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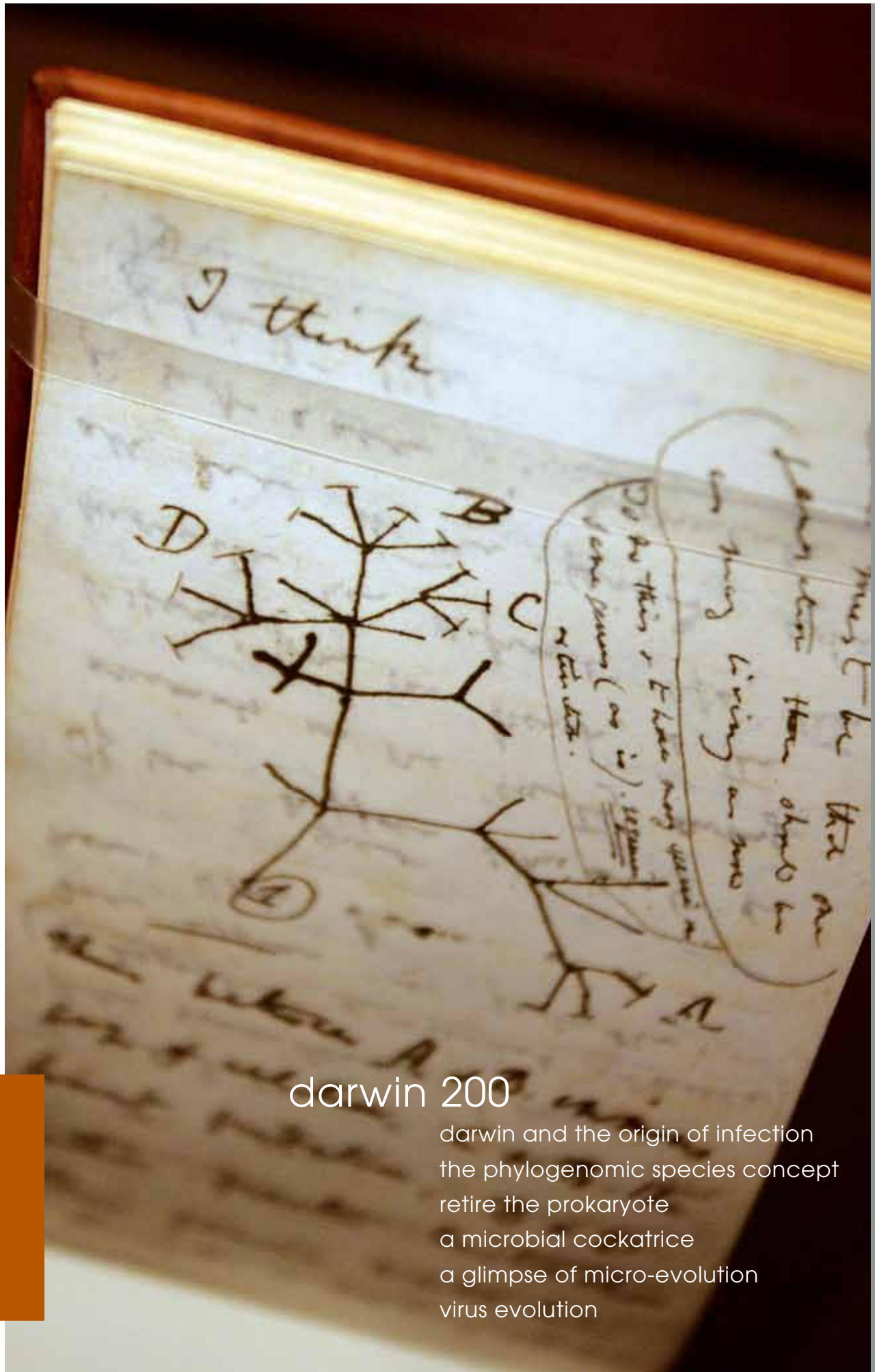

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Cover image A 'tree of life' sketch from one of Darwin's notebooks. *Mario Tama / Getty Images*

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Journals

Journal back archive project completed!

April saw two significant milestones in the project to put the entire back content of the Society's journals online. The entire archive of *Microbiology/Journal of General Microbiology*, back to volume 1 issue 1 in January 1947, and *Journal of Medical Microbiology*, back to volume 1 issue 1 in August 1968, went live on the journals' HighWire sites at **http://mic.sgmjournals.org/** and **http://jmm.sgmjournals.org/**, respectively. Around 125,000 pages of back content had to be scanned and assembled for *Microbiology/JGM*, and a further 25,000 pages for *JMM*. Each article is present as a full-text PDF, and research articles have HTML headers (titles, authors, abstracts, etc.), which had to be re-keyed, allowing compilation of an HTML table of contents for each issue. The archives also contain PDF 'front' and 'back' matter: covers, advertising, editorial boards, instructions to authors, original tables of contents, indexes and conference proceedings. Over the next few weeks, full text searching of the article PDFs will be installed.

These retrospective conversion projects are not just a matter of packing up the volumes and sending them off for scanning, but involve an immense amount of work in checking for accuracy and sorting out a variety of questions about what goes where, and some amazing historical idiosyncrasies of journal makeup. Not least, all errata, addenda and corrigenda had to be linked to the corrected articles. I'm grateful to Robin Dunford and his colleagues in the editorial offices for their skill, patience and industry, and for detecting and solving a number of problems.

The back archives of *Journal of General Virology* and *International Journal of Systematic and Evolutionary Microbiology* had already been placed online, so this completes the project. All the archive material is freely accessible, without access controls, as part of SGM's charitable remit to support microbial science. Thanks are also due to the many individuals and libraries who donated back runs of all four journals for scanning.

***Ron Fraser**, Chief Executive*

The 'Nature' of *IJSEM* back issues

The launch of online access to the entire back content of *International Journal of Systematic and Evolutionary Microbiology* last November was marked by a one-page feature in *Nature Reviews Microbiology*. It noted that the availability of the archive would be a '*boon for scientists, historians, and the public*' and made a good job of raising the profile of SGM and its publishing activities.

SGM introduces new pricing model for institutional journal subscriptions from 2010

In 2010, SGM is changing the way it charges for its journals to make pricing fairer and to offer greater flexibility of access to readers and libraries.

Like many publishers, SGM has historically operated a 'one price for all' model for its journal subscriptions to institutions. But, as journal readers increasingly access articles online, the traditional licensing agreements that accompany such a model are becoming out-dated. Students and researchers want to be able to access journals from multiple campuses including, for example, the university medical school, which might be located in a completely different city from the central library.

Under the new tiered pricing model, the price customers pay will depend on the type and size of organization and how many sites they want to be able to access journals from. Librarians will be able to purchase subscriptions with online access in up to two cities as standard, rather than having to enter into negotiation for access for additional sites. This new model also ends the inequality that saw a small college paying the same amount for an online journal subscription as, for example, a large corporation.

Publishing is an industry that is changing rapidly. SGM is making the move to a tiered pricing structure now, ahead of many other smaller publishers, to stay at its forefront and to protect its journals' futures.

'*As a not-for-profit publisher we've always worked hard to minimize the costs of our journals, which are among the most inexpensive and yet highly cited in microbiology, and our prices remain lower than many competing titles produced by commercial publishers*' commented Dr Ron Fraser, Chief Executive of SGM. '*Our model seeks to deliver a fair price based on the value of our journals to any one institution, with the flexible licensing terms that libraries need in order to maximize the value of their purchase.*'

Open access – a serial killer?

