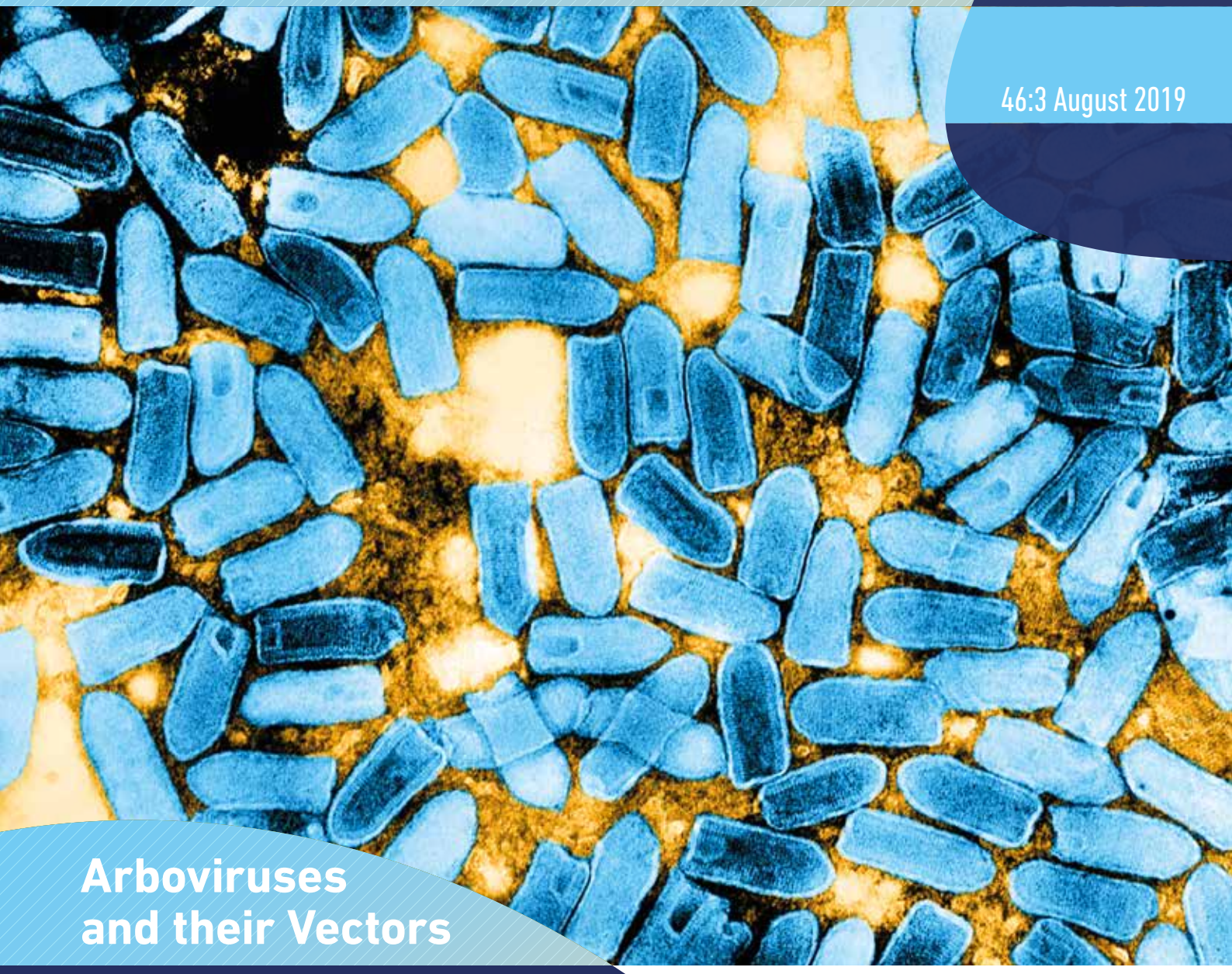
Microbiology TODAY

46:3 August 2019



Arboviruses and their Vectors

Plant arboviruses: major threats to food security
Crimean-Congo haemorrhagic fever virus
Dengue: a self-limiting acute disease
Wolbachia – applications of an antiviral bacterium
Engineering transgenic mosquitoes to prevent disease transmission

MICROBIOLOGY SOCIETY

Editorial

The impact of arboviruses on the world cannot be underestimated, and recent outbreaks caused by arboviruses such as the Zika virus have raised public awareness of their importance. This group of viruses transmitted by arthropods are able to infect plants, animals and humans, and are found in a wide range of arthropods distributed across the globe. In the August edition of *Microbiology Today* our authors address the diseases caused, diagnostic tests available and the treatments used, as well as highlighting some of the cutting-edge research moving our understanding of arboviruses forward.

Whole Picture

Starting with a look into food security, John Carr, Ken Fening, Paul Kuria, Alex Murphy, Josiah Musembi Mutuku, Jane Wamaitha Mwathi and Mildred Ochwo-Ssemakula explain why crop-based agriculture is vulnerable to arbovirus infection. A vast range of arboviruses are capable of infecting plants; this means that virtually all crops are vulnerable to attack. The control of these viruses has traditionally been through vector-based control and the use of insecticides; however, with the rise of resistant vectors and new restrictions on insecticides, it is unclear how crop productivity will be affected. An alternative method of protecting plants has been through the genetic modification of plants, to contain virus-resistant genes. Although effective, there has been limited use of these techniques, and John's team explore the possibilities for using natural vector deterrents emitted by plants.

Moving from plants to people and to a disease identified by the World Health Organization as an under-researched pathogen, Roger Hewson provides us with an insight into Crimean-Congo haemorrhagic fever. Spread by ticks and having originally been isolated and identified in two separate places (hence the name), this virus can be transmitted between humans once they are infected, giving rise to potential outbreak situations. Roger provides insight into research focused on improving diagnostics and also investigating the potential for vaccines.

Another arbovirus with a substantial impact on human health is the dengue virus – found in tropical and sub-tropical regions across the globe. Although often self-limiting, the virus can cause a severe form of disease thought to be related to cross-reactivity between different dengue viruses. Kevin Maringer explains how this cross-reactivity impacts disease severity and complicates vaccine development. With no specific treatments currently available, research into the disease-carrying mosquitoes might be a route by which disease transmission could be reduced in the future.

When thinking about the control of virus transmission through mosquito vectors, the abilities of the antiviral bacterium *Wolbachia* are of great interest. Ewa Chrostek provides an insight into how these insect-associated bacteria have potential to protect mosquitoes from virus infection and in doing so break the cycle of virus transmission and disease. The ability of *Wolbachia* to increase its frequency within a population as well as decrease vector susceptibility to virus infection are some of the reasons why *Wolbachia* is being used in field trials across the globe.

The potential benefits of another arbovirus control strategy – this time involving the use of genetically modified mosquitoes – is illustrated by Christine Reitmayer, Priscilla Tng and Luke Alphey. Explaining how population suppression or modification can be used to reduce the transmission of disease, they suggest possible targets for modification and highlight the challenges associated with this sort of strategy.

The Comment piece by Rennos Fragkoudis and Barry Atkinson discusses the global impact of arboviruses and how they have helped shape history. Touching on the variety of factors which have changed and continue to alter the range and impact of arboviruses, the authors give us an insight into the dynamic nature of these microbes and the complications involved in predicting what might come next.

Rowena Jenkins
Editor
r.e.jenkins@Swansea.ac.uk

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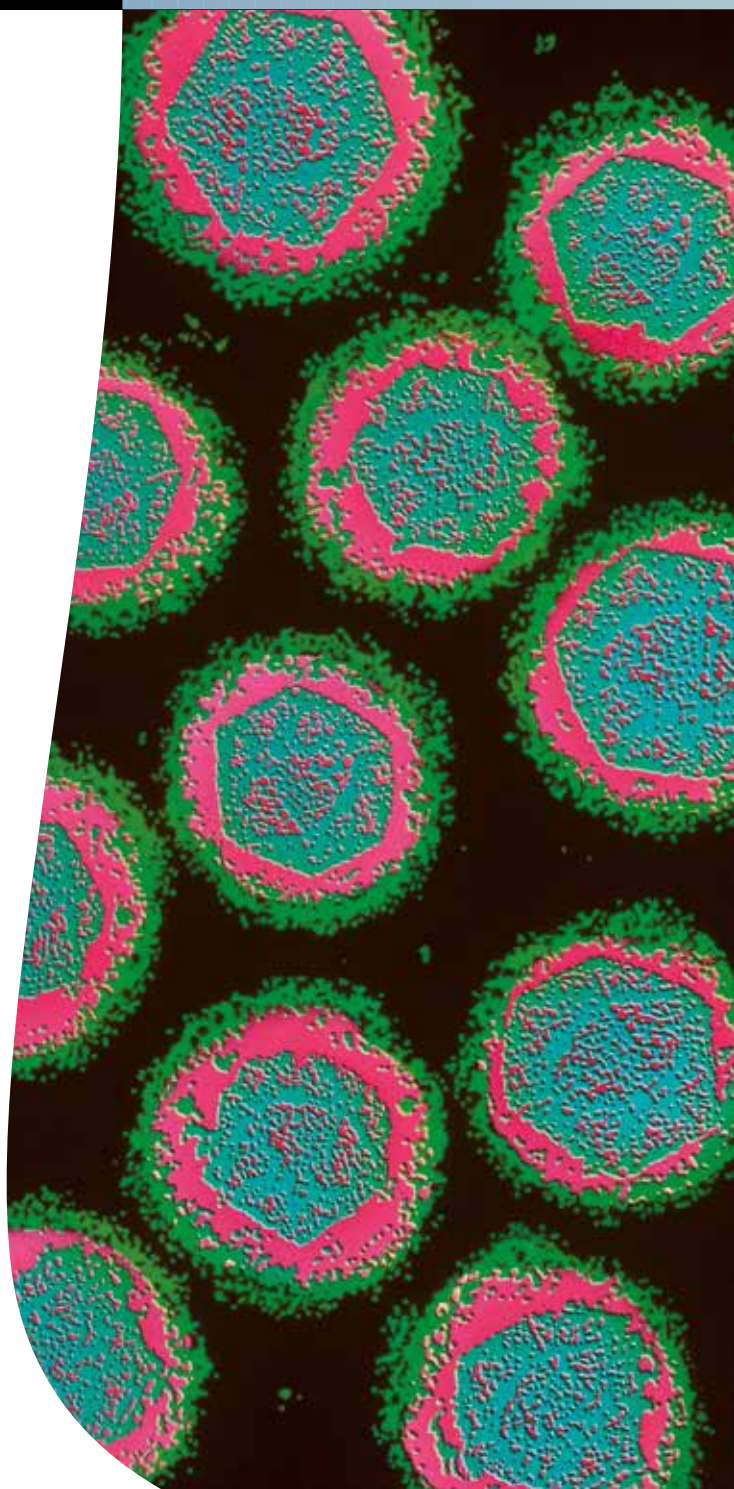

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Features

Regulars

Address **Microbiology Society, Charles Darwin House, 12 Roger Street, London WC1N 2JU** T **+44 (0)20 7685 2683** E **mtoday@microbiologysociety.org**
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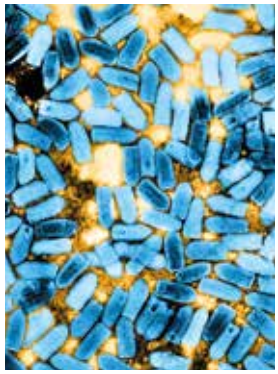

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Negatively-stained transmission electron micrograph showing the presence of numerous negative-sense, single-stranded RNA vesicular stomatitis virus (VSV) virions. Science Source/Science Photo Library

MICROBIOLOGY SOCIETY

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Department of Biochemistry, University of Oxford, South Parks Road, Oxford OX1 3QU; **president@microbiologysociety.org**

General Secretary – Professor Maggie Smith

Department of Biology, Wentworth Way, University of York, York YO10 5DD; **maggie.smith@york.ac.uk**

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School of Biological Sciences, Faculty of Biology, Medicine and Health, Manchester Academic Health Science Centre, Michael Smith Building, University of Manchester, Manchester M13 9PT; **i.s.roberts@manchester.ac.uk**

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School of Molecular and Cellular Biology, University of Leeds, Leeds LS2 9JT; **n.j.stonehouse@leeds.ac.uk**

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The Roslin Institute, Easter Bush Campus, Edinburgh, Midlothian EH25 9RG; **amy.pickering@ed.ac.uk**

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Policy Committee – Professor Paul Kellam

Imperial College London, Faculty of Medicine, St Mary's Campus, Norfolk Place, London W2 1PG; & Kymab Ltd; **p.kellam@imperial.ac.uk**

Professional Development Committee – Dr Tadhg Ó Cróinín

Health Science Centre, University College Dublin, Belfield, Dublin 4, Ireland; **tadhg.ocroinin@ucd.ie**

Publishing Committee – Professor Jodi Lindsay

Institute of Infection and Immunity, St George's, University of London, Cranmer Terrace, London SW17 0RE; **jlindsay@sgul.ac.uk**

Scientific Conferences Committee – Professor Mick Tuite

School of Biosciences, University of Kent, Canterbury CT2 7NJ; **m.f.tuite@kent.ac.uk**

Elected Members

Professor David J. Blackbourn (Chair of Equality, Diversity and Inclusion Ambassadors)

The School of Biosciences and Medicine, 14 AX 01, Edward Jenner Building, Faculty of Health & Medical Sciences, University of Surrey, Guildford, Surrey GU2 7XH; **d.blackbourn@surrey.ac.uk**

Professor Deirdre Devine

School of Dentistry, University of Leeds, St. James' University Hospital, Leeds LS9 7TF; **d.a.devine@leeds.ac.uk**

Professor Charles Dorman

Department of Microbiology, Moyne Institute of Preventive Medicine, Trinity College Dublin, Dublin 2, Ireland; **cjdorman@tcd.ie**

Dr John Morrissey

School of Microbiology, University College Cork, Ireland; **j.morrissey@ucc.ie**

Professor Tracy Palmer

Centre for Bacterial Cell Biology, Baddiley-Clark Building, Medical School, Newcastle University, Newcastle upon Tyne NE2 4AX; **tracy.palmer@ncl.ac.uk**

Professor George Salmond

Department of Biochemistry, Hopkins Building, University of Cambridge, Tennis Court Road, Cambridge CB2 1QW; **gpcs2@cam.ac.uk**

From the President

A key part of science is networking, to aid collaboration, broaden knowledge and engage with others in your field. I hope you can take advantage of the range of ways the Society enables you to build your network. Annual Conference in April is a hub of activity where you can meet with others, as is the ECM Forum Summer Conference in June, and the Society supports and runs a number of other events throughout the year which you can take part in and where you can showcase your research.

The annual Focused Meeting series, which this year started in June, features events on specific areas of microbiology. The upcoming events in September and October are on arboviruses and their vectors, microbes in medicine, and antimicrobial drug discovery from traditional and historical medicine. Find out more about these events on page 130. In September we will also celebrate the achievements of our Young Microbiologists of the Year as part of our Annual General Meeting, which you are invited to attend. Information about the finalists can be found on page 133.

The Federation of Infection Societies Conference 2019, which the Society is hosting this year in Edinburgh, collaborating with 16 societies, is another fantastic opportunity to showcase your research if you work in infectious disease and clinical microbiology. Read more about this event on page 132. The Society is also organising an event with the Healthcare Infection Society to build links between academics and clinicians.

My Roadshow events will be in Dublin in October, and Plymouth and Reading in November. These events bring microbiologists together in their local area to meet other members and Society staff and learn about forthcoming Society activities to get involved in. I will be presenting at the events and I hope to see you there. Book your free place via the website: **microbiologysociety.org/events**.

Society-Supported Conference Grants help fund a range of events that are taking place all over the world in 2019, such as the UK Cellular Microbiology Network: Exploring the host-bacterial interface event, the *Pseudomonas* 2019 event in Malaysia and the Bacterial Morphogenesis Survival and Virulence 2019 event in South Africa. The Society offers funds to members who organise events, and members can also submit proposals for future Focused Meetings. Find out more on page 131 and on our website.

Annual Conference 2020 in Edinburgh will be a special and celebratory affair with an extended five-day programme. I am looking forward to hearing from world-renowned scientists including Paul Nurse from the Francis Crick Institute, Stirling Churchman from Harvard University and Eddie Holmes from the University of Sydney at the Fleming Showcase on the first day of Conference. Registration for Annual Conference 2020 will open soon. Book your place and submit your abstract if you are planning to present your research. Details can be found on page 128.

You can also be in our 75th anniversary celebrations in 2020 by submitting images to the Microbiology Images project that is currently running and by taking part to our A Sustainable Future project. There will also be more activities taking place during the anniversary year and further President's Roadshow events, including one in Cambridge in April 2020.

In late April 2020 the Society will be running a meeting in Montreal in Canada on *Candida* and candidiasis. You can now submit your abstract and book your place for this event online. The 2020 Focused Meeting series will also be announced next month. I hope you get chance to attend one of these upcoming events to connect with your fellow microbiologists.

Judith Armitage
President
president@microbiologysociety.org

From the Chief Executive

I have just celebrated my five-year anniversary at the Microbiology Society, so I have been looking back at what has happened in that time and thinking about what we can achieve in the next five years. There are too many achievements to list them all but we have balanced the Society's budget to make us sustainable for the future; launched an innovative new journal in *Access Microbiology*; ensured that Annual Conference is an unmissable experience; embedded the Early Career Microbiologists' Forum; made some amazing visual, digital, audio and video content; expanded our professional development offering in response to feedback from members; dramatically reduced the time it takes to publish articles at a lower cost and had some of the Society's first significant policy successes.

Measuring success is not easy when the point of an organisation is to forge connections and build communities, but we must be doing something right because the number of members is rising steadily, as more and more microbiologists recognise the value of being part of the Microbiology Society community.

Looking forward with any certainty is even harder, partly because it's impossible to predict the things that are outside of our control. How will Brexit affect the research community? Will changes to the way scientific publication is paid for turn out to be a threat or an opportunity for a community publisher like the Microbiology Society? Will the political process take a keener interest in the big challenges where microbiology can make a significant contribution, like food security and climate change?

What I can say with confidence is that the Microbiology Society is well placed both to respond to these developments, but more importantly to play a part in leading and defining them. The work we have done in the last few years has given us renewed confidence in the part that we as a community can take.

The big global challenges are an example. The Microbiology Society's project about the role of our discipline in meeting the United Nations Sustainable Development Goals (UN SDGs) – A Sustainable Future – is forging a community that links the unique depth and breadth of knowledge that you – as members of the Society – can bring, with the politicians and non-governmental organisations that see themselves as responsible for ensuring the SDGs are delivered. The launch event in Westminster brought together soil microbiologists, medical microbiologists and environmental microbiologists with civil servants, doctors, educators and others as an early step in bringing these communities closer together.

