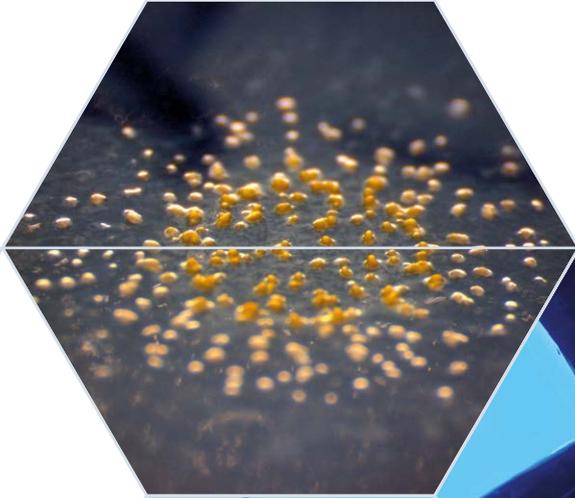


# microbiologist



Seeing  
the world  
with microbial  
eyes



CRISPR-Cas9:  
game changer



Why do  
bacterial names  
change?

# microbiologist

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## Who killed Kenny?



Microbiology has already dominated 2020, with Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2), first identified in Wuhan City, China, putting life on hold across the world and an episode of an American animated sitcom getting clever with the microbiome.

Global experts, governments and health officials rapidly came together to expand scientific knowledge and provide advice to countries and individuals on measures to protect health and prevent the spread of this pandemic.

You can read incoming SfAM President Professor Brendon Gilmore's interview with Dr Connor Bamford, a virologist from Queen's University Belfast on page 32. Connor answers questions including 'How far away might a suitable vaccine be?' and 'What is the evolutionary history of coronaviruses and in particular those affecting humans?'

Reaching as many people as possible with the applications of microbiology is the aim of many of us and navigating the communication gap between a non-expert public and scientists can be exceptionally tricky. Scientific research is often hyped and overstated when presented to the public and this compromises the accuracy of scientific studies and negatively impacts people's trust in science.

Research into the human microbiome is one topic that often falls into this category and science communicators struggle to get all the complicated and important messages across.

I urge you to watch the TV series *South Park*, episode 'Turd Burglars'. Kyle's dream, about his microbiome, leads to a revelation in a hilarious episode that manages to stretch out a simple joke about poo for 20 minutes. It is clear that thorough research around the microbiome has been conducted and the show still manages to educate and engage the public.

For those of us trying to communicate the benefits of microbiology, applying the concept of comedy and storytelling to our research does not come naturally. Journals and conference speakers are generally not the highlight of one's downtime and successful ways in which we explain our work within popular culture are few and far between. But when they turn up, they can be game changers.

The *Microbiologist* would love to hear from any readers that may have wacky ideas to communicate applied microbiology and can guide them to funding opportunities to help make those ideas a reality.

Stay safe, and stay in touch.

**Paul Sainsbury**

Editor

I am always excited to meet scientists who are living with local communities

Megan Hine

Survival consultant

## News

- 02** Contact point
- 03** Editorial  
Who killed Kenny?
- 06** A President speaks  
Recognition for a technique born out of microbiology
- 07** Harper's postulates  
Supporting and shaping the future
- 08** Shaping the future  
ECS social and symposium
- 09** ECS Research Symposium 2020  
(Event cancelled)
- 10** Fellowship Award 2020  
(Event cancelled)
- 10** New members of the Society
- 11** Nominations to our Executive Committee
- 11** A tribute to Andrew Miller

## Features

- 12** Going wild with infection control
- 16** CRISPR-Cas9: game changer
- 18** Why do bacterial names change?
- 24** Hiding in plain sight: the elusive candidate phyla radiation

## People & Places

- 28** Meandering in microbiology
- 32** An interview with Dr Connor Bamford
- 36** London's microbiota: pickle and preservation
- 39** Parliamentary Links Day 2020

## Policy & Public Affairs

- 40** BioFocus: Increasing the impact and reach of the biosciences
- 42** Introduction to the new Policy and Public Affairs Manager
- 45** Plant-Microbe Interactions 2020  
(Event postponed)

## Must-read Articles

- 46** *Journal of Applied Microbiology*
- 47** *Microbial Biotechnology*

## Education & Public Outreach

- 48** Seeing the world with microbial eyes
- 51** WH PIERCE PRIZE: Nominations are now open

## Industry

- 52** Happy 100th Birthday to NCTC
- 54** The latest news, views and microbiological developments



## A PRESIDENT SPEAKS

# Recognition for a technique born out of microbiology

The science and discipline of microbiology has often been at the forefront of new technologies and developments in terms of emerging techniques and methods.

We have seen the rise of a number of techniques such as microbial metabolomics manipulation, gene transfer and recombinant DNA technology, and synthetic biology in the form of the production of 'next-generation biofuels' or more recently the development of 'synthetic microbial life' as attempted by Craig Venter's group. However, few of these breakthroughs and developments have been as far-reaching through most of bioscience as CRISPR-Cas9. This technology is fantastic in that it allows the editing of genomes, alteration of DNA sequences and potentially, modification of gene function. This powerful tool has been extensively used in the realm of microbiology but also outside of our subject area. It has been found to have potential applications and roles in areas such as treating and preventing the spread of diseases, correcting genetic defects, right through to helping to improve crop strains. This has been a fantastic development led by a supremely talented group of scientists including Emmanuelle Charpentier and Jennifer Doudna. Doudna and Charpentier were the first to propose that the CRISPR-Cas9 system from bacteria could be used for programmable editing of genes in other systems.

We are very proud at SfAM to be able to offer Jennifer Doudna an SfAM fellowship for her contribution to the exploitation of CRISPR-Cas9 technology, a development described as one of the most significant discoveries in the history of biology. Professor Doudna has been recognised by a number of bodies in the scientific community, as well as being named as one of the *Time 100* most influential people, along with Emmanuelle Charpentier, and was a runner-up for *Time's 2016 Person of the Year* with the other CRISPR scientists. In 2020, Professor Doudna will become a fellow of the Society for Applied Microbiology, a fellow of whom we can be rightly proud for all her achievements and for her role in the development of CRISPR-Cas9 technology.

Thank you Professor Doudna and colleagues.

### Mark Fielder

President of the Society for Applied Microbiology

## HARPER'S POSTULATES

# An uncertain spring

Every year, we look forward to connecting with the wider early career scientist community at the annual ECS Research Symposium. I am extremely proud that we have supported this event for nearly a decade now: I use the word support very deliberately as this is an event run by ECS members of the Society, for ECS members and students.

Our ECS committee always create an event with a supportive environment for those who may have never experienced a conference before. This symposium is for all early career scientists with applied microbiology-related occupations/studies.

The event has a unique energy and atmosphere of collaboration and is always a fantastic opportunity for early career researchers to present their work in a supportive environment, fostering genuine and potentially career-long relationships. This year was to be no exception and would have been the biggest in its 9-year history.

However, given the growing concerns around SARS-CoV-2/COVID-19, the Executive Committee of trustees has taken the difficult decision to cancel this year's ECS Research Symposium, as well as the Fellowship event at which we'd intended to honour Professor Jennifer Doudna, our new Fellow. An incredible amount of hard work and effort has been invested by our talented team and ECS into creating these events, so the decision to cancel was not an easy one and was reached after a lot of careful thought and consideration.



Both events will remain part of the SfAM events calendar and we will ensure you are updated once plans for future events are confirmed (you can read details regarding the date of next year's ECS Research Symposium in the 'Shaping the future' article by ECS Member Alli Cartwright).

The current SARS-CoV-2/COVID-19 pandemic has provided an opportunity for us to explore alternative ways of operating – including more home-working for the team. Also, you'll remember that we updated our Articles of Association last year to include the provision for virtual trustee meetings and this current situation will no doubt be the catalyst to putting the theory behind these changes into practice. All these changes will make no significant difference to the way you can get in touch with us, so please do contact us through the normal routes.

As I write this, the outcome of this pandemic remains uncertain, but in the meantime, I wish all our members well and look forward to engaging with you at a future SfAM event.

### Lucy Harper

Chief Executive of the Society for Applied Microbiology



## Making the tough decision

Cancellation of the ECS Research Symposium was a tough call to make as it is an incredibly important event for SfAM and a lot of hard work was put into it by the ECS Committee, but we need to prioritise the health and safety of our delegates, exhibitors and everyone else who makes the symposium such a special event.

We explored delaying the symposium until later in the year, but as the situation with SARS-CoV-2 is unpredictable we felt that cancelling the event was the only option.

We remain committed to hosting the symposium in the city of Cardiff; the Mercure Hotel, where the 2020 event was to be held, have been amazing and allowed us to transfer our booking to next year without any penalties. So, we already have a provisional date of **17 March 2021** for the **10th Anniversary ECS Research Symposium Spectacular** – we promise to make this event extra special for you and look forward to seeing you there.

Meeting with the next generation of microbiologists is one of the highlights of what we do and this year we will still provide an ECS Symposium-inspired virtual experience for our community in lieu of the event itself. We're also planning other ways for early career scientists to get together later in the year through a combination of hosted events, videos and potentially some live-streamed content. We will share additional details on our plans through the SfAM website, monthly newsletters and Twitter. In the meantime, thanks for your patience and understanding.

**Alli Cartwright**

ECS Communications Officer

Members of the ECS committee and membership also attend meetings throughout the year to discuss matters relating to microbiology, our events and being an ECS member. Best of all we also get to hang out, meet new people and have a laugh. Earlier this year we went to a board-game café under Waterloo Station. It was a surprise, but I was thrilled – I love board and card games! The first game we played was *The Resistance*, a game in which spies have the chance to fail secret missions. In the third round I was a spy and I had to work carefully, lying to my friends and pretending to be innocent. I had to leave my SfAMily just as they decided to play one called *Pandemic*. Who knew.

It also gave us a chance to welcome our attending new members, Kate Bamford (Policy Officer), Nasmille Larke-Mejia (Welfare Officer), Joseph Kirk (Podcast Editor) and Elitsa Penkova (Undergraduate Officer), who will be helping us with the preparations for the 2021 Symposium amongst other things.



## Early Career Scientist RESEARCH SYMPOSIUM 2020

All events  
are postponed until  
further notice.

This is an evolving  
situation and this page  
is therefore subject  
to review.

<b>09:30</b>	Welcome allocation of presentation topics and registration	<b>14:00</b>	Professor Julian Marchesi The human microbiome: a new clinical frontier or just another 6-pack scheme?
<b>10:15</b>	Opening of the symposium <b>Dr Lucy Harper</b> and <b>Dr Tom Ellis</b> Imperial College London Microbes – growing materials from microbes with DNA-programmed properties	<b>14:30</b>	Break and posters
<b>10:30</b>	Early Career Scientist oral presentations. <b>Alba Pacheco Moreno</b> How do barley plants communicate with beneficial roots-associated <i>Pseudomonas</i> ? <b>Natalia Miguel-Vitor</b> From <i>Streptomyces</i> to <i>Pseudomonas</i> : Identifying and harnessing the biosynthetic pathway of anti Gram-negative antibiotic bicyclomycin <b>Rachael Slater</b> Discovering the scent of the equine faecal mycobiome: an integrated -omics approach <b>Hannah Pugh</b> RND efflux pump conservation across the pangenome of <i>Escherichia coli</i> <b>Anete Krista Salmene</b> Use of textiles for attached cultivation of red marine microalgae <i>Porphyridium purpureum</i>	<b>14:50</b>	Workshops: Delegates will be split into 4 different groups and given a microbiology issue. They will then rotate around 4 different stations to learn how to communicate this issue in 4 different contexts. The stations are: • POLICY • PRESENTATION SKILLS • PUBLIC SCIENCE COMMUNICATION • PRESS RELEASE
<b>11:40</b>	Flash presentations x10	<b>15:50</b>	Break and posters
<b>11:55</b>	Lunch and posters	<b>16:10</b>	Workshop presentations
		<b>16:40</b>	Closing of the symposium, prizes
		<b>17:00</b>	End

# Fellowship Award 2020

## Professor Jennifer Doudna



Jennifer Doudna is the Li Ka Shing Chancellor's Chair and a Professor in the Departments of Chemistry and of Molecular and Cell Biology at the University of California, Berkeley, as well as an Investigator of the Howard Hughes Medical Institute. Her co-discovery of CRISPR-Cas9 genetic engineering technology, with collaborator, French scientist Emmanuelle Charpentier, has changed human and agricultural genomics research forever. This genome-editing technology enables scientists to change or remove genes quickly, with a precision only dreamed of just a few years ago. Labs worldwide have re-directed the course of their research programmes to incorporate this new tool, creating a CRISPR revolution with huge implications across biology and medicine.

In addition to her scientific achievements and eminence, Doudna is also a leader in public discussion of the ethical and other implications of genome editing for human biology and societies, and advocates for thoughtful approaches to the development of policies around the use of CRISPR-Cas9. She has received many prizes for her discoveries, including the Japan Prize (2016), the Kavli Prize (2018) and the LUI Che Woo Welfare Betterment Prize (2019). In 2015, Doudna was named by *Time* Magazine as one of the 100 most influential people in the world.