Most learned societies depend on income from publishing journals to carry out their charitable aims. In recent years the issue of free open access to research papers has become a threat to the current business model on which such publishing operations are based. The Biosciences Federation, which represents 35 organizations, set up a subcommittee to investigate the impact of open access, amongst other pertinent topics. They carried out a survey of member societies and the researchers who belong to them to find out their policies on open access and self-archiving by authors, and to gather information on the financial contribution made by the societies to their disciplines. In addition, society members were invited to complete an online questionnaire on their experience and views on open access publishing and self-archiving. SGM Chief Executive Dr Ron Fraser has been helping to lead this initiative.

The survey is now complete and the results have been published in *Serials*, a journal read by librarians and people working in the publishing industry. The article was written by Sue Thorn, Sally Morris and Ron Fraser. The findings show that member societies contributed twice as much financially in the form of grants and awards to UK higher education institutions than they received in publication sales from this source. None of the societies currently offers full open access, but all provide delayed free access, mostly after 12 months. Researchers appear to be very confused about open access journals altogether. The full article is available at:

http://serials.uksg.org/openurl.asp?genre=article&issn=0953-0460&volume=22&issue=1&spage=39
(doi:10.1629/2239)

First SGM Prize Medallist receives award

Dr Stanley Prusiner, the first winner of the Society's new Prize Medal, is seen below being presented with his medal by SGM President Robin Weiss. He also received a certificate and £1,000.

Dr Prusiner's lecture – *Prion biology and disease* – was delivered to a packed lecture theatre at the Harrogate meeting, where it was greeted with much acclaim.

The medal was specially struck for the event and was based on a design by SGM Design Manager Ian Atherton. The prize is to be awarded annually to a microbiologist of international standing whose work has had a far-reaching impact beyond microbiology.

Antibiotics in history

The Harrogate meeting was themed around the Legacy of Fleming, to mark the anniversary of the discovery of the publication of penicillin. Kevin Brown, curator of the Fleming Museum, kindly supplied some posters telling the story.

The scientific session entitled *Production, formulation and delivery of biotherapeutics*, organized by Frances Burke, Chris Hewitt and Stuart Stocks, with welcome support from commercial colleagues, covered the theme from an industrial perspective. As well as looking back, speakers considered the latest developments in the field.

The accompanying poster session included some displays on the history of the development of various antibiotics, mainly penicillin. Two offprints were available to delegates: *People, Penicillin and Pursuit of Excellence: Eli Lilly and Co Ltd Speke Operations* and *The Life and Work of Guy Newton (1919–1969)*. Spare copies are still available for members unable to attend the Harrogate meeting. Contact Janet Hurst (j.hurst@sgm.ac.uk) if you would like one.

SGM Council

February meeting highlights

Election of new SGM Council Officers from September 2009

The President reported on the deliberations of the subcommittee he had chaired to discuss nominations for the Council Officer posts that fall vacant in September. After considering their recommendations, Council agreed to approach the following members.

President: **Professor Hilary Lappin-Scott**
Bangor University

General Secretary: **Dr David Blackbourn**
University of Birmingham

Publications Officer: **Professor Howard Jenkinson**
University of Bristol

Education and Public Affairs Officer: **Professor Joanna Verran**
Manchester Metropolitan University.

Professor Hilary Lappin-Scott, the outgoing SGM Scientific Meetings Officer, was present at the Council meeting and was delighted to accept the Presidency to much acclaim. Subsequent to the Council meeting, all of the other newly elected officers were contacted by the President and accepted their roles. From September 2009, Council will be working in the transitional stage to its new structure, which has 6 officers and reducing to 6 elected members by September 2011.

Dr Evelyn Doyle, University College, Dublin, was appointed as Deputy Scientific Meetings Officer from September 2009 and she will attend Council meetings by invitation.

Honorary Membership

Council decided unanimously to offer Honorary Membership to **Dr Rita R. Colwell**, Chairman, Canon US Life Sciences, and Distinguished Professor, University of Maryland College Park and Johns Hopkins University Bloomberg School of Public Health, for her significant contribution to microbiology worldwide and her support of SGM.

SGM Prizes

A draft document outlining revised procedures for nominating and awarding SGM Prizes, prepared by Ulrich Desselberger and Janet Hurst, was discussed and accepted with minor amendments. From 2009 onwards the timing of nominations and Council decisions will be moved forward to enable the President to approach the prize-winners at an earlier stage and to give SGM meetings organizers more time to make appropriate arrangements for the delivery of the prize lectures. Details of Prizes to be awarded in 2010 are on p. 70.

Scientific meetings

Professor Hilary Lappin-Scott, the Scientific Meetings Officer, reported on a meeting of the SGM Divisions in London. Topics discussed included meeting the needs of academic clinical virologists at Society conferences and how to improve cross-theme working within the organizational planning matrix. Good progress was made on both fronts.

Finances

Council was pleased to accept the Treasurer's Financial Report for the year ended 31 December 2008. They also heard about the presentation given on the previous evening at Treasurer's Committee by Mr Willie Hartley Russell, the SGM's Investment Manager. SGM's portfolio has lost value, in line with the poor global economic circumstances. Council discussed the situation and will continue to monitor it closely.

The income from commercial journal subscriptions, which enables SGM to fund many of its charitable activities, was reviewed and in general considered to be satisfactory. Council was interested to learn about the new tiered pricing system for journal sales, which had been extensively discussed at Treasurer's Committee. After discussion, they accepted the recommendation to implement the new system.

European Society for Virology

The Inaugural Meeting of the European Society for Virology (ESV) took place in Rome on 24 April 2009. Our President **Professor Robin Weiss FRS** was a keynote speaker. After some discussion, Council decided to support ESV in general and become a corporate member but they hoped that future eurovirology congresses would be scheduled to avoid clashes with the SGM's spring meetings.

Biosciences Federation (BSF) and Institute of Biology (IoB) merger

Council noted the provisional business plan for the proposed merger of the BSF (of which SGM is a Member Organization) and the IoB. It is hoped that the new Society of Biology will provide UK bioscientists with a single and authoritative voice on issues relating to scientific, educational, economic and social aspects of biology. In principle Council supported the initiative, but felt that more detailed information should be made available to member organizations of the BSF about their liabilities if the merger took place.

***Ulrich Desselberger**, General Secretary*

People

American Academy of Microbiology

The following SGM members have been elected Fellows of the American Academy of Microbiology:
Mark J. Buttner, John Innes Centre, Norwich
Gordon Dougan, The Wellcome Trust Sanger Institute, Cambridge
David W. Holden, Imperial College London

Congratulations to …

Microbiology Today Editor **Matt Hutchings** (left) and his wife Cerian on the birth of baby Noah Benjamin on 29 January 2009. Noah weighed in at 7lb 4oz and is doing very well.

Professor Roger Pickup, on appointment to a chair in the Biomedical and Life Sciences Division, Lancaster University.

Professor Tracy Palmer, University of Dundee on her election to Fellowship of the Royal Society of Edinburgh.

Professor David Baulcombe, Department of Plant Sciences, University of Cambridge, on his appointment to the Council of the Biotechnology and Biological Research Council.

Professor Maria Zambon who has been appointed Director of the Health Protection Agency's Centre for Infections at Colindale, London.

Deaths

The Society notes with regret the deaths of **Miss Mairin Clarke**, County Louth, Ireland (member since 1975) and **Dr Ronald M. Keddie**, formerly of the University of Reading (member since 1949). We are also sad to note that **Professor Rob Goldbach**, a former Editor of *Journal of General Virology* and Head of the Laboratory of Virology, University of Wageningen, has died in a tragic accident whilst on holiday.

SGM staff

We bid farewell to Staff Editor **Nicolas Fanget**, who is taking up a new post as a copy-editor on *Nature*. Nico has worked mainly on *JGV* where his input has been much appreciated.