In the world of publishing, which generates most of the Society's surplus income from which we fund our programmes, we are taking a lead, as the economic model is rapidly changing in response to the needs of funders. The Microbiology Society is at the heart of the process as new deals are structured and new policies developed, so that the public gets a fair deal for the money it invests in science, the research community has a fair choice of where to publish its work so that it reaches the right audience and not-for-profit publishers like the Microbiology Society can serve the needs of our community.

Next month, the Microbiology Society will move its headquarters to new premises. We need more space, and more importantly we need facilities that match our level of ambition. The strategy that the Society's Council and staff are pursuing begins with the words: 'microbes are everywhere and affect almost all aspects of our lives'. The transformative potential of microbiology to change people's lives for the better is almost unlimited, and the members of the Microbiology Society have a unique contribution to make. We have achieved a great deal together in the past five years and I look forward to being ever more ambitious in the next five. Please let me know about the opportunities you see where we can have an impact by ensuring that the science of microbiology provides maximum benefit to society.

Peter Cotgreave
Chief Executive
p.cotgreave@microbiologysociety.org

News

Connect with the Microbiology Society on social media:

@MicrobioSoc

Annual General Meeting and Showcase of the Society's Achievements

The Society is pleased to confirm that this year's Society Showcase and Annual General Meeting will take place on 12 September 2019, at The Law Society, 113 Chancery Lane, London WC2A 1PL. Visit the website (**microbiologysociety.org/AGM**) for more information.

Article and journal metrics

Microbial Genomics has received its first journal metrics and we would like to thank all our editors, authors and reviewers who have supported the journal since its launch in 2015. As a signatory to the San Francisco Declaration on Research Assessment (DORA) we believe that while metrics form part of a holistic assessment of research, no metric should be used in isolation to assess the value of research. To this end, we have created a page on the journals platform (**microbiologyresearch.org/authors/metrics**) to show a range of metrics about all our journals.

IMAV 2019: International Meeting on Arboviruses and their Vectors

5–6 September 2019, University of Glasgow, UK

Last call – if you work in this discipline, this Focused Meeting offers a unique opportunity to interact with arbovirus field experts from different disciplines very unlikely to meet outside such a meeting. If you haven't already registered, visit **microbiologysociety.org/IMAV19** to secure your place today.

Taxonomy profiles in *Journal of General Virology* and *Microbiology*

The *Journal of General Virology* publishes ICTV Virus Taxonomy Profiles – concise, review-type articles that provide overviews of the classification, structure and properties of novel microbes and individual virus orders, families and genera. The ICTV Virus Taxonomy Profiles include *Parvoviridae*, a family of small, resilient viruses that infect vertebrates including humans. *Microbiology* now also publishes Microbe Profiles, which include *Pseudomonas syringae*, a plant pathogen that is implicated in a range of diseases in annual crops. Visit the journals platform (**microbiologyresearch.org**) to find out more.

Grant deadlines

Date	Grant
1 September 2019	Travel Grant – for eligible members wishing to present at conferences or attend training events taking place between 1 October and 31 December.
	Careers Conference Grant – to support Undergraduate Student members wishing to attend the Royal Society of Biology Bioscience Careers Day.
30 September 2019	ECM Forum Event Fund – for ECM members requiring sponsorship for local events.
1 October 2019	Education and Outreach Grants – for eligible members requiring support for projects to communicate or teach microbiology.
	International Development Fund – for eligible members wishing to contribute to the development of microbiology in low- and lower-middle-income countries.
	Research Visit Grants – for eligible members wishing to make a research visit to a collaborator.

For more information please visit the website (**microbiologysociety.org/grants**).

FIS 2019

11–14 NOVEMBER, EICC, EDINBURGH, UK

HOSTED BY

MICROBIOLOGY SOCIETY

Focusing on the themes of treatment and management of infectious diseases as well as epidemiology and prevention, this exciting four-day programme will bring together some of the best and most thoughtful minds from around the world to participate and inform.

Registration and full programme details can be found on **microbiologysociety.org/FIS19**

#FIS19
@MicrobioSoc

Geertje van Keulen

Chair of the Prokaryotic Division

Geertje van Keulen

The Society's four Divisions (Eukaryotic, Prokaryotic, Virology and Irish) consist of members who support the organisation and plan sessions and symposia for the Society's events programme. Each Division Chair and Chair-Elect sits on the Scientific Conferences Committee, and the Chair reports into Council, the Society's governing body. In this article we find out about the work of Geertje van Keulen, Chair of the Prokaryotic Division.

I am Associate Professor in Biochemistry at Swansea University. My lab group is focused on my favourite actino prokaryote, *Streptomyces*, which is used as inspiration for researching manufactured, natural/environmental and living materials, and for biochemical engineering, thereby adopting a true interdisciplinary approach.

When did you first decide you wanted to do science (and why)?

I was first inspired to do science by my chemistry teacher in secondary school, while my dad taught me about electrical engineering. I enjoyed chemistry and the molecular aspects of biology from the first day I learnt about these disciplines. When studying chemistry at university, I developed wide-ranging interests in biochemistry, organic, polymer and structural chemistry, as well as chemical engineering. I eventually chose to specialise in biochemistry, which is where my passion for molecular biology, particularly transcription regulation, started as a researcher. My interest in and passion for science and technology, not necessarily high grades in school or university, led me to become a researcher, with a career now as an interdisciplinary microbiologist.

When did you join the Society and why did you join?

My first stint as a member was as a PhD student while working in The Netherlands, to benefit from reduced registration fees for the Spring/Autumn Conferences, now Annual Conference. When I moved to the UK as Marie Curie Intra-European Fellowship (IEF) fellow, I re-joined to connect with the large microbiology network in the UK and for the many member benefits. Now, I encourage our students to join the Society to equally benefit.

Please describe your role on the Division.

Following election as a Prokaryotic Division member and then Chair-Elect, I am now Chair of Division, with a variety of roles. My main role is leading a large group of senior and early career prokaryote microbiologists to come up with topic ideas to attract top conference speakers for the communities we serve and ensuring the scheduling of sessions works for all delegates. I have also developed a mentoring document for Early Career Microbiologists' (ECM) Forum Co-Chairs, which explains their roles and expectations.

What motivated you to be part of the Division?

I joined the Division as a member with a remit for environmental microbiology, which I thought at the time was not represented as well as it could be. Over time I also helped set up the Forums, which created more presentation opportunities for ECMs, and organised the first of the Focused Meetings series which was on the topic of Soil Microbiology.

If you're a member and would like to join one of the Divisions, visit the website (**microbiologysociety.org/divisions**) to find out more. You can gain insight into the work of the Society and first-hand experience of Council and Committee activities by taking part of the Council and Committees shadowing scheme (**microbiologysociety.org/shadowingscheme**).

Plant arboviruses: major threats to food security

John P. Carr, Ken Okwae Fening, Paul Kuria, Alex M. Murphy, Josiah Musembi Mutuku, Jane Wamaitha Mwathi and Mildred Ochwo-Ssemakula

Arthropod-borne viruses are a major and growing threat to crop-based agriculture and native plant communities. Almost half of the emerging infectious agents threatening plants are viruses.

In some cases, this is because viruses are inadvertently spread or introduced into new areas by human activity, but climate change is playing an increasing role by altering the geographic ranges of viruses' arthropod vectors. Climate change, by increasing ambient temperature and carbon dioxide levels, may also decrease a plants' ability to resist infection by viruses and colonisation by arthropod vectors. Higher temperatures also enhance vector reproduction rates. Most viruses – an estimated 60–70% – that infect land plants are vectored by arthropods, the vast majority of vectors being insects. Leaf chewing or puncturing herbivorous insects (such as beetles and thrips) transmit several viruses, some of which are very important, but the most common vectors are hemipterans – insects like aphids, whiteflies and leafhoppers that have piercing, needle-like mouthparts called stylets. Stylets enable these insects to penetrate plant cells and tissues and extract nutrients. During this feeding process, virus particles are easily acquired from virus-infected plants or deposited into new hosts.

Which types of viruses attack plants and how do they interact with vectors?

Most plant viruses have RNA genomes and relatively simple particle structures. A smaller number have DNA genomes but these include the geminiviruses (named for their 'twinned', dumbbell-shaped particles), that are mostly transmitted by whiteflies and leafhoppers, and which cause devastating losses to important crops such as cassava. Most plant viruses do not infect their arthropod vectors. For example, most viruses transmitted by aphids (the largest group of vectors) are carried for a fairly brief time on the stylet ('non-persistent' transmission). Others are taken up through the aphid's gut wall and circulate within the insect until particles reach the salivary glands and can then be injected into a plant host ('persistent' transmission). In most cases of persistent transmission by aphids, the viruses do not replicate in the insect's cells. The process is further remarkable in that safe passage of virus particles from gut to salivary gland is dependent upon a protein ('symbionin') that is released by bacterial endosymbionts living within specialised cells of the aphid.

However, a few plant viruses with double- or single-stranded RNA genomes do infect their insect vectors. These are therefore animal as well as plant viruses. Perhaps not surprisingly, these viruses belong to groups better known for causing disease in humans: reoviruses, rhabdoviruses and tospoviruses (members of the virus family *Bunyaviridae*). The relationships of these plant viruses to vertebrate-infecting viruses is one line of evidence indicating that insects are not only effective vectors but also 'bridges' that have facilitated the cross-Kingdom adaptation and evolution of new viruses.

Which regions and crops are at risk from plant arboviruses?

The short answer to this question is everywhere and all of them. In more developed countries arthropod-transmitted viruses have been controlled with variable success by using insecticides to kill the vectors. Unfortunately, this drives the evolution of insecticide-resistant vectors and the unintended damage caused by insecticides to beneficial insects, such as pollinators or natural predators of pests, has led to restrictions or bans on certain chemicals. For example, turnip yellows virus is persistently transmitted by aphids and can cause serious losses to oilseed rape and sugar beet crops. In the UK its transmission was controlled effectively using neonicotinoid insecticides. However, neonicotinoids can be deleterious to bees and so their use was recently curtailed. It is uncertain what impact this will have on the productivity and sustainability of

Top left panel shows a bean leaf infested with aphids, one of the most important types of plant arboviral vectors. Left lower panel, setting up vector traps in an experimental field plot in Kenya. Right panel shows a maize plant with maize lethal necrosis disease, which is caused by co-infection by two arboviruses.
John P. Carr

crops protected using this insecticide family.

The most severe effects of plant arboviruses on crop production are seen in tropical or subtropical regions where the abundance of vectors is greatest. Africa provides some of the most important and challenging plant arbovirus problems. The leafhopper-vectored geminivirus maize streak virus is a problem throughout Africa, and in eastern and central Africa invasive whiteflies spread geminiviruses that cause cassava mosaic disease and may be spreading westwards. A number of important diseases result from mixed infections, in which two or more viruses 'synergise', causing more serious symptoms than a single infection by one of the partners. Typically, the viruses are unrelated and are carried by different vectors. This is true for some well-established diseases such as sweet potato virus disease (capable of causing yield losses of more than 90%) that is caused by a synergistic infection by an aphid-transmitted and a whitefly-transmitted virus. The current serious outbreak of maize lethal necrosis disease in east and central Africa, which can cause total loss in infected maize fields, is caused by a synergistic double infection by indigenous strains of sugarcane mosaic virus (transmitted by aphids) in combination with the beetle- or thrips-transmitted maize chlorotic mottle virus, which was inadvertently introduced from Asia. Our work in Kenya and Ghana indicates that introduced viruses may also be threatening legume and brassica crops, respectively.

Perhaps the most 'successful' invasive arbovirus is the tospovirus tomato spotted wilt virus that infects not only tomato but also over 1,000 other plant species, including many crops. The virus is transmitted by thrips, especially the western flower thrips. The virus also infects thrips, causing changes in feeding behaviour on plants that enhance inoculation efficiency. Tomato spotted wilt was first described in Australia 100 years ago but, along with its thrips vector, has now spread worldwide. In Uganda, for example, this virus has become a greater concern for tomato production than the indigenous whitefly-transmitted geminiviruses, which already cause serious losses.

Can we control plant arboviruses?

As already mentioned, although insecticides can be effective crop protectants, problems arise from off-target effects on beneficial insects and from the evolution of resistant vector strains. Fortunately, there are a significant number of natural plant resistance genes that can be bred into crops to protect against the viruses. There are also a few examples of resistance genes that work against vectors. Unfortunately, conventional crop breeding is a time-consuming process and is unable to move resistance genes between different plant species.

Genetic modification of plants, for example, by engineering them to express RNA molecules that induce destruction of viral nucleic acids (RNA silencing), provides extremely effective virus resistance. A similar approach can also protect against vectors. More recently, gene editing has been used successfully to mutate genes encoding host factors needed by viruses to replicate in plants. Unfortunately, despite the effectiveness of these approaches there is a reluctance to use these technologies, in large part due to a public perception that plant genetic engineering is intrinsically harmful or because large corporations were involved in development of the technology. A possible way forward is the treatment of plants with synthetic RNA molecules to induce RNA silencing against viruses, which may prove more acceptable since no genetic engineering is involved.

An approach that some of us have been investigating is to better understand the volatile chemical signals ('semiochemicals') emitted by plants that attract or deter vectors. Virus infection can alter the composition of the volatiles emitted by plants and this may engender changes in vector–plant interactions that will enhance transmission. Understanding how these chemical signals influence vector behaviour could provide a means of protecting against arboviruses by decoying or trapping vectors or warding them away from crops.

Further reading

Cillo F, Palukaitis P. Transgenic resistance. *Adv Virus Res* 2014;90:35–146.

Canto T, Aranda MA, Fereres A. Climate change effects on physiology and population processes of hosts and vectors that influence the spread of hemipteran-borne plant viruses. *Glob Change Biol* 2009;15: 1884–1894.

Hull R. *Plant Virology*, 5th edn. New York: Academic Press; 2014.

Jones RAC. Plant virus ecology and epidemiology: historical perspectives, recent progress and future prospects. *Ann Appl Biol* 2014;164:320–347.

Mauck KE. Variation in virus effects on host plant phenotypes and insect vector behavior: what can it teach us about virus evolution? *Curr Opin Virol* 2016;21:114–123.


John Carr

John P. Carr

e **jpc1005@hermes.cam.ac.uk**

John Carr has been a member of the Microbiology Society for over 20 years. He teaches plant virology and plant–microbe interactions at the University of Cambridge. John's collaborations with the co-authors have been facilitated via the GCRF-CONNECTED Network (**connectedvirus.net**).


Paul Kuria

Paul Kuria

e **kuriapk@gmail.com**

Paul Kuria is a research scientist from the Kenya Agricultural and Livestock Research Organization in Nairobi, Kenya. His research is focused on understanding transmission, molecular mechanisms of host resistance and interaction of viruses in cassava, maize and fruit trees.


Josiah Musembi Mutuku

Josiah Musembi Mutuku

e **j.mutuku@cgiar.org**

Josiah Musembi Mutuku is a scientist at the Biosciences eastern and central Africa-International Livestock Research Institute (BecA-ILRI) Hub in Nairobi, Kenya, and a Visiting Scientist at the Plant Sciences Department, Cambridge, where he researches aphid-vectored plant viruses of legume crops.


Jane Wamaitha Mwathi

Jane Wamaitha Mwathi

Jane Wamaitha Mwathi is a scientist at Kenya Agricultural and Livestock Research Organisation working on arboviruses causing maize lethal necrosis disease (MLND). Jane works on outreach in east and central Africa to aid farmers in MLND management and mentors young African scientists through training and research exchanges.


Ken Okwae Fening

Ken Okwae Fening

e **kenof2@yahoo.com**

Ken Okwae Fening is a Senior Research Fellow (Agricultural Entomologist) from the Soil and Irrigation Research Centre (SIREC), and the African Regional Postgraduate Programme in Insect Science (ARPPIS), University of Ghana and his UK collaborative work was facilitated by a CAPREx Cambridge-Africa Fellowship and a GCRF Impact Acceleration award.


Alex Murphy

Alex M. Murphy

e **amm1013@hermes.cam.ac.uk**

Alex Murphy is a Senior Research Associate at the University of Cambridge and carries out research on plant–arbovirus–insect interactions and antiviral resistance mechanisms.


Mildred Ochwo-Ssemakula

Mildred Ochwo-Ssemakula

e **mknossemakula@caes.mak.ac.ug**

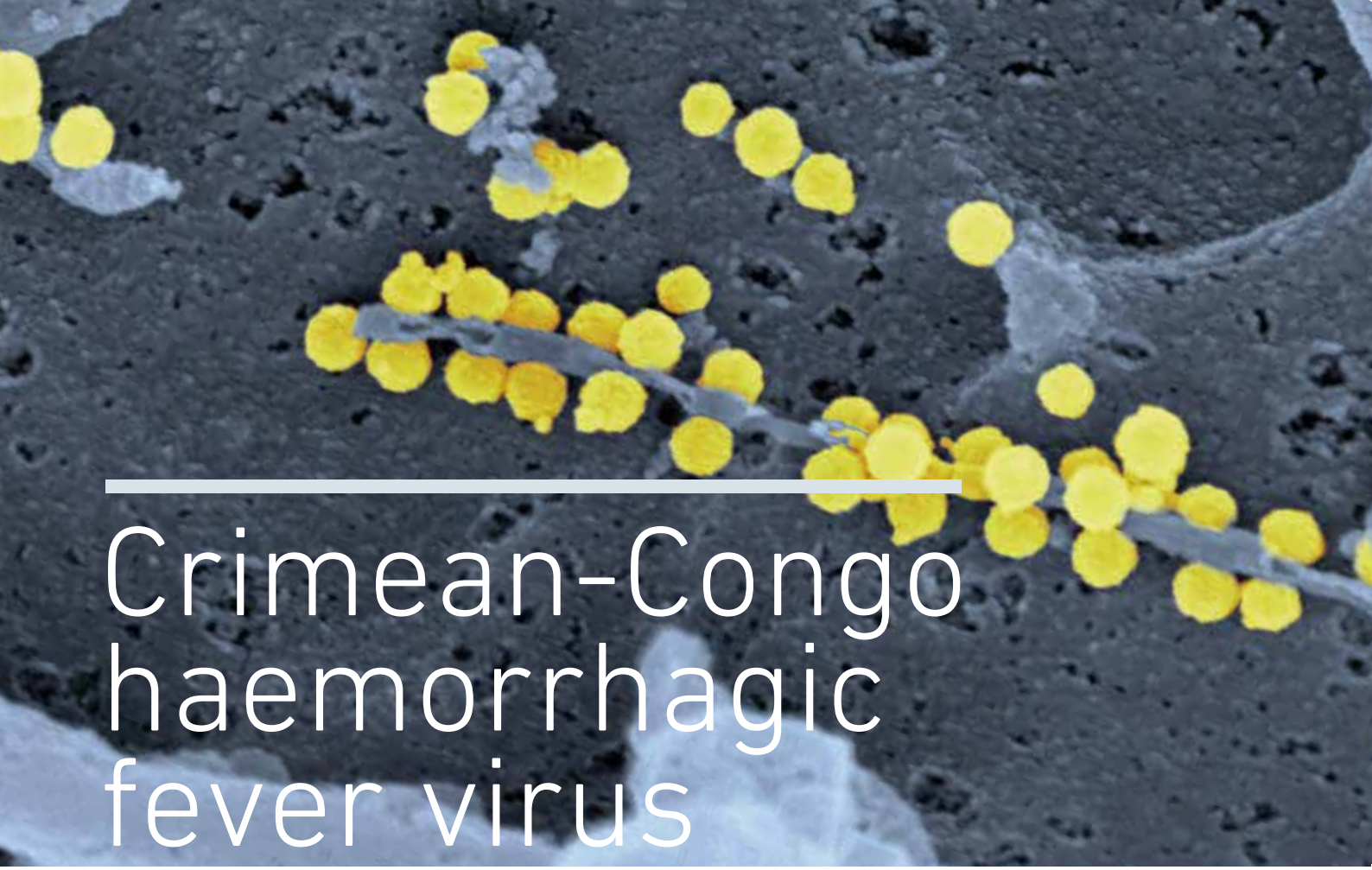
Mildred Ochwo-Ssemakula is a Senior Lecturer in Plant Pathology at Makerere University, Uganda. Mildred works on viral diagnostics and host–vector–pathogen interactions and development of strategies for management of diseases affecting horticultural and staple crops in Uganda.

