefits & Options

Benefits

The Society for Applied Microbiology is the voice of applied microbiology within the UK and was founded in 1931. Society Members play a leading role in shaping the future of applied microbiology, and enjoy many benefits, including:

- The opportunity to apply for one of our many grants or funds.
- Access to our five peer-reviewed journals: *Journal of Applied Microbiology* (JAM), *Letters in Applied Microbiology* (LAM), *Environmental Microbiology*, *Environmental Microbiology Reports* and *Microbial Biotechnology*.
- Free access to the entire collection of digitized back files for JAM and LAM dating back to 1938.
- A topical quarterly magazine, *Microbiologist*.
- Substantially reduced rates for attendance at SfAM meetings and conferences.
- Networking with worldwide professionals in over 80 countries
- Access to private Members' area of the SfAM website.
- Monthly email bulletins with the latest news from SfAM.
- Invitation to the annual *Environmental Microbiology* and *Journal of Applied Microbiology* lectures.
- Fostering cross disciplinary research.
- A 35% discount on the extensive Wiley-Blackwell collection of titles.

Detailed information about all these benefits and more can be found on the Society website at: www.sfam.org.uk/membership.

GRANTS & AWARDS

Many grants, awards and prizes are available to Members including the W H Pierce Memorial Prize and prizes for student oral presentations and posters at the Summer Conference. In addition to these substantial awards, the Society has funds to assist Members in their careers as microbiologists. These include the President's Fund, Conference Studentships, Sponsored Lecture Grants and the popular Students into Work Scheme.

Full details of all the Society's grants and awards, together with application forms, can be found on the website at www.sfam.org.uk/grants.

JOURNALS

The Society publishes two monthly journals: *Journal of Applied Microbiology* and *Letters in Applied Microbiology*. We also produce this quarterly colour magazine, *Microbiologist*, which contains features, topical news stories and full details of our meetings. The Society is also a partner with Wiley-Blackwell in the monthly journals: *Environmental Microbiology*, *Environmental Microbiology Reports* and *Microbial Biotechnology*. See more at www.sfam.org.uk/journals.

All Full and Student Members receive free access to the online versions of the Society's journals, and can also submit papers to our journals via an online submission service.

MEETINGS

We hold three annual meetings: the Winter Meeting is a one-day meeting with parallel sessions on topical subjects; the Spring Meeting is a one-day meeting tailored for personnel in clinical microbiology; and the Summer Conference is held every June/July and comprises a main symposium, a poster session, the AGM and a lively social programme. All Members are invited to our prestigious annual lectures held to commemorate the success of two of our journals: *Environmental Microbiology* and the *Journal of Applied Microbiology*. We also hold *ad hoc* meetings on topical subjects and enter into joint ventures with other organizations on topics of mutual interest.

WEBSITE

www.sfam.org.uk is the best source of detailed information on the Society and its many activities. It has a fully interactive Members-only area (www.sfam.org.uk/membersonly) where you can find archive issues of *Microbiologist*, exclusive SfAM documentation and much more.

Membership OPTIONS

- > **Full Ordinary** gives access to our many grants and awards, online access to the *Journal of Applied Microbiology*, *Letters in Applied Microbiology*, *Environmental Microbiology*, *Environmental Microbiology Reports* and *Microbial Biotechnology*, copies of *Microbiologist*, preferential registration rates at Society meetings, and access to the Members-only area of the website.
- > **Full Student** confers the same benefits as Full Membership at a specially reduced rate for full-time students not in receipt of a taxable salary.
- > **Associate** is only open to those with an interest in applied microbiology without it being a prime aspect of their job. For example, school teachers and those taking a career break, on maternity leave, or working temporarily in other areas. It does not provide access to any journals or Society grants and awards.
- > **Honorary** membership of the Society is by election only and this honour is conferred on persons of distinction in the field of applied microbiology. Honorary Members have access to our online journals.
- > **Retired** is available to Full Members once they have retired from their employment. Retired Members are entitled to all the benefits of Full Membership except grants and access to the Society's journals.
- > **eAffiliate:** this category of membership is open to microbiologists residing in Band I developing countries and is free of charge. It is an online only membership and provides access to the eAffiliate bursary only.
- > **eStudent:** this category of membership is open to undergraduate students only. It is an online only membership and is free of charge. This category of membership does not provide access to the Society's grants or journals.
- > **Corporate** is open to all companies with an interest in microbiology. Corporate Members benefits include:
 - Quarter page advertisement in each issue of *Microbiologist* (which can be upgraded to a larger size at discounted rates).
 - The opportunity to publish press releases, company news, etc., in each issue of *Microbiologist*.
 - FREE banner advert on the Society website with a direct link to your company site.
 - Up to three Members of company staff attending Society meetings at Members' rate (this means a 50% discount on non-Member registration rate).