## NEW MEMBERS OF THE SOCIETY

- |  |   |  |   |   |
|--|---|--|---|---|
| <b>Egypt</b><br>M. Almoghazy             | <b>Nepal</b><br>K. Thapa  | I. Nwike<br>A. Awanye<br>O. Bankefa<br>H. Olaleye<br>B. Opawale<br>O. Aromolaran | S. Aiyedun<br>E. Gardener<br>K. Gupta<br>R. Macmillan<br>J. O'Grady<br>E. A. Mulhall<br>G. Duffield<br>A. Nedelea<br>A. Cowan<br>J. Haystead<br>M. Wu<br>M. Sulonen<br>F. McCuaig<br>F. Hodges<br>M. Raut<br>R. McCarthy<br>D. Kirzakova<br>E. Lauguico<br>J. Teneb | V. Heath<br>A. Ehibhathiomhan<br>D. Alkhder<br>G. McVicker<br>A. Pacheco Moreno<br>K. Lavender<br>M. Rothwell<br>M. Jones<br>F. Alli<br>Z. Alfahl<br>J. Winter<br>N. Gray<br>M. Leach<br>L. Kerr<br>F. Ukachukwu<br>W. O'Neill<br>A. Fuller |
| <b>France</b><br>S. Mahmood              | <b>Nigeria</b><br>O. Chukwuma<br>I. Asogwa<br>O. Nduka<br>B. Oduntan<br>B. Alagha<br>T. Duche<br>T. Ugwu<br>P. Ezeobi<br>L. Adamu<br>E. Omah<br>C. Eze<br>S. Fakoya<br>J. Bamidele<br>A. Soretire<br>A. Akerele | <b>Thailand</b><br>F. Xie  | <b>United Kingdom</b><br>K. Cozens<br>E. Walker<br>R. Harsent<br>I. Maziar<br>R. Weiser<br>C. Brennan-Richardson<br>H. Dane<br>D. Ogundijo  |   |
| <b>India</b><br>L. Archana<br>P. Bhaskar |   |  |   |   |
| <b>Iraq</b><br>N. Ghaffar                |   |  |   |   |
| <b>Ireland</b><br>C. Trigueiros          |   |  |   |   |
| <b>Malaysia</b><br>N. Kamal              |   |  |   |   |

## Nominations to our Executive Committee

The Executive Committee (EC) of trustees plays a vital role in forming SfAM's strategy and guiding our programme of activities.

The EC of trustees meets three times a year and is responsible for steering the strategic direction and overseeing the running of the Society for Applied Microbiology. It provides ideas and initiatives to support applied microbiology and microbiologists. The EC provides input to our strategic campaigns, receives updates on the Society's financial position, and assesses the governance and risk that the Society may be exposed to.

Many people don't think they have the right skillset to be a member of the EC. We disagree. If you are passionate about promoting the applications of microbiology, then you have the skills we need.

In terms of microbiological interest area, we are looking for more people working in:

- industrial microbiology
- microbial biotechnology
- pharmaceutical microbiology
- agricultural microbiology
- water microbiology.

Nominations are invited from current members of the Society (must be over 18 and based in the UK) and will be reviewed by the EC, who will draw up a list of candidates for election. The election will take place in May 2020 and successful applicants will serve on the EC from July 2020 for an initial period of three years.

Nominations are accepted via the SfAM website. To be considered for a 2020 appointment, SfAM must receive the nominating information by 1 April 2020. Should you wish to discuss the role of a trustee in more detail, please email [lucy@sfam.org.uk](mailto:lucy@sfam.org.uk).

## A tribute to Andrew Miller died 24 December 2019



SfAM would like to pay tribute to the late Andrew Miller, former MP for Ellesmere Port and Neston, who died recently on Christmas Eve. Andrew, former and first ever Chair of the House of Commons Science and Technology Select Committee, was instrumental in helping SfAM to establish our Science Policy Subcommittee.

We began our work with Andrew in 2016, when he took part in a policy workshop as a policy expert panel member, which ran as a precursor to our annual conference. Andrew provided us with some real insight into the world of science policy that set us on a path to work more closely with him. Following various discussions, we were delighted that Andrew agreed to become a special advisor as we set up our Policy Subcommittee, and he gave generously of his time, and his extensive knowledge. Many suggest that policy and the workings of Parliament are shrouded in mystery, but Andrew helped us to understand clearly how SfAM could make a difference, and how best to engage with different kinds of opportunities, but importantly to also know our limitations. Since then we have provided written evidence to various select committee and other inquiries, we have hosted a series of policy discussions framed around food safety after Brexit and published the outcomes, engaged with members of both Houses by hosting an 'evidence pod' during Evidence Week at Parliament, pitched a microbiology topic to the My Science inquiry and strengthened our Policy team at SfAM. I am in no doubt that all of this was made possible by our work with Andrew, and his enthusiasm and generosity in sharing his expertise.

# Going wild with infection control

**Megan Hine**

*Survival consultant*

I spend 10 to 11 months of each year overseas either leading expeditions or consulting for some of the biggest adventure and survival shows on TV. My job on these shows is both as a producer; coming up with content and journeys for on-screen talent as well as safety; stunt rigging and keeping the film crews safe. Wherever we go, we require new content and one of my absolute favourite aspects has always been learning skills from local peoples, whether it is how to make fire by rubbing pieces of bamboo together or which plants have edible and medicinal properties. To these native peoples, the environments they live in are very much a part of them in a way us in the modern world have lost touch with. Their awareness of the seasons, of change within their environment is instinctual and intuitive and their ability to spot the signs of plants and animals is incredible to

behold. Many years ago, I spent several months living and working with a San Bushman tribe in Namibia, I would accompany the women out foraging. Often, we would be looking for the Bush potato, a tuber which grew even in these dry climes. The women were looking for a thin vine like plant which the potato put up out of the ground twining around the scrub. There was something in how these vines looked that signalled that the potato was a good size to eat or was ripe. Much to the hilarity and often frustration of the women, I frequently received a clip around the head from one of the elder women's digging sticks, even after several months I couldn't see this.

Sadly, many traditional skills and knowledge including herbal medicine are being lost. Many native peoples do not write down their knowledge. To do so would be highly

Wherever we go, we require new content and one of my absolute favourite aspects has always been learning skills from local peoples, whether it is how to make fire by rubbing pieces of bamboo together or which plants have edible and medicinal properties

disrespectful. Their knowledge is passed on orally. With many younger people leaving their native communities in search of work and of a 'better' way of life so much knowledge has already been lost. I am always excited to meet scientists who are living with local communities to learn more about the chemical properties of the plants. There are many plants and animal products which I have come across which I have seen what I believe is evidence of healing and infection fighting properties. Here are a few I have come across in my travels.

## Pine sap

This sticky resin is so messy when handling the wood from the tree, particularly in early spring when the sap is rising, it can take days and hard scrubbing to get it off. A few years ago, when guiding a trip in winter in Norway, I accidentally cut my hand quite deeply with my knife. In the extreme cold, my experience is that it is hard for cuts, particularly such straight knife cuts to bind together, plus I use my hands a lot, which doesn't leave a lot of time for healing. I had heard of the antimicrobial properties of spruce sap and I figured it was so sticky I would see if I

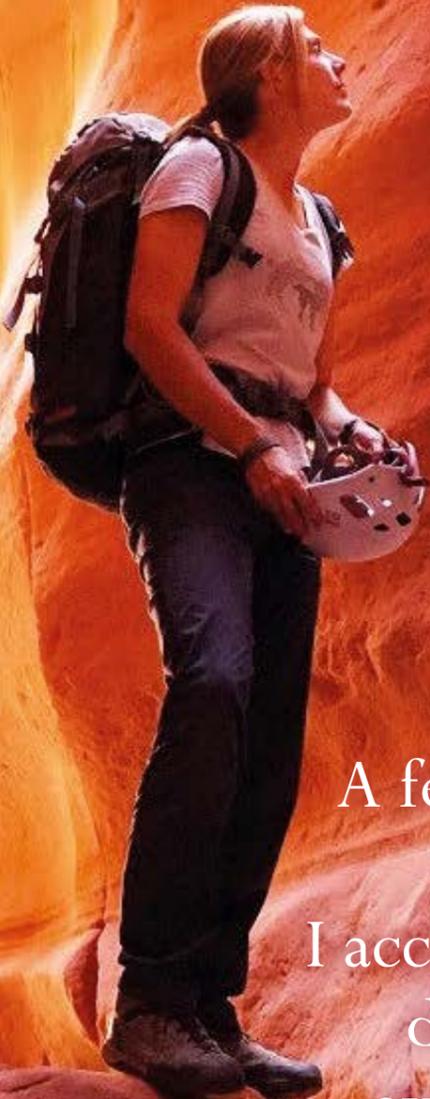


could stick the cut back together. I consequently had no issues with it becoming infected and the wound stuck together well. The only thing I was aware of was that it is so sticky not only does it stick your hand to your gloves but dirt can stick to it too. I was very conscious of this and ensured I washed the dirt away each evening with melted snow. It is possible to collect sap without damaging the tree and it is also an excellent fire starter, both in its harder resinous state and as the sticky sap. I have seen the harder resin being ground up and sprinkled onto wounds, supposedly having antimicrobial and antifungal properties.

**Charcoal**

This may be currently fashionable but on survival shows, where I have been dropped with nothing but a machete, I have used charcoal, bamboo charcoal in particular, to clean my teeth. Complications with teeth on expedition can be incredibly troublesome and very hard to deal with; without someone with training in how to manage them they can often result in evacuation. I am always very meticulous with dental hygiene to avoid these scenarios. I have also used charcoal in improvised water filters to filter out microbes. However, on remote expeditions in particular, ingesting contaminated water can have very severe consequences and, although the times I have improvised water filters I haven't become sick, this is not something I would encourage. In a survival scenario, if you have a container to boil your water in, always boil it.

A few years ago, when guiding a trip in winter in Norway, I accidentally cut my hand quite deeply with my knife. In the extreme cold, my experience is that it is hard for cuts, particularly such straight knife cuts to bind together



**Ant pincers**

This is a technique I have seen both in various jungle environments and used in African communities. Ants with larger pincers are used as sutures to close open wounds. Although not antimicrobial, they do close wounds. The technique is to position the ant over the wound so it bites and then twist its body off, leaving its head in place. I have tried the technique on the back of my hand to see what it felt like. It is a rather painful process. I am also unsure of the cleanliness of the mandibles of the ant but this is a technique that has been used for thousands of years.

**Witchety grubs**

These are a fantastic source of protein, both in survival scenarios and for the Aboriginal communities of Australia. They have a creamy inside that tastes slightly of Primula cheese. Once you get past the Western aesthetic aversion for anything that isn't a vacuum-packed chicken breast, these taste really good. I have seen these grubs, dried and ground up into a powder and then made into a paste, either with spit or with water, as a healing salve for wounds.

**Maggots**

As you are most likely aware, maggots have been used for many years to fight infected wounds; they eat the dead tissue and supposedly secrete an antibacterial substance. I have seen these used on various occasions. The one that sticks in my mind the strongest is on a man in Brazil who had been bitten by a fer-de-lance snake.

These snakes have a haemotoxic venom, which kills tissue rapidly. The maggots were being used to help fight this. I very much doubt the man survived this as without immediate medical intervention, anti-venom being administered and a sterile environment, a bite from this snake is usually deadly.

**Plantain**

In the UK, so much of our herbal medicinal knowledge was lost with the burning of the witches. When I taught bushcraft in the UK I was fortunate enough to work with a medicinal herbalist who was investigating the knowledge we do still have access to and exploring the properties of plants whose uses have been lost. Many people from the local village would come and visit her for her remedies. I had been working in the Alps and had taken a fall, embedding mica, a very thin glasslike layer of rock, into my knee. As much as I had cleaned it out and pulled out as much as I could with tweezers, my knee was incredibly painful and swollen with infection. I came straight off this job and back into the woods to teach bushcraft and after a few days the swelling had not subsided.

After taking a look at me, the herbalist gave me a poultice of broadleaf plantain, a tiny but prolific plant we have growing all over the UK, and packed it onto my knee, wrapping a bandage around it. The poultice truly appeared to draw out the infection and within a couple of days it was healing nicely. Now, whenever I am in the UK and have a small infected cut when I am out in the wilds, I will chew up some plantain and place on the wound site. The seeds are also very effective in cases of constipation.



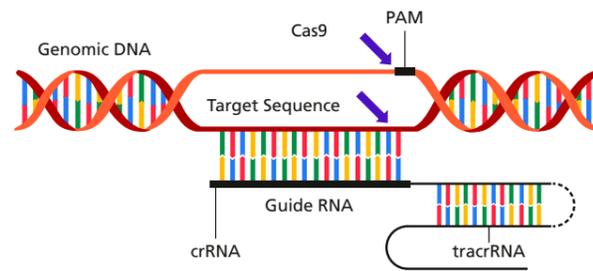
# CRISPR-Cas9: game changer

**Robert Millar**  
Society for Applied Microbiology

Coming from a biotechnology background, CRISPR-Cas9 has been part of my everyday vocabulary for several years now. Since it first became known to the scientific community, the question 'Have you considered using CRISPR?' has been a mainstay of conferences, meetings and casual conversation. It's not just scientists who are talking about it either – the mainstream media have been talking about it for several years now as well. So, why has this technique got everyone a-buzz? We've been able to edit DNA for a long time, so what is it about CRISPR-Cas9 that sets it apart from everything else? This short article should shed some light on the subject.

CRISPR-Cas9, which is often nicknamed 'CRISPR', is a technique that can edit DNA. The system has two parts: an enzyme and a guide. When introduced to a cell, the enzyme (Cas9) will cut DNA in a specific location determined by the guide. When CRISPR-Cas9 was discovered, these guides were CRISPRs, which stands for clustered regularly interspersed short palindromic repeats. These guides are used to fight off viruses; if a virus infects a cell, CRISPRs guide Cas9 to the DNA of the virus and cut it apart, killing it.

Whilst the use of CRISPR-Cas9 by archaea and bacteria as a sort of immune system against viruses is very interesting – and there's still lots of research being done on the subject – the real interest in CRISPR-Cas9 for most people is the fact that you can tailor the guide to any DNA sequence in any organism. This basically means you have a system with only two components that you can design to cut any sequence of DNA you might need to, and that's what has got scientists excited.



## Covering all bases

So, what's so great about being able to cut DNA? Well, put simply, cutting is the first step to making a change. In its simplest form, using this technique to cut DNA in a cell forces the cell to try and repair the break, which often introduces errors that we call mutations. This can be very useful for research to find out what a particular piece of DNA does, as by changing the DNA sequence we can change the function of whatever it codes for, and observing these changes can improve our understanding.