Why does microbiology matter?

John Carr: The activities of microbes including viruses make all other life possible and most fundamental discoveries in biology have had their beginnings in microbiological and virological research.

What is the most rewarding part of your job?

John Carr: Hearing the news that a former student or postdoc has started their own lab.



Crimean-Congo haemorrhagic fever virus

Roger Hewson

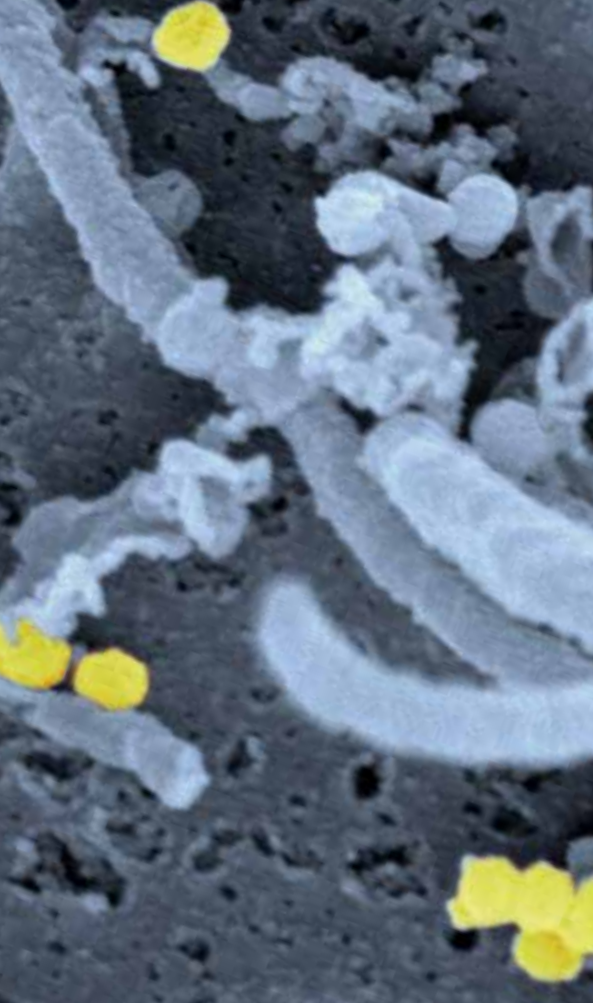
Crimean-Congo haemorrhagic fever virus (CCHFV) is a neglected virus identified as a key research target by the World Health Organization (WHO). Following the unpredicted size, speed and reach of the Ebola virus outbreak in West Africa in 2014, the WHO assembled a broad coalition of international experts to develop a research and development (R&D) Blueprint for action to prevent future disease epidemics caused by under-researched pathogens. This Blueprint highlights the importance of increased research investment into CCHFV by researchers, pharmaceutical communities and governments.

Coloured scanning electron micrograph of CCHF viral particles (yellow) budding from the surface of cultured epithelial cells from a patient.
National Institute of Allergy and Infectious Diseases, NIH/Science Photo Library

CCHF is a rare tick-borne disease spread to humans from animals and causes high human fatality rates. It is caused by a negative-sense single-stranded, segmented RNA virus classified within the *Orthonairovirus* genus of the family *Nairoviridae*. The virus is particularly associated with *Hyalomma* ticks, which act as both reservoirs and vectors. Because of this association, it is the most widely distributed agent of severe haemorrhagic fever known, endemic over much of Asia, and with focal endemic areas over Africa and Europe where it continues to emerge.

History and politics

Classical evidence points to a probable description of CCHF in the territory now occupied by Tajikistan as early as 1100 AD, in reports of patients with bleeding symptoms that were linked to blood-sucking ticks. The first



modern medical account of disease was made much later in 1944 during an outbreak affecting over 200 Soviet troops assisting in war-devastated Crimea. This disease was named Crimean haemorrhagic fever (CHF) and was shown to be distributed across the Soviet Republics. While it was established that a virus was the cause of this disease, it was not isolated and sent for registration by the Soviet scientists until 1968. During the registration process, CHF virus was recognised as identical to an African virus – Congo virus – that had been isolated in 1956 and registered in 1961 by virologists from the Congo, USA and UK. It came as a great surprise to Soviet virologists that a virus causing an African disease, that did not even have a name before 1961, could be associated with CHF which had been recognised and studied for nearly three decades in the USSR. Surprise turned to shock when, by convention, it was advised that the official name should be Congo virus, since this virus had been described and registered in the catalogue of arthropod-borne viruses before CHF virus. Shock among the Soviet virologists turned to outrage since they had used a different name for the disease for many years and they refused to use the new nomenclature. This was the time of the Cold War and although the International Committee for Taxonomy of Viruses suggested the compromise name of Congo-Crimean

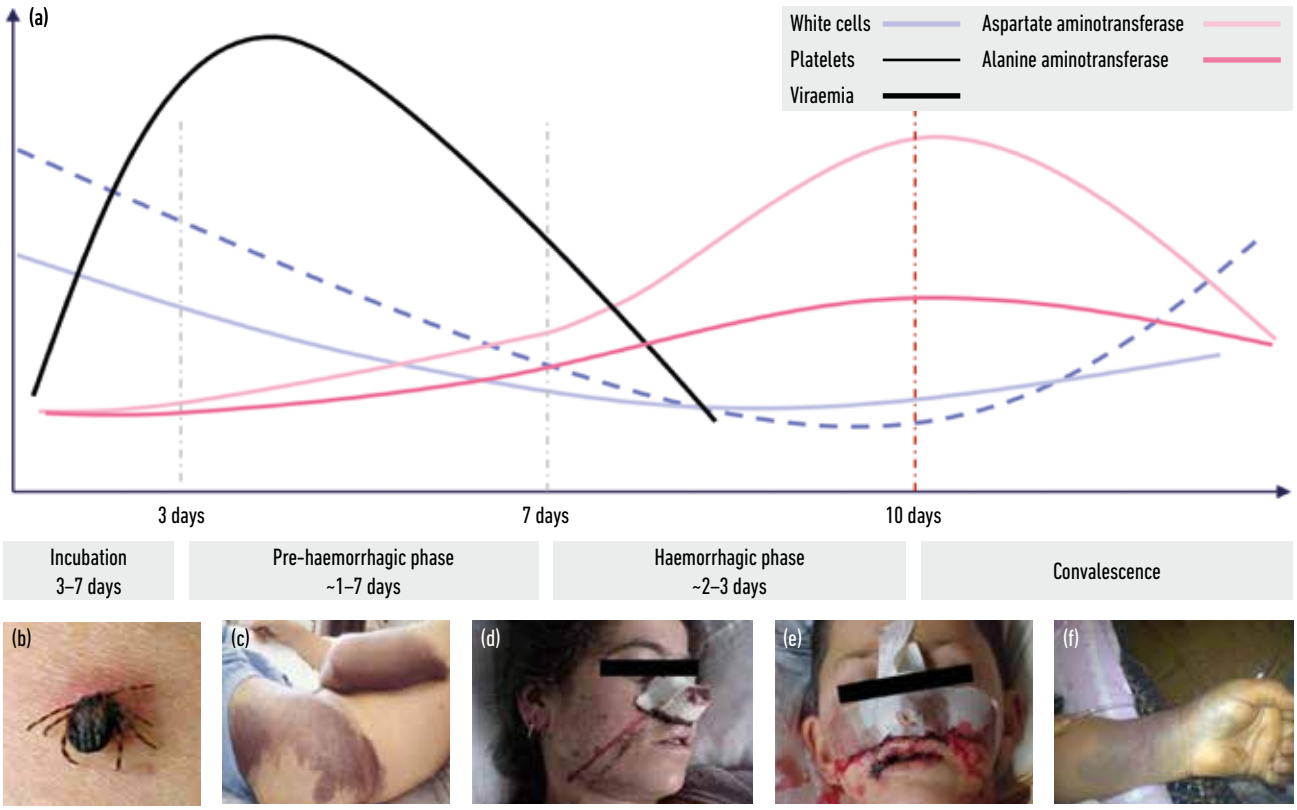


Fig. 1. (a) The general clinical features of CCHF infection can be defined into four distinct phases: incubation, a pre-haemorrhagic phase typified by fever, myalgia, nausea; a haemorrhagic phase typified by bruising, epistaxis and haematemesis; followed by convalescence. Patients do not always develop haemorrhagic symptoms. Some infections are mild and subclinical infections are also reported. Diagnosis by RT-PCR follows viral load. (b) Embedded tick, removed from a CCHF patent. (c–f) Bruising, ecchymoses and haemorrhagic features of fatal disease. Graph modified from Ergonul 2006. Pictures from collaborators: Prof. Salih Ahmeti, Kosovo & Farida Tishkova, Tajikistan

haemorrhagic fever virus, the deadlock was not resolved until 1973 when the Soviet compromise 'Crimean-Congo haemorrhagic fever virus' was finally agreed.

Human disease and basic biology

CCHFV infects a wide range of domestic and wild animals, such as cattle, goats, sheep, hares and rodents, which all serve as asymptomatic amplifying hosts for the virus. Humans are incidental hosts which often acquire the virus through tick bites. Unlike many other tick-borne viruses, CCHFV is also transmitted by direct contact with infected tissues and body fluids of animals and humans. Human-to-human transmission is a common hallmark of infection which can lead to population-based and nosocomial outbreaks. Clinical features commonly include an abrupt onset of fever, myalgia, headache and thrombocytopenia which can progress to haemorrhage, multiorgan failure and death (Fig. 1). Case fatality rates (CFRs) correlate with the mode of transmission: tick bites lead to CFRs of 10–30% but incidents of up to 80% are often reported following nosocomial transmission. Human transmission resulting from the butchering of viraemic animals is also common and can lead to high mortality. Increased episodes and small outbreaks have been noted to coincide with religious festivals that involve the slaughter of (viraemic) animals. This is expected to play an important role in increased transmission in the future, as the dates of such festivals overlap with increased tick feeding activity and viraemic animals.

CCHF is nevertheless a rare disease, with approximately 2,000 cases per year globally. Early diagnosis is important for the implementation of adequate infection control and contributes to a favourable outcome through the general supportive management of symptoms. Administration of the antiviral ribavirin is thought to be effective if used early in infection, but this is based on observational studies; a large placebo-controlled, randomised control trial is lacking, and evidence of the efficacy of ribavirin for the treatment of CCHF infections remains inconclusive. Likewise, there are no effective vaccines licenced for use against CCHF. In consequence, the Advisory Committee on Dangerous Pathogens in the UK classifies the virus as a hazard group 4 pathogen, which mandates that all work with infectious materials be carried out at maximum biological containment in specialist containment level 4 (CL4) facilities. Corresponding classifications apply in other parts of the world and generally the availability of such resource-heavy laboratory infrastructure is a bottleneck to basic research. Consequently, knowledge of CCHFV has lagged behind that of other pathogens and the poor payback on investment required for applied research into therapeutics and vaccine development for such a rare disease has been a major impediment to progress.

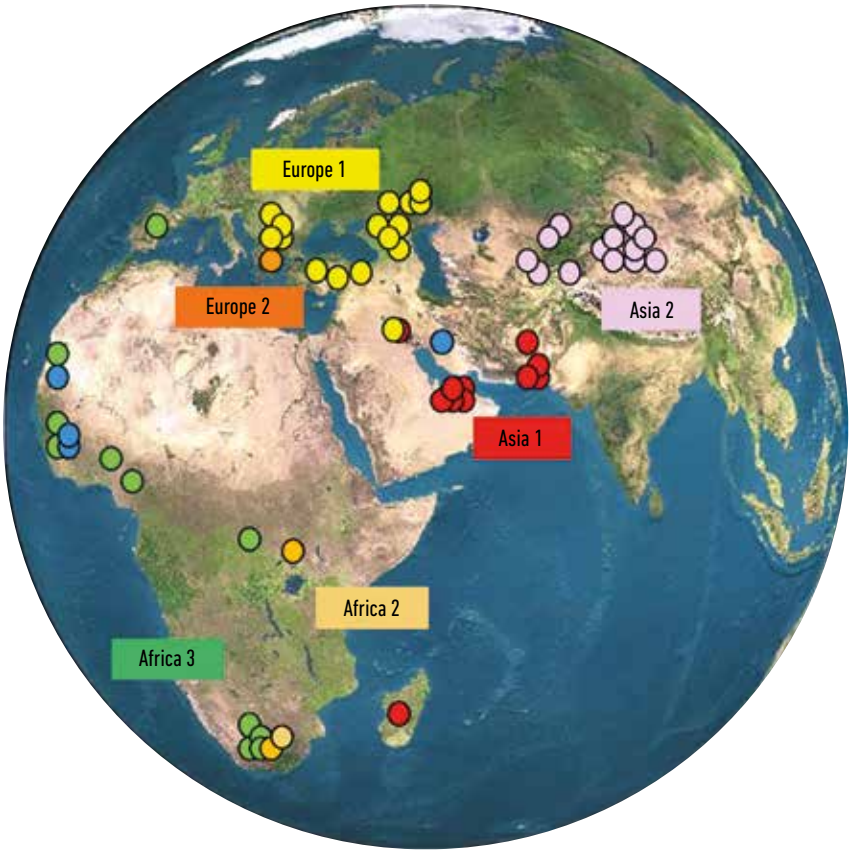


Fig. 2. Geographical correlation of genotypes. When superimposed onto the globe the phylogenetic grouping of S RNA segments illustrates that the pattern of genetic diversity observed is largely related to the geographical distribution of the viruses. Similar genotypes are sometimes found in distant geographical locations, highlighting long-distance carriage of virus in infected ticks during bird migration and or trade in livestock. The recent emergence of CCHF in Spain is thought to be the result of bird migration from West Africa. Roger Hewson

Nevertheless, some aspects of CCHFV's biology are known or can be inferred from work on similar orthonairoviruses. Its genome consists of three single-stranded, negative-sense RNA molecules, termed S (small), M (medium) and L (large), encoding the N-protein (S-segment), the viral glycoprotein (M-segment) and the viral RNA-dependent RNA polymerase (RdRp) (L-segment). Infection starts with viral attachment to an unknown cell-surface receptor and entry via endosomes. Viral fusion with the host cell membrane is thought to be pH-dependent, releasing the viral ribonuclear-protein-complex into the cytoplasm. L- and S-segment mRNAs are translated by free ribosomes while M-segment mRNA is translated by membrane-bound ribosomes and is co-translationally cleaved to yield two glycoproteins, Gn and Gc. These accumulate in the Golgi, where virions assemble and bud, being released after fusion with the plasma membrane.

Molecular epidemiology diagnostics and vaccine interventions

While serological methods have been important in determining the breadth of CCHF distribution, these approaches do not readily differentiate between alternative strains of CCHFV. To characterise viral strains in more detail and facilitate a global epidemiological study, molecular methods based on partial and complete sequence data of the S-segment have been used to identify certain S-segment genotypes. These genotypes show a strong relationship to the geographical area of isolation of the parent virus, leading to the terminology Asia 1, Asia 2, Europe 1, etc. These studies also show that similar genotypes are found in distant geographical locations (Fig. 2), supporting the idea that the virus or infected ticks may be carried over long distances during bird migration. Anthropogenic factors, such as the trade in livestock, also appear to play a role in the dispersal of CCHF viruses.

With the increasing applicability of whole genome sequencing to the many different strains of virus it has become clear that CCHFV shows enormous variety. While simple genetic drift and recombination play important roles, segment reassortment seems to be a key driver of genetic variation, with current evidence pointing to the greater exchange of M-segments between viruses. Co-infections of multiple CCHFV strains are a prerequisite of such variation and most likely the optimal environments occur within ticks, where lasting virus infections persist for extended periods, and superinfection with a second or third strain during blood meals may be quite common. These observations provide support for a global and dynamic reservoir of CCHFV and underpin the importance of maintaining diagnostics that keep pace with such variation. This is important so that all known circulating strains can be promptly identified and, in the case of human infection, rapidly controlled before infection spreads.

While vaccine interventions for CCHFV are currently unavailable, this research area is now highly active, and several approaches are being developed. One of the most advanced is a viral-vector approach based on the highly successful Modified Vaccinia Ankara approach which drives the expression of CCHFV-GP. Phase I clinical trials should commence early in 2020.

Roger Hewson

e **roger.hewson@phe.gov.uk**

Roger Hewson is Scientific Leader for Viral Haemorrhagic Fevers and Arboviruses at Public Health England – Porton Down and Head of the institute's WHO Collaborating Centre for Virus Research and Reference.

What does a typical day or week look like for you?

The Virology & Pathogenesis Laboratory studies a wide range of zoonotic and vector-borne viruses, many of which are new and emerging, including to the UK. A typical week involves lab meetings and one-to-one discussions on current research projects, the preparation and finishing touches to scientific reports for publication, including the supervision of MSc and PhD students. International collaborations and laboratory networks, including with partners in endemic disease regions, is an important aspect of our work and we need to be involved in workshops and occasionally field work to support our basic capability – travel or planning for such activity is a central theme of the laboratory. Advancing our research through new proposals and grant applications for new sources of funding to sustain capacity is a constant necessity.

What advice would you give to someone starting out in the field?

Follow your interests, develop trustworthy experimental capability, develop a niche and keep pace with technological advances.

Dengue: a self-limiting acute disease

Kevin Maringer

The World Health Organization (WHO) considers dengue to be the most important vector-borne viral disease affecting humans. The disease is widespread across tropical and subtropical regions of the world, with almost half of the global population living in affected areas and public health systems strained by epidemics of increasing frequency, severity and geographic reach. However, hyperbolic statements like these hide the true personal and societal impact of a disease, and I find a more human illustration of the importance of dengue in the public consciousness of affected regions to be the existence of a rock band called 'Dengue Fever'.