AGM 2009

The Society AGM will be held on **Tuesday, 8 September 2009** at the Society Meeting at Heriot-Watt University, Edinburgh. Agenda papers, including reports from Officers and Division Chairs and the Accounts of the Society for 2008 will be circulated with the August issue of *Microbiology Today*.

New Outreach Award

The new Education Division has instituted an annual prize to be awarded for excellence in outreach work in microbiology. Yakult Ltd have kindly agreed to sponsor this prize for the first 3 years, which consists of £250, a certificate and free attendance at an SGM meeting.

Jo Heaton of University of Lancashire was given the award for 2009 in recognition of her enthusiastic promotion of microbiology to school children. She is pictured here being presented with her cheque by Linda Thomas, Science Director of Yakult Ltd, at the Gala Dinner in Harrogate.

Yakult

New *Cronobacter* international collaboration

In 2008, biogroups of *Enterobacter sakazakii* were placed in the new genus *Cronobacter*. These bacteria, which are widespread in the environment, have been linked to the incidence of infant meningitis and necrotizing enterocolitis, probably caused by post-process contamination of milk-based infant formula or feed. This important threat to the health of neonates was the theme of the 1st International Conference on *Cronobacter* held at University College Dublin in January. SGM was pleased to provide support for speakers via the Joint Meetings Scheme. SGM's Irish Division members provided significant input. The event attracted 200 delegates from around the world and was opened by Mr Brendan Smith, TD, Ireland's Minister for Agriculture and Food. At the close of the conference, Peter Ben Embarek of the WHO announced that the UCD Centre for Food Safety had been designated the first laboratory to be a WHO Collaborating Centre for *Cronobacter*. See **www.ucd.ie/crono09** for details.

Information on the SGM's Joint Meeting Scheme is available at **www.sgm.ac.uk/meetings/JointMeetingsForm.doc**

SGM Prize Lectures

A range of prestigious awards is made by the Society in recognition of distinguished contributions to microbiology. Nominations are now sought for the 2010 prize lectures. The award panel will consider the submissions in the autumn and take their recommendations to November Council for approval. The outcome will be announced in the February 2010 issue of *Microbiology Today*. Prize lecture rules and a nomination form are on the SGM website: **www.sgm.ac.uk/about/prize_lectures.cfm**

Fleming Award – This is awarded annually for outstanding research in any branch of microbiology by a young microbiologist in the early stages of his/her career. The winner receives £1,000 and gives a lecture based on his/her work to a Society meeting. The text is usually published in a Society journal.

Marjory Stephenson Prize Lecture – The Society's principal prize, awarded biennially for an outstanding contribution of current importance in microbiology. The winner receives £1,000 and gives a lecture on his/her work at a Society meeting. The lecture is usually published in a Society journal.

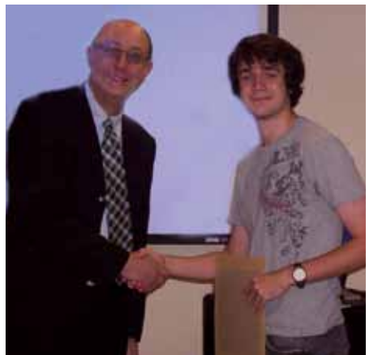
Peter Wildy Prize for Microbiology Education – This is awarded annually for an outstanding contribution to any area of microbiology education. The winner receives £1,000 and gives a lecture on a topic of his/her choice at a Society meeting.

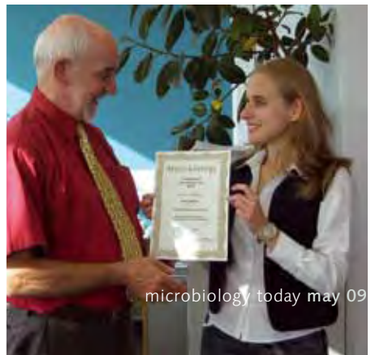
Completed nomination forms, together with supporting documents, should be sent to Ulrich Desselberger, c/o SGM HQ. Closing date for all nominations is **30 September 2009**.

Undergraduate Microbiology Prizes

The prizes aim to encourage excellence in the study of microbiology by undergraduate students and to promote scholarship in, and awareness of, microbiology in universities. The prizes are awarded annually to the undergraduate student in each qualifying institution who performs best in microbiology in their penultimate year of study for a Bachelor's degree. Each winning student will be awarded £150, a certificate and a free year's undergraduate membership of the SGM. One prize is available to each university in the UK and Republic of Ireland offering a degree course with a significant content of microbiology. The university chooses the assessed microbiological work for which the prize is awarded. The submission should be supported by formal marks, not an informal assessment. Winning students should have attained at least 2(I) overall in their degree examinations at the stage at which the award is made. Universities are now invited to nominate a student for a 2009 SGM Undergraduate Microbiology Prize. Submissions can only be accepted on the form which has been sent to all institutions. The full rules and further copies of the form may be downloaded from the SGM website or obtained from the Grants Office at Marlborough House. The closing date for nominations is **28 August 2009**.

▼ Two recipients of 2009 UG prizes receiving their certificates – Graham Hood, University of Reading (left), and Marta Kaleta, London Metropolitan University (right).





Grants

SGM has a wide range of grant schemes to support microbiology. See **www.sgm.ac.uk/grants** for details and closing dates.

Enquiries should be made to the: Grants Office, SGM, Marlborough House, Basingstoke Road, Spencers Wood, Reading RG7 1AG (t 0118 988 1821; f 0118 988 5656; e grants@sgm.ac.uk).

Check out the current schemes, to ensure that you don't miss any deadlines.

Scientific Meetings Travel Grants

This scheme offers members who are early-career scientists limited grants to present their work at scientific meetings. Applicants in the following categories are eligible to apply: postgraduate students, resident and registered for a higher degree in a country in the EU; postdoctoral scientists within 3 years of their first appointment in a country in the EU, graduate scientists within 3 years of their first appointment to a microbiological post in the UK or Republic of Ireland; university lecturers (LA or equivalent) within 3 years of appointment to their first post in the UK or Republic of Ireland.

International schemes

International Development Fund

The fund exists to provide training courses, publications and other assistance to microbiologists in developing countries.

President's Fund for Research Visits

The fund enables early career scientists, as defined in the scheme rules, to visit any other country for 1–3 months to carry out a defined piece of microbiological research. Grants contribute towards travel, subsistence and some consumables.

The Watanabe Book Fund

Members who are permanently resident in a developing country may apply for funding to acquire microbiology books for their libraries. These annual awards are available as a result of a generous donation from Professor T. Watanabe of Japan.

The closing date for these international schemes is **25 September 2009**.

Student schemes

Postgraduate Student Meeting Grants

Grants cover travel and accommodation expenses for attendance at ONE SGM meeting each year. Applications for a grant to attend the Heriot-Watt meeting (7–10 September) must be submitted by **4 September 2009**.

GRADschool Grants

Awards to contribute the full course fees of a UK GRAD national (personal or career development) residential course. Applicants must be resident and registered for a PhD in the UK.

Medical Microbiology Support Grants

Elective grants

Funding for UK/Ireland medical/dental/veterinary students to work on microbiological research projects in their elective periods.

Trainee support grants

Funding for SGM members carrying out small lab-based microbiology projects during either foundation or specialty postgraduate medical training. Up to £3,000 is available towards the consumables costs of a project.

The closing date for these schemes is **25 September 2009**.

UK Society of Biology to go ahead

Members of the UK's two leading biology organizations, the Institute of Biology (IoB) and the Biosciences Federation (BSF), have voted overwhelmingly in favour of unification to form a single organization, the Society of Biology. This positive development takes the IoB and BSF a step closer to the creation of an organization that combines the expertise of the learned societies and other biology organizations with the professional skills of the IoB and its individual members. Professor Dame Nancy Rothwell, Chair of the Interim Council said, '*The Society of Biology will have a sufficient critical mass to enable it to speak with authority over the breadth of topics covered by modern biology*'. SGM, as a member of the BSF, voted in favour of the merger.