Taking it a step further, imagine now that you used two guides for your Cas9. This would mean two breaks that need fixing and there's a chance that when things are put back together, everything between the two breaks is removed. This is called a deletion and is extremely useful to us. Deleting a gene (a section of DNA that codes for a protein) can be used to better understand the gene (i.e., seeing how the cell behaves without the gene and assuming that whatever has changed is related to the gene that has been deleted) but can also be used in biotechnology to delete genes that are counterproductive to whatever you want your organism to do.

Imagine you had a type of brewers' yeast that made a beer with a bitter aftertaste, but otherwise was a great beer. After a bit of research, you find that the yeast is making a chemical that tastes bitter, so using CRISPR-Cas9 you cut out the part of the DNA that codes for the pathway that makes the bitter chemical. Apart from that one change, the yeast is exactly the same, so in theory you

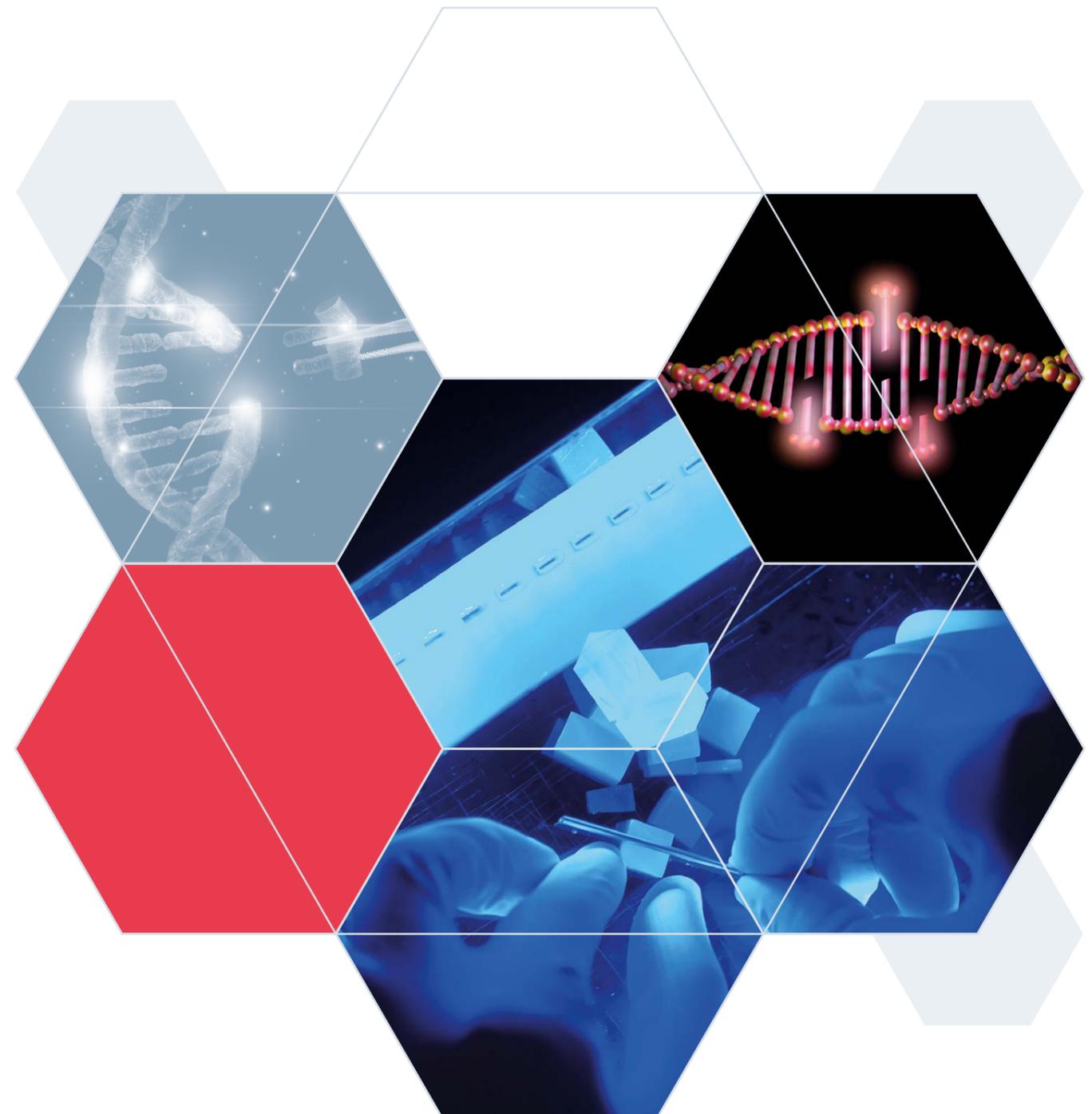
should get the same great beer but with no aftertaste. All using a simple and quick technique.

## Controversy

CRISPR-Cas9 has drawn some controversy in the news and not entirely without reason. Because of its versatility, CRISPR-Cas9 can be used in all sorts of organisms – not just microbes – including humans. This can have huge benefits, such as theoretically deleting the DNA sequences that cause Huntington's, or editing pre-cancerous cells to ensure they never develop into cancer. Of course, as is

often the case when DNA editing hits the mainstream media, there are always concerns about 'how far is too far'. Is it right to edit the DNA of embryos so that they never develop disease? How about changing eye colour? These ethical questions are probably beyond the scope of this article, but have prompted calls in government for the halting of CRISPR research in humans.

CRISPR-Cas9 is a powerful tool for biotechnology, medicine and almost all biological research. No other DNA-editing technique is as fast and versatile, or holds the potential to completely change the way we go about research.



# Why do bacterial names change?

**Barry Holmes**

Retired Head of The National Collection of Type Cultures (NCTC)

## Introduction

In microbial taxonomy, one must first **classify** one's unknown strains and determine whether they represent a new taxon. One can then propose a **name** and formal description of the new taxon. One is then set to **identify** future unknowns to this new taxon. Prior to 1980 (in fact, since 1 May 1753), a proposal of a new genus and/or species could be published in any microbiological book or journal. It was mainly only the authors of relevant sections of the successive editions of *Bergey's Manual of Determinative Bacteriology* who attempted to give a complete list of the members of any particular genus or higher group. Such authors would list characters for differentiating between taxa and assess their taxonomic position. Frequently, type strains would be unavailable and an organism would be known only from a published description. This caused great difficulty for those proposing new species and all too often another worker would later discover that the same organism had been previously described under a different name.

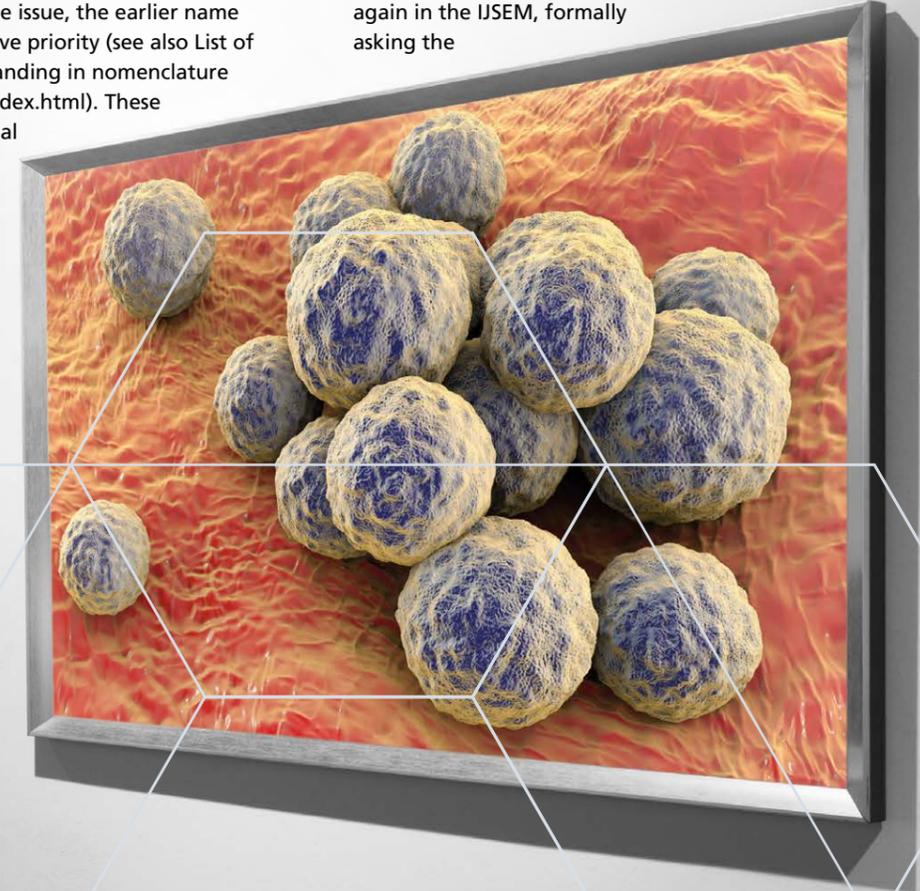
To overcome these problems a new starting date was chosen of 1 January 1980 at which time, on behalf of the Judicial Commission of the International Committee on Systematic Bacteriology, the *Approved Lists of Bacterial Names* would be published. Only those names included on 'the Lists' would have standing in nomenclature and organisms were only to be included if they were

adequately described and a type strain was available (every new species must now have a designated type strain to which the name belongs; the type must be deposited in at least two recognised culture collections in different countries). The Lists would make life much easier as those describing new taxa subsequently would need only to show that their new taxon differed from those on the Approved Lists. Also, type and other reference strains would be available with which to make the necessary comparisons. Naturally, if any worker felt that an organism omitted from the Lists should have been retained then it was possible to revive the name, as was done for *Pseudomonas cepacia* (now more commonly known as *Burkholderia cepacia*).

Although proposals of new taxa could continue to be made in any journal, for the future, in order to obtain standing in nomenclature all new names would have to be published in the *International Journal of Systematic Bacteriology* [IJSB; now *International Journal of Systematic and Evolutionary Microbiology* (IJSEM)], either in the text of

the journal, or, where the description had been published in a different journal, by inclusion in the (validation) lists of such names at the back of each issue. In the event that a name were to appear in the text of the journal and a different name for the same organism in the validation lists at the back of the same issue, the earlier name (that in the text) would have priority (see also List of prokaryotic names with standing in nomenclature <http://www.bacterio.net/index.html>). These rules for governing bacterial

nomenclature are given in the *International Code of Nomenclature of Prokaryotes* (ICNP, formerly the *Bacteriological Code*). Where strict adherence to 'the Code' would cause nomenclatural problems it is open to any worker to publish a Request for an Opinion, again in the IJSEM, formally asking the



Judicial Commission to make an exception to the rules. For example, the previous type strain of *Proteus vulgaris* differed substantially both biochemically and chemotaxonomically from typical strains of the species and a case was made to replace it with a more typical strain; this request was subsequently acceded to.

All bacterial names with standing in nomenclature are in the IJSB/IJSEM issues from January 1980 onwards. To determine a complete list of such taxa, whether they be new taxa or new combinations for previously described taxa, one must start with the 1980 Approved Lists. An update was published for the period 1 January 1980 to 1 January 1985, at least. However, from 1 January 1985 to July 1991 it is necessary to look at individual issues of the journal and to search *both* the text and the validation lists at the back. From July 1991 it is only necessary to look at the rear of the journal as, following the validation list for new names or combinations published outside IJSB/IJSEM, there is a separate list of new names and combinations appearing in the text of the journal.

The genetic information in bacterial cells is expressed at four different levels (example techniques for studies at each level given in parentheses): 1. the genome (DNA–DNA hybridisation, 16S rRNA gene sequencing, whole-genome analysis); 2. proteins (serology and gel electrophoresis); 3. cell components (cell wall composition, lipid analysis, pyrolysis gas-liquid chromatography, pyrolysis mass spectrometry, MALDI-TOF); and 4. morphology and behaviour (physiology, nutritional requirements, enzyme tests). Since the genome encodes the synthesis of cell proteins it is not surprising that studies at level 2 most

closely reflect the findings of studies at level 1. However, as we move down the various levels there will be more instances when results do not correlate closely with the findings of studies involving the genome. Many bacteria were classified at a time when studies could only be carried out at level 4. As our abilities to study the genetic information in bacterial cells at increasingly higher levels have developed, so bacterial classification has had to change. As classification changes, so does the nomenclature of the organisms concerned.

### Changing classifications

Many of the early classifications, based mainly on studies of morphology and behaviour, have stood the test of time. For some organisms, however, there have been major changes. The genus *Flavobacterium* for example, comprising yellow-pigmented oxidase-positive organisms, was found on the advent of mol percent guanine plus cytosine (mol % G+C) content determinations, to be divisible into high and low G+C content groups. In the 7th, 1974, edition of *Bergey's Manual of Determinative Bacteriology*, *Flavobacterium* was divided into two sections. Since the type species of the genus, *Flavobacterium aquatile*, fell in the low G+C section I, all the high G+C content species in section II had ultimately to be moved into other genera.