Dengue is caused by four viruses within the *Flavivirus* genus in the *Flaviviridae* family, dengue virus (DENV) serotypes 1 through 4 (DENV-1, DENV-2, DENV-3, DENV-4). These viruses are grouped together based on antigenic cross-reactivity and the clinical manifestations of disease. On a sequence level the four dengue viruses are more divergent from one another than some other flaviviruses considered distinct species; and marked differences in the behaviour of different DENV serotypes have been observed at the molecular, cellular and epidemiological level. While there have been reports of a potential fifth serotype, the primary supporting data has yet to be published in the peer-reviewed academic literature.

Dengue disease

DENV infects up to 390 million people each year, with one in four of these developing clinical signs of disease. Dengue fever is a self-limiting acute disease typified by severe flu-like symptoms, with fever, joint and muscle pain, severe headache, retro-orbital pain (pain behind the eye) and rash. These acute symptoms last approximately one week, but patients can continue to experience severe fatigue for over a month. A small minority of symptomatic patients (fewer than 5%) develop 'severe dengue', formerly and sometimes still referred to as dengue haemorrhagic fever (DHF) or dengue shock syndrome (DSS). The clinical manifestations of severe dengue can include vascular permeability, haemorrhage, plasma leakage, shock and organ failure. Severe dengue is fatal in 2.5% of cases if left untreated.

A major factor implicated in cases of severe dengue is the antigenic

cross-reactivity between the four dengue viruses. Primary infection with any given DENV serotype results in life-long homotypic protection against symptomatic disease from that same serotype, but only temporary heterotypic protection against other serotypes. Notably, the chances of developing severe dengue are increased by the presence of non-neutralising cross-reactive antibodies, either during secondary infection with a different serotype or during primary infection in children harbouring cross-reactive maternal antibodies transferred through breastfeeding. These non-neutralising antibodies bind to the surface of the DENV particle and, upon recognition by Fc receptors, enhance viral entry into macrophages. Since macrophages are one of the cells in which DENV replicates, the result is an increased viral load in the patient, along with a dysregulated production of cytokines and chemokines thought to contribute to vascular permeability. Epidemiologically, one of the factors contributing to the increased number of severe dengue cases has been the global spread of all four serotypes, so that multiple DENV strains now co-circulate almost everywhere that dengue is present, increasing the chance that individual patients infected with DENV already harbour antibodies to a different serotype. It should though be noted that life-threatening dengue is also

Dengue affects people living in both urban and rural tropical and subtropical regions. Kevin Maringer

possible during primary infection, with additional contributing factors including patient age, as well as viral and human genetic differences.

Diagnosis, treatment and vaccines

The symptoms of dengue fever are similar to those of other diseases, including Zika fever, chikungunya fever and malaria, which complicates the clinical diagnosis of dengue. Diagnosis can be confirmed using laboratory tests, including reverse transcriptase-PCR (RT-PCR) for detecting viral RNA, and enzyme-linked immunosorbent assays (ELISAs) for detecting DENV-specific immunoglobulin M (IgM) antibodies or the viral protein NS1 in patient serum. Severe dengue is diagnosed by its clinical signs, including thrombocytopaenia, haemorrhagic manifestations and other signs of vascular leakage, leukopenia, liver damage, hypovolaemic shock and organ failure. It is not possible to predict which dengue patients will develop life-threatening complications, making treatment difficult and straining public health systems while large numbers of patients, many of whom do not develop life-threatening disease, are monitored in hospital.

There are no specific antiviral therapies available to treat dengue. Patients that develop severe dengue are treated with fluid replacement therapy to prevent hypovolaemic shock. While this supportive therapy reduces the case fatality rate from 2.5% to 1%, not all patients have access to the necessary medical facilities and expertise.

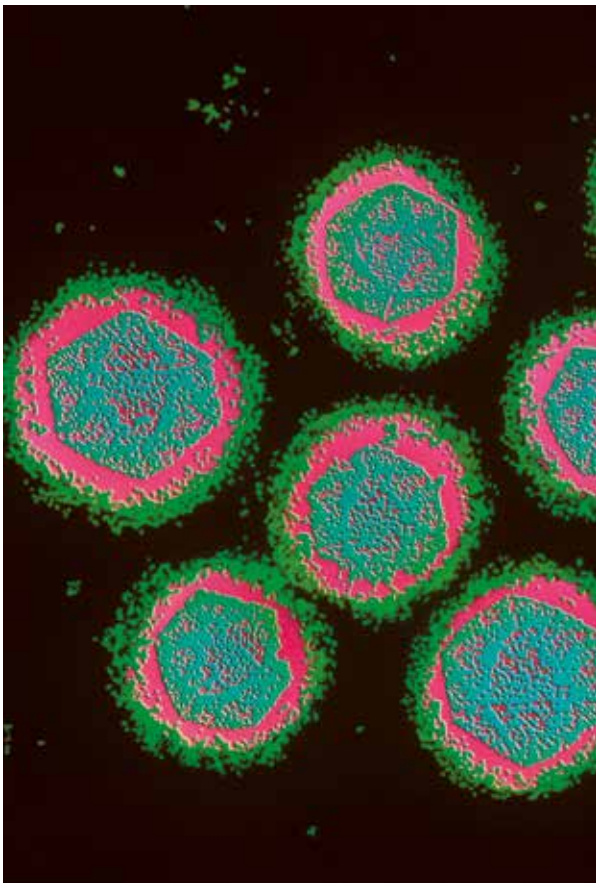
The first licensed dengue vaccine became available in 2015 and is designed to target all four DENV serotypes. The WHO considers this vaccine safe and protective in seropositive people who have experienced a prior DENV infection. However, the vaccine increases the likelihood of naïve individuals developing severe dengue disease upon primary infection with DENV. While this limits use of the vaccine to regions of high dengue endemicity, the vaccine is nevertheless a valuable tool for helping to reduce the global public health burden of dengue.

Mosquito vectors

DENV is transmitted by the two mosquito species, *Aedes aegypti* and *Aedes albopictus*. Infection through blood-borne routes, organ transplantation and breastfeeding is possible, but the vast majority of cases result from mosquito-borne transmission. *Ae. aegypti*, known colloquially as the 'yellow fever mosquito', is the primary vector for DENV in urban settings, due to its close association with humans. This tropical mosquito species feeds almost exclusively on humans and prefers to breed in artificial containers, resulting in high mosquito population densities capable of sustaining DENV transmission cycles in the urbanised tropics. *Ae. albopictus*, known colloquially as the 'Asian tiger mosquito', is less closely associated with humans, but is highly invasive in many parts of the world and more cold-tolerant. For these reasons, *Ae. albopictus* is an important vector for DENV in rural areas and in subtropical environments.

Prior to the availability of the vaccine, dengue control efforts largely focused on the mosquito vector. Insecticides have been effective at reducing mosquito populations to reduce DENV transmission, but with insecticide resistance on the rise, alternative approaches such as *Wolbachia* transinfection and genetic strategies for controlling mosquito populations (both covered elsewhere in this issue) are becoming increasingly important.

There is also an increasing interest in how virus–vector interactions contribute to the transmission and emergence of arboviruses like DENV. Mosquitoes are not simply mechanical vectors of DENV, but rather the virus must go through sequential cycles of replication in various tissues of the insect, including the midgut immediately after consumption of an infectious blood meal, and the salivary gland prior to the injection of virus-containing saliva into the human host. Factors such as viral entry receptors, vector immune responses and the vector



Colour-enhanced transmission electron micrograph of dengue virus (*Flaviviridae*), which causes dengue fever and dengue haemorrhagic fever. Magnification, x103,000. Chris Bjornberg/Science Photo Library

microbiome (including the virome) have been shown to affect arbovirus replication and transmission. By gaining a better understanding of the interactions between arboviruses like DENV and their respective vectors, our lab and others aim to develop alternative methods of controlling the spread of arboviral diseases by modifying (genetically or otherwise) vectors to reduce their capacity for virus transmission.

Looking to the future

A better vaccine, specific antivirals and diagnostic tools for predicting which patients will develop severe disease are desperately needed. More work is also needed on virus–vector interactions, and how DENV is affected within individual patients, vectors and at an epidemiological level by the presence of, or coinfection with, other arboviruses with similar geographic distributions and vector specificities, such as chikungunya virus and Zika virus. With local DENV transmission recently observed for the first time in Spain and other southern European countries, it will also be important to understand how climate change will affect vector ranges, viral transmission and the geographical distribution of dengue.

Further reading

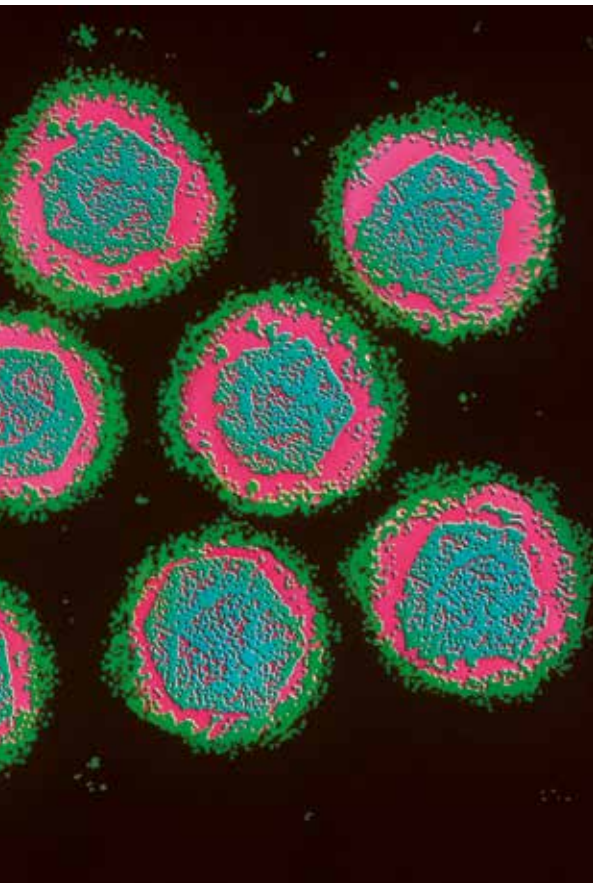
Castro MC, Wilson ME, Bloom DE. Disease and economic burdens of dengue. *Lancet Infect Dis* 2017;17:e70–8.

Katzelnick LC, Coloma J, Harris E. Dengue: knowledge gaps, unmet needs, and research priorities. *Lancet Infect Dis* 2017;17:e88–e100.

Pang T, Mak TK, Gubler DJ. Prevention and control of dengue – the light at the end of the tunnel. *Lancet Infect Dis* 2017;17:e79–e87.

World Health Organization. Dengue control; 2019. https://www.who.int/denguecontrol/en [accessed 31 May 2019].

World Health Organization. Dengue and severe dengue; 2019. https://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue [accessed 31 May 2019].



Kevin Maringer

Lecturer in Microbiology, Department of Microbial Sciences, Faculty of Health and Medical Sciences, University of Surrey, Guildford, Surrey GU2 7XH, UK

e **k.maringer@surrey.ac.uk**

MaringerLab

@MaringerLab

maringerlab

Kevin Maringer graduated with a BSc in Medical Microbiology and Virology from the University of Warwick, and obtained a PhD in herpesvirus assembly in the lab of Gill Elliott at Imperial College London. He has worked on dengue virus–host interactions since his Sir Henry Wellcome postdoctoral fellowship, hosted by Ana Fernandez-Sesma (Icahn School of Medicine at Mount Sinai, New York, USA) and Andrew Davidson (University of Bristol), and now runs his own research group studying arbovirus–host interactions at the University of Surrey. Kevin has been a member of the Microbiology Society since 2009.

What is your greatest achievement to date?

I felt very privileged to be part of some great teams working on Zika virus during the early months of the recent outbreak in the Americas. At the time, very little was known about Zika virus or the disease it causes, and it felt like even relatively minor scientific advancements were making important contributions to help better inform patients and governments.

What is the most rewarding part of your job?

Seeing the students in my lab learn and grow as scientists is very special. It's wonderful to share their excitement when they first get a technique to work, or when they generate their first piece of data.

Wolbachia – basic science and applications of an antiviral bacterium

Ewa Chrostek

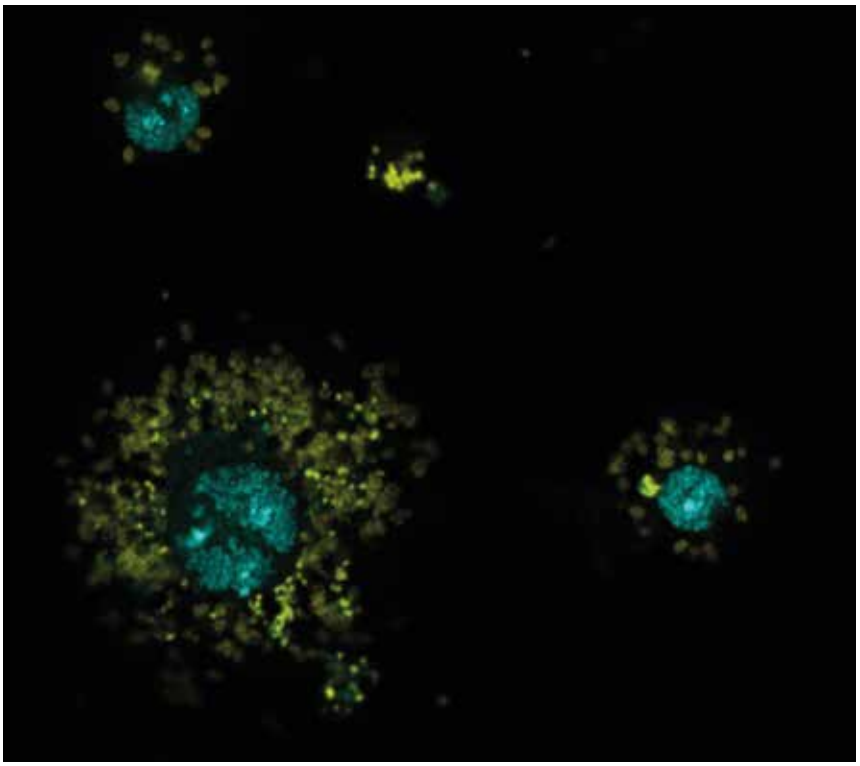
Mosquitoes cause a lot of human suffering – every year over one million people worldwide die from mosquito-borne diseases. *Wolbachia*, an intracellular, insect-associated bacterium, can protect mosquitoes from viruses and reduce their numbers. If mosquitoes are either virus-free or absent, they cannot infect humans. Therefore, *Wolbachia* holds a promise for the successful control of many mosquito-borne diseases.

As the applied use of *Wolbachia* and potential public health benefits have drawn a lot of media attention and research funding, the basic research which has led to these developments has often been forgotten. *Wolbachia*-conferred antiviral protection was initially discovered in the fruit flies, *Drosophila melanogaster*. Fruit flies were also the donors of an antiviral *Wolbachia* for the *Aedes aegypti* mosquito, the main dengue, Zika and chikungunya vector. The research on *Wolbachia* in and from *Drosophila* both founded and continues to inform the field initiatives. Applied *Wolbachia* research, aimed at using it to fight diseases, and the basic research, aimed at understanding how *Wolbachia* works, are not two separate worlds, but rather complementary programmes.

What is *Wolbachia* and how can it help?

Wolbachia is the most prevalent intracellular bacterium on the planet. It naturally infects most insect species, and it is transmitted from the mother to the offspring inside insect eggs. This microbe can spread through a population of insects through 'cytoplasmic incompatibility', where females without the bacterium are effectively sterilised by mating with males harbouring it. *Wolbachia*-infected females (that are immune to this sterilisation) can then produce more offspring every generation, and this is how *Wolbachia* increases in frequency. The likely mechanism of this phenomenon, relying on the *Wolbachia*-produced toxin and antitoxin, has been recently described based on studies in *Drosophila*.

In addition to cytoplasmic incompatibility, *Wolbachia* infection often alters the susceptibility of insects to viruses. Commonly, insects carrying *Wolbachia* are less sensitive to attack by a particular group of viruses. This group includes dengue, Zika, West Nile and chikungunya viruses



Insect cells infected with *Wolbachia*. Fluorescent microscopy image showing *Wolbachia* bacteria (yellow) surrounding *Drosophila* cell nuclei (blue). Ewa Chrostek

causing human vector-borne diseases. However, how *Wolbachia* produces this effect is poorly understood. To understand the mechanism of *Wolbachia*-induced pathogen blocking we need to develop new research tools and techniques. Meanwhile, approaches using *Wolbachia* in the wild are in trials globally, with the aim to reduce the burden of arboviruses in humans.

Killing mosquitoes with *Wolbachia*

Wolbachia-induced mating incompatibilities can be used to reduce the number of certain insects or even eradicate them completely. In this case, fewer-to-no mosquitoes means less-to-no disease. In practice, this strategy involves artificial rearing (in the laboratory insectaries and mosquito factories) and releasing *Wolbachia*-infected mosquito males, which mate with wild females, that then produce no offspring. If a sufficient number of incompatible males are released, the population of the disease vector may even collapse. This strategy was first applied in 1967 to eradicate the vector of filariasis in one village in Myanmar. The approach was re-established forty years later to target other diseases and mosquito species in French Polynesia and the USA.

Unlike pesticide alternatives, *Wolbachia* release does not damage non-target insects and leaves no environmental chemical residue that may harm human health. If mosquito populations cannot be eradicated, repeated releases, often year by year, can be performed to suppress populations. One challenge this strategy faces though is separating mosquito males from females on a large scale. This process is error-prone, and if enough *Wolbachia*-infected females are released, then the population suppression strategy will cease to work (as infected females can produce offspring with infected males).

Making mosquitoes virus-free

As with many other breakthrough discoveries, the discovery of *Wolbachia*-conferred antiviral protection was first made in the fruit fly. After challenge with pathogenic viruses, *Wolbachia*-infected flies had lower viral load and survived better than their *Wolbachia*-free counterparts. *Drosophila* and mosquitoes are closely related, so shortly after the experiments from flies were repeated in *Aedes aegypti*, the vector of dengue, Zika, West Nile and chikungunya viruses. And with success: *Wolbachia* could reduce both viral load and transmission in mosquitoes. Pilot releases of *Wolbachia*-infected virus-resistant *Aedes aegypti* have now been undertaken in Australia, Indonesia, Vietnam, India, Sri Lanka, Brazil, Colombia, Fiji, Vanuatu, Kiribati and Mexico. Early data are encouraging, and the upcoming years will establish the success of these field trials.

And there is a twist to this story. As *Aedes aegypti* mosquitoes do not harbour natural *Wolbachia* infections, *Wolbachia*

from *Drosophila* has been introduced there artificially in the laboratory, with the fruit fly as the first *Wolbachia* donor in this interspecies *Wolbachia* transplant. Although many other insects have also served as a source of *Wolbachia* for *Aedes aegypti*, *Wolbachia* from *Drosophila melanogaster* is dominating the field releases lead by The World Mosquito Program.