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You can apply for membership online (www.sfam.org.uk/join) or offline. To apply offline, please contact the Membership & Finance Co-ordinator, Julie Wright on +44 (0)1234 326846, or email julie@sfam.org.uk.

I distinctly remember being told about age 12 that the choices I made for my GCSEs were important, as they could impact on what I did with my life. At that age I had my suspicions that I would like to do something with maths or science but if someone suggested a geomicrobiologist I would most likely have looked at them confused, especially as my 12-year-old-self considered biology the least interesting of the sciences and did not study it beyond age 16, instead choosing mathematics, chemistry and geology for A levels.

My interest in geology, and how the Earth works, led me to choose Earth sciences at university. It was not until my final year project that I had my first laboratory encounter with microorganisms. My project focused on structures in ancient rocks that are comparable to modern biofilms. As a geologist I did not really know what a modern biofilm should look like, let alone an ancient one, so I found a helpful microbiologist in the plant science department to help me grow some. I spent more time in the plant science labs and started to neglect my rock thin-sections; my fascination with microorganisms began.

I spent my PhD looking for life in ice, and found a lot. However, the focus of my work involved developing methods in the lab so they could be used in the field. This took me to some awesome places, including under a glacier in Norway, and it led to nine weeks of DNA extractions, real-time PCR, fluorescence cell counts and ATP bioluminescence measurements about 100 m from the Greenland icecap. We brought along a dedicated lab tent and I spent much of my time sitting cross-legged on the floor doing 'science'. Through my PhD, I developed a deep respect for the ability of microorganisms to survive and even thrive in environments that humans would consider inhospitable.

I did not get a research job straight after my PhD but worked as a tutor, in early years education using Lego robots (unfortunately not for Lego) and as a support worker. My fascination with microbes did not stop and to satisfy my curiosity I embarked on a Master's in Biotechnology. This gave me a good foundation in microbiology, but mostly made me realize how much I did not know and how much more there was to find out.

CAREERS



From rocks to bugs and back again

My current position is a geomicrobiologist at the British Geological Survey (BGS), which has brought me back to the rocks I neglected many years previously. There are four geomicrobiologists at the BGS and I am the newest member of the team. I have been here just over a year and when people ask what I do my response depends on what day it is. Some of my work involves keeping the laboratory running, like changing gas cylinders on the anaerobic cabinet or maintaining live anaerobic cultures. The majority of my time is spent in the lab running experiments, or in the office writing up the results. I am part of the Radioactive Waste team but work on research projects across the BGS. The radioactive waste research involves trying to understand the impact that microorganisms may have if radioactive waste is disposed of in the deep subsurface within a specially engineered facility. Of particular interest is understanding whether microbes could play an important role 'consuming' (eating) the gases produced by the waste as it decomposes over time.

The rest of my work also involves trying to understand how the interactions between microorganisms and their subsurface environment might be of benefit or hindrance to society. However, one project has led me to the surface. A few months after starting I was given some Ziploc® bags of red mud (waste left over from aluminium processing). These mud samples contain high concentrations of rare Earth elements (REE) which are critical in modern technology and 'green energy' solutions. I was tasked with cultivating microbes to

assess their potential for use in biomining of REE. Extraction and separation of REE requires energy and harsh chemicals and the use of microbes could offer a cleaner and more energy efficient method for the extraction and processing of these ores. This was my first opportunity to isolate microbes of my own as most of my previous work had been with molecular biology. After some background reading I selected three different media with antibiotics and anti-fungals and plated out a range of dilutions of the sediment and incubated these at two different temperatures. After three weeks I had one colony. Trying a new medium and increasing the pH led to about 50 different colonies. Eliminating duplicates and looking for microbes that changed the pH led to four microbial isolates, and each was tested to see if they could mobilize REE from the original sediment. None of these four were the golden goose, but I am now ready for the next batch of sediments which should be coming from Madagascar as part of a NERC-funded grant to understand the movement of REE in the environment (SoS RARE).

My work at the BGS means I am involved in a wide range of research projects, and as the importance of geomicrobiology grows, I hope my search for understanding life will expand into new environments, and even to other planets. However, this will mean more time explaining to geologists that although the rocks may not have changed in the many millions of years since their formation, the microbes probably have.



Megan Barnett

Geomicrobiologist, British Geological Survey, Keyworth

Membership CHANGES

We would like to warmly **welcome** the following new Members to the Society.