For more information, see **www.newbio.info**

Public Inquiry into South Wales *E. coli* O157 outbreak

Former SGM President Hugh Pennington has completed his inquiry into the outbreak of *Escherichia coli* O157 which affected at least 157 people in South Wales in 2005. Tragically, one 5-year-old child died.

The work took 2 years to complete and the report concluded that cooked meats that had become contaminated with the pathogen due to severe breakdowns in good food hygiene practice at a catering butcher business were the cause of the outbreak.

The full report is available at **www.ecoliinquirywales.org**

microshorts

Jane Westwell takes a look at some recent microbiological stories

As *Microbiology Today* went to press, a new influenza A H1N1 virus from Mexico hit the headlines. Jane Westwell tracks some of the reactions to this new 'swine 'flu' as it began to spread around the world.

Swine 'flu – the story so far

Ten days after the first case of swine 'flu was announced in Mexico on 24 April, over 1,000 cases had been reported worldwide. In Mexico, over 700 cases were recorded; 26 resulting in death and in the USA almost 300 cases of the virus had been reported across 36 states, whilst in Canada about 100 cases were confirmed. In 16 other countries, the virus was infecting far fewer people (between 1 and 3) with highest number of occurrences in Spain (54) and UK (32).

In Alberta, Canada, the first case was recorded of the H1N1 virus passing from human to another species when a farm worker infected over 200 pigs after returning from a holiday in Mexico. The WHO called for increased surveillance of pig-farms in countries with H1N1 infections in humans due to concern that repeated transmission of the virus between humans and pigs may increase the chances of it mutating into a form that could lead to a higher mortality rate in humans.

The WHO increased the state of alert to level 5 and was monitoring a surge of reported cases in Spain just as measures to counteract spread of the virus were being relaxed in Mexico.

Just how ready were we?

Across the globe, levels of individual countries' preparedness varied enormously. Some had significant stocks of antiviral drugs laid-by and had clear plans to deal with outbreaks. A few countries were less well-prepared and are only now forming task-forces to plan responses to disease outbreaks.

Actions to control spread of the disease were also diverse. The UK government put in place a communications campaign advising people to '*catch it, bin it, kill it*' – good advice for preventing spread of any cold or 'flu infection. They also, along with other countries, adopted a 'containment' approach to dealing with outbreaks: isolate the infected person and those they have been in contact with then administer anti-viral drugs to the patient and contacts. There is not very much evidence that this approach works but it does have the advantage of reducing severity of symptoms and shortening the illness if 'flu does develop. Authorities in China have taken the containment approach to a much further extreme – enforcing quarantine conditions on Mexican nationals. Guests in a hotel where one case of H1N1 was identified have been confined to the hotel irrespective of whether they display symptoms of the infection. In Vietnam, visitors from affected countries are to be isolated on arrival. Other approaches to preventing outbreaks include a cull of all pigs (in Egypt) and bans on pork imports from affected countries despite no evidence to suggest that H1N1 can be transmitted by eating pig-meat.

Economic impact

One thing is certain, the outbreak of H1N1 is already having economic consequences. Airline share prices fell sharply after the news broke. Holiday companies temporarily withdrew planned trips to Mexico where concern is growing over the potential loss in income from the tourist trade. The pig-farming industry in 'flu-affected countries is also facing economic losses due to trade bans imposed by several countries. On the other hand, opportunists started to cash in on the outbreak by selling 'miracle cures' and products claimed to prevent transmission of the virus.

Media coverage

Coverage of H1N1 in the UK media has been extensive and fairly balanced. Newspaper and TV website users can download maps illustrating outbreaks and read regular news updates, commentary and background information from scientific experts (including several SGM members). Interactivity of websites has encouraged people to express their fears and opinions. Those airing eccentric views or attitudes to the situation have received vigorous responses from other members of the public. Twitter has recorded over 10,000 tweets per hour on the subject – some might say a case of information overload. As time has progressed, the media coverage is lessening and on day 11 website updates were far less frequent than in earlier days of the story. This is probably a reflection that swine 'flu has not yet reached pandemic proportions and the symptoms are far less severe than first feared.

What next?

Experts predict that a new wave of cases could appear in the autumn, if the present outbreak dies down as expected over the summer months. Will there be a pandemic or not? Will microbiologists win the race to produce an effective vaccine quickly? Watch this space…

www.independent.co.uk/life-style/health-and-wellbeing/health-news/network-of-flu-friends-could-help-says-health-ministry-1679713.html

www.independent.co.uk/news/world/americas/swine-flu-snake-oil-web-sites-get-roasted-by-fda-1679187.html

www.newscientist.com/article/dn17049-expert-analysis-mexican-swine-flu--the-story-so-far.html

http://news.bbc.co.uk/1/hi/world/americas/8022516.stm

http://news.bbc.co.uk/1/hi/world/americas/8034284.stm

Fighting counterfeit fungi

Italian and French researchers are unravelling the secrets of truffles. The black truffle (*Tuber melanosporum*) genome has been sequenced and is expected to be followed by the white truffle (*Tuber magnatum*) later this year. For decades scientists have assumed that there is very little genetic variation between truffles growing in different regions. The black truffle genome has areas with variable amounts of repetitive DNA which have been used as markers in genetically fingerprinting 200 truffles from 13 different regions of southern Europe. This has revealed regional varieties of genetically distinct truffles rather than the monoculture that was previously assumed to exist. Preliminary data on 300 white truffles, from 26 different areas, indicate that they also form distinct regional variations.

Such a rare and high-value product attracts counterfeiters who mix a small amount of 'true' black truffle with more plentiful (and cheaper) varieties. Whilst DNA analysis has been used to identify 'imposter' species, researchers are planning to refine the fingerprinting to establish whether it is possible to distinguish between truffles of the same species from different regions. This technique will be vital if governments adopt a controlled geographical origin system, similar to the wine industry, which would require authentication of where a truffle was harvested.

www.sciencemag.org/cgi/content/fllsci;323/5917/1006

Hand washing, not isolation, controls MRSA

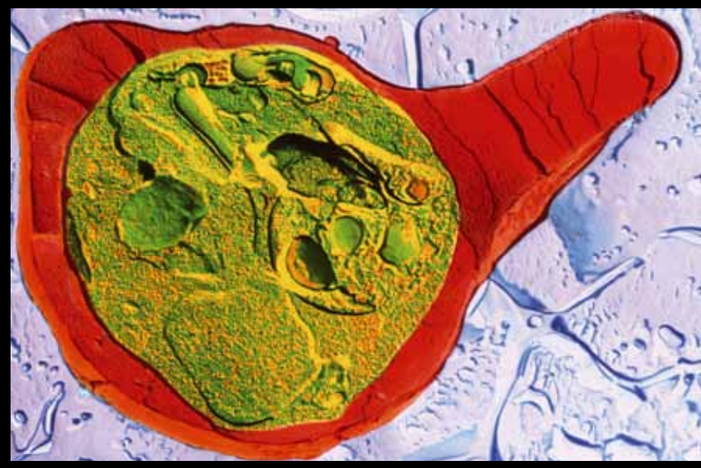
A recent study, by UK researchers, has shown that careful hand hygiene among staff on hospital intensive care units (ICUs) could be the best way to halt the spread of MRSA among patients. ICU wards tend to have higher levels of MRSA than general wards and patients with the infection are often isolated in separate wards to minimize the risk of cross-infecting other patients. However, some experts argue that moving infected patients carries a risk. The study took place over a year; for 6 months patients with MRSA were moved to isolation wards and for the remainder of the year they were not moved. Throughout the study, staff were encouraged to wash their hands and frequency of hand-washing was monitored. The findings show that rates of cross-infection with MRSA were similar during both periods. At the end of the study there were no differences in cross-infection rates, suggesting that isolating patients does not substantially reduce the risk of infection.