The advent of DNA–DNA hybridisation allowed a proper definition of a bacterial species (strains belonging to the same species should be 70–100% related, with less than 5% loss of thermal stability due to sequence divergence) and cast some surprises. Some 'species' proved to be merely

biovars (biotypes or biochemical varieties) of a single genomic species. Thus '*Klebsiella aerogenes*', '*Klebsiella edwardsii*', '*Klebsiella ozaenae*', '*Klebsiella pneumoniae*' and '*Klebsiella rhinoscleromatis*' are a single genomic species that should be regarded as a single species, *K. pneumoniae*. However, because *K. ozaenae* and *K. rhinoscleromatis* are associated with particular clinical conditions they continue to be accorded separate species status. '*K. aerogenes*' and '*K. edwardsii*', on the other hand, have lost standing in nomenclature as they were not included in the Approved Lists (it is an accepted convention to place such names in quotation marks) and such strains should now be called *K. pneumoniae*. Similarly, *Escherichia coli* and *Shigella* species are also a single genomic species, as are *Neisseria gonorrhoeae* and *Neisseria meningitidis*, but are afforded separate generic status for historical and medical reasons. In the case of *Yersinia pestis* and *Yersinia pseudotuberculosis* it was found that the two 'species' were so closely related that they should be regarded as subspecies of a single species with the name *Y. pseudotuberculosis*. However, the proposal, though scientifically valid, generated so much concern over possible confusion in the identification of plague organisms that the Judicial Commission formally rejected the name *Y. pseudotuberculosis* subspecies *pestis* and retained instead the name *Y. pestis*.

DNA–DNA hybridisation data, conversely, also showed some species to be heterogeneous and to comprise two or more different genomic groups, even though such species had proved relatively homogeneous in studies of their morphology and behaviour. In some cases, phenotypic

characters were found to correlate with the new genomic data and this led to the description of many genomic groups as new species, often within existing genera. Thus, yellow-pigmented strains failing to ferment sorbitol and regarded as variants of *Enterobacter cloacae* proved to be a separate genomic group closely related to *E. cloacae*, but now known as *Enterobacter sakazakii* (and more recently as *Cronobacter sakazakii*). Where no phenotypic tests can be found to correlate with genomic differences then such separate genomic groups are retained, for the time being at least, in the original named species. Many new species have been determined and many new genera have been recognised as a result of DNA–DNA (and rRNA–DNA) hybridisation studies. The creation of a new genus has sometimes led to a proposal for the transfer of additional species from one genus to the new one, necessitating a change in the genus name of such species.

The advent of rRNA–DNA hybridisation and, later, 16S rRNA gene sequence comparisons then whole-genome analysis, facilitated genomic studies at the genus and suprageneric levels. These studies have led to an 'explosion' of proposals of new genera in recent decades. It was known, for example, that the various rRNA homology groups of *Pseudomonas*, some as distantly related phylogenetically to each other as they were to *E. coli*, could be subdivided into several new genera. *Pseudomonas maltophilia* belonged to *Pseudomonas* rRNA homology Group V, along with *Xanthomonas*, and given certain common features it was eventually proposed that the organism become *Xanthomonas maltophilia*. Further studies showed that despite their shared features, *X. maltophilia* nevertheless



showed some significant differences to the other *Xanthomonas* species. It was therefore proposed that a new genus be created. This resulted in a second move, the latest proposed name being *Stenotrophomonas maltophilia*.

**It cannot be stressed enough that new names are only proposals and their use is not mandatory.**

Any name published in the *IJESM* and in accordance with the *International Code of Nomenclature of Prokaryotes* (ICNP, formerly the *Bacteriological Code*) is validly published. There is no such thing as a 'correct name' for a bacterium; all validly published names are 'correct' and it is a grave mistake to think one has to meekly accept the latest proposal as soon as it is published. Although it is generally advisable to adopt new names and to keep abreast of nomenclatural changes it is ultimately the scientific community that determines whether a new name comes into general acceptance; it is not automatic. As examples, numerical classifications based on phenotypic tests and later DNA–DNA hybridisation studies showed that, despite its motility, *Enterobacter aerogenes* should be placed in the genus *Klebsiella*. Since, at that time, there was already a '*Klebsiella aerogenes*' the specific epithet also needed to change. The latest proposal is of *Klebsiella mobilis*. However, the name *K. mobilis* has never been widely used and the organism is still generally referred to as *Enterobacter aerogenes*. The genus name *Fluoribacter* was proposed to accommodate certain species hitherto placed in the genus *Legionella*. However, *Legionella bozemanii*, *Legionella dumoffii* and *Legionella gormanii* are the names most widely used today; their names as placed in *Fluoribacter* have never found widespread usage. The proposed reclassification of *Vibrio fischeri*, *Vibrio logei*, *Vibrio salmonicida* and *Vibrio wodanis* as belonging to the genus *Aliivibrio* caused an instant problem of confusion between abbreviated forms of *Aliivibrio salmonicida* (*A. salmonicida*) and *Aeromonas salmonicida* (*A. salmonicida*). These two bacteria cause two important diseases in the same species of farmed fish, mainly salmonids, in the same areas often at the same time. However, given that it is not mandatory to follow each new proposal and that it is up to the scientific community to decide which name to use (assuming such names are validly published), field workers are at liberty to continue using the name *Vibrio salmonicida* (and the less confusing abbreviation *V. salmonicida*).

A change in genus name rarely causes a change in the specific epithet. Slight changes may occur to reflect a different gender of the new genus, thus *Flavobacterium breve* became *Empedobacter brevis*. Occasionally, a new name may be published and only then be found to have the incorrect ending. The corrected name can then be published. *Campylobacter laridis*, for example, was corrected to *Campylobacter lari*. A complete change in the species epithet is rare, but can occur when it is proposed that an organism be moved to a new genus in which there is already a species with the same epithet. As well as the example given above with regard to *Enterobacter*

*aerogenes*, a further example is that *Cytophaga aquatilis* was to be transferred to the genus *Flavobacterium*, whose type species is *F. aquatile*. On transfer, *C. aquatilis* required a new specific epithet as well as a change in genus name; it is now *Flavobacterium hydatis*.

Prior to publication of the Approved Lists in 1980, names would also change when authors found an older name and description which they proposed as corresponding to a later described organism; thus '*Acinetobacter anitratus*' became known as *A. calcoaceticus*. However, whilst *Citrobacter koseri* became known as *Citrobacter diversus*, the Judicial Commission subsequently rejected the latter name, leaving the name *C. koseri* to stand. Such complete changes of specific epithets are rare now as so many older names lost standing in nomenclature on publication of the Approved Lists. Occasionally, however, it is observed that two names have been given to the same organism, as with *Cytophaga marina* and *Flexibacter maritimus*; in such cases the earlier name will normally take priority.

Where two names for the same organism appeared on the same validation list at the back of an issue of the *IJSB/IJSEM* the position was less clear. *Klebsiella trabulsii* was named later than *Yokenella regensburgei*, yet the former appeared first on a validation list by virtue of alphabetical order. Although *K. trabulsii* could be construed as technically having priority over *Y. regensburgei* by virtue of its earlier listing in the journal, the latter is generally regarded as having priority and has gained widest acceptance. The Approved Lists did not set out to judge on synonymy so there are still some nomenclatural issues remaining to be resolved. For example, *Serratia marinorubra* and *Serratia rubidaea* are both on the Approved Lists and are clearly synonyms as they have the same type strain.

### Importance to public health

A key aspect of medical, public health and diagnostic microbiology laboratories is the accurate and rapid reporting and communication regarding infectious agents of clinical significance. Microbial taxonomy in the age of molecular diagnostics and phylogenetics, however, has created changes in taxonomy at a rapid rate, further complicating this process. All the major pathogens of public health importance have been defined through various taxonomic studies over a long period of time. In foodstuffs we find *Listeria monocytogenes*, pathogenic *E. coli* and *Salmonella* species. In meat processing at slaughter there is frequent contamination with a number of pathogenic bacteria such as Shiga toxin-producing *E. coli* (STEC) O157. Other significant pathogens from food samples include *Shigella* species, enteroinvasive *E. coli* (EIEC) and enterohaemorrhagic *E. coli* (EHEC). Toxigenic *Vibrio cholerae* and *Legionella pneumophila* are significant waterborne pathogens. *Staphylococcus aureus*, especially clones that resist methicillin (MRSA), have caused a medical and public health problem worldwide.

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Molecular studies have sometimes shown, as already mentioned, that certain species, considered separate in the past, are genomically a single species. A further example is the organism described by clinical microbiologists as *Pseudomonas multivorans*, which plant pathologists had earlier named *Pseudomonas cepacia* as a cause of onion rot. The former name has priority and this organism is now included in a new genus as *Burkholderia cepacia*. Conversely, as already mentioned, molecular studies have sometimes shown the existence of multiple species within what was once regarded as a single species. It is important to discern these new species as they may have an association with certain infections or a predilection for particular patient groups. Thus, the majority of *C. sakazakii* cases are adults, but low-birth-weight pre-term neonatal and older infants are at highest risk. The disease is associated with a rare cause of invasive infection in infants with historically high case fatality rates (40–80%). Most neonatal *C. sakazakii* infections have been associated with the use of powdered infant formula. Whilst all other *Cronobacter* species have been linked retrospectively to clinical cases of infection in either adults or infants, the species *Cronobacter condimenti* has not. In the case of the genus *Obesumbacterium*, a brewery contaminant not pathogenic to man, there is but a single species, *Obesumbacterium proteus*, but it has two defined

biogroups (1 and 2). These two biogroups are actually distinct species that are phenotypically different and only distantly related by DNA–DNA hybridisation. *O. proteus* biogroup 1 is actually a biogroup of *Hafnia alvei*, now referred to as *H. alvei* biogroup 1.

'Why do they have to keep changing names?' is a charge levelled against taxonomists. It happens not just in the bacterial world but also for fungi (some strains of *Aspergillus niger* have been reclassified as *Aspergillus brasiliensis*) and also in higher animals (the lion, once *Felis leo* is now classified in a later proposed genus as *Panthera leo*). From the discussions above it is hoped that the reader appreciates that taxonomy is dynamic and name changes are not without foundation, but reflect advances in our scientific knowledge. As newer methodologies become available and are applied to taxonomy, so new knowledge is gained and this is then reflected in changing classifications and nomenclature. The name we give to an organism is universal, so facilitates accurate communication worldwide, enabling workers in particular fields to ensure they are referring to the same organism. This is particularly important in public health; the recognition of a new species from human clinical specimens, such as *Staphylococcus cornubiensis* in 2018, enables others to recognise it and to therefore, in time, establish its pathogenic potential.



## Hiding in plain sight: the elusive candidate phyla radiation

**Xuesong He**

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The candidate phyla radiation (CPR) is a diverse monophyletic group of bacteria that has been found in many environments from the human body to oceans, freshwater, soil and deep subsurface sediments. Most of the information about CPR comes from the reconstruction of genome sequences from metagenomic surveys. Based on the analysis of concatenated protein sequences, CPR has been estimated to contain anywhere between 15% and 50% of the total phylum-level bacterial diversity on earth, with the most recent estimates placing this figure at not more than 26.3%. The diversity of 16S rRNA sequences has led to the division of CPR into 65 or more different phyla. However, a recently proposed approach to taxonomy using 120 concatenated protein sequences and normalising for lineage-specific rates of evolution changes this picture completely. This 'Genome Taxonomy Database' reclassifies the CPR as a single phylum and proposes the name 'Patescibacteria'.

So, what do CPR or Patescibacteria look like? How do they grow? Why are they so difficult to culture? The first clues lie in the genome sequences themselves. These sequences reveal a widespread lack of metabolic pathways that are essential for independent cellular growth. Yet there are genes that are enriched in the CPR including those for type IV pili and a system for the uptake of extracellular DNA. These systems hint at an obligate symbiotic or parasitic lifestyle, where CPR attach to host cells using adhesins such as type IV pili and scavenge key nutrients such as nucleotides.

Based on the analysis of concatenated protein sequences, CPR has been estimated to contain anywhere between 15% and 50% of the total phylum-level bacterial diversity on earth

If the genomes are small, are the cells small too? In 2015, Jillian Banfield and colleagues answered this question by passing groundwater through an  $\sim 0.2 \mu\text{m}$  filter and examining the filtrate. Metagenomic analyses indicated that the vast majority of microorganisms in the filtrate were CPR bacteria. Cells were visualised by cryo-electron tomography and shown to possess periodic surface layers (S-layers) and, in many cases, pili-like structures of varying length and sizes. Occasionally, these pili appeared to link small cells to larger cells including spirochaetes.

Perhaps the most important breakthrough came from myself and Floyd Dewhirst at the Forsyth Institute in Boston, USA, and collaborators, also in 2015. Recognising that genome sequences of CPR bacteria contained an unusual base substitution in the 16S rRNA gene, this group predicted that the TM7 phylum (now Saccharibacteria) within the CPR would be resistant to streptomycin. Using streptomycin enrichment, they were able to obtain co-cultures of a saccharibacterium (now known as '*Nanosynbacter lyticus* TM7x') with *Actinomyces odontolyticus*. This was the

*Nanosynbacter lyticus* TM7x (small cells) attached to their *Actinomyces odontolyticus* host. Image kindly provided by Xuesong He, Forsyth Institute, USA.



first time that any CPR bacterium had been cultured and provided a unique opportunity to explore the biology of the species. In keeping with the Banfield study, the cultured TM7x were only 200–300 nm in diameter and were obligate epibionts, relying on their host for key nutrients. Further characterisation has shown that TM7x can infect naive host strains of *A. odontolyticus*, rapidly killing the majority of host cells but leaving a reservoir of uninfected cells. The association quickly evolves into a stable relationship where TM7x only infects and kills a relatively small subpopulation of *A. odontolyticus*, with little impact on the overall rate of growth of the host.

Armed with a better understanding of CPR and the confidence that they can be cultured, the Forsyth group has developed a protocol for isolating Saccharibacteria in association with host strains by a combination of filtration, ultracentrifugation and co-culture ([http://www.homd.org/ftp/doc/Saccharibacteria\\_Isolation\\_and\\_Cultivation.pdf](http://www.homd.org/ftp/doc/Saccharibacteria_Isolation_and_Cultivation.pdf)). At an inaugural symposium on 'The Uncultivable Bacteria' at the Forsyth Institute, this technique was successfully employed on willing workshop participants to culture a range of novel Saccharibacteria isolates. Other groups are hot on their heels in the race to culture the uncultured members of the human oral microbiota. In 2019, Mircea Podar and colleagues reported a 'reverse genomics' approach to engineer antibodies against Saccharibacteria and other uncultured bacteria. They were able to culture three novel Saccharibacteria isolates as well as another previously uncultured lineage termed SR1. The Saccharibacteria were all obligate epibionts of Actinobacteria.