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B. Djeghout

ARABIAN GULF

K. Hussein

AUSTRALIA

*G. Holds
O. Ogbughalu*

BANGLADESH

T. Hossain

BURKINA FASO

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S. Jarraud

GUATEMALA

J. R. Menchu

INDIA

A. Bhardwaj

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A. Fox
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J. Graca
L. Hannon
B. C. Holohan
I. O. Ikoyi
A. McGurrin
G. Pozdeev
C. Walsh
D. Ziuzina*

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F. De Filippis

KENYA

C. Kitonde

KUWAIT

I. Alsaif

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K. Kalutay

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*F. Corbino
B. Rayamajhee
C. Sujakhu*

NIGERIA

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O. A. Adedeji
O. Adeleke
G. Adeshina
J. D. Ajah
F. I. Alzau
J. Echem
J. O. Enya
C. O. Ibiam
O. B. Ibingha
A. G. Nwachukwu
F. S. Okeleke-Kooper
S. Olofinsae
C. Opara
C. Osilo
O. V. Uchenna
J. Udo
A. C. Ukonu*

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*F. Hasan
S. Sehar*

PORTUGAL

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A. M. R. G. Varela*

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C. A. Achu
O. Adebambo
M. Agbaje
N. Al Waili
M. Al Zadjali
Y. Alabdali*

*S. Al-Aidy
Q. Ali
A. Allen
I. Andrade
S. Baho
S. Bailey
A-M. Balan
R. Barthakur
J. Bayles
A. Bazaid
H. Begum
D. Boampong
N. Bravo
J. Burns
H. Chan
H. Ciesielczuk
K. Coates
J. Coelho
M. Conwell
S. Cordon
A. Couchman
S. Coupe
A. Curilovs
Y. Darkbloom
C. Dixon
T. Do
L. Fernandez-Martinez
K. Fraser
N. Gerits
S. Girvan
N. Goeders
R. A. Goncalves da Silva
A. Gorchs Rovira
B. Harari
C. Havranek
E. Hayhurst
A. Henstra
J. Herbert
T. Hickey
K. Hitri
D. Holt
H. Hoosen
M. Hrubinova
J. Hussain
E. Hutton
A-M. Ionescu
J. Jervis
D. Johnson
R. S. Jones
H. Jones
G. Kapatai*

*A. Kelly
P. Krahn
T. Law
M. Lister
H. K. Maity
S. Malmalawadu
Fernando
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B. D. Shlla
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I. Swinscoe
E. Sypianska
C. Thompson-Whyte
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L. Toman
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J. Vassallo
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H. J. Wileman
C. E. Williamson
K. Wilson
S. Worsley
S. M. Yousaf*

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O. Berhilyvch

USA

*H. DeMoras
K. Mitchell
J. Oliver
M. O'Seaghdha
C. Williams*

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DEATHS

We were saddened to learn of the deaths of the following Members of the Society:

*Bernard M. Mackey
M.R. Kimmitt*

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The latest news, view and microbiological developments from our Corporate Members

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The genesig q16 is a 16 well real-time quantitative PCR machine. Although small (it has a 12 cm footprint) and incredibly easy to use this real-time PCR machine matches larger machines in performance.

An affordable price (£3995) opens up the possibility of more laboratories benefiting from the speed and accuracy of qPCR.

With over 400 detection kits the genesig 'Easy' kits contain all the components required to run a qPCR. Simply rehydrate the reagents, mix with your extracted nucleic acid and press go. The automated data analysis programme makes interpretation easy.

To find out more about these new products and how they can help in your laboratory testing please visit the BioConnections website, alternatively contact us by email or by telephone.

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Spiral plating made simple with the new Whitley WASP Touch

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Screening for *Streptococcus agalactiae*

Medical Wire has recently launched Sigma GBS™, a swab based device for the direct collection and rapid processing of screening specimens for *Streptococcus agalactiae* (Group B Streptococcus), a leading cause of serious illness in newborn babies. The organism may be carried asymptotically by the mother, but then passed onto the baby during labour. Policies vary, but some countries have a screening programme to identify carriers with a view to offering antibiotics during labour. Other countries may not have universal screening, but there is still increased testing of those deemed to be at most risk of being carriers.

The Sigma GBS™ device consists of a vial of Lim broth enrichment medium and a swab which can be snapped into the vial. The swab is used to collect specimen in the normal way from vagina or rectum. The vial is incubated at 37°C before inoculation onto a suitable chromogenic agar medium for the direct detection and identification of *Streptococcus agalactiae*.