Basic and applied *Wolbachia* research – two sides of the same coin

Basic research on the fruit fly, *Drosophila melanogaster*, has initiated the efforts to eradicate diseases by making mosquitoes disease-proof. Now, studies on *Wolbachia*-induced effects could improve current or initiate novel antiviral interventions.

Drosophila is a great model to study mechanisms of pathogen blocking by *Wolbachia*. Flies, in contrast to mosquitoes, can be reared easily (for example, they can complete their life cycle in a single small vial, and they do not need to eat blood). They also do not try to bite you all the time! Further, as a natural *Wolbachia* host, *Drosophila* may be a good model to study the antiviral protection by itself, without all the additional effects observed in *Aedes* due to the recent *Wolbachia* transplantation.

Although the general mechanism of *Wolbachia*-conferred protection remains unknown, studying *Wolbachia* from *Drosophila* has taught us a lot about its applications in vector-borne disease control.

1. Not all *Wolbachia* strains are the same. Strains differ in the strength of the antiviral protection they induce, in their sensitivity to heat stress, and in their ability to spread through populations. Choosing the best strain for the field applications is important, as once any *Wolbachia* gets established in the population, mating incompatibilities will prevent its easy replacement with another *Wolbachia* strain.
2. The more *Wolbachia* in an insect, the stronger the antiviral protection. Yet, this leads to a higher burden on the insect – more 'mouths to

Mosquito rearing cages. Ewa Chrostek

***Drosophila melanogaster*, the fruit flies.** Krzysztof Kuś

feed'. The choice of optimal *Wolbachia* strain for field interventions has to include the cost-to-benefit ratio.

3. Antiviral effects are complex. How much virus blocking occurs depends not only on *Wolbachia* but also on the host, the virus and the environmental conditions. All of these can change over time. Without knowing exactly how protection occurs, it is hard to predict how efficiently this strategy will operate in the wild.

Basic research on the mechanisms of *Wolbachia*-induced effects, especially the mechanism of pathogen blocking, could improve current or initiate novel strategies aimed at eliminating arboviruses. The knowledge gained could be used to the benefit of humans extending far beyond the control of vectors and vector-borne diseases.

Further reading

Chrostek E, Marialava MSP, Esteves SS, Weinert LA, Martinez J. *Wolbachia* variants induce differential protection to viruses in *Drosophila* melanogaster: a phenotypic and phylogenomic analysis. *PLoS Genet* 2013;9:e1003896.

Lindsey ARI, Bhattacharya T, Newton ILG, Hardy RW. Conflict in the intracellular lives of endosymbionts and viruses: a mechanistic look at *Wolbachia*-mediated pathogen-blocking. *Viruses* 2018; 10:141.

Teixeira L, Ferreira A, Ashburner M. The bacterial symbiont *Wolbachia* induces resistance to RNA viral infections in *Drosophila melanogaster*. *PLoS Biol* 2008;6:e1000002.

The MosquitoMate Program USA. https://mosquitomate.com/?v=3.0 [accessed 3 June 2019].

The World Mosquito Program. https://www.worldmosquitoprogram.org [accessed 3 June 2019].

Ewa Chrostek

FEBS Fellow (until 2019) and Marie Skłodowska-Curie Fellow (from 2019), Institute of Integrative Biology Biosciences Building, University of Liverpool, Crown Street, Liverpool L69 7ZB, UK

e **echrostek@gmail.com**

@EwaChrostek

ewa-chrostek-0474971a

I gained my master's degree in Biotechnology (Jagiellonian University, Krakow, Poland) and PhD in Host–Microbe Interactions (Instituto Gulbenkian de Ciencia, Oeiras, Portugal). Subsequently, I was an EMBO Fellow at the Max Planck Institute for Infection Biology (Berlin, Germany). Since March 2018, I have been working at the University of Liverpool, UK.

What inspired you to become a microbiologist?

I am a child of a microbiologist and a biochemist. We had a lot of biology textbooks at home and I loved to visit labs, with all of the interesting machines, colourful science posters, and nice people. Beyond any doubt, my parents inspired me to become a scientist.

How do you see this field changing in the future?

I hope more work will be done on the genomic dark matter – genes and proteins we know nothing about. Many of these are essential to keep cells alive. Others may have very specific functions in processes we cannot predict or imagine. I think a lot of fascinating biology is still out of our reach, and we need systematic approaches to address this at a large scale.

Coloured scanning electron micrograph of a male *Aedes aegypti*. Eye of Science/Science Photo Library

Engineering transgenic mosquitoes to prevent disease transmission

Christine Reitmayer, Priscilla Tng and Luke Alphey

Mosquitoes vector a variety of arboviruses, such as chikungunya, dengue and Zika viruses. Increasing international travel and trade has contributed to the spread of mosquito species into locations from which they were historically absent. The effects of climate change are also predicted to change the distribution of suitable habitats for species capable of transmitting arboviruses (such as *Aedes* and *Culex* species); diseases that have predominantly been associated with countries in tropical and subtropical regions, now also have the potential to become a serious threat to countries further from the equator.

The most effective way to prevent arbovirus infection is management of their insect vectors. Pesticides are still the most effective means of mosquito population control currently available; however, pesticide resistance and the environmental impact of the extensive use of insecticides urges research into alternative strategies for preventing arbovirus transmission. Such alternative strategies include genetic modification of mosquitoes – with the aim of either population suppression or population replacement.

Reducing disease transmission via population suppression or population modification

Population suppression strategies aim to reduce the number of vector mosquitoes in a certain area, to a level that will inhibit disease transmission. An example is genetically modified mosquitoes engineered by Oxitec that carry a repressible lethal gene. Males carrying this gene are released into the field. If they successfully mate with a wild-type female, offspring will die – if sufficient males of sufficient quality are released, the target population will decline and collapse. For this technology to be successful, certain conditions need to be met: quite a large number of male mosquitoes needs to be released in order to achieve the desired effect, though this number can be reduced once the target population has been suppressed; the released males need to successfully compete with wild-type males for a mating partner; males need to be released on a spatial scale appropriate for their dispersal distance – for *Aedes aegypti* this is typically less than 100 m, though may be higher for other mosquito species. Releases of such males have been successfully conducted in locations such as Brazil, Grand Cayman and Malaysia. Other means of sterilising males, such as the use of cytoplasmic incompatibility, have similar properties, though with some differences in detail. In theory, and in laboratory cage experiments but not yet in the field, infertility may be spread through a target population more aggressively by the use of gene drive systems (a genetic strategy for achieving super-Mendelian inheritance). Such approaches potentially require much lower release numbers, so deployment may be much cheaper, but they are also harder to control, i.e. limit or reverse after release, so regulatory and social issues will likely be more problematic.

Population modification strategies

Population modification strategies, also known as population replacement, aim to spread a gene into vector populations that reduces the vector competence of mosquitoes without killing them; if successful, the vectorial capacity of the population would be reduced without substantially reducing the number of mosquitoes. While such 'refractory' genes could be introduced by mass-release of modified mosquitoes, for long-term persistence and economic reasons relating to release numbers, it is generally assumed that for large-scale use, the refractory gene(s) will need to be coupled to a gene drive, though initial trials might use simple mass release.

What gene or genes might we use to reduce vector competence? One such genetic system, conveniently coupled to a gene drive system, has been found in nature. *w*Mel, a strain of *Wolbachia* found in fruit flies, protects the flies from some pathogenic viruses. Artificially transplanted to *Aedes aegypti* mosquitoes, it reduced the ability of such mosquitoes to transmit dengue virus. *Wolbachia* is maternally inherited and uses various tricks to bias inheritance in its favour, thereby representing one of the many gene drive systems found in nature. Though the molecular basis of the virus-suppressing activity, and indeed of the gene drive mechanism, is poorly understood, this gene drive-plus-refractory system has entered field trials in several countries.

Many other gene drive systems are known in nature and have inspired attempts to develop synthetic ones. None have yet reached field trials, partly because of the difficulty of engineering robust gene drives and partly because of regulatory and social issues around the use of recombinant DNA methods that *Wolbachia*-based methods have to date avoided.

Several additional aspects affecting gene drive function will require further field work to resolve, particularly issues around the field ecology and population structure of mosquitoes. *Aedes aegypti*, an important disease vector, is more than happy to spend its whole life in one's backyard where it usually finds all it needs – mating partners, a blood source (such as the human occupants of the house), an energy source (nectar from flowering plants) and breeding grounds (any standing water, for example bird feeders). Low mobility may increase the need for human intervention to spread a gene, where this is desired, but can, however, also be an advantage when an effect is only aimed to be achieved in a certain area at a particular point in time, perhaps for targeted population suppression. In such a case, a highly targeted reduction of a mosquito population could be achieved with minimal environmental impact and off-target effects to other species.

Possible targets for genetic modifications in mosquitoes

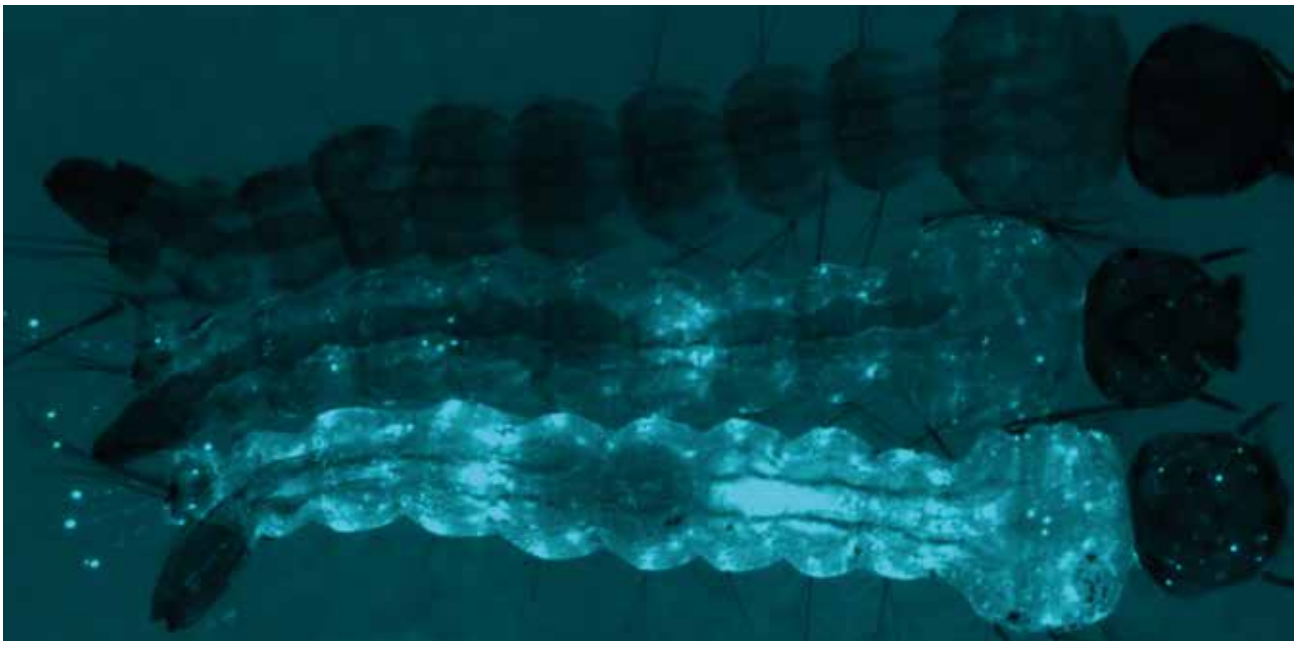
Let's assume for a moment that we would have a gene drive that works in the desired way – what would then be a desired trait to drive through a mosquito population? For anti-virus traits, that would depend on the mosquito species (as different species are vectors for different arboviruses) and perhaps also the intended area for use (as different arboviral diseases or combinations of those are endemic in different areas of the world). Even for a given vector–

virus combination, there are a range of potential approaches to engineering refractoriness, as well as the possibility of co-opting existing ones, as with *Wolbachia*. Most strategies developed so far aim to utilise antiviral insect immune pathways, especially RNA interference (RNAi), which is a major antiviral immune response in insects. Mosquitoes expressing long hairpin versions of virus sequences showed good resistance against dengue virus. Similarly, systems expressing small interfering RNAs have been developed to confer resistance against specific viruses (namely Zika, dengue and chikungunya) in transgenic mosquitoes.

Other elements of the insect immune system can also be used, for example the JAK/STAT pathway. Modulations of this pathway have been shown to provide reduced susceptibility to dengue virus infection; however, this approach was to date not found to be effective against chikungunya or Zika viruses. This might reflect a lesser importance of the JAK/STAT pathway in the antiviral immune response in insects compared to the RNAi pathway.

Entirely exogenous factors may also be useful, for example expression of specific single-chain antibodies, which have been used to reduce vector competence for both viral and cellular pathogens. Immune effectors from other species, such as antimicrobial peptides, have also been shown to be effective in some cases.

A significant challenge to geneticists developing such systems is to achieve the desired effect without adversely affecting the mosquito. Off-target effects of various types might impose a fitness cost on transgenic mosquitoes. If this is the case, mosquitoes carrying the desired trait have a (potentially significant) disadvantage compared to their wild-type counterparts. This might manifest through any of a range of traits such as development time, longevity, mating competition or fecundity, and perhaps only under certain conditions. Off-target effects and fitness costs can potentially be reduced by restricting expression of system components to key tissues for virus infection and transmission, especially the adult female midgut and salivary glands. This may be achieved using tissue-specific promoters for the expression of the gene of interest, such as using a carboxypeptidase promoter which is induced by a bloodmeal and the expression is restricted to the midgut. This means that the payload gene would only be expressed at a time point in a female's life – only females blood feed – when there is the potential that it acquires an arbovirus infection (through an infectious bloodmeal) and would be restricted to the body tissue that is the first defence barrier against arbovirus



Homozygote (bottom) and heterozygote (middle) transgenic mosquito larvae carrying a blue fluorescent whole body marker next to a non-transgenic (top) mosquito larvae not expressing any fluorescent protein. Michelle Anderson

infection in mosquitoes. Despite some notable successes with such systems, the range of promoters and other tools for mosquito synthetic biology is still very limited, which restricts the possibility for rational design of both gene drive and pathogen-refractory systems, correspondingly increasing the amount of trial-and-error and time required. Although many questions are still unanswered and there are many challenges to overcome, genetic modification of mosquitoes has the potential to ease the burden of arboviral diseases imposed on millions of people worldwide, while at the same time reducing the environmental footprint and health implications that come with the extensive use of insecticides.

Further reading

Alphey L. Genetic control of mosquitoes. *Annual Review of Entomology* 2014;59: 205–224.

Buchman A, Gamez S, Li M, Antoshechkin I, Li HH *et al.* Engineered resistance to Zika virus in transgenic *Aedes aegypti* expressing a polycistronic cluster of synthetic small RNAs. *Proc Natl Acad Sci* 2019;116:3656–3661.

Gantz, VM, Jasinskiene N, Tatarenkova O, Fazekas A, Macias VM *et al.* Highly efficient Cas9-mediated gene drive for population modification of the malaria vector mosquito *Anopheles stephensi*. *Proc Natl Acad Sci* 2015;112: e6736–e6743.

IUCN Task Force on Synthetic Biology and Biodiversity Conservation. *Genetic frontiers for conservation: an assessment of synthetic biology and biodiversity conservation*. Gland, Switzerland: IUCN; 2019.

National Academies of Sciences, Engineering, and Medicine. *Gene Drives on the Horizon: Advancing Science, Navigating Uncertainty, and Aligning Research with Public Values.* Washington, DC: The National Academies Press; 2016.

Christine Reitmayer

The Pirbright Institute, Ash Road, Woking GU24 0NF, UK

e **christine.reitmayer@pirbright.ac.uk**

Christine Reitmayer joined the Arthropod Genetics Group at The Pirbright Institute as a postdoctoral research scientist in 2018. She is engaged in research designing transgenic mosquitoes less capable of transmitting viral diseases and is interested in novel strategies of vector control as a means of preventing disease transmission.

Priscilla Tng

The Pirbright Institute, Ash Road, Woking GU24 0NF, UK

e **priscilla.tng@pirbright.ac.uk**

Priscilla Tng is a research scientist in the Arthropod Genetics Group at Pirbright Institute, developing viral refractory genes for gene drives. She obtained her Diploma in Biology from the University of Würzburg and worked for six years at DSO National Laboratories, Singapore, in combat care. She joined the Pirbright Institute in 2016.

Luke Alphey

The Pirbright Institute, Ash Road, Woking GU24 0NF, UK

e **luke.alphey@pirbright.ac.uk**

Luke Alphey works in the emerging field of genetic pest management, particularly on synthetic biology approaches in mosquitoes – building engineered sterile males, gene drives and mosquitoes less able to transmit viruses. Professor Alphey was selected as a Technology Pioneer of the World Economic Forum in 2008 and BBSRC Innovator of the Year 2014.

What is the best career decision you have ever made?

Christine: It was definitely the decision to undertake my PhD project at the University of Southampton, which was the first step towards a research career and also ended up being a very pleasant experience. I was supervised by two incredibly dedicated and motivated supervisors, who not only taught me many useful skills, but also shaped my understanding of science and the responsibility that comes along with working in research.

Why does microbiology matter?

Christine: It sheds light on an otherwise invisible world which is crucial to understanding health and wellbeing.

Annual Conference **2020** #Microbio19

30 March–3 April 2020 – Edinburgh, UK

The Microbiology Society celebrates its 75th anniversary in 2020. To mark the anniversary the Society's Annual Conference will – for one time only – be extended to a five-day event, from Monday 30 March to Friday 3 April 2020. This prestigious meeting will be held at the Edinburgh International Conference Centre (EICC).

Work is currently underway on programme development and the global line-up of expert speakers is being confirmed. The meeting will, as always, consist of symposia, workshops, forums, poster sessions and a trade exhibition. It is designed to offer ample opportunities for formal and informal networking for both early career and established microbiologists.

Fleming Showcase lectures

The Microbiology Society's Fleming Prize is awarded each year to an early career researcher who has achieved an outstanding research record within 12 years of being awarded their PhD. As part of the celebrations for the anniversary, Annual Conference will include an additional Fleming Showcase day on Monday 30 March 2020 and will be followed by the standard four days of scientific sessions.

The Fleming lectures will be used as an opportunity to formally observe the legacy of past Fleming Prize winners and has been organised by a committee of them, chaired by Sir Paul Nurse.