So far, the culture of CPR bacteria has been restricted to the human oral microbiota. We are beginning to build a picture of the Saccharibacteria, although many basic questions about their cell structure and biology remain unanswered. Importantly, it is not yet known how these organisms contribute to human health or disease or to biogeochemical processes in the environment. One key challenge is to transfer our knowledge about isolation procedures to capture CPR from other environments such as the oceans or soil. A first step will be to identify hosts that support growth and enable laboratory culture. This will be critical if we are ever to appreciate the full range of microbiology on planet earth.

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*Nanosynbacter lyticus* TM7x (small cells) attached to their *Actinomyces odontolyticus* host. Image kindly provided by Xuesong He, Forsyth Institute, USA.

We are beginning to build a picture of the Saccharibacteria, although many basic questions about their cell structure and biology remain unanswered

1 µm

EHT = 3.00 kV  
WD = 3.0 mmSignal A = SE2  
Width = 7.500 µmMag = 40.27 K X  
Image Pixel Size = 3.662 nm



## Meandering in microbiology

In 1973, the UK joined the EEC (EU), Billie Jean King won the 'Battle of the Sexes' tennis match, beer cost less than 10p a pint and I began studying microbiology at University College London. I worked hard but did not have much confidence and, after qualifying, had no idea what to do next or that I would have a career in microbiology spanning over 40 years – with periods in the NHS, academia and industry. Not the result of any grand plan but serendipity and circumstances.



This posed photo was for an e-learning module on prokaryotic diversity I wrote when at Cardiff.

### Linda Thomas

Society for Applied Microbiology Executive Committee

After graduating (and getting married), my first 'proper job' was in the Central Public Health Laboratory (now Public Health England) at Colindale. Here, having grown in confidence, I badgered to do a PhD (on the virulence of enterotoxigenic *E. coli*) on top of my routine work identifying enteric pathogens. My pregnancy during this came as rather a surprise. Picture Dopey in *Snow White* with his oversized coat trailing on the floor – me in a lab coat, trying to work as long as possible before maternity leave. After having my son, I realised full-time work was not an option for me, so returned part-time, working every morning to keep experiments going. Based on this experience, I would advise: (i) not to write up a PhD on maternity leave (your brain is not fully focused); and (ii) to minimise the costs/fatigue of travel by working fewer but full days.

Shortly after getting my PhD I had another child, at which point childcare costs were higher than my earnings, so I did not return to work. This was back in the dark ages – I had to pay back the little maternity pay I had received. After my eldest had started school, however, an invitation to the lab's Christmas lunch resulted in a return, where I worked on extending the *Aeromonas* serotyping scheme. I enjoyed

my time at Colindale and learnt a lot, including how to write better scientific papers. My first attempt (hand-written of course – the dark ages...) came back covered in red ink. Must do better.

Following our move to Wales, a chance conversation with a lady (a Professor's wife) at my son's nursery resulted in postdoc research at Cardiff University. This was a very different lab, home to several PhD students with a remarkable vocabulary of swear words as well as disgusting smells (usually due to their experiments). I was using gradient plates to investigate how multiple factors inhibit food pathogens, so I had to ensure that no one (including staff) sat on my bench or ate in the lab. When I became funded by the European Union, I started to travel abroad, with my first international presentation in Norway. We used the term 'propinquity' to describe distance between colonies as I was investigating the effects of this on lactic acid bacterial inhibition of pathogens. Thinking

the word might be unfamiliar, I had photographed the relevant dictionary page and, on the day, nervously read out the first word on the slide. 'Condom?' I squeaked, not realising the page had started with the definition of 'prophylaxis'. But the audience were amused and became more interested, eager for my next comedy moment.

I was considering returning to full-time work when, out of the blue, one of my EU collaborators phoned asking me to visit his labs in Dorset. This resulted in my move to industry, heading a team developing novel natural food preservatives, focusing on nisin and natamycin. I was now liaising with researchers in Denmark, Germany and the USA, so still travelling abroad frequently. (Feedback from one US meat manufacturer after a talk of mine: 'Gee Linda, I don't know what the hell you were talking about but it sure sounded good.' Never mind the science, my accent had convinced.) We devised food models to test our new preservative combinations and had a particularly

## Hysterical time at the University of Plymouth facilities making hot dogs inoculated with *Listeria*



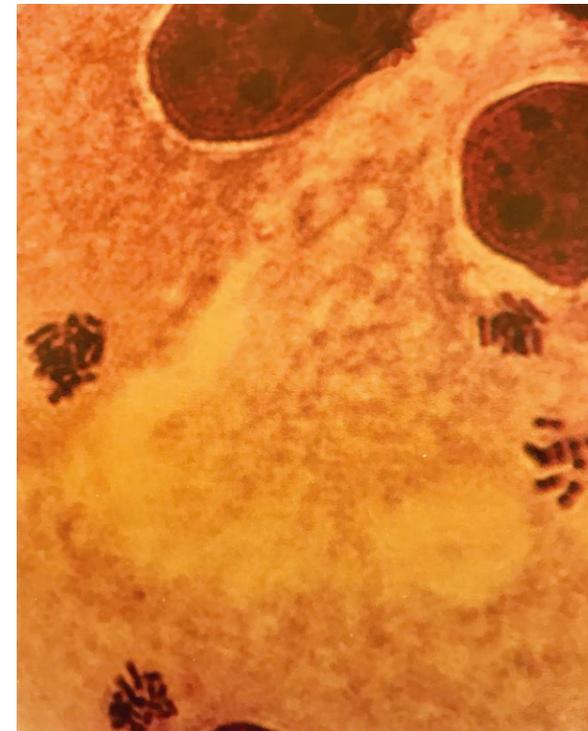
I have always loved microbiology, with its combination of practical and theory work and its impact on all aspects of life. This and my workaholic tendency helped me progress even though working part-time

**Above**

An enterotoxigenic strain of *E. coli* (serotype O25:H42) showing the virulence fimbriae that facilitate its adhesion to the human gut (×32,000)

**Right**

A higher resolution negative stain of the above fimbriae (×100,000)



Pattern of adherence of an enterotoxigenic strain of *E. coli* (serotype O114:H14) adhering to a human intestinal cell line.

hysterical time at the University of Plymouth facilities making hot dogs inoculated with *Listeria*. I also started to file patents, an interesting process that delayed but did not prevent scientific publication.

I reached the level of Principal Senior Scientist but going further probably meant working abroad. With both sons grown and a husband working in London, I decided to move there for my next job. The probiotic company Yakult, where I became Science Director in the UK, suited my experience of 'good' and 'bad' bacteria but it was a wrench to be no longer in a lab. The Japanese work 'culture' (pardon the pun) was also very different. I was surprised by the range of research with the *Lactobacillus casei* Shirota strain and enjoyed working on clinical trials on infections ranging from *Clostridioides difficile* to the common cold, and diseases ranging from cirrhosis to constipation. I was not so crazy about dealing with the press regarding their probiotic headlines and was also involved in regulations during a difficult time for probiotic health claims, organising conferences and producing educational material for healthcare professionals. I left after 11 years when I felt I had achieved all I could and the weekly commute from Dorset had become too much.

My 'retirement' has been busy. I spent two years as Chief Editor of the *International Journal of Dairy Technology*, still organise the British Society of Gastroenterology's 'Gut Microbiota for Health' expert panel and do some consultancy and lecturing. I have also enjoyed my time on the Executive Committee and Policy Committee of SfAM; I appreciate their support of Early Career Scientists as well as their equality, diversity and inclusion initiatives.

My tips for those starting out:

- DEMONSTRATE YOUR KNOWLEDGE**  
I established myself in new fields by writing reviews and chapters, and managed to produce a constant flow of research papers. Publications clearly show achievements to prospective employers. Before interviews, read up about the organisation, the interviewer and the topic. I asked all Yakult applicants to define 'probiotic' – it was disappointing how few could.
- WRITE FOR YOUR READER**  
In industry, you report to busy people who may not be scientists and/or not have English as their first language. Don't blind them with science. Explain concisely and clearly what results mean in terms of further work and potential for the company. Follow company guidelines in terms of layout.
- GIVE PRESENTATIONS**  
I was terrified but good preparation and an ability to act can see you through. Analyse what makes a good presenter and a good talk at conferences, then follow these examples.
- BUILD A NETWORK OF CONTACTS**  
You never know who may help you in the future. Conversations with scientists from different backgrounds also spark new ideas and collaborations.
- USE YOUR SOCIETY**  
Attend SfAM conferences and check out their grants, which range from support of conference attendance to research. Consider serving on an SfAM committee (a great way to network) or write articles or blogs.
- BE PASSIONATE ABOUT YOUR WORK**  
I have always loved microbiology, with its combination of practical and theory work and its impact on all aspects of life. This and my workaholic tendency helped me progress even though working part-time. Enthusiasm and genuine interest in a topic convince potential employers.
- DO AS YOU WOULD BE DONE BY**  
I have been helped and encouraged by countless people throughout my career, many of whom had no reason to do so. I am very grateful to them and hope I have followed their example.



Professor Brendan Gilmore  
SfAM Vice President

An interview with



Dr Connor Bamford

## Dr Connor Bamford

Virologist and Wellcome ISSF Early Career Research Fellow  
at the  
Wellcome-Wolfson Institute for Experimental Medicine at Queen's University Belfast

At the end of 2019 in the city of Wuhan, China, an outbreak of viral pneumonia of unknown cause led to the discovery of a new human coronavirus. As of 15 March 2020, SARS-CoV-2 is known to have infected 153,517\* people, in 143\* countries killing 1,775\*. There is no known cure or vaccine against coronavirus disease 2019 (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus.

\* World Health Organization Situation Report (15 March 2020).

### **Connor, can you tell us a little bit about your background and in particular your interests in coronavirus research?**

I am a virologist working on antiviral immunity, in particular in the lung. I am currently working on looking at immune aspects of influenza virus infections. I completed my PhD in molecular virology at Queen's University Belfast in 2014 before going to the MRC-University of Glasgow Centre for Virus Research for my postdoc to investigate antiviral proteins where I got interested in signalling proteins called interferons that help defend us against infection. I recently moved back to Belfast to continue this work but in the lung, which is kindly supported by an independent Wellcome-ISSF Early Career Fellowship. As viruses can infect our lungs and kill us, I am particularly interested in this new coronavirus.

### **What is the evolutionary history of coronaviruses and in particular those affecting humans?**

Coronaviruses (named due to their crown-like morphology when observed using electron microscopy) are a large and diverse group of viruses that infect many birds and mammals, like humans. Some coronaviruses cause serious disease, including those of veterinary importance such as infectious bronchitis virus of chickens, and of importance to humans like SARS-CoV-2, which is actually the seventh

human coronavirus. Other human coronaviruses (CoVs) include the causative agents of SARS and MERS that cause fatal pneumonia and come from animals but also four CoVs that are endemic in humans and are responsible for common cold-like symptoms in most people. Intriguingly, most CoVs can trace their origins to bats, from which they likely jump species into humans and other animals.

### **What are the similarities between this virus (SARS-CoV-2) and other emerging coronaviruses such as SARS and MERS? Why is it novel?**

SARS and MERS-CoVs are two viruses of great concern. SARS-CoV emerged into humans from bats (via civet cats) in southern China in the early 2000s, infected nearly 8,000 people and killed 10% of those in 26 countries before being eradicated. MERS-CoV is a camel common cold virus that continuously jumps into humans in the Middle East where it can cause severe disease. SARS-CoV-2, while bearing genetic similarity to SARS-CoV (and to a lesser extent to MERS-CoV, and also the common cold CoV 'HKU1') is considered a distant cousin only and thus 'novel'. SARS-CoV-2 is not SARS-CoV.

People with severe disease are more likely to be male, older and have significant other diseases, such as heart disease or diabetes

### **What are the clinical symptoms of COVID-19 in humans and how is it spread between hosts?**

COVID-19 was first picked up as a cause of severe viral pneumonia, with characteristic symptoms such as cough, fever and shortness of breath. More in-depth analysis revealed more symptoms in a smaller amount of people. Severe pneumonia can lead to a disease called acute respiratory distress syndrome, which is very hard to treat and can be fatal. People with severe disease are more likely to be male, older and have significant other diseases, such as heart disease or diabetes. It is thought that the majority of COVID-19 infections result in mild cold-like symptoms. We don't know how the virus was initially transmitted to humans but it is now capable of spreading from one person to the next. COVID-19 affects the lungs and is spread via the respiratory route via coughing, sneezing or contact between respiratory fluids containing viruses between people.

### **What makes a virus like this deadly?**

We don't really know the answer to this but likely it is a combination of multiple factors, such as the ability to infect cells deep in the lung and for the virus to evade our own immune system that is trying to clear it. Often, a major contributor to viral disease is the host's own immune response to infection that can sometimes cause most of

the symptoms. It doesn't help us that we do not have a vaccine nor any antiviral drugs against COVID-19.

### **There has been much talk about the $R_0$ of SARS-CoV-2. What does that mean and can you place it into the context of other communicable viral diseases?**

The  $R_0$  value of SARS-CoV-2 is hard to measure due to the challenge in identifying people who are infected but it has been estimated to be 1.4–3.8, which means that approximately three people could be infected for every infected person. This is a significant number as anything above an  $R_0$  of 1 means that the infection could sustain itself in the absence of any interventions. To put this number in context, the  $R_0$  values of other viruses are as follows: SARS-CoV 2–4, seasonal influenza 1.4–1.6 and measles 12–18. It is worthwhile to remember that  $R_0$  is an average and the variability could be large with most infections leading to zero new infections while the minority could pass on the most infection during so-called 'super-spreader' events. The goal of any strategy to control communicable diseases is based around driving the  $R_0$  to <1.