www.telegraph.co.uk/health/healthnews/5077135/Handwashing-more-effective-at-controlling-MRSA-than-isolating-patients.html

Old microbes of the sea

Scientists have discovered evidence of an ancient microbial community that has survived for more than 1.5 million years under the Antarctic ice. Analysis of brine (four times more salty than ordinary seawater), flowing through a crack in the wall of the Taylor Glacier, indicated a complete absence of oxygen, but did reveal presence of microbial life beneath the ice. Scientists believe that the microbes have evolved from marine organisms that became trapped in a landlocked briny pond that was subsequently covered by the glacier. The pond currently lies 1,300 feet below the ice. In darkness and without oxygen, the microbes have survived by using minerals and decayed organic matter as nutrient sources and respired anaerobically with iron as the terminal electron acceptor. The microbes found in the brine are genetically closely related to modern marine micro-organisms.

www.independent.co.uk/news/science/microbes-that-breathe-iron-are-found-in-antarctic-1669966.html



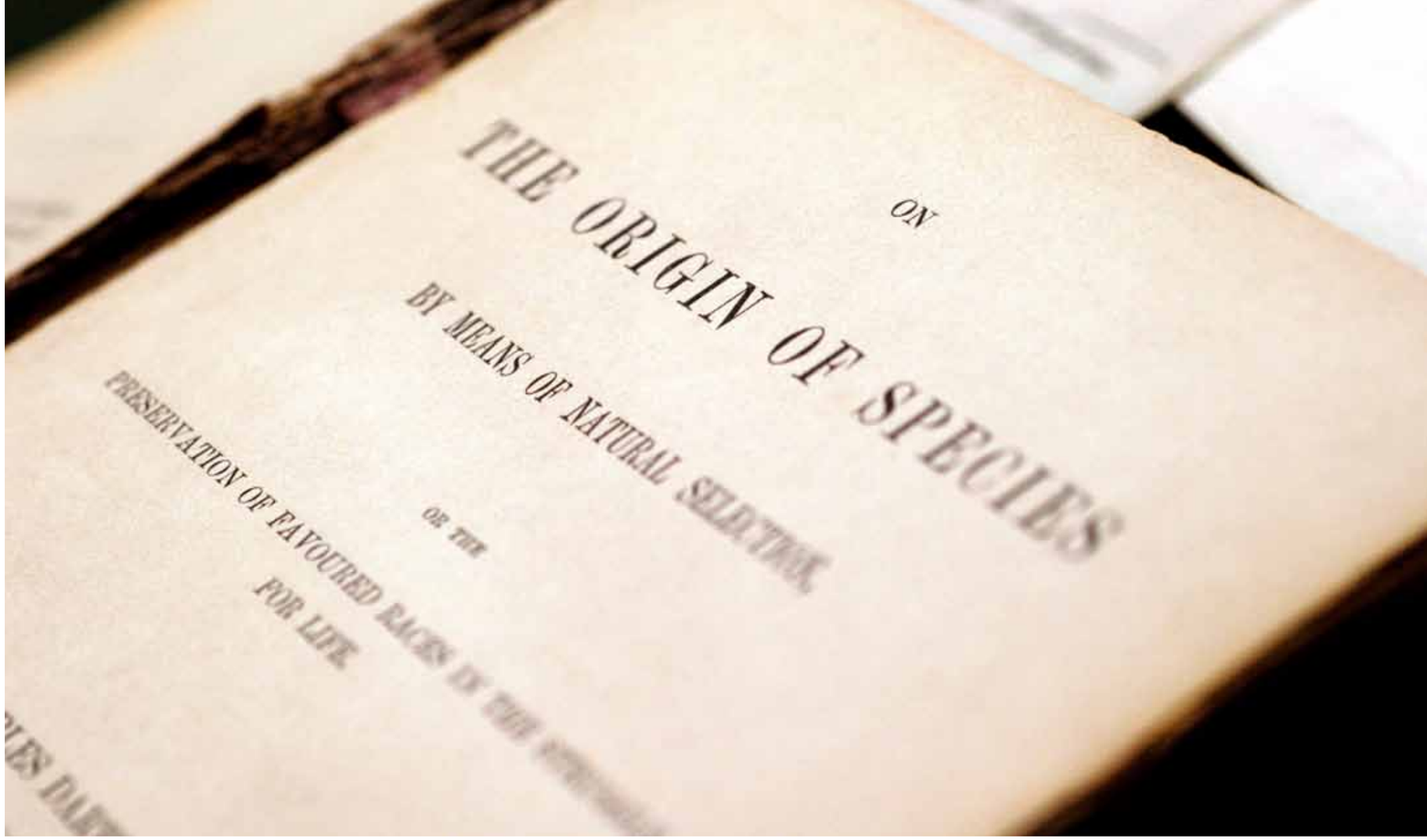
▲ Coloured freeze-fractured TEM of a section through a red blood cell infected with a malaria parasite (*Plasmodium* sp.). *Dr Tony Brain / SPL*

Combating malaria with a lab-on-a-chip

Scientists at University of Glasgow have developed an electronic chip which identifies individual species of malaria. In April, the team tested their malaria chip and it correctly identified a test sample of human blood infected with *P. malariae* provided by the Scottish Parasite Diagnostic Laboratory. The researchers were greatly encouraged by this initial result and are working on further tests that aim to produce a chip to test for the presence of malaria and indicate drug resistance in less than 60 minutes. At present, the most accurate way to diagnose malaria is by examination of a blood smear by skilled personnel – a time-consuming process – and there is no rapid test for drug resistance in use. A 2008 study by the UK Health Protection Agency showed that in recent years there has been an increase in cases of the most dangerous forms of malaria being brought back by travellers from overseas.

news.bbc.co.uk/1/hi/scotland/glasgow_and_west/8015241.stm

Darwin: from the origin of species to the origin of infection



In this special issue of *Microbiology Today* to mark the two Charles Darwin anniversaries in 2009, **Mark Pallen**, a Darwin enthusiast, explores the links between the great man and microbiology.

2009 marks the bicentenary of the birth of Charles Darwin and the 150th anniversary of the publication of *On the Origin of Species by Means of Natural Selection*. The impact of Darwin's theory of evolution by natural selection is felt throughout biology and even beyond it — in disciplines as diverse as computer science and cosmology. Darwin's theory is widely touted as '*the best idea anyone ever had*' and arguably ranks as the most influential change in human thought in modern times (although as microbiologists, we may wish to claim that the germ theory of infection is of more practical significance).

What about Darwin and microbiology? Antibiotic resistance is widely cited as a tangible example of Darwinian evolution. But Darwin himself lived through the birth of our discipline, so it is not surprising to learn that there are links between Darwin and the founding fathers of microbiology.

Darwin and natural selection

Charles Darwin was born and schooled in Shrewsbury, an English market town close to the Welsh border. He tried, and ducked out of, a medical education in Edinburgh, then studied at Cambridge with a view to joining the clergy. But his reputation as a naturalist earned him a place on a round-the-world trip on *HMS Beagle*, which primed him for his revolutionary ideas on evolution. He started to formulate his thoughts on evolution shortly after his return from the *Beagle* voyage, recording a riot of ideas, sometimes earthy or even vulgar, in a series of notebooks. For inspiration on his ideas of the struggle for existence and natural selection, he drew on the work of Robert Malthus, who had suggested that human populations always eventually out-run the means to sustain them. Darwin outlined his theory in a 'pencil sketch' of 1842 and an essay of 1844, but, preoccupied with other work, delayed publication until the late 1850s, when he was spurred into action by the rival work of Alfred Russel Wallace.