The vial is compatible with all current automated processing platforms, while if a more rapid diagnosis is required, the specimen can be tested using molecular methods.

Further Information

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NCIMB kicks-off new research collaboration

NCIMB is collaborating with the Robert Gordon University in a new KTP-funded research project to screen *Streptomyces* species for the production of novel natural products.

Streptomyces species play an important role in organic matter decomposition, and are responsible for the familiar earthy smell of soil. They also have an

enormously important role in antibiotic production, producing most of the clinically-used antibiotics of natural origin.

The National Collection of Industrial Food and Marine Bacteria was established in the 1950s and today includes more than 10,000 strains, isolated from a variety of sources and geographical locations. Since the collection was created, there have been huge developments in the tools available to study microorganisms, that pave the way to revealing properties and potential uses that could not have been predicted by the scientists who discovered some of our earlier deposits.

Streptomyces' complex secondary metabolism made them an obvious choice for this project, which aims to look for compounds that have potential for use in pharmaceutical products such as antimicrobials, anti-tumour or anti-inflammatory medication, as well as compounds relevant to other industry sectors. We hope that the project will make a valuable contribution to a programme of work that adds value to the culture collection through the provision of more information about the strains within it.

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Recent developments with our Great Basin molecular testing range include the full identification of Staphylococci with resistance detection, Shiga toxin detection, group B Streptococci and enteric screening.

Microbank of course remains the method of choice for the long term storage and retrieval of bacteria and fungi. Please visit the new website at www.pro-lab.co.uk to request your free copy of the recently updated Worldwide Performance Portfolio, now covering 25 years of successful storage data from many laboratories around the world. Contributions are always welcome, as are pictures of our long serving cute mascot for the "Where in the World am I?" Calendars.

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Protos 3 Colony Counter and Rapid ID System from Symbiosis

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Symbiosis has introduced a vibrant new automated colony counting and chromogenic identification system, Protos 3. This system allows walk-away colony counts, as well as accurate identification of colonies cultured on chromogenic plates.



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The stylish, yet practical Protos 3, which comes in bright red, attaches easily to a computer and requires minimal training to set up. Users simply input their plate identification and click. The Protos 3, featuring a highly sensitive CCD camera combined with unique three colour LED lighting, rapidly images an infinite number of colony colours on one plate and detects colonies as small as 0.043mm.

The Protos 3's powerful software then generates true to life counts and plate images, which can be transferred and stored in Excel. This GLP compliant process, with its full audit trail eliminates keying and image transfer errors providing accurate, objective data, which can be reviewed anywhere and anytime.

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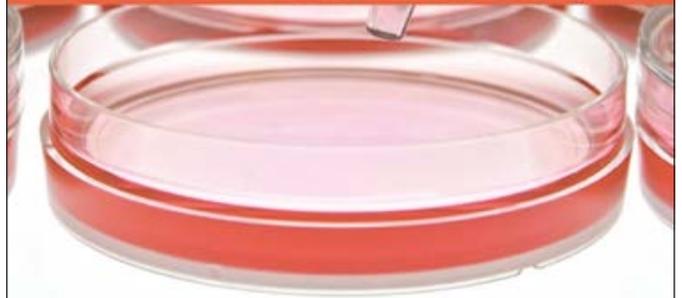
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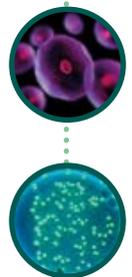
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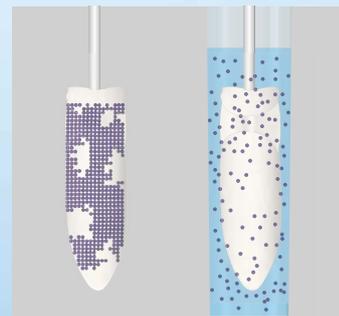


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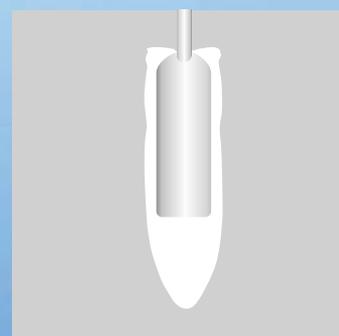
The ultimate in environmental sampling



- Premoistened foam sampling device
- Self-contained and portable
- Swab securely attached to quick-open cap
- Paddle inside foam for precision control of sampling
- Superb catch and release of microorganisms
- Hi-white foam and shaft for easy visualisation of colorimetric changes
- Premoistened with neutralising buffer



Catch and Release



Paddle Structure



Hi-White Foam Tip and Shaft



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