There are lots of different kinds of masks, some more effective at this than others, for example, some masks don't make a tight seal nor do they have an actual filter installed

#### **How far away might suitable diagnostics vaccines and antivirals be?**

Global governments, the WHO and authorities across the world are doing everything they can to stop the virus. Global responses include public health measures but also in the development of critical diagnostics, vaccines and antivirals.

Health interventions take time to develop until they are accurate, sensitive, safe and efficacious. This is especially true for viruses that we didn't really know existed nor cared about before December 2019. SARS-CoV-2 falls within this category. However, due to China's rapid sharing of the genome sequence of SARS-CoV-2, within weeks of discovery, researchers across the world had developed PCR-based diagnostics for the virus. Because of SARS and MERS, scientists have been testing antiviral drugs against these coronaviruses including SARS-CoV-2 and have already found some promising leads that are effective in cell culture and animal models. Some of these are being tested in clinical trials as we speak. Vaccines take longer and we have not developed a human coronavirus vaccine before, although we know how we might do that. Similar to antiviral drugs, thanks to SARS and MERS there has been

scientific interest and funding support for experimental coronavirus vaccine platforms, which can be focused now on SARS-CoV-2. This will likely take months to reach a human for safety and efficacy testing.

#### **How prepared is the UK for this pandemic?**

Prime Minister Boris Johnson published the UK's government's 27-page action plan for tackling COVID-19 on 3 March 2020, which is available and updated "<https://www.gov.uk/government/publications/coronavirus-action-plan>" here. However, given that the data are still emerging, we are still uncertain of the impact of the outbreak. In certain scenarios, up to one-fifth of employees may be absent from work during peak weeks.

The government has warned that because COVID-19 is a new virus, meaning the population lacks immunity, it has the potential to spread extensively. We are all susceptible to catching this disease and the UK will be significantly affected. The current plan details the stages of how the authorities would respond as infection spreads and the current thought is that the outbreak will escalate in April and peak in May or June, with a tapering from July and August.

#### **How effective have the Chinese government measures been in 'locking down' this outbreak (what have they done etc.)? How about travel bans – do they work?**

As we don't have a vaccine or antivirals against COVID-19 the only way to stop this outbreak from developing further is to block transmission, i.e. driving the  $R_0$  to below 1. After its experience with SARS and avian influenza outbreaks, China knows how devastating these epidemics can become and has taken strong measures to counteract the virus. As it appears many infections are spread when people have mild symptoms, there is significant transmission within the community. One way to stop transmission from this kind of infection is to prevent the interaction of infected people with non-infected individuals by encouraging social isolation and inhibiting transport within and between affected regions and countries, such as by applying travel bans, which is what we are seeing now in many countries. Travel bans can be effective in stopping transmission but may also hinder the response and can have economic and political costs associated. Only time will tell how effective these measures will be but the infection has already spread to many other countries across the world where local spread has begun.

#### **Is mask use outside of the clinical setting likely to have any effect?**

Yes and no but in reality probably not likely. Masks stop the inhalation/exhalation of small particles from your nose and mouth. There are lots of different kinds of masks, some more effective at this than others, for example, some masks

don't make a tight seal nor do they have an actual filter installed. Most masks you see people wearing are the former, less effective kind. To protect yourself you would likely have to wear even the good masks all the time, to change them very often, and remove them without accidentally infecting yourself. Outside of social isolation, which can be effective, there are better preventative measures that revolve around encouraging good hygiene practices, such as covering your mouth and nose when you sneeze and cough, and washing your hands regularly before touching your face.

#### **This is the third major coronavirus outbreak in the past two decades. How likely is it that we will see future outbreaks of novel coronaviruses?**

After SARS and MERS, COVID-19 is the third in 17 years. Likely other endemic human coronaviruses emerged in similar ways. We have to thus expect these outbreaks to be the norm and may even be increasing in frequency as the human population grows and we interact more with wild or farmed animals either through deliberate hunting and consumption or through environmental disturbance. Furthermore, there have been parallel outbreaks of zoonotic bat-borne coronaviruses in farmed pigs in Asia. This phenomenon is not restricted to coronaviruses either and there other emerging, zoonotic infections in humans and animals such as influenza from birds, Ebola, Hendra and Nipah from bats, and monkeypox viruses from rodents.

*China, Chengdu, Yinghui Rd. January 23, 2020: Coronavirus epidemic in China. People wearing face masks.*



# London's microbiota: pickle and preservation

**Martin Adams**

*SfAM President 2011–2014*

In 1819, two former school friends, Thomas Blackwell and Edmund Crosse, were apprenticed to a firm making pickles and sauces at premises in King Street near present-day Shaftesbury Avenue. They excelled to the extent that, 10 years later, they bought the business for £600 and the partnership, thereafter known as Crosse & Blackwell, came into being.



Substantial expansion began in 1838 with the purchase of the former residence of Lady Cornelys at 21 Soho Square. Socially speaking, Soho was an area in relative decline as the wealthy minor gentry moved westwards and craftsmen, manufacturers and tradesmen moved in to create a vibrant area of small businesses and domestic housing. In the 1850s, when the pioneering nurse Mary Seacole was moving into lodgings at 15 Soho Square, Crosse & Blackwell were acquiring and converting a number of surrounding

buildings spreading between Soho Square and Crown Street (now Charing Cross Road). In nearby Little Denmark Street, a building and yard were bought for the production and warehousing of jams, fruit preserves and confectionery. They established a vinegar brewery off the Caledonian Road, installing one of the largest vats of the time, holding 115,000 gallons (more than half a million litres), to supply their ever-growing needs. Wharves in Millwall and Battersea were acquired for the transport of ingredients and products.

In an era predating scientific understanding of microbial activity in food spoilage and foodborne illness, the company's product range was based largely on traditional recipes and an empirical approach to shelf life and stability. Today, food microbiologists would describe the pickles, sauces and jams they produced as examples of the hurdle concept of food preservation, where combinations of suboptimal factors such as reduced water activity, low pH and weak organic acids inhibit microbial growth and spoilage.

Understanding of the scientific basis of this approach came much later when the essential physiology of foodborne microorganisms was explored. Knowing how microorganisms respond to different environments allowed the development of quantitative predictive models as practical tools for formulating safe and stable foods. This really

began in the USA in the 1920s with Esty and Meyer's mathematical treatment of microbial inactivation in canning and has continued through to the current ComBase models describing both growth and inactivation under a variety of conditions. Along the way, formulas specifically predicting the composition of stable pickled products were also developed. The most elaborate of these, from the Unilever laboratories in the Netherlands, is known as the CIMSCEE code (the acronym deriving from the French title of the European Sauces Trade Association):

$$15.75 (\% \text{ undissociated ethanoic acid}) + 3.08 (\% \text{ salt}) + (\% \text{ hexose}) + 0.5 (\% \text{ disaccharide}) = \Sigma.$$

In the equation, each term represents one of the principal antimicrobial factors and their relative contribution. These are simply added together to give a value,  $\Sigma$ . Readers may recall that in *The Hitchhiker's Guide to the Galaxy*, the supercomputer 'Deep Thought' was asked the answer to the 'Ultimate Question of Life, the Universe and Everything'. After 7½ million years, it came up with an answer: 42. Well, for pickle and condiment makers, who admittedly may



have more limited horizons, the answer turns out to be 63. If, applying the CIMSCEE formula,  $\Sigma$  exceeds 63 then a sauce will be microbiologically stable without refrigeration, even after opening.

Relying on traditional empiricism, however, Crosse & Blackwell grew throughout the nineteenth century, supplying expanding urban markets and creating international brands. From the very beginning they were adept at promotion, obtaining a royal endorsement from Queen Victoria and employing celebrity cooks, starting with a former chef to Napoleon, Senor Qualiotti, who introduced several new products including, for Christmas 1832, 'Piccalilli'. The company also diversified its range to reflect the influence of the Empire with, for example, 'Captain White's Oriental Pickle' and 'Colonel Skinner's Mango Relish', and they acted as agents for Lea and Perrin's 'Worcestershire Sauce' – another product inspired by the Indian subcontinent. With the celebrity chef Alexis Soyer, they ventured into French cuisine including *inter alia* the intriguingly named 'Soyer's Sauce for Ladies'. The relatively new technology of canning was not overlooked, with the acquisition of the Bermondsey canning company founded by Donkin, Hall and Gamble, a salmon cannery in Ireland and production of a variety of thermally processed potted meats.

The problems of operating in central London eventually told and in 1921 the company began to move

manufacturing away from Soho Square to a former machine-gun factory in Branston, near Burton upon Trent – a move that inspired another new product, 'Branston Pickle'. In 1960, Crosse & Blackwell was acquired by Nestlé and is now owned by companies in Europe and the USA. The Branston brand is owned separately by a Japanese company.

Following the company's move to Branston, much of its existing property in the West End was sold off. A warehouse on Charing Cross Road was redeveloped, later becoming the site of the Astoria, a legendary music venue in the capital until its closure in 2009. Its subsequent demolition in the Crossrail redevelopment of Tottenham Court Road Station allowed Museum of London archaeologists the opportunity to conduct an excavation of the area, expertly described in a recent book (see further reading panel).

The excavation unearthed a cornucopia of food packaging from an era before plastics, including a variety of glazed earthenware and stoneware vessels, glass bottles and jars, lids and stoppers, as well as a few tin cans (fabricated locally in premises on Dean Street). Though many are quite decorative, sadly most will be relegated unseen to museum storerooms. Perhaps we should emulate Athens, where archaeological artefacts (admittedly older) are displayed at the local metro stations? I wait with bated breath for others to join me in a campaign to celebrate our illustrious pickling heritage more visibly. Bring out the Branston!

FURTHER READING

Jeffries N, Blackmore L, Sorapure D.  
*Crosse and Blackwell 1830–1921: a British food manufacturer in London's West End.* (Museum of London Archaeology, 2016)



# Parliamentary Links Day 2020

Tuesday 14 July 2020

**All events are postponed until further notice. This is an evolving situation and this page is therefore subject to review.**

Contact the RSB events team for further details at [events@rsb.org.uk](mailto:events@rsb.org.uk)





## Increasing the impact and reach of the biosciences

One of the things we often celebrate here at the RSB is the diversity of roles across the biosciences, and the undeniable impact of bioscientists and their work. We want to help others recognise that biologists occupy a wide range of roles and influence so many areas of everyday life, by no means restricted to academia or research.

We started the year by celebrating some of our Fellows who were recognised in the 2020 New Year's Honours List for their services to science – from medical research, to animal welfare, to radioactive waste management, this year's recipients really highlighted the breadth of disciplines within the biosciences.

Our second current-affairs style programme in partnership with ITN Productions is now online, which looks to capture how biology impacts everyday lives. Short films from organisations such as the University of Oxford, UWE Bristol and Karus Therapeutics tell different stories of how their biosciences work affects the wider world. You can find the programme over on our YouTube channel – be sure to check out some of the amazing work these organisations do.

We recently launched our new Industry Skills Certificate, designed to support the employability of scientists who wish to move from other areas into industry. The certificate recognises skillsets such as programming, quality management, training delivery and leadership, and is designed for anyone who wishes to kick-start a career in

industry. Moving into industry can seem like a big leap, but with this certificate, biologists, including SfAM members, should feel more confident in making the transition.

We've also launched our new Apprentice of the Year award, in recognition of bioscience apprentices who demonstrate the impact apprentices can make within the bioscience sector. Apprenticeships increase the accessibility



Children celebrating at the Education Awards Ceremony

**Mark Downs** CSci FRSB

Chief Executive of the Royal Society of Biology



of the sciences for those who don't pursue more traditional routes into science, bringing new minds and a greater diversity of talents into the sector. Nominations close at the end of March, so do consider putting forward the names of any apprentices you think deserve recognition.

One of the benefits and strengths of our diverse membership base, including SfAM and our other membership organisations (MOs), is the expertise upon which we can draw when developing policy positions and offering advice to government. To increase accessibility to our bioscience-related policy outputs, we've launched our new Policy Resource Library, which includes over 800 documents produced by the RSB and MOs, including SfAM. We hope the platform becomes a one-stop shop for those working or interested in exploring biosciences policy.

As always, we are seeking to inspire the bioscientists of the future – in 2019, our outreach and engagement team spoke to more than 10,000 people, attending numerous events often in partnership with SfAM and other members of the Outreach and Engagement Working Group.

The RSB team has already kicked off their 2020 calendar of events, spending a weekend in February at the Suffolk Science Festival and delivering activities on plant health, marine plastics and anatomy. The team are always looking for volunteers to get involved and help deliver their events; details of the schedule is on the RSB website.

Our anniversary year celebrations began last October, and since then, we have seen a flurry of activity as we celebrate 10 years of the Society in its current form, and the 40 years of its Royal Charter. These activities would not be possible without the generous support of our sponsors, including SfAM, who is one of our valued Anniversary Partners.

As part of our wider anniversary celebrations, we'll be highlighting the diversity of bioscientists' roles with our *Pioneers of Biology* talk series. Delivered in partnership with our branches, we'll be running a series of talks on some truly influential bioscientists of our time, and the impact they have had on society. Our first event, held as part of the Northern Ireland Science Festival in February, was all about medic and engineer duo Professor Frank Pantridge and Professor John Anderson, who developed the portable defibrillator.