In *On the Origin of Species by Means of Natural Selection*, first published in 1859, Darwin eloquently (and presciently, given its subsequent influence on antibiotic resistance) emphasizes the remarkable power of natural selection:

> '*We have seen that man by selection can certainly produce great results, and can adapt organic beings to his own uses, through the accumulation of slight but useful variations, given to him by the hand of Nature. But Natural Selection, as we shall hereafter see, is a power incessantly ready for action, and is as immeasurably superior to man's feeble efforts, as the works of Nature are to those of Art.*'

Later, in *The Descent of Man*, despite his ignorance of the nature of inheritance, Darwin points out that the variation that is a prerequisite of natural selection originates independently of the selection itself.

In the decades after his death, while Darwin's ideas of evolutionary change and common ancestry were widely accepted, his principal mechanism for change, natural selection, was not. However, in the mid-20th century, Darwin's intellectual legacy was reconciled with Mendelian genetics in what is often called 'The Modern Synthesis'. As part of this reconciliation, bacteria were brought into the broader evolutionary genetic framework, principally through the experiments on the genetics of phage susceptibility published by Salvador Luria and Max Delbrück in 1941. In their famous fluctuation test, Luria and Delbrück confirmed Darwin's hunch that variation precedes selection, rather than arising in response to it, and thrust bacteria centre stage as biological entities with fully-fledged genetics. A few years later, in 1945, Milislav Demerec repeated the fluctuation test on penicillin resistance in *Staphylococcus aureus*, showing for the first time the awesome power of natural selection to curtail our biochemical victories over micro-organisms.

Darwin and Pasteur

Shortly after Darwin published *The Origin*, in Paris, Louis Pasteur performed a series of experiments that demolished the theory of spontaneous generation. Darwin was well aware of the on-going controversy. In 1860, in a letter to his friend Lyell, he refers to the work of Pasteur's rival Pouchet:

> '*I have seen something about the infusorial experiments in Paris: Quatrefage objected to their accuracy. Some old experiments were several years ago tried in Germany with astonishing precautions (air all passed through sulphuric acid & caustic potash) and infusoria never appeared.*'

A few years later in 1863, he wrote to the English botanist George Bentham:

▲ Title page from an early edition of *On The Origin of Species*, first published in 1859. *GustoImages / Science Photo Library*

'*I am very glad that you are going to allude to Pasteur; I was struck with infinite admiration at his work.*'

In disproving spontaneous generation, Pasteur might be seen as undercutting Darwin's theory of evolution by removing a mechanism for the generation of the first life forms. However, Darwin was sharp enough to realize that the conditions under which life first originated were likely to be quite different from those around today. In 1871, he wrote to his botanist friend Joseph Hooker:

'*It is often said that all the conditions for the first production of a living organism are now present, which could ever have been present. But if (and oh! what a big if!) we could conceive in some warm little pond, with all sorts of ammonia and phosphoric salts, light, heat, electricity, etc., present, that a proteine* [sic] *compound was chemically formed ready to undergo still more complex changes, at the present day such matter would be instantly devoured or absorbed, which would not have been the case before living creatures were formed.*'

As far as I am aware, Pasteur never made any direct reference to Darwin, although he opened his 1864 address to the Sorbonne on spontaneous generation with these expressive lines:

'*Great problems are in question today, keeping every thinking man in suspense: the unity or multiplicity of human races, the creation of man 1,000 years or 1,000 centuries ago; the fixity of species, or the slow and progressive transformation of one species into another…*'

Half a century later, an essay in *Science* magazine concluded:

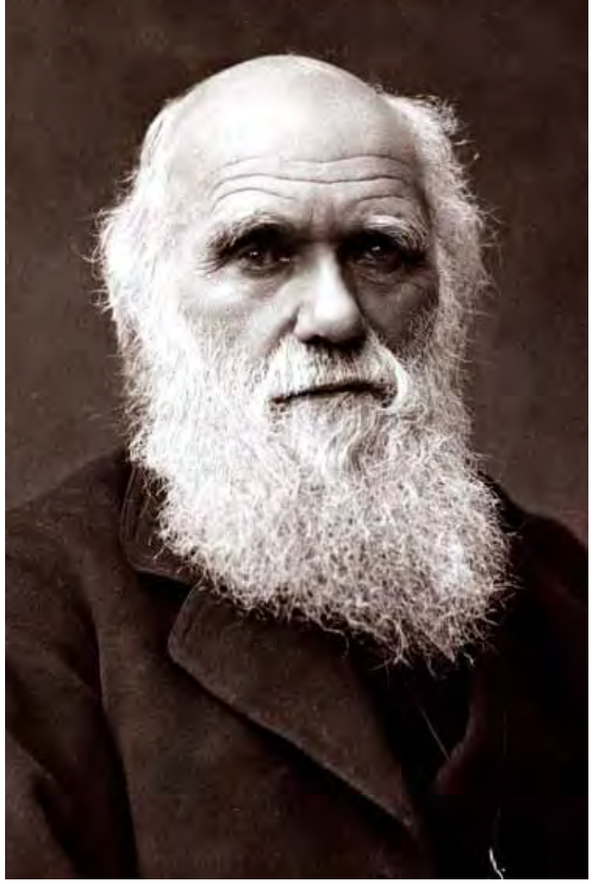
'*Darwin, master of the organic world sleeps near Newton, master of the inorganic, in the great [Westminster] Abbey, among the most famous of his race. Pasteur rests alone in the chapel of his laboratory … Both rest forever among the immortals. the last half of the nineteenth century may well be called their age "the Age of Darwin and Pasteur".*'

Darwin, Cohn and the origin of infection

Darwin maintained an extensive network of correspondents. Among them was the German Jewish botanist and bacteriologist, Ferdinand Cohn (1828–1898), who is widely recognized as the father of bacterial taxonomy. Cohn was the first to classify bacteria according to their microscopic appearance and the first to describe sporulation in *Bacillus*. He was instrumental in publishing Robert Koch's work on *Bacillus anthracis*.

From 1874 until 1882, Darwin and Cohn maintained a lively correspondence, principally on botany. On 26 September 1876 Darwin writes to invite Cohn and his wife to visit him at Down House. And then, the very next day, Darwin writes to his son Frank, saying that he hopes they will not come! Apparently the subsequent visit was a success.

However, for microbiologists, one particular exchange of letters stands out. In January 1878, Cohn writes to Darwin, discussing Koch's recent discovery of the anthrax bacillus.



▲ Charles Darwin in old age. *Popperfoto / Getty Images*

Darwin's response is a triumphant celebration of the birth of medical microbiology:

'*I thank you sincerely for your most kind letter and I return your wishes for the New Year with all my heart. Your letter has interested me greatly. Dr Sanderson showed me some admirable photographs on glass by Dr Koch of the Organisms which cause Splenic Fever. But your letter and the valuable work which you have given me make the case much clearer to me. I well remember saying to myself between 20 and 30 years ago, that if ever the origin of any infectious disease could be proved, it would be the greatest triumph to Science; and now I rejoice to have seen the triumph.*'

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Further reading

Darwin, C. (1859). *On The Origin of Species By Means of Natural Selection*. London: John Murray.

Pallen, M. (2009). *The Rough Guide to Evolution*. London: Rough Guides.

Creager, A.N.H. (2007). Adaptation or selection? Old issues and new stakes in the postwar debates over bacterial drug resistance. *Stud Hist Phil Biol Biomed Sci* **38**, 159–190.