The following Fleming talks have been confirmed:

- My life in science
  Paul Nurse Francis Crick Institute, UK
- Genetic control of mosquitoes
  Luke Alphey The Pirbright Institute, UK
- Predatory *Bdellovibrio* Bacteria – 58 years of understanding them as allies against AMR infections
  Liz Sockett University of Nottingham, UK
- Visualizing bacterial nanomachines *in situ* by electron cryotomography
  Grant Jensen California Institute of Technology, USA
- The expanding virosphere
  Edward Holmes University of Sydney, Australia
- Palaeomicrobiology: what ancient DNA can tell us about pathogens from the past
  Mark Pallen Quadram Institute, UK
- Orchestrating gene regulation across the genome and across the cell
  Stirling Churchman Harvard University, USA

EICC

Keep up-to-date with events on Twitter: **@MicrobioSoc**

rabbit75_ist/Thinkstock

Abstracts

Annual Conference attracts over 1,600 attendees for the UK's largest annual gathering of microbiologists. It is designed to cover the breadth of microbiology research and its oral abstracts and posters reflect this comprehensive scientific programme.

Abstract submissions will be opening soon so don't miss out on this opportunity to showcase your microbiological work and research to this broad scientific community.

Annual Conference 2020 abstract submissions open **week commencing 19 August 2019.**

Submissions close on **9 December 2019.**

Notifications of acceptances will be made from **14 January 2020**.

Conference Programme 2020

You can view the current 2020 programme on the Society's website, including a list of the invited speakers and their talk titles and abstracts. The scientific sessions will cover the following:

Main symposia:

- AMR
- Back to the future
- Bacteroidetes
- Bioproduction and biomaterials
- Dynamic cell
- Epigenetics
- Exploring the eukaryotic tree of life
- Marine microbiology
- Novel eukaryotic drug targets
- Outer layers of microbiology
- Phage biology
- Public health microbiology
- Skin-full of viruses
- Starve the (livestock) pathogen, feed the world
- The secret life of mobile genetic elements
- Toxins and antitoxins
- Virus modulation of cell stress

Eukaryotic and prokaryotic forums:

- Environmental and applied microbiology forum
- Genetics and genomics forum
- Infection forum
- Microbial physiology, metabolism and molecular biology forum

Virology workshops:

- Cell stress and viruses
- Clinical virology
- DNA viruses
- Negative-strand viruses
- Positive-strand and double-stranded RNA viruses
- Retroviruses

Professional development sessions:

- Bioinformatics
- Entrepreneurship
- Fellowship
- Teaching in higher education
- Unconscious bias

Visit the Society website to view all the information about the Annual Conference (**microbiologysociety.org/annualconference**) and follow the Twitter hashtag **#Microbio20** for regular updates.

Destination Edinburgh

The Society is returning to one of its most popular Annual Conference destinations. Edinburgh is globally recognised as a world-leading authority in the sciences and is home to some of the leading centres of microbiological research in Europe.

Annual Conference will take place at the EICC. This award-winning venue is a centre of excellence for world class events and conferences and is situated in the heart of Edinburgh. Its impressive facilities include adaptable auditoria, break-out suites and spacious exhibition and reception areas, which will all be for the exclusive use of the Microbiology Society and its delegates during the week of Annual Conference 2020.

Travel and accommodation

Visitors to Scotland's capital are served by two major railway stations, an airport providing UK and international flights and an extensive road network. See the event details on the Society's website for further information.

Edinburgh is a popular destination and the Society encourages all delegates to secure accommodation and to make travel plans as early as possible as hotel rooms fill-up quickly.

To support you in securing your accommodation we provide links to our booking and accommodation services via Reservation Highway. This travel and venue agency have secured negotiated rates at hotels to suit a broad range of budgets. If you require any further information for personal or group hotel bookings, please call **01423 525577** (during office hours) or email **admin@reservation-highway.co.uk** at any time.

Focused Meetings 2019

Our Focused Meeting programme continues in September and October with **IMAV 2019: International Meeting on Arboviruses and their Vectors**, **Microbes In Medicine: A Century Of Microbiology At Trinity College Dublin** and **Antimicrobial drug discovery from traditional and historical medicine**. The 2020 Focused Meeting programme will be announced later in the year.

IMAV 2019: International Meeting on Arboviruses and their Vectors 2019

#IMAV19

5–6 September 2019 | University of Glasgow, UK


Erik Kartis/Thinkstock

The Society is delighted to be hosting the third IMAV meeting. It will be a great occasion to come together and hear about new research and developments. As always, the event will include highly recognised invited speakers and opportunities to network with colleagues and interact with potential new collaborators.

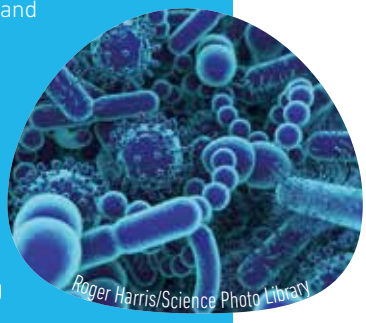
Key topics include pathogenesis, immunology and vaccines, virus–host interactions, virus replication and vector biology.

Microbes In Medicine: A Century Of Microbiology At Trinity College Dublin

#MicroMed19

24–25 October 2019 | Trinity College Dublin, Ireland

This meeting brings together scientists who share an interest in the contribution of microbes to human and animal medicine, with a focus on recent advances in understanding pathogenic mechanisms and in the use of microbes and microbial products to treat and prevent disease. The programme features keynote speakers who are international leaders in their fields and will also give early career stage researchers an opportunity to present their recent research findings as offered oral presentations.


Roger Harris/Science Photo Library

Key topics include the use of genomics to study antibiotic resistance and virulence, gene regulation in pathogens, antibiotic persistence in bacteria, microbiota in health and disease, and microbial surfaces.

The discipline of Microbiology at Trinity College Dublin celebrates its centenary in 2019 and this meeting will have an historical dimension, together with a celebration of the strength of the field today.

Antimicrobial drug discovery from traditional and historical medicine

#AMRmeds19


Mikola249/thinkstock

29 October 2019 | Ashmolean Museum, Oxford, UK

Researchers from a diverse range of fields, including microbiology, chemistry and botany, will be attending this pilot one-day meeting to scope what is needed in order to build an effective research network. The number of places at the meeting is limited so early registration is advised.

Microbiology Society members receive a discount when registering for events. Visit our website (**microbiologysociety.org/events**) for further event details and registration information.

The Focused Meeting programme is determined by our membership through our proposal scheme. Visit our website (**microbiologysociety.org/proposals**) to find out more about how the programme is devised.

Keep up-to-date with events on Twitter: **@MicrobioSoc**

Society-Supported Conference Grants

The Microbiology Society is pleased to announce that the following meetings have been awarded Society-Supported Conference Grants for events taking place in 2020.

Event Name	Date of Event	Location
JAM Talks	Multiple dates in 2020	Birmingham, UK
Biofilms in nature, industry and environment: impact and implications	1 January 2020	Kolkata, India
Recently Independent Virology Researchers (RIVR) 2020	9–10 January 2020	Leeds, UK
Galleria mellonella Workshop	15–17 May 2020	Frascati, Italy
19th International Symposium on the Biology of Actinomycetes (ISBA 2020)	21–25 June 2020	Toronto, Canada
MedVetPathogens 2020 Conference – 6th Prato Conference on Animal Bacterial Pathogenesis	12–15 October 2020	Prato, Italy

Visit our website (**microbiologysociety.org/ssconferences**) for a full list of Society-supported conferences.

If you are organising an event in any field of microbiology and meet the eligibility requirements, don't miss out on the opportunity to receive up to £2,000 to cover invited speakers' costs. Applications are welcomed for any meetings taking place in 2020 and the next closing date is Monday 16 December 2019. Visit our website (**microbiologysociety.org/ssconference grants**) for further information and application guidelines.

MICROBIOLOGY SOCIETY

FOCUSED MEETING 2020

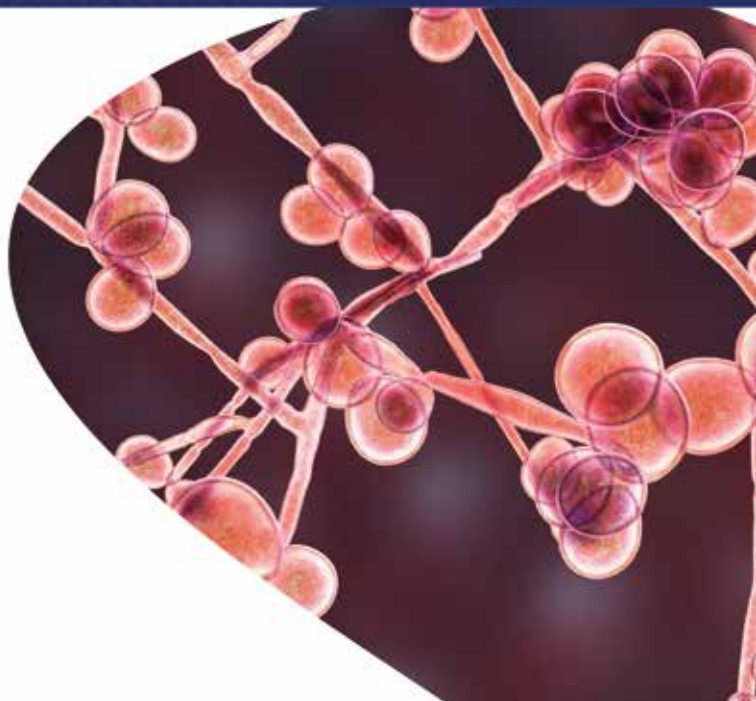
Candida and Candidiasis 2020

SAVE THE DATE

19–23 April 2020, Montreal, Canada

Find out more at microbiologysociety.org/candida2020

@MicrobioSoc
#Candida2020



Federation of Infection Societies Conference 2019

EICC Edinburgh, 11–14 November 2019

#FIS19

The Microbiology Society are delighted to be hosting the Federation of Infection Societies Conference 2019 in Edinburgh this year. Professor Sheila Patrick tells us all why this is a meeting not to miss.

"The Federation of Infection Societies' annual conference represents a unique collaboration of societies across the UK with interests in multiple aspects of Infectious Diseases. FIS conferences provide the opportunity for Microbiology Society members to interact with and present their research through offered oral or poster presentations to infectious disease and clinical microbiology specialists, biomedical scientists, infection control nurses and pharmacists, all at one conference, while attending sessions covering the most important current issues facing infectious disease control, prevention, diagnosis and treatment. The conference usually attracts over 600 delegates and is being held at the Edinburgh International Conference Centre (EICC) from 11 to 14 November 2019."

Find out more about the event by watching our video with Sheila Patrick (**microb.io/FIS19video**) on YouTube.

Late breaker: abstract submission (poster presentations only)

Abstract submission for oral presentations is now closed. We welcome abstract submission for poster presentations until Monday 9 September. Visit the website (**microbiologysociety.org/FIS19**) for a full list of topics.

Registration

Visit our website (**microbiologysociety.org/FIS19**) to register for the event. The following is included in your registration fee:

- Admission to all sessions
- Admission to industry events
- Full access to the trade exhibition
- Full access to scientific poster sessions
- Hot buffet lunch
- Tea and coffee breaks
- Two drinks during the evening receptions and poster presentations
- A delegate bag and conference material
- A conference programme guide
- Access to an online abstracts book
- Certificate of attendance
- Access to CPD points

Dinner and dance

The Hub, Edinburgh EH1 2NE

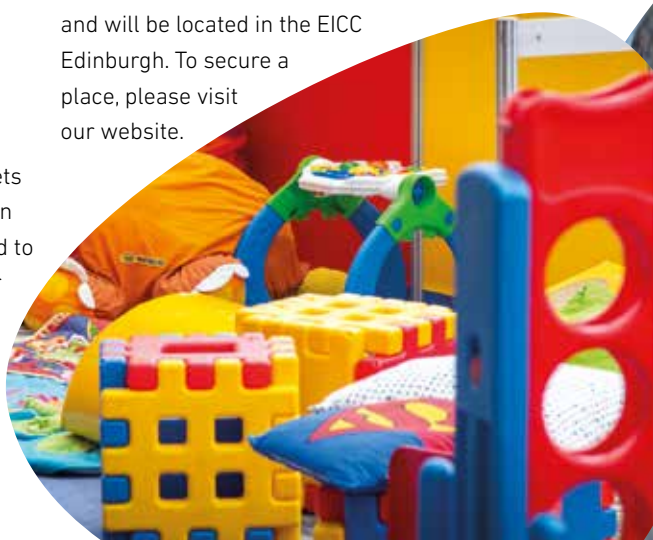
This year delegates can join us for a two-course dinner, followed by a traditional Ceilidh and live band. Tickets are £45 per person and full details can be found on our website. You will need to secure your tickets when you register for the conference and if you would like to bring a guest please email us at **conferences@microbiologysociety.org**.

Continuing professional development (CPD) accreditation

At present, FIS 2019 has been accredited by the Royal Society of Biology (84 CPD credits), the Royal College of Pathologists (41 CPD credits) and the Institute of Biomedical Science (category: Professional Activity). Those wishing to claim CPD credits should sign a daily register held at the help desk, which is located by the registration desk. Email **profdev@microbiologysociety.org** for further information.

Crèche

The Society is again teaming up with Nipperbout to provide a free crèche during FIS 2019. The crèche will be available to all children of delegates between the ages of 0 and 12 years, on a first-come, first-served basis, and will be located in the EICC Edinburgh. To secure a place, please visit our website.



Early Career Microbiologists' Forum Update: the importance of networks

The 2019 Annual Conference in Belfast was hugely successful for Early Career Microbiologists' (ECM) Forum members. It's clear that the presence of the Forum is increasing year on year, and it's heartening to see that the new President of the Society, Judith Armitage, is keen to continue the positive steps that her predecessor, Neil Gow, took to cement the role of early career members at the heart of the Society.

From a pool of 81 posters, the ECM Forum Executive Committee awarded their Annual Conference Poster Prize to Emily Warman, University of Birmingham, for her work on the properties and directionality of intragenic promoters in *E. coli*. David Sünderhauf from the University of Exeter was highly commended for his submission. One of my favourite ECM Forum activities, the Conference co-chairing scheme, is increasing in popularity year on year, with 28 ECM Forum members taking advantage of this opportunity in Belfast.

A highlight for me is always the pre-Conference networking event. Initially organised by Society staff, the Executive Committee took on this event when they first formed, and it has received increasingly positive feedback. Following this year's event, I reflected on just how important it is to construct and maintain a network of your peers that you can rely on for support and guidance (and maybe the occasional glass of 'sorry your experiment failed again' wine). For some, these networks come ready-made. I am fortunate to work in a large group with several PhD students at the same stage as I am, and from talking to people during the event it was evident that others are also lucky enough to be in the same boat.

This is not the case for everyone though. If your cohort is small, you have recently relocated or you just don't share the interests of those around you, then it can make the early stages of your career feel isolating and considerably more difficult than they should be. Imposter syndrome, for example, is thought to affect a large proportion of PhD students. This can lead to, or be exacerbated by, mental health conditions such as depression, anxiety and obsessive-compulsive disorder. These feelings can be made worse if the act of strengthening your network or finding a support group feels challenging.

To offer a solution to this, we have set up a LinkedIn group exclusively for ECM Forum members. This group is free to join once you are a member of the Forum (which is also free for Microbiology Society members!). We hope that this will become a platform for early career microbiologists to meet one another, share their experiences in applications and interviews and ask for experimental tips and troubleshooting … whatever you like! To join, simply send a request to the group after you have signed up to the Forum and a member of Society staff will approve it within a few days (Monday–Friday). We hope to meet you all there soon.

As always, if you have any questions or suggestions for the Forum then please do get in touch!

Rebecca Hall
Communications Representative,
ECM Forum Executive Committee

Are you an ECM Forum member? Join the Microbiology Society Early Career Microbiologists' Forum LinkedIn group: **microb.io/ECMForumLinkedIn**.

Careers Focus: managing a research laboratory

During this year's Annual Conference, we hosted an 'Essential Skills' session on managing a research laboratory. The day covered all aspects of managing a lab: project management, managing assets, health and safety and managing people. Here we give an overview of each component; to find out more, members can access the full presentations on Mi Society.

Managing projects

Managing a research lab means managing competing deadlines for many different tasks, as well as maintaining a good work-life balance. Nicola Stonehouse, Professor of Molecular Virology at the University of Leeds and Chair of the Communications Committee, outlined how leading a lab involves dealing with a multitude of functions that can lead to converging deadlines.

While the research record is often the main reason for group leaders being recruited, it was acknowledged that 'research' is a complex job and includes many tasks: supervising lab members, writing grant applications and managing budgets as well as overseeing the team's work. Teaching, including lectures and marking, is a requirement of many group leaders, but also demands a lot of time to plan and evaluate modules. On top of contracted responsibilities, external responsibilities are essential for your own career development, and include participating in grant panels, reviewing, and sitting on other external committees such as the Microbiology Society's Council. These activities can be rewarding both personally and professionally; for example, attending conferences to network can lead to new collaborations and subsequent grant applications for more funding.

But all these tasks lead to conflicting deadlines and need to be prioritised! Attendees were given a scenario reflecting a real-life demanding day in the office. They were asked to prioritise the issues needing attention as either 'Urgent' or 'Important', helping them to see how to manage competing issues realistically and reasonably and emphasising the importance of using all the tools available to get things done.

Finally, Nicola reminded attendees to ensure that time is preserved for a personal life and hobbies to keep you balanced while running a research lab.

Managing assets

The next section, 'Managing assets', by Nigel Brown, Emeritus Professor of Molecular Microbiology at the University of Edinburgh and former Society President, provided an overview of the different types of funding available to group leaders. Nigel focused on what makes a successful grant application: as well as high-quality research, a checklist was provided for attendees to use when writing a grant application.

As well as emphasising the responsibility to maintain resources and stay in budget, Nigel ended the session noting the importance of reporting appropriately. Different funders may have different concluding requirements, but reporting results appropriately also helps define future strategic funding decisions, as well as being a useful self-reflection exercise.

Best practices

Our penultimate section, 'Best practices in Lab Management', was delivered by Lindsay Murray, Health and Safety Manager at the University of Edinburgh. Lindsay provided a brief overview of the Health and Safety Executive (HSE) and summarised how the health and safety compliance process works, focusing on how COSHH regulations interact with other HSE regulations. The unrecognised hazard

Grant application checklist

- ☐ Is the case for support clearly written?
- ☐ Has an expert read it?
- ☐ Has someone who doesn't know the area in detail read it?
- ☐ Have you fully justified the resource required?
- ☐ Have you indicated where your application matches the funders priorities?

of late and lone working was covered, as well as the impact of stress on individual researchers' health, something which is quite often overlooked. Attendees were also given some interesting case studies showing the need to plan thoroughly; for example, with scheduled maintenance of equipment to avoid unnecessary disasters in the laboratory.

Getting the most out of your team

The day concluded with Lindsay Hall, Research Leader at the Quadram Institute, outlining factors to consider when forming a research group. Lindsay introduced attendees to the process of recruiting staff and students and noted the importance of setting different expectations for individuals based on career stage and contracted work commitments. The group used questionnaires on personality and learning styles to think about how they work with different types of people.