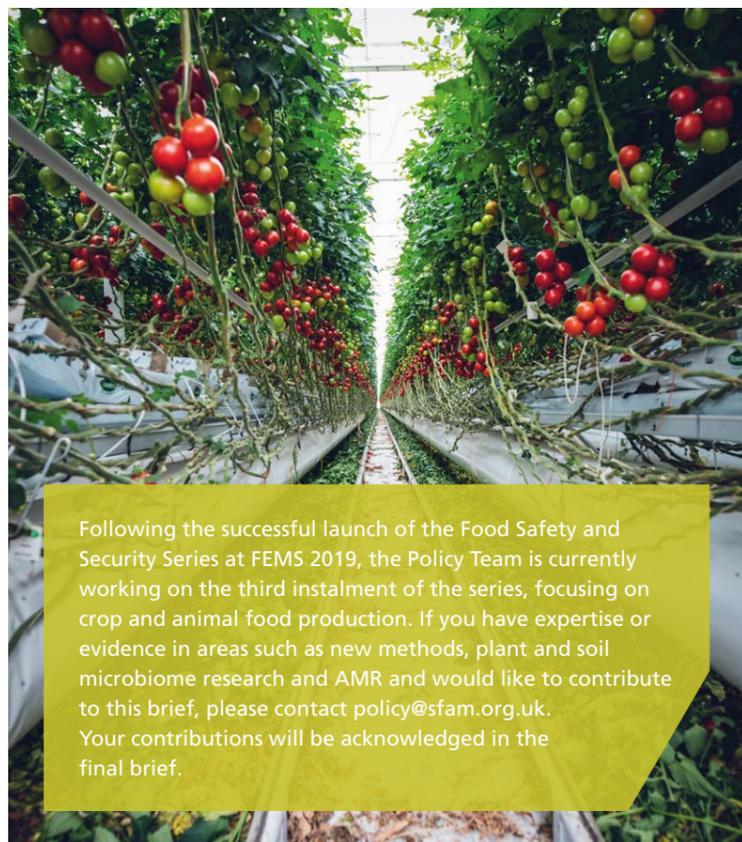
This month we had our Anniversary Gala Dinner, and celebrated the lifetime achievements of our Honorary Fellow Sir David Attenborough CBE Hon FRSB, with a keynote also from Sir Paul Nurse FRS Hon FRSB. Both of these individuals have had an enormous impact on the biosciences community and we are grateful that both are honorary fellows of the RSB.

The rest of the year will continue to be busy – upcoming dates for your diary include our annual Voice of the Future event held at Westminster on 10 March, our AGM on 6 May, and a whole host of other events up and down the country. Please join us as we continue to celebrate the biosciences as a whole, and share the impact our diverse and wide-reaching sector has across all walks of life.



Teacher of the Year  
**Gemma Singleton**





Following the successful launch of the Food Safety and Security Series at FEMS 2019, the Policy Team is currently working on the third instalment of the series, focusing on crop and animal food production. If you have expertise or evidence in areas such as new methods, plant and soil microbiome research and AMR and would like to contribute to this brief, please contact [policy@sfam.org.uk](mailto:policy@sfam.org.uk). Your contributions will be acknowledged in the final brief.



### Equality, Diversity and Inclusion in Science and Health

We are thrilled to announce that we are now a member of Equality, Diversity and Inclusion in Science and Health (EDIS). EDIS is a powerful coalition of 17 organisations that aims to advance Equality, Diversity and Inclusion in Science and Health. To find out more visit our ED&I activities page on the SfAM website.

Society for Applied Microbiology
Science notes for policy 1 November 2018

THE CHANGING ENVIRONMENT
PRESERVING & PROTECTING OUR OCEANS

## The marine microbiome

# Marine microbiology campaign

Following the success of our Marine Microbiome Briefing in 2018 and ahead of the UN Decade of Ocean Science, the SfAM policy subcommittee is embarking on a new marine microbiology campaign for 2020 – Marine Microbes Matter. If you are interested in getting involved in the Marine Microbes Matter campaign, contact the SfAM policy team ([policy@sfam.org.uk](mailto:policy@sfam.org.uk)).

**Further information**

If you are interested in learning more about the Society's policy work and want to get involved, get in contact with the SfAM policy team.

[policy@sfam.org.uk](mailto:policy@sfam.org.uk)



# Plant–Microbe Interactions

COMING SOON



**All events are postponed until further notice. This is an evolving situation and this page is therefore subject to review.**

Plants interact in a variety of ways with microorganisms, whether through symbiotic associations leading to environmentally specific fitness benefits or biotic insults orchestrated by pathogens. Plants have evolved a myriad of complex and highly coordinated mechanisms to deal with such interactions, which will be the focal point of the 2020 Plant–Microbe Interactions meeting. This event will take a comprehensive view of the multidisciplinary field of Plant–Microbe Interactions, to demonstrate how it offers solutions to fundamental questions in biology and provides potential applications in agriculture, biotechnology, and conservation.

This one-day event will be of interest to microbiologists and plant scientists addressing questions relating to the plant microbiome, co-evolution or the improvement of plant traits through microbial-mediated means, in either an academic or industrial setting.

The programme offers a range of diverse topics to highlight the breadth of research emerging from this exciting field. The event will include a poster session and a commercial exhibition offering excellent opportunities for networking.

**SfAM and SfAM ECS Members who wish to present a poster must submit an abstract via the website. Successful presenters will have their registration fees covered and up to £100 toward travel expenses.**

Non-members	£250	(£200 early bird*)
SfAM members	£150	(£120 early bird*)
SfAM ECS poster presenters REG FEES COVERED		

\*See our website for further details

For further details, abstract submission and registration information please visit [sfam.org.uk](http://sfam.org.uk)





A method to evaluate factors influencing the microbial reduction in domestic dishwashers.

Brands B, Schulze Struchtrup S, Stamminger R, Bockmühl D. (2020), A method to evaluate factors influencing the microbial reduction in domestic dishwashers. *Journal of Applied Microbiology* 2020 doi:10.1111/jam.14564.

Available from

<https://sfamjournals.onlinelibrary.wiley.com/doi/epdf/10.1111/jam.14564>

Since many infections are foodborne and acquired within the domestic setting, the hygienic cleaning of dishes that have probably been in contact with pathogens is highly important. While the dishwasher thus might serve as an efficient means to remove germs, there have also been reports on the survival of microorganisms in automated dishwashing and of microbial communities in dishwashers for household use. However, no cases of infection via dishwashers have been reported so far. There are standards to determine the cleaning performance and energy use of dishwashers and others that regulate the minimum reduction needed in commercial-use dishwashers, but to

date, there is no standard method to determine the microbial reduction in domestic appliances. The current study does not aim to fix a minimum microbiological reduction for household dishwashers, but rather tries to deliver a method to measure the reduction achieved by a certain dishwasher programme or dishwasher. Therefore it will provide a possibility to directly compare the hygienic performance of dishwasher programmes and to identify possibly critical cycles. As a consequence, the findings can be used to find a balance between the needs for lower energy and water consumption and the necessity for a certain level of hygiene.

**Dirk Bockmühl**

Rhine Waal University of Applied Sciences, Kleve, Germany



The home clinic or All in a day's work of Dr. Fics.

Timmis, K. The home clinic or All in a day's work of Dr. Fics. *Microbial Biotechnology* 2020; 13, 3–10

Available from

<https://sfamjournals.onlinelibrary.wiley.com/doi/epdf/10.1111/1751-7915.13520>

Telemedicine has been extensively discussed as a means of improving key issues of healthcare, namely access, equity, quality and cost-effectiveness, in both developed and developing countries ([https://www.who.int/goe/publications/goe\\_telemedicine\\_2010.pdf](https://www.who.int/goe/publications/goe_telemedicine_2010.pdf)).

More recently, the role of computation and artificial intelligence in patient data acquisition, handling and diagnosis has gained traction and the potential for do-it-yourself medicine as a health system complement/component for the primary healthcare setting has been explored. Central to the effective exploitation of telemedicine in general, and DIY in particular, is the discovery and application of new health- and disease-relevant biomarkers, the development of easy-to-use molecular diagnostic tests and instruments, and the creation of a coherent informatic framework that integrates robot-assisted patient interrogation/diagnosis procedures and prophylaxis/therapy recommendations, with existing patient records and advanced diagnostic algorithms in a national data analytics centre, and with existing clinical services.

In this humorous, forward-looking article on the future home clinic, served by the remote, online clinical robot, Dr. Fics (fourth-generation interactive clinical server) and complemented by same-day home deliveries of diagnostic, prophylactic and therapeutic materials, some plausible routine diagnostic options are explored, including automated sampling, sample work-up and analysis by a Personal Health Station (PHS). In the case of the PHS described, a smart lavatory, which can carry out a wide range of biomarker analyses in urine and faeces, including pathogen detection and faecal microbiota profiling, the emerging association of gut microbiota and mental/stress disorders, and conceivable remedies, are discussed. Finally, the issue of patient perceptions of interactions with a robot *vis-à-vis* a human physician is explored.

**Ken Timmis**

Technical University Braunschweig, Germany

## Seeing the world with microbial eyes

**Mark O. Martin**

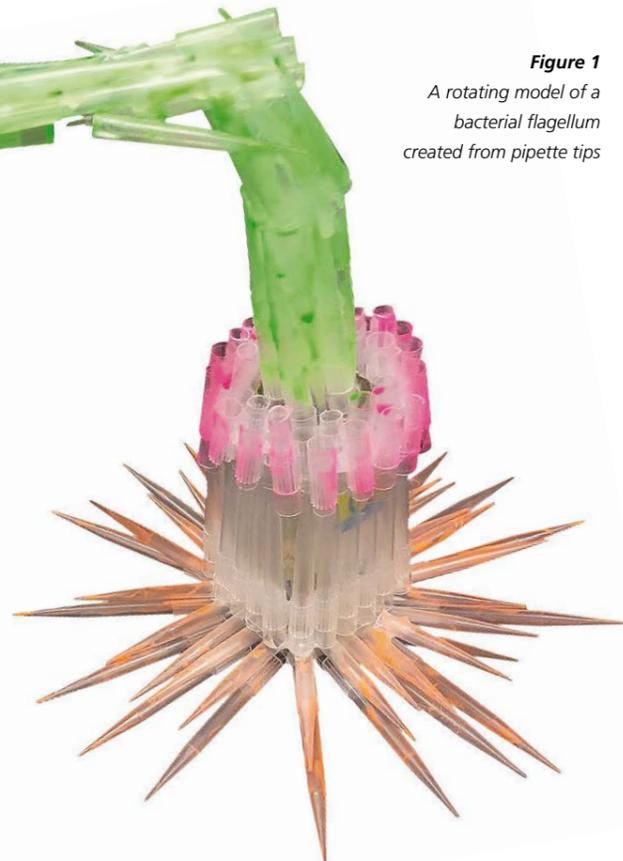
University of Puget Sound, Tacoma, Washington, USA

Most of my life, I have adored the microbial world. A tattoo on my right forearm reads 'Avete parvuli Domini' in Latin, or 'All hail the small masters'. Thus, it is a dream come true for me to promote what might be called 'microbial centricity' to my students at the University of Puget Sound here in Tacoma.

My institution is an undergraduate-only university; we graduate perhaps 50 seniors a year. Our classes are small and collaboration between students – I call mine #Micronauts – and professors is valued greatly. Still, I am the only person teaching microbiology at my institution. Just one course, taught once per year. I only get that one opportunity to convince my students of the centrality and wonders of the microbial world.



**Figure 2**  
A cartoon illustrating the microbiology of *Thiomargarita*



**Figure 1**  
A rotating model of a bacterial flagellum created from pipette tips

Over the past decade or so, I have been using a number of unusual approaches to hook students into seeing their world with 'microbial eyes'. I find that allowing students to be creative in their approaches not only enriches my classroom, but improves ownership, enthusiasm and concept retention. Let me share some examples.

In every exam, I allow students to earn points by creating a cartoon that illustrates a specific concept we have discussed in class. As you can see in Figure 2, this can yield solid pedagogical benefits; the student-artist clearly retained the fact that *Thiomargarita* (despite its large size) has a small cytoplasmic volume and a large internal compartment containing nitrate for anaerobic respiration. The humour is just a bonus.

Not all students are creative in terms of drawing or painting. I often ask students to create microbial haikus. Figure 3 shows the value of this approach, with the student squeezing the overall concept of arabinose operon regulation into a 5:7:5 structure!

Even the modern mania of memes can be harnessed to encourage student learning, as you can see in Figure 4. It is rewarding for me to see that concepts I discuss in class are within the brains of my students, and not just trivial jokes but solid concepts! Given their creativity and enthusiasm, I am not surprised.

I also work hard to explore with my #Micronauts the, um, inaccurate ways that microbes are portrayed in the popular media, creating a lens of 'angel', 'devil' and 'indifferent' microbes as can be seen in Figure 5. This helps students to think critically and they often send me sample articles that

fit one of these categories. I even discuss the silliness of what I term #SwabStories that describe items in everyday life as teeming with 'germs' (as if we are all not moving through a sea of microbes at all times).