Sedgwick, W.T. (1923). Darwin and Pasteur: an essay in comparative biography. *Science* **52**, 286.

http://darwin-online.org.uk/ – The complete works of Charles Darwin online.

www.darwinproject.ac.uk/ – Darwin Correspondence Project

The tree of life is based on phylogeny which infers the evolution of lineages of organisms by the analysis of the sequences of their macromolecules, in particular genes and proteins. The 16S rRNA gene sequences used in the hierarchical classification of *Bacteria* and *Archaea* from domain to genus are too highly conserved to be of taxonomic use at the species level and **Jim Staley** proposes an alternative approach.

The phylogenomic species concept

Speciation is the process whereby organisms evolve to form new strains and species. Like speciation in plants and animals, bacterial speciation is driven by ecological and geographical factors. For example, consider the bacteria that have evolved to become pathogens of specific plant and animal species. These pathogenic bacterial species are illustrative products of ecological speciation.

Geographic separation in which divergence to form new species is caused by mutation, selection and genetic drift, is common in animals and plants. Evidence for the effect of geographic factors on bacterial speciation has been more difficult to establish. Recently, however, Rachel Whitaker and colleagues showed that *Sulfolobus islandicus*, a thermoacidophilic archaeon isolated from globally separated hot springs, forms different clades depending on the their location. Strains isolated from hot springs in Iceland differ from those from Yellowstone (Fig. 1) and Lassen National Parks of North America, and these groups differ from strains isolated from Kamchatka, Russia. This finding indicates that geography also plays a role in bacterial speciation and quite probably a major one, although more research is needed to better understand the importance and commonality of it among bacteria and archaea.

Taxonomy of bacteria and archaea

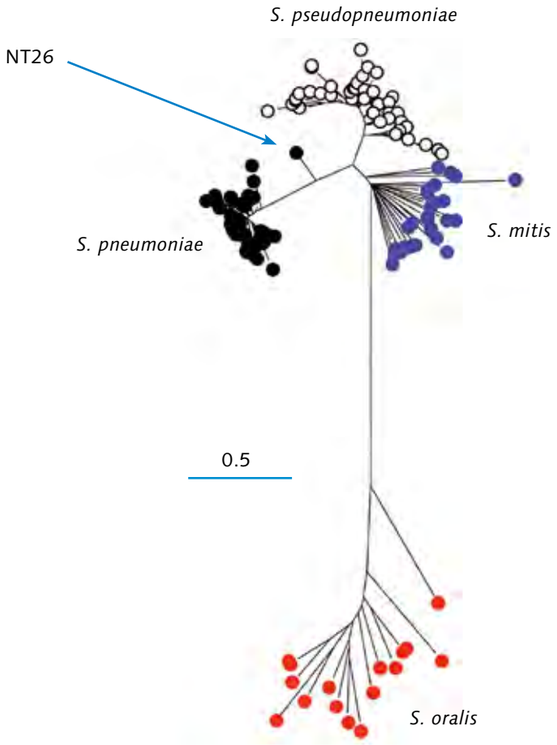
Early classifications of bacteria depended entirely on the expressed or phenotypic properties of the organism. Each species has its characteristic phenotypic attributes, such as temperature and pH range for growth, carbon sources utilized, habitat, Gram stain, size and shape, etc.

In the 1960s molecular characterizations were introduced. These included DNA base composition (mol% G+C content) and DNA–DNA hybridization. The combination of DNA hybridization with phenotypic features has culminated in the currently accepted polyphasic species definition used for bacteria and archaea. Two strains that have distinctive phenotypes and show greater than 70% DNA hybridization between them are considered to be members of the same species, whereas those that exhibit less than 70% are considered to be different species. The introduction of DNA hybridization and the polyphasic species definition brought uniformity to the species definition and has served bacteriologists very well since its adoption in the 1980s. However, the current definition is not conceptual and DNA hybridization has two major drawbacks:

1 the difficulty of conducting the DNA hybridization assay, and
2 its inability to assess speciation, the evolutionary process whereby organisms form species.

The 1980s brought protein and RNA sequencing as well as phylogeny into taxonomy. Most importantly, phylogenetic analyses of the 16S rRNA genes of bacteria and archaea, and

► Fig. 1. A view of Norris Geyser Basin, Yellowstone National Park, which was the source of several strains used in the biogeographic study of the thermoacidophile, *Sulfolobus islandicus*. *US National Park Service*.



▲ Fig. 2. An MLSA phylogenetic tree showing the positions of numerous strains of *Streptococcus pneumoniae*, *S. pseudopneumoniae*, *S. mitis* and *S. oralis*. Note that one strain, NT 26, lies between *Streptococcus pneumoniae*, *S. pseudopneumoniae*, and therefore cannot be identified. The bar indicates 0.5 substitutions per 100 nucleotides. *Reproduced with permission from Hanage* et al. *(2006),* Phil Trans R Soc B ***361****, 1917–1926*

the 18S rRNA genes of eukaryotic organisms revealed that there were three primary lines of descent in the tree of life. These major phylogenetic divisions, now called domains, are *Bacteria*, *Archaea* and *Eukarya*. This led to changes in bacterial taxonomy. In Volume 3 (1989) of the first edition of *Bergey's Manual of Systematic Bacteriology* (www.bergeys.org), the *Archaea* (*Archaeobacteria*) were the first to be classified taxonomically on the basis of 16S rRNA gene sequence analyses. In the second edition of the *Manual*, 16S rRNA is being used as the basis for the entire classification of the *Bacteria* and *Archaea* from domain to genus.

There was initially great anticipation that the 16S rRNA gene could be used for identifying species as well. But, alas, this was not to be. Unfortunately, it is too highly conserved to identify species. For this reason this article proposes a phylogenomic species concept that entails the use of less highly conserved genes for the identification of species as well as genomic approaches.

The phylogenomic species concept (PSC)

The time has arrived for bacteriologists to adopt a concept for species. The PSC relies on phylogenetic and genomic information to identify species. Genes that are less highly conserved than 16S rRNA are selected for phylogenetic analysis to determine the relatedness among a group of strains. In addition, genomic information, which includes all gene sequences, information on synteny (the arrangement of genes), and the use of DNA hybridization and expression approaches, supplement the phylogenetic analyses.

The advantages of the PSC are:

- it is based on phylogenetic theory which infers the evolution of an organism from the sequence of its macromolecules;
- it is pragmatic in that it relies on phylogenetic analyses that have been developed to assess the relatedness among macromolecules of different strains;
- PSC information is archival;
- PSC information is portable and can be transferred anywhere electronically;
- it has the potential to be universally applied to all organisms.

The PSC in practice

Actually, the PSC is already being used to identify bacterial species. Brian Spratt's laboratory has pioneered the use of multiple locus sequence analysis (MLSA) as a phylogenetic method to identify strains of many pathogenic bacteria including the genera *Streptococcus*, *Neisseria* and *Burkholderia*.

The MLSA approach relies on assessing the sequences of typically five to eight genes from each strain. The sequences of each gene are concatenated (linked together end to end) prior to phylogenetic analyses. The result is a phylogenetic tree of the strains of a species (Fig. 2).

The work on *Sulfolobus islandicus* discussed previously also used the MLSA approach. The 16S rRNA gene was included in that study, but it was too highly conserved to be useful. However, eight genes selected for analysis by MLSA indicated that the strains from each geographic location formed separate clades.

Genomic approaches are now becoming important in the study of speciation. Kostas Kontaninidis and James Tiedje have led this effort. Not only do genomes provide all of the organism's genes, but they provide the arrangement of the genes, or synteny, and hybridization and expression microarrays can be applied to compare strains.

Genomic approaches require that complete sequences are available of several strains of a species and its close relatives. Although this might appear to pose a major problem, it may not be such a significant issue in the future, because even now, literally hundreds of strains of some pathogenic bacterial species are being sequenced.