The session ended with examples of tried and tested team activities that Lindsay used to build her team's rapport, such as scheduled dinners and using public engagement activities to get people working together. Finally, managing a team also involves difficult conversations which produce positive outcomes when done effectively, so Lindsay took attendees through dealing with 'unspoken thoughts and feelings' vs 'what we actually say and do', and provided tips to prepare for difficult conversations.

There is so much to consider when managing a research lab and these are general themes illustrated by the personal examples of some of our members. Establishing a good work-life balance, planning for incoming funding, establishing routine health and safety practices and developing nuanced ways of working with team members are all essential parts to start with to successfully lead your research laboratory.

Young Microbiologist of the Year 2019 Competition: meet the finalists

The Microbiology Society is pleased to announce the finalists of the 2019 Sir Howard Dalton Young Microbiologist of the Year competition, which takes place during our Annual General Meeting (AGM) in September.

The prize, which recognises excellence in science, is awarded each year to an early career Society member as part of the Society's mission to advance understanding of microbiology and champion the contribution made by microbiology, its members and their work in addressing global challenges.

For this year's competition the finalists were shortlisted by the Society's Divisions, from entrants who presented at our 2019 Annual Conference and 2018 Irish meeting. The finalists will each give a 15-minute presentation on their research to a panel of judges chaired by the Society's Professional Development Committee Chair. The titles of the shortlisted presentations are below.

Finalists for the 2019 Young Microbiologist of the Year competition

Eukaryotic Division

- **Davis Laundon** Marine Biological Association, UK
  Shining new lights on chytrid cell biology: Quantitative live cell imaging of rhizoid development in an early-diverging fungus
- **Laura Petch** University of Kent, UK
  The impact of natural genetic variation on protein aggregation in *Saccharomyces* species

Irish Division

- **Christine Jordan** Imperial College London, UK
  Understanding how bacterial products from the microbiota enter the host, determining where they aggregate, and their influence over immune cells at these sites
- **Gareth Raynes** Aberystwyth University, UK
  Investigating correlations between endophytic bacteria halotolerance and salt stress mitigation in their host plants

Prokaryotic Division

- **Sarah Worsley** University of East Anglia, UK
  The chemical ecology of protective microbiomes in plant roots and leafcutter ants
- **Naoise McGarry** Trinity College Dublin, UK
  Characterisation of *rpoS* alleles in UPEC strain CFT073

Virology Division

- **Daniella Lefteri** University of Leeds, UK
  Modulation of arbovirus infection by mosquito saliva
- **Michaela Conley** University of Glasgow, UK
  Assembly of a portal-like structure in Feline calicivirus following receptor engagement

This year, the finalists will be joined by 2018 finalist, Paula Seoane (Eukaryotic Division), who was unable to present at last year's AGM due to technical difficulties.

- **Paula Seoane** University of Birmingham, UK
  Exploring the effects of Interferon α on *Cryptococcus neoformans* infection

Promoting your work

In the last issue of *Microbiology Today* we wrote about open research as an extension of Open Access. In this article we discuss different ways to promote your research (open or otherwise) to help raise your profile as a scientist.

Once your article has been published – whether in a journal or as a preprint – you naturally want to draw attention to your work. There are many ways to do this, from the traditional sharing of PDFs and emails to social media and lay summaries. We suggest that you start by making sure that you have a comprehensive bibliography online, either through your institutional webpage or via ORCID* (**orcid.org**). ORCID provides a persistent digital identifier that distinguishes you from every other researcher and, through integration in key research workflows such as manuscript and grant submission, supports automated linkages between you and your professional activities ensuring that your work is recognised.

You'll probably want to start a conversation about your work, which means sharing it widely. Social media can be your friend here (check out our Top Tips) but you should also think about platforms which allow a deeper conversation. One we particularly like is ScienceOpen* (**scienceopen.com**), a free search and discovery engine which goes beyond search to let users add new articles, create public collections, review articles, write plain language summaries, and even track the impact of their work. Our publishing team have been using ScienceOpen for over a year to boost the impact of activities like the Microbiome collection, and you can check out our publishing page (**microb.io/2WHvMqZ**) if you want to explore ScienceOpen.

Top tips for social media

Keep it simple With millions of posts being shared across social media platforms every day it's best to keep your post simple. Use keywords that will grab attention and think about interactive formats such as polls or questions that might help start a conversation. Don't forget to include a hyperlinked DOI, taking the reader to the full text of your article!

Use hashtags Hashtags emphasise your post's relevance and are a great indicator of what is topical or interesting. If your article is particularly timely or topical find the appropriate hashtag and use it – and if nothing else, use the hashtag for the journal your article was published in.

Use mentions Mentions help highlight your post to specific users. If you mention your institution, or a co-author, they might share the post with their followers. Don't forget to mention **@MicrobioSoc** on Twitter and we'll share your tweet with our growing community of 35,000+ followers.

Include images A picture is worth a thousand words, so find an image relevant to your work and include it in your posts. According to a study conducted by Twitter, tweets with images get 35% more retweets than those without.

Get involved Social media is a great way to connect with fellow scientists and interested members of the public. The more exposure you have the more likely people are going to see what you're posting, so get involved in discussions and share posts when relevant. This is also a great way of increasing your network.

Share the love Finally, remember to support the scientific community. If you read an article that you find particularly interesting, do your part to promote that research group's work too!

Platforms like ResearchGate, Academia.edu and ScienceOpen allow you to share your papers widely, but please be careful! While the Microbiology Society journals permit authors to share accepted manuscripts on the day of publication, some publishers are much more restrictive and several of the very large publishers have been trying to have research removed from these platforms.

Outreach is an important part of the research cycle and that means you might want to consider writing plain language summaries for your articles. We've found that Scholarcy* (**scholarcy.com**) can be helpful here, using machine learning technology to digest papers into flashcard-style summaries. Another great option is Kudos* (**growkudos.com**), which lets researchers explain their work in simple language and track the impact through a dashboard, showing the effects of communication plans. The Kudos team say that sharing these plain language summaries can help boost readership by around 23%.

Last but not least, don't overlook the value of blogs and press releases. These longer-form pieces of content allow you to write more about your research, explaining what the work is about and why it is important in a way that complements both the article and your shorter-form social media activities.

Further reading

Fry N, Marshall H, Mellins-Cohen T. In praise of preprints. *Access Microbiology* 2019;1:e000013. doi:10.1099/acmi.0.000013

**We do not receive revenue from these initiatives and are promoting them only because our team truly believes they are useful tools for our members.*

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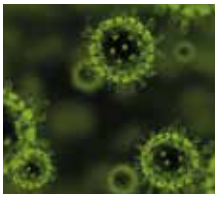

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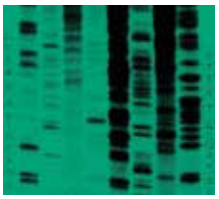

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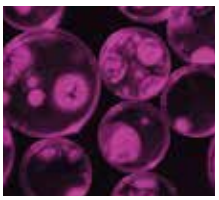

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We hope that you're finding these articles useful. If there is a topic you would like us to address, email us at **journals@microbiologysociety.org**.

UK-PHRST:
the UK's novel approach to outbreak response

The 2013–16 epidemic of Ebola virus disease in West Africa underscored the shortcomings of the international community to both respond to outbreaks and conduct critical research in complex humanitarian crises.

Training in Nigeria (Taq Array Card loading with mock samples). Dr Emeka Ndodo (NCDC)

To address these concerns the UK Public Health Rapid Support Team (UK-PHRST), funded by UK Aid from the Department of Health and Social Care, was formed. The UK-PHRST is a collaboration between Public Health England and the London School of Hygiene & Tropical Medicine, with the University of Oxford and Kings College London as academic partners. The UK-PHRST has a novel triple mandate to work in low- and middle-income countries (LMICs) to carry out the following tasks:

1. Respond to outbreaks.
2. Conduct innovative research on outbreak-prone diseases both during and between outbreaks in order to generate evidence on best practice.
3. Build capacity for LMIC outbreak response.

The UK-PHRST has taken a unique approach in fulfilling its tripartite mandate by tackling outbreaks and outbreak-associated activities in a holistic manner. This has been achieved via the recruitment of a multidisciplinary core deployable team of experts consisting of microbiologists, epidemiologists, clinical researchers, social scientists, data scientists, infection prevention and control experts and logisticians – each specialisation adding knowledge, practical skills and technical expertise to help tackle dynamic problems in the field. The UK-PHRST is a member of the World Health Organization's (WHO) Global Outbreak Alert and Response Network (GOARN) and can deploy under their processes, via direct requests from an LMIC government or in support of UK-Emergency Medical Teams (UK-EMT) or other international stakeholders, all within 48 h of a formal request. To date, the UK-PHRST has responded to a wide array of requests for support for an outbreak response, including to Madagascar (pneumonic plague), the Democratic Republic of the Congo (Ebola virus disease), Nigeria (Lassa fever), Bangladesh (diphtheria), Nigeria (meningitis), Ethiopia (acute watery diarrhoea/cholera) and Sierra Leone (enhanced surveillance for waterborne disease after heavy rains and landslides).

In addition to providing rapid and robust outbreak responses, the UK-PHRST also implements and supports a range of research and capacity-building projects. The challenge is to make these two aspects work synergistically, thus helping to not only provide answers to important research questions, but also to concurrently build in-country outbreak-related research and diagnostic capacity. Examples of research projects with capacity-building elements currently underway include effective diagnostics and laboratory outbreak capability for gastrointestinal pathogens in Sierra Leone; application of metagenomics to outbreaks of undifferentiated febrile illness in Sudan; identification by TaqMan array card system and MinION sequencing of co-circulating pathogens that are clinically indistinguishable from Lassa fever during seasonal Lassa outbreaks in Nigeria; phylogenetic and cluster analysis of human monkeypox samples from the 2018–19 outbreak in Nigeria and rapid response molecular diagnostics for Crimean-Congo haemorrhagic fever.

To help support the ever-growing need for trained specialists to deploy rapidly in response to outbreak callouts, the UK-PHRST has begun to establish a reserve cadre from across the UK that will provide surge capacity and enhanced expertise to the core deployable team. Reservists will remain employed by their primary organisation and be released only when required to deploy. The UK-PHRST issues calls for reservists periodically and is always interested in recruiting high calibre scientists, especially French speakers (a valuable skill for work in francophone Africa), with experience in diagnostics, high-containment microbiology and field work in LMICs. Any interested individuals are encouraged to contact **ukphrst@phe.gov.uk**, or the authors directly, for more information.

Acknowledgements

The views expressed in this publication are those of the author(s) and not necessarily those of the UK National Health System, the National Institute for Health Research or the Department of Health & Social Care.

Jonathan W. Ashcroft and Ben W. Gannon

UK Public Health Rapid Support Team: Public Health England, Porton Down, UK, and London School of Hygiene and Tropical Medicine, London, UK

jonathan.ashcroft@phe.gov.uk

Obituary

Professor Derek Burke 1930–2019

Professor Derek Burke, Honorary Fellow of the Society and President from 1987 to 1990, died in Norwich on 15 March.

Derek trained in natural products chemistry, at the University of Birmingham and then at Yale University, working on steroids and arabinosides. He returned in 1955 to the National Institute for Medical Research with the objective of determining the nucleic acid composition of influenza virus. He was supervised by Alick Isaacs in the Virology Division and James Walker in Chemistry and was clearly inspired by Isaacs who, with Jean Lindenmann, had just discovered the anti-viral protein interferon. During five years of research, Isaacs taught Derek virology, and when he took a Lectureship at Aberdeen University in 1960 he was able, with great energy, to establish a laboratory for virus and interferon research in the Department of Biological Chemistry.

Nine productive years later he was recruited to be founding chair of Biological Sciences at Warwick University. There, while building a new department, he retained his enthusiasm for research on interferon induction by viruses and antibody-affinity purification of the protein. He was elected to membership of the European Molecular Biology Organization (EMBO) in 1980 and was recognised as a world-leading expert in interferon research.

In 1982 he joined the largest biotech company in Canada, Allelix Inc., as Vice-President and Scientific Director, fulfilling an ambition to apply his scientific knowledge commercially. In 1986, Allelix separated its Agriculture and Pharmaceutical Divisions and the former was taken over by a US company.

Derek returned to the UK in 1987 to become Vice-Chancellor of the University of East Anglia (UEA) and his energy and enthusiasm were re-directed to the success of the university. By all accounts he transformed UEA. In 1989, he organised a major building programme for student residences and academic accommodation.

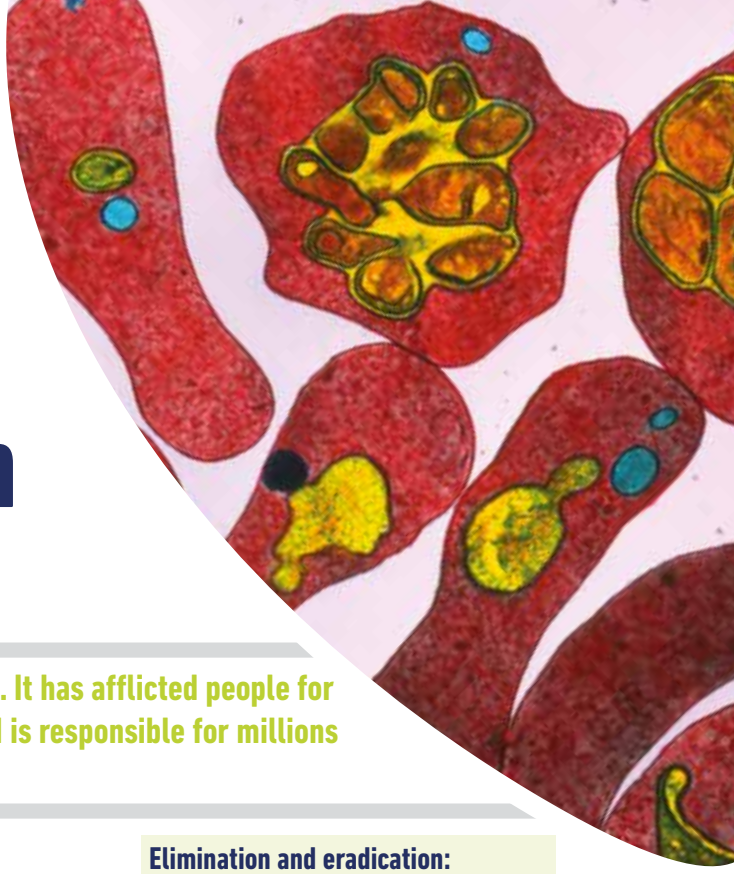
He strongly encouraged interactions between the university and the research institutes in Norwich and supported the development of a science research park next to the university. He promoted a site for the new Norwich hospital next to the university campus and the success of his bid was eventually an important factor in the establishment of a new medical school. Between 1987 and 1995 student numbers at UEA almost doubled and its research grant income tripled.

Throughout this period, Derek was involved in numerous advisory boards and committees outside the university. Notably, he was a member of the Health and Safety Executive Advisory Committee on Genetic Modification between 1987 and 1995, and of the Advisory Committee on Novel Foods and Processes of the Department of Health and Ministry of Agriculture, Fisheries and Food from 1989 to 1997. He was active in debate about the safety and ethics of GM foods and crops and was a member of the Archbishops' Medical Ethics Advisory Group. On retirement in 1995 he continued in many of these positions and until 2001 he was specialist advisor to the House of Commons Select Committee on Science and Technology.

He received honorary doctorates from the Universities of Aberdeen and East Anglia, he was Deputy Lieutenant of Norfolk in 1992 and was awarded a CBE in 1994, richly deserved honours that recognised a lifetime of outstanding leadership and successful commitment to science, education and society.

John Skehel
john.skehel@crick.ac.uk

The role of global advocacy in the eradication of malaria



Malaria is one of the world's oldest and deadliest diseases. It has afflicted people for centuries, contributed to the fall of the Roman Empire, and is responsible for millions of deaths.

Malaria is caused by five species of a single-celled protozoan parasite called *Plasmodium*, transmitted by female mosquitoes. It typically results in flu-like symptoms, which, if left untreated, can progress into severe illness and death. Today almost half the world's population is at risk from malaria, despite it being treatable and preventable. The burden is concentrated in Africa where a child dies every two minutes from the disease – young children are at greater risk from malaria as they have not yet developed natural immunity.

Malaria eradication – the ultimate aim

Over the past 70 years, global advocacy has played an important role in reducing the global burden of malaria. In 1955 the World Health Organization (WHO) launched the Global Malaria Eradication Programme (GMEP). Through this campaign, countries in Europe, America and Asia eliminated malaria, largely through indoor residual spraying with insecticides (primarily dichlorodiphenyltrichloroethane, known as DDT) and mass drug administration of the antimalarial chloroquine. However, in 1969 amidst growing mosquito resistance to DDT, parasite resistance to chloroquine, resurgence of a malaria epidemic in Sri Lanka following failed attempts to eliminate it and funding shortages, the GMEP was abandoned. No major progress had been made in sub-Saharan Africa. The World Health Assembly was forced to admit that in certain regions the approach should revert back to 'malaria control with the ultimate aim of malaria eradication'.

In the following decades, global support and investment in malaria control stalled. Europe, with its developed public health infrastructure, was able to capitalise on the progress made and was officially declared to have eliminated malaria in 1975. However, many poorer countries experienced increased malaria cases and deaths. By the 1980s malaria had returned to parts of Europe, highlighting the fragility of malaria elimination.

One of the harsh lessons from the failure of the GMEP was the need for better understanding of malaria, and for new interventions for malaria control. The scientific community responded with the development of insecticide-treated bed nets to protect people at night when the mosquitoes are active, artemisinin-based combination drug therapies, and rapid diagnostic tests.

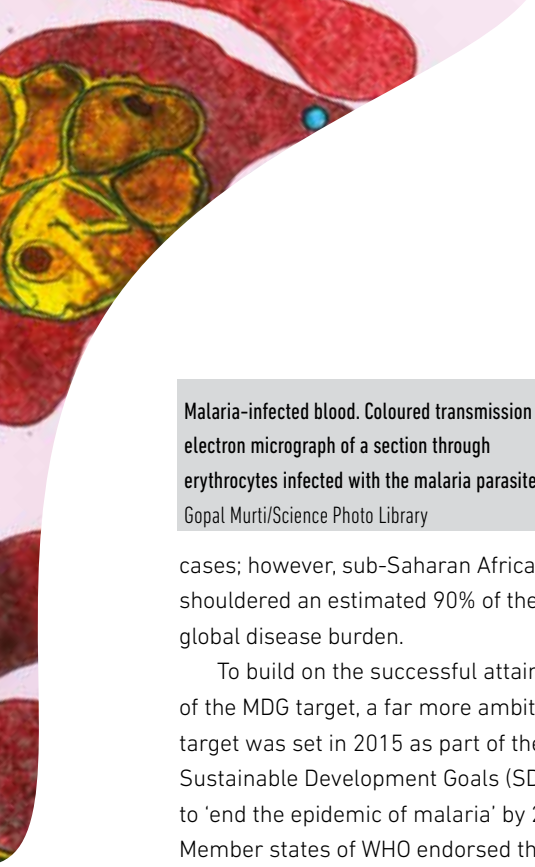
Elimination and eradication: WHO definitions

Malaria elimination – reduction to zero of the occurrence (incidence) of infection caused by a specified malaria parasite in a defined geographical area as a result of deliberate efforts.