Finally, I encourage my students to explore some aspect of microbiology from our course creatively. I have seen #Micronauts produce amazing videos, poems, paintings, sculptures and other wonders each time I teach. For example, a student modified the stage play *Thoroughly Modern Millie* to *Thoroughly Modern Microbes*, complete with many concepts from class. Figure 1 is a rotating model



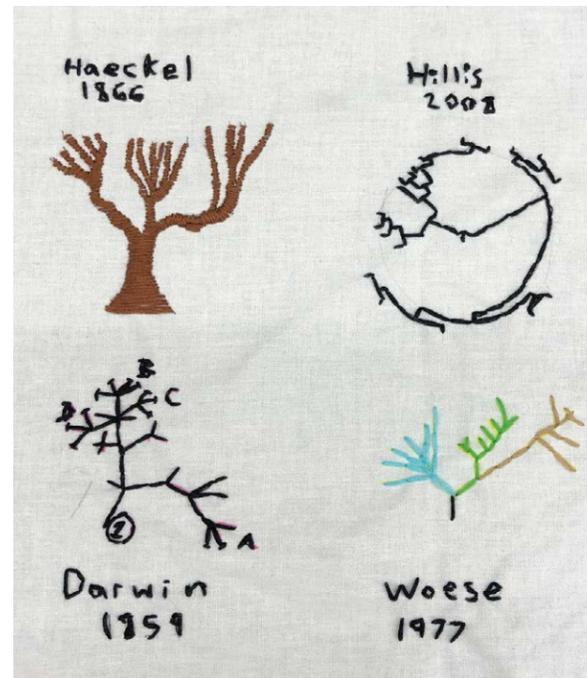
**Figure 4**  
A microbial meme

**Figure 3**  
A microbial haiku poem

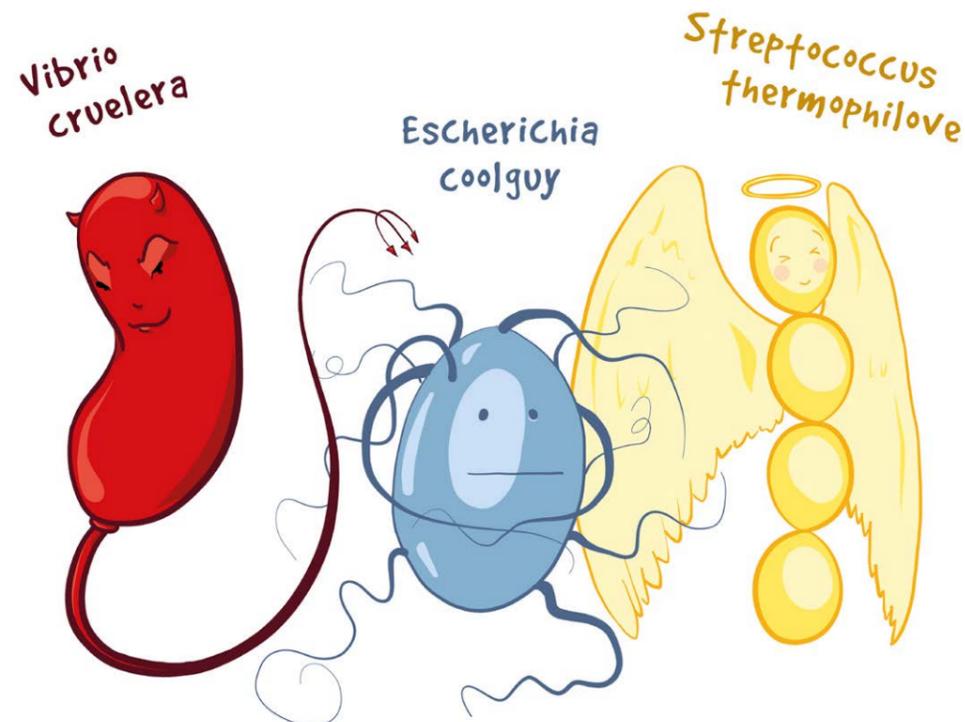
of a bacterial flagellum created from pipette tips (the artist lamented there was not an internal channel in the filament through which pipette tips could travel to self-assemble at the tip!). Figure 6 shows a lovely bit of needlepoint illustrating how views of phylogeny have changed, primarily because of microbial giants such as Carl Woese.

I encourage any and all readers to try this approach with their own students, at any stage. For me, the key to learning is engagement, enthusiasm and hard work. Ownership assists with all of these. I usually scaffold the student efforts so that each #Micronaut has time to think, consider and re-evaluate their work (and make certain that their masterpiece does indeed mesh with course concepts); I also encourage students to discuss their projects with one another. Collaboration is key to effective education.

I have an office and laboratory filled with wonderful microbial artefacts to cheer my days. But what is more rewarding is the certain knowledge that those students finished my course with an appreciation not just for the facts of microbiology, but the feeling of microbial wonder that drives us all.



**Figure 6 (above)**  
Needlepoint illustrating changing views of phylogeny



**Figure 5 (left)**  
Exploring how microbes are portrayed in the popular media via pictorial versions of 'angel', 'devil' and 'indifferent'

I have been using a number of unusual approaches to hook students into seeing their world with 'microbial eyes'

# WH PIERCE PRIZE

## Nominations are now open



This prestigious prize is awarded each year to a microbiologist who has made a substantial contribution to the science of applied microbiology. It is worth £6,000.

The award was instituted in 1984 by the directors of Oxoid to commemorate the life and works of the late WH (Bill) Pierce, former Chief Bacteriologist of Oxo Ltd and a long-time member of the Society. Application is

through nomination by members of the Society only. To nominate a candidate, members should log in to the website and use the form to submit a name. The recipients do not have to be existing SfAM members.



## Happy 100th Birthday to NCTC

NCTC has been in operation for 100 years, surviving a world war, six relocations and acute financial hardship. Nevertheless, the collection is thriving and making a significant contribution to our understanding of infectious diseases and how to overcome them.



NCTC holds nearly 6,000 historically and microbiologically significant live bacterial strains, most of which have caused infections in humans or animals. Scientists from around the world have come to NCTC for 100 years to request cultures of strains, and more recently extracted DNA, so they can undertake tests and mine the associated data. The collection has always captured the imagination of the people who look after it and keep it relevant, and the scientists who contribute to it range from less well-known microbiologists to world-famous Nobel Prize winners.

NCTC was established in 1920 to 'provide a trustworthy source of authentic bacteria for use in scientific studies'. We can speculate as to whether the founders knew that the collection would hold answers to so many scientific questions over the next 100 years or imagine that the strains would be used so widely in fields such as drug discovery, vaccine development and method advancement. NCTC cultures are now a mainstay in ensuring results from

clinical diagnostic microbiology tests are accurate and internationally comparable.

The bacteria held in NCTC provide windows into the past, as well as providing data for present scientists to deliver benefits for people's health and well-being. The NCTC type strains are arguably the collection's most important strains because they are the first isolates of a new species that every other strain of the species will be compared against. The names of new species must be published in the *International Journal for Systemic Bacteriology*, together with a strain description and designation of the type strain. There are nearly 1,000 type strains in NCTC, and many new type strains are deposited every year.

The history of NCTC reflects changes in taxonomy, nomenclature and identification. Traditionally NCTC curators made a major contribution to international proceedings for bacterial nomenclature and taxonomy. Routine identification of bacteria in the early 20th century was from morphological and biochemical tests, later supplemented by serotyping and antimicrobial susceptibility patterns. By the 1960s, NCTC scientists led the field in numerical (computer) taxonomy used to determine the degree of similarity between different bacteria using a wide spectrum of tests. During the 1970s gas-liquid chromatography (GLC) was explored to assess bacterial metabolites and compare differences between different species.

The 1980s hailed the development of enzyme analysis and molecular identification using gel electrophoresis methods to separate nucleic acids. By the 1990s 16S ribosomal RNA sequencing was being introduced and methods such as PCR and amplified fragment length polymorphism (AFLP) analyses followed later. To date, the most important development in the 21st century resulted from a successful collaboration between NCTC and the Wellcome Sanger

**Established in 1920, the UK's National Collection of Type Cultures is one of the longest established collections of medically relevant microorganisms in the world. It is a global provider of authentic bacterial strains and associated biological materials to the international biomedical, research and control community.**

<p><b>Products</b></p> <ul style="list-style-type: none"> <li>Over 5500 strains of bacteria including historic, contemporary and antimicrobial resistant isolates</li> <li>Strains specified by quality control guidelines such as EUGAST and UK Standards for Microbiology Investigations</li> <li>Many strains with whole genome sequence data, phenotypic data and isolation metadata</li> <li>Bacteria available as pure live cultures or as DNA extracts</li> <li>An expanding collection of bacteriophage</li> </ul>	<p><b>Services</b></p> <ul style="list-style-type: none"> <li>Contract freeze-drying</li> <li>Active accessioning of bacteriophage and bacterial strains of medical significance</li> <li>Bespoke DNA and LENTICULE Disc production</li> <li>A recognised collection that supports the description of novel bacterial species</li> <li>Safe and patent depositing</li> </ul>
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Institute, that ran from 2013 to 2018 and delivered long-read whole-genome sequence data for more than 3,000 NCTC strains, including most of the type strains preserved in the collection at that time. This genomic data is freely available and will be mined by microbiologists and bioinformaticians for years to come. NCTC scientists are currently using genome sequence data in conjunction with proteomic analysis techniques to gain insight into the mechanisms of antimicrobial resistance in *Neisseria gonorrhoeae*.

The teams operating NCTC over the past 100 years have always been dedicated to using new technologies to create innovative means for scientists to interact with the collection. In addition to advances in microbiology, this also includes the application of newer communication technology, digital imaging and social media. We create networks of scientists and scientific communicators, engage with programmes like British Science Week to spread the message about the value of collections like NCTC, and work with artists and writers to raise awareness of what we do, and why. NCTC is committed to developing global relationships to help meet 21st century challenges to people's health and to create new commercial opportunities to help assure the collection's continued longevity.

The future looks bright as we move into NCTC's second century of providing 'authentic bacteria for scientific studies'.



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# The latest news, views and microbiological developments

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## Cherwell delivers bespoke environmental monitoring solutions

Cherwell Laboratories has been providing bespoke solutions for microbiological environmental monitoring and control for over 30 years. Many of these innovations have become standard requirements for the pharmaceutical and medical device industries. The most obvious of these include the now ubiquitous irradiated triple wrapped agar contact plate in its many forms and variations.

Prompted by an increasing concern from regulatory inspectors and internal quality assurance professionals, the increased emphasis on risk assessment and consequent risk reduction in aseptic manufacturing has required many small changes to accepted best practice. The latest type of project to make this transition from single customer enquiry to routine industry demand is the Cherwell settle plate stand.

The risk from settle plates on the floor are several and the consequences of stepping on an agar plate include:

- Personal injury – slips and falls
- Contamination of wider surfaces with agar residue
- Loss of essential monitoring data

In addition, there is the concern about the 3 dimensional location of settle plates in relation to the risk assessment of process contamination.

Cherwell laboratories now routinely supply all stainless steel stands for one or two settle plates in a range of heights from 115 to 1000mm.

For more information visit [www.cherwell-labs.co.uk](http://www.cherwell-labs.co.uk) or to discuss your environmental monitoring requirements email [sales@cherwell-labs.co.uk](mailto:sales@cherwell-labs.co.uk) or call +44 (0)1869 355500.

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## A new chapter in media and sample preparation

Don Whitley Scientific (DWS) announced recently that they will be the new UK distributors of Alliance Bio Expertise (ABE) media and sample preparation equipment.

### New and innovative designs

The ABE range includes two sizes of media preparators (MEDIWEL 10 and 30), a diluter (DILUWEL), pourer stacker (DISTRIWEL), peristaltic pump (DOSYWEL) and homogeniser (MIXWEL). Intuitive, sturdy, reliable and providing full traceability, this equipment automates



some of the most tedious tasks that lab technicians have to undertake on a daily basis.

### Benefits of buying from DWS

As well as providing other products for laboratory use, DWS has service support that is second to none, with a team of ABE-trained service engineers located throughout the UK. All DWS engineers carry a comprehensive range of spare parts to endeavour to perform a first-time fix to reduce downtime.

UKAS validation and calibration is also offered on a variety of heat sterilisation equipment, temperature controlled processes and temperature indicators.

Automated media and sample preparation devices have always been one of our staple areas and this new chapter with ABE provides our customers with a quality range of laboratory products. A full range of equipment is available for demonstrations and trials.

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## GENETIC PCR SOLUTIONS™

An outbreak of pneumonia, epidemiologically linked to the Huanan Seafood Wholesale Market in Wuhan, was notified to WHO on 31-Dec-2019 by the Chinese Health Authorities. SARS-CoV, MERS-CoV, avian influenza, influenza and similar viruses were ruled out.

Chinese scientists were able to isolate a novel coronavirus, named COVID-19 by the WHO, on 7-Jan-2020 and a first genome was provided. The COVID-19 is a  $\beta$ -CoV of group 2B with at least 70% similarity in genetic sequence to SARS-CoV.

A week later, scientists from Germany, Hong Kong, and China (CDC) developed two multiplex PCR protocols (ORF1ab and N gene) designed to detect COVID-19. Because only a single genome was available, the assays are also reactive to SARS-CoV and bat SARS-like coronavirus.

As of 19-Jan-2020, 13 other genome sequences from 6 different labs were released on to GISAID. Our laboratory, Genetic PCR Solutions™ (GPS™), analysed the set of data and designed primers and probe fully specific for this new coronavirus. The real time PCR (qPCR) was adapted to our innovative MONODOSE format, single PCR reaction tubes which contain all reagents (dehydrated) to which only

samples need to be added. To our knowledge, launched at the end of January, this is the first COVID-19 qPCR kit commercially available.

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## Halophiles from the world's oldest salt mine and a strain with plant-pathogen control potential now available from NCIMB

Recent additions to the National Collection of Industrial, Food and Marine Bacteria include three moderate halophiles and a strain with potential as a biocontrol agent.

Moderate halophiles NCIMB 15224 *Aquisalibacillus elongatus*, NCIMB 15225 *Salinicoccus sesuvii* and NCIMB 15226 *Halomonas aquamarina*, were all isolated from saline soil of the Khewra salt mine in Pakistan, and deposited at NCIMB by scientists from the Fatima Jinnah Women University. The Khewra salt mine, reported to be the oldest salt mine in the world, is known for production of pink Khewra salt. Salt mines are a popular destination for microbiologists with an interest in industrial biotechnology, as halophiles have recently been the focus of interest as a low-cost platform for bioprocessing.

NCIMB 15235 *Serratia inhibens* was isolated from a potato rhizosphere and deposited in the NCIMB collection by scientists from the University of Copenhagen. A draft genome sequence has been published in Microbiology Resource Announcements. The authors state that the application of rhizosphere biocontrol bacteria to control plant-pathogenic fungi is an alternative approach to the use of chemical agents, and that the genomic data provide insight into the genetics underpinning the activity of this strain. For more information about purchasing any of our strains contact [enquiries@ncimb.com](mailto:enquiries@ncimb.com) or visit our website [www.ncimb.com](http://www.ncimb.com).

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