Malaria eradication – the permanent reduction to zero of the worldwide incidence of malaria infection caused by all species of human malaria parasites.

Unprecedented progress

In 2000, malaria was placed back on the global agenda, but this time with a more cautious goal. The disease was recognised as one of the largest barriers to global development and, to address this, world leaders committed to "halt and reverse the incidence of malaria" by 2015, under target 6c of the UN Millennium Development Goals (MDGs). Concerted international efforts over the next 15 years, using these new interventions and accompanied by huge increases in global funding for malaria control, resulted in unprecedented progress – a 37% global decline in the rate of new malaria cases, and a 60% decrease in the global malaria death rate, amounting to 6.2 million fewer malaria deaths. Europe once again reported zero indigenous malaria



Malaria-infected blood. Coloured transmission electron micrograph of a section through erythrocytes infected with the malaria parasite. Dr Gopal Murti/Science Photo Library

cases; however, sub-Saharan Africa still shouldered an estimated 90% of the global disease burden.

To build on the successful attainment of the MDG target, a far more ambitious target was set in 2015 as part of the Sustainable Development Goals (SDGs); to 'end the epidemic of malaria' by 2030. Member states of WHO endorsed the vision of a world free of malaria and developed a 'Global Technical Strategy for Malaria 2016–2030' to provide a framework to move towards this vision – including targets to reduce malaria case incidence and mortality by 90%. This strategy highlighted the need for "unremitting political commitment, substantial and predictable financing, and increased regional collaboration" in order to meet the ambitious targets set. Now malaria eradication is back on the global agenda.

A wake-up call

Worryingly, in 2017 progress on malaria control was reported to be in decline. After years of reduction, global malaria cases have risen since 2015, and all 10 of the highest-burden African countries reported increases. Investment in malaria control, although relatively stable falls far short of what is required to meet the WHO targets.

> *"If we continue with a 'business as usual' approach – employing the same level of resources and the same interventions – we will face near-certain increases in malaria cases and deaths"*. Dr Tedros Adhanom Ghebreyesus, WHO Director-General, World Malaria Report 2017.

WHO called for a new country-led approach, 'High burden to high impact' to accelerate progress against malaria in the countries it hits hardest.

What happens next?

Earlier this year, RTS,S (Mosquirix) the first-ever vaccine that has shown a protective effect against malaria in young children, was rolled out in Malawi as part of a vaccine pilot programme. Although in clinical trials the vaccine only prevented 40% of cases, this has the potential to save many lives and contribute to malaria eradication. The development of this vaccine by GlaxoSmithKline took 32 years and was funded by a public–private partnership with the Path Malaria Vaccine Initiative with support from WHO, and various international non-profit organisations.

As with the MDG malaria target, it took sustained global political will, significant financial investment and scientific innovation to develop a malaria vaccine. It remains to be seen over the next decade whether this renewed call for action against malaria, along with the use of new interventions, is translated into the global advocacy needed to achieve the SDG target, and progress towards a world free of malaria.

A Sustainable Future

In recognition of the complementary roles of microbiological innovation and global advocacy, the Microbiology Society's A Sustainable Future project aims to highlight the role of microbiology in addressing the SDGs. To find out more about the project please visit our website (**microbiologysociety.org/SDGs**) or contact **policy@microbiologysociety.org** with any questions.

Funding for malaria

Malaria disproportionately affects poorer countries. As a result, funding for malaria control and R&D is largely delivered by the international public and not-for-profit sectors. For example, in 2017, of the US$ 3.1 billion was invested globally in malaria control, 72% of this was provided through international financing; the USA government contributed 39%, the UK government contributed 9%, and the Bill and Melinda Gates Foundation contributed 2% of the total.

The UK government have committed to spend £500 million a year to tackle malaria from 2016 to 2021.

Further reading

Roll back Malaria Partnership: Progress and Impact Series. Eliminating Malaria: Learning From the Past, Looking Ahead; 2011. https://path.azureedge.net/media/documents/MCP_rbm_pi_rpt_8.pdf [accessed 4 June 2019].

World Health Organization. Achieving the malaria MDG target: reversing the incidence of malaria 2000–2015; 2015. https://www.who.int/malaria/publications/atoz/9789241509442/en [accessed 4 June 2019].

World Health Organization. Global Technical Strategy for Malaria 2016–2030; 2015. https://www.who.int/malaria/publications/atoz/9789241564991/en [accessed 4 June 2019].

World Health Organization. World Malaria Report 2017; 2017. https://apps.who.int/iris/bitstream/handle/10665/259492/9789241565523-eng.pdf?sequence=1 [accessed 4 June 2019].

World Health Organization. High burden to high impact: a targeted malaria response; 2019. https://www.who.int/malaria/publications/atoz/high-impact-response/en [accessed 4 June 2019].

Being a member of the Microbiology Society

Whether it's career support for early career microbiologists, networking opportunities for those keen to step up or opportunities for established career microbiologists wanting to give something back, being a member of the Microbiology Society provides a platform.

Still studying?

Financial support is available through our grants programme and there is career support to help identify future career paths.

- Apply for grants to enhance your transferable skills, visit colleagues and attend conferences.
- Access 'How-to' guides to help answer key career questions and connect with others through the Members' Directory.
- Attend special events such as the networking session before Annual Conference to meet senior society members who can share their experience.

The early careers opportunities and access to funding are great.
Francesec Coll I Cevezo

Membership is a great way to access FEMS benefits too.
Katherine Ansbro

It's a brilliant opportunity as a member, to present my work and get feedback.
Salina Thapa

I particularly like the journals and the opportunities these bring.
Dinesh Subedi

Early career?

Building your networks, demonstrating your capabilities, improving your skills and looking for additional career opportunities are important.

- Apply for a grant including conference attendance and travel grants; research visit grants and Early Career Forum member support.
- Receive discounts on article processing charges for the Society's journals.
- Get more involved and develop transferable skills by becoming a Society Champion.
- Access Federation of European Microbiology Societies' (FEMS) grants.

We can help you raise your professional profile; develop skills and meet other microbiologists from a wide range of specialisms, countries and backgrounds.

Established career?

Perhaps you're looking to support early career members, to have a deeper relationship with the Society and take on an additional role or continue to build your networks and share your experience.

- Apply for Travel Grant support and Research Visit Grants.
- Receive discounts on article processing charges for the Society's journals.
- Build your network through the Members' Directory.
- We can help you raise your professional profile and meet other microbiologists from a wide range of specialisms, countries and backgrounds.

We provide opportunities to give something back and to lead, through closer involvement in Society working groups and committees, shadowing schemes and networking opportunities.

Membership gives access to a wide variety of disciplines.
Mike Merrick

Membership has allowed me a deeper and more fulfilling understanding of the Society.
Stephen Tuffs

Have a general interest in microbiology?

Keep in touch through our regular member e-newsletter, *Microbiology Today* magazine, Mi Society pages on the website, and social media via Twitter, Facebook and LinkedIn.

Whatever your background, career stage, level of interest or specialism, there are opportunities as a member of the Society. We would encourage you to shape your interest, development, career and involvement as far as you would like to. Contact **members@microbiologysociety.org** if you would like more information

**Please be aware benefits vary by membership grade.*

Member Q&A

This is a regular column to introduce our members. In this issue, we're pleased to introduce Sarah Abdulrahamn Almahboub.

Sarah Abdulrahamn Almahboub

Where are you currently based?

In Jeddah, Kingdom of Saudi Arabia. I'm a postdoctoral fellow at the Vaccine and Immunotherapy Unit at King Fahd Medical Research Center, King Abdulaziz University

What is your area of specialism?

Currently, my research focuses on developing virus vaccines using biotechnological approaches.

And more specifically?

My work focuses on the development of a plasmid-based vaccine against Middle East respiratory syndrome coronavirus (MERS-CoV). This virus first emerged in Saudi Arabia in 2012 and continues to circulate, and no licensed vaccines or approved treatments are available for human use yet. Developing such a vaccine would help protect millions of people and prevent the spread of the virus.

Tell us about your education to date

I have a bachelor's degree and a master's degree in Microbiology from King Abdulaziz University. I received a scholarship from the King Abdullah scholarship programme to complete my doctoral degree in Ireland and completed my PhD at the School of Biomolecular and Biomedical Science at University College Dublin. I was under the supervision of Professor Kevin O'Connor and my project focused on designing a biocatalyst for synthesis of unnatural amino acids for biomedical application.

Where did your interest in microbiology come from?

From the first time I used a light microscope.

What are the professional challenges that present themselves, and how do you try to overcome them?

When I start to learn a new skill or technique, it is challenging in the beginning but training and reading different sources of information enable me to achieve the desired goal.

What is the best part about 'doing science'?

That you wake every morning trying to prove your hypothesis and you are answering lots of questions. Science is about finding connections between things; sometimes it is frustrating but worth it in the end.

Who is your role model?

No one person. Passionate people!

What do you do to relax?

Walk on the beach.

What one record and luxury item would you take to a desert island?

My cup of coffee.

Tell us one thing that your work colleagues won't know about you.

I'm a good barista.

If you weren't a scientist, what would you be?

A writer.

If you would like to be featured in this section or know someone who may, contact Paul Easton, Head of Membership Services, at **p.easton@microbiologysociety.org**.

Reviews

Viruses of Microorganisms

Edited by Paul Hyman and Stephen T. Abedon
Caister Academic Press (2018)
£199 ISBN 978-1-910190-85-2

Viruses of micro-organisms (VoMs) are viral pathogens of single-celled bacterial, archaeal or eukaryotic organisms such as algae and protozoa. Collectively, VoMs are the most abundant yet overlooked species in virological research. *Viruses of Microorganisms* is a monograph edited by two prominent members of the International Society for Viruses of Microorganisms, Paul Hyman and Stephen T. Abedon, and collates the totality of VoMs research into a timely and compact volume.

In the introductory chapter, good-naturedly titled 'Viruses of Microorganisms: What are They and Why Care?' Hyman and Abedon introduce VoMs and succinctly explain some of the ambiguities of nomenclature within VoMs. Following this introduction is an examination of the genomics of VoMs along with evolutionary and higher-order genomic relationships by Evelien M. Adriaenssens. The bulk of the book covers the ecology and diversity of VoMs. As someone who uses metagenomic approaches to characterise virus communities, explanations of the ecological processes of VoMs in modifying microbial communities and descriptions of VoMs in marine or soil environments were fascinating and well-executed. Painstaking effort has also been put into providing the most recent understanding of VoMs diversity. Of note is the chapter on 'Protozoal Giant Viruses' which reproduces remarkable electron micrographs of these VoMs.

To round the monograph out, the final chapters cover broad biotechnological applications of VoMs, such as virus-mediated biocontrol, along with a comprehensive discussion of methods and approaches to study VoMs in aquatic environments.

Viruses of Microorganisms would be a valuable addition for scientists and postgraduate researchers working within microbial ecology and metagenomics and an at-hand reference for those considering potential biotechnological applications.

Rhys H. Parry
University of Queensland, Australia

For more reviews, please visit the online issue of *Microbiology Today* at **microbiologysociety.org/microbiologytoday**.

Comment

Arboviruses: what will bite next?

Rennos Fragkoudis and Barry Atkinson

Arthropod-borne viruses (arboviruses) pose an increasing threat to both human and animal health worldwide. By definition, arboviruses are transmitted to susceptible vertebrates through the bites of haematophagous arthropod vectors such as mosquitoes, ticks, biting midges and sand flies in which active viral replication must occur. Over the last decades, and due to a variety of causes – environmental change, globalisation, animal trade, migration – numerous emerging/re-emerging arboviruses of medical and veterinary importance have expanded their geographic range and caused large outbreaks with significant impact in terms of both human and animal health.

Most arboviruses belong to the RNA virus families *Flaviviridae*, *Reoviridae*, *Rhabdoviridae* and *Togaviridae* and the order *Bunyavirales*. To date, the only known animal DNA arbovirus is African swine fever virus (*Asfarviridae*). Viruses with RNA genomes have a high mutation rate and can be associated with a broad host range (allowing them to efficiently replicate in vertebrate and invertebrate hosts) and high zoonotic potential.

Close-up of an *Aedes aegypti* mosquito on leaf. frank600/iStockphoto

Tomato plant infected with tomato-spotted wilt virus (TSWV). Miyuki Satake/iStockphoto

In humans (which are a dead-end host for many, but not all, arboviruses), arboviruses cause a spectrum of disease including:

(i) Asymptomatic; most human infections are asymptomatic/subclinical. A typical example is West Nile virus, where 80% of infections are asymptomatic.

(ii) A mild, febrile, self-limiting illness characterised by symptoms such as fever, myalgia, arthralgia and rash, for example Sindbis virus.

(iii) Neurological/CNS (encephalitis) or arthrogenic (arthritis) disease, for example tick-borne encephalitis virus, Venezuelan equine encephalitis virus and chikungunya virus.

(iv) Haemorrhagic fever, for example dengue virus, Rift Valley fever virus and Crimean-Congo haemorrhagic fever virus.

***Ixodes ricinus* tick on a plant.** Thomas Marx/iStockphoto

It is noteworthy that many of the symptoms are often associated with multiple viral diseases, making differential diagnosis challenging. Furthermore, in general, the most severe forms of disease are observed in a small percentage (1–2%) of infected individuals. However, many arboviral diseases incur a significant economic impact (hospitalisation, persistent sequalae etc.).

The ability of arboviruses to invade new territories depends on two major factors: the presence of competent vector species, which is affected by a multitude of factors that might also affect virus replication, dissemination and transmission, and the abundance of susceptible vertebrate hosts. It is not an exaggeration to say that arboviruses and their vectors have often dramatically changed the course of human history. A characteristic example is that of *Aedes aegypti* (often called the yellow fever mosquito), an anthropophilic mosquito which was introduced into (circa 1500s) and established in (circa 1650) the New World as a result of the slave trade from West Africa. *A. aegypti* is the major urban vector for yellow fever virus which has caused vast human outbreaks. More British and French soldiers succumbed to yellow fever infection than were killed in the battlefield, affecting the outcome of the American War of Independence. Later, the construction of the Panama Canal was interrupted as a result of a yellow fever outbreak. Most recently, *A. aegypti* has been associated with the spread of viruses with significant medical and socio-economic impact such as dengue, chikungunya and Zika viruses.

Ticks are competent vectors (and often a significant reservoir) for numerous arboviruses such as Crimean-Congo haemorrhagic fever, Huaiyangshan banyangvirus (formerly severe fever with thrombocytopaenia syndrome [SFTS] virus) and, most importantly for Europe, tick-borne encephalitis virus (TBEV). TBEV is transmitted to humans predominantly through the bite of an infected *Ixodes ricinus* tick. Annually, approximately 3,500 cases are reported in Europe and in recent years TBEV (now endemic in 27 European countries) has spread into new territories (northwards and to higher altitudes). This correlates with the introduction of *I. ricinus* ticks in these areas, a result of climate change. Transmission has a strong seasonality correlating with tick activity. Like other arboviruses, it is estimated that two thirds of TBEV infections are asymptomatic.

Arboviruses also have a major impact on domesticated animals of economic importance; an example of such viruses is bluetongue virus (BTV; *Reoviridae*) known to infect sheep, goats, cattle and deer. The geographical distribution of BTV is directly linked to the presence of competent *Culicoides* (biting midge) vectors. At present BTV is endemic in many tropical, sub-tropical and temperate regions of the world, between the latitudes 40°S and 53°N, with transmission occurring during times of the year that are optimal for vector activity. The effects of climate change are thought to have supported the expansion northwards of vector midge species (for example, *Culicoides imicola*) into new areas in southern Europe. BTV has also become established in Europe, which despite single serotype and short-lived incursions, was previously regarded as predominately BTV-free. Outbreaks of bluetongue disease can have a great economic impact, as demonstrated over the last two decades in Europe, where the emergence of BTV-8 and BTV-4 have caused overt clinical signs in cattle as well as sheep. As a World Organisation for Animal Health listed disease, restrictions of animal movements disrupt normal trade routes used by livestock industries, adding to the primary economic burden caused by the loss of productivity, death of production animals and the cost of control efforts.

In plants, a variety of arthropods, including aphids and thrips, have the ability to transmit viruses that pose a serious threat to vegetable crops. In many cases transmission is mechanical, but examples of 'classical' arbovirus transmission are known. A well-known example is that of the thrips-transmitted tomato-spotted wilt virus (*Tospoviridae*) that affects economically important crops such as tomatoes, peppers and lettuce.

As highlighted, the effect of arboviruses on life worldwide is immense, and it is impossible to predict when, where and which virus will cause the next big outbreak. Despite this, there is often inadequate surveillance and a substantial lack of data on epidemiology, arbovirus–vector–host interactions and within-vector dynamics to elucidate how these affect virus pathogenesis and transmission. To address these issues and to assess the emergence/re-emergence potential of arboviruses, it is imperative that further research in these areas is carried out. Finally, novel and more efficient methods for the control of arthropod vectors in the field are essential to limit the burden of arboviral diseases.


Rennos Fragkoudis

Rennos Fragkoudis

School of Veterinary Medicine and Science, University of Nottingham, Sutton Bonington Campus, Leicestershire LE12 5RD, UK

e **rennos.fragkoudis@nottingham.ac.uk**

Rennos Fragkoudis is a Senior Research Fellow in arbovirus pathogenesis at the University of Nottingham. His research focuses on elucidating the interactions between arboviruses, their arthropod vectors and their vertebrate hosts, and developing novel intervention methods.


Barry Atkinson

Barry Atkinson

The Pirbright Institute, Ash Road, Pirbright, Woking, Surrey GU24 0NF, UK

e **barry.atkinson@pirbright.ac.uk**

Barry Atkinson is a postdoctoral researcher at The Pirbright Institute. His current research focuses on methods to reduce the capacity for mosquitoes to transmit high-consequence viruses to humans.

What inspired you to become a microbiologist?

Rennos: I always knew I wanted to be a biologist, but it was not until I had my first lectures on viruses as an undergraduate student that I decided to become a virologist (the movie Outbreak was out around that time too!). I found – and still find – microbes fascinating; some are so small that one is unable to see them even under a light microscope, but they can manipulate a host, evade the immune system and cause so much damage. I strive through my research to help reduce the impact of arboviral diseases on human and animal health.

What skills are required in your position on a day-to-day basis?

Rennos: As a virologist, other than the necessary laboratory skills, you need to develop a plethora of transferable skills such as the ability to effectively mentor, communicate and manage people, deal with funding and budgets, and disseminate the outcomes of your research through appropriate channels.

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