The issue of horizontal gene transfer

One of the most perplexing issues confronting bacterial taxonomists is that of horizontal gene transfer (HGT). Evidence for HGT is found at all levels of classification from domain to species. For example, at the inter-domain level, homologues for genes such as those for eukaryotic α- and β-tubulins that are responsible for forming microtubules, have been reported in *Prosthecobacter*, a bacterial genus in the phylum *Verrucomicrobia* (Fig. 3). Since these genes have been found only in this single genus of the *Verrucomicrobia*, the most likely explanation is that they were transferred to this group from a eukaryote millions of years ago.

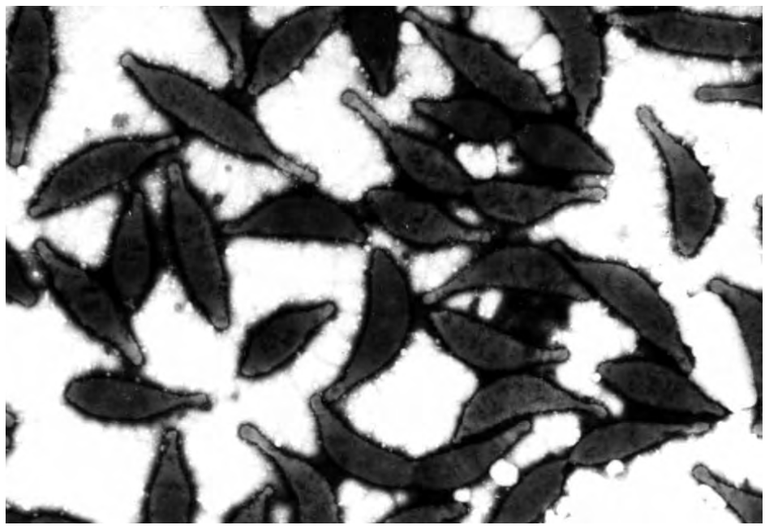
There is even greater evidence for HGT at the species level than there is at higher taxonomic levels. Clearly, if HGT is too extensive, it can lead to ambiguous classifications and potentially an erasure of the evolutionary pathway. This phenomenon might in part help explain the fuzzy species that are sometimes encountered when MLSA is used. HGT affects not only phylogenetic classifications but those based on phenotypic properties as well.

However, as thorny an issue as HGT is, it does not appear to be an overwhelming problem for phylogeny. It seems probable that genomic studies will help lead to a clarification of the likely potential source and nature of genes that have been transferred from other organisms.

Universal PSC

The PSC is applicable to all living organisms, so its espousal by biologists could lead to the establishment of a complete hierarchical taxonomy of all life on Earth. If the PSC were adopted, it could, like the tree of life, serve as a unifying step for all biology.

▼ Fig. 3. An electron micrograph showing numerous cells of *Prosthecobacter debontii*. The bacteria in this genus contain BtubA and BtubB, which are homologues for eukaryotic α- and β-tubulin. Although it is a hallmark feature of all members of the *Eukarya*, this is the only known example of tubulin-containing bacteria. *J.T. Staley*



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Further reading

Bishop, C.J. & other authors (2009). Assigning strains to bacterial species via the internet. *BMC Biol* **7**, 3 (doi:10.1186/1741-7007-7-3).

Feil, E J. & Spratt, B.G. (2001). Recombination and the population structures of bacterial pathogens. *Annu Rev Microbiol* **55**, 561–590.

Hanage, W.P., Fraser, C. & Spratt, B.G. (2005). Fuzzy species among recombinogenic bacteria. *BMC Biology* **3**, 6–13.

Jenkins, C. & other authors (2002). Genes for the cytoskeletal protein tubulin in the bacterial genus *Prosthecobacter*. *Proc Natl Acad Sci U S A* **99**, 17049–17054.

König, H. & Stetter, K.O. (1989). Section 25 – *Archaeobacteria*. In *Bergey's Manual of Systematic Bacteriology*, vol. 3, pp. 2171–2173. Edited by J.T. Staley & others. Baltimore: Williams & Wilkins.

Konstantinidis, K.T. & Tiedje, J.M. (2005). Genomic insights that advance the species definition for prokaryotes. *Proc Natl Acad Sci U S A* **102**, 2567–2572.

Konstantinidis, K.T., Ramette, A. & Tiedje, J.M. (2006). The bacterial species definition in the genomic era. *Phil Trans R Soc B* **361**, 1929–1940.

Staley, J.T. (1989). On using the Manual. In *Bergey's Manual of Systematic Bacteriology*, vol. 3, pp. xix–xxi. Edited by J.T. Staley & others. Baltimore: Williams & Wilkins.

Staley, J.T. (2006). The bacterial species dilemma and the genomic–phylogenetic species concept. *Phil Trans R Soc B* **361**, 1899–1909.

Whitaker, R.J., Grogan, D.W. & Taylor, J.W. (2003). Geographic barriers isolate endemic populations of hyperthermophilic archaea. *Science* **301**, 976–978.

It's time to retire the prokaryote

Norman R. Pace believes that the term 'prokaryote' is an anachronism in modern biology. Here he explains why and seeks the help of microbiologists in stopping its use.

Experimental results rarely upset the common wisdom of a scientific discipline, but that happened to biology late in the 20th century. The common wisdom in deep evolution and how we classify organisms was rendered sorely in need of modernization. And that modernization is happening too slowly.

The anachronism here is the notion of 'prokaryote' and the model of biological organization and evolution that it elicits. This model, which I term the 'prokaryote–eukaryote' model, posits that fundamentally there are two kinds of organisms, prokaryotes and eukaryotes, defined by the presence or absence of a nucleus (more properly nuclear membrane). Additionally, the model proposes that prokaryotes gave rise to eukaryotes, as shown in the figure overleaf.

The problem, however, is that the prokaryote concept has been undermined critically by sequence-based phylogenetic results. Indeed, the notion of prokaryote was scientifically illogical from the beginning because the definition, an 'organism without a nucleus', is a negative definition. No one can tell you what a prokaryote is, they can only tell you what it is not. Yet, institutional biology embraced the notion of prokaryote and it came to dominate textbooks, journals and discourse in matters of deep evolution. But the hypothesis of the prokaryote was never tested.

◀ 'Prokaryotes' heading into the sunset. *Medical R.F.Com / Science Photo Library (bacteria); Photos.com/Jupiter Images (sunset)*

Where it came from – the very short history of prokaryote

It is important to understand that the concept of prokaryote is not based on scientific results. Rather, it is based on historical conjecture. To simplify the history considerably, I think that prokaryote had its origins in evolutionary models of the late 1800s, with 'monera' at the origin of a tree of complex eukaryotes. Monera persists today at the base of the five-kingdom classification scheme, which was introduced in the 1960s and is popular in current textbooks. Also in the 1960s, the name 'monera' became interchangeable in the textbooks with 'prokaryote'. It is curious that the nomenclature of 'monera' never caught-on among earlier microbiologists, whereas 'prokaryote' was immediately incorporated into the lexicon. But in fact, prokaryote was never much more than a name-change from monera, a 19th century notion based on far more limited knowledge than is now available.

The disproof of prokaryote

The idea of prokaryote was disproved in 1977, with Carl Woese's discovery of archaea and the first articulation of a rudimentary molecular phylogenetic tree that related the most diverse forms of life. Woese saw through comparisons of ribosomal RNA (rRNA) sequences that life's diversity is composed not of two deeply related groups, prokaryote and eukaryote, but rather three such groups. These three phylogenetic 'domains' came to be called *Bacteria*, *Eukarya* (eukaryotes, which indeed proved monophyletic) and *Archaea*. Woese originally named the latter group *Archaebacteria*, but this was changed to *Archaea* when it became clear they are fundamentally distinct from Bacteria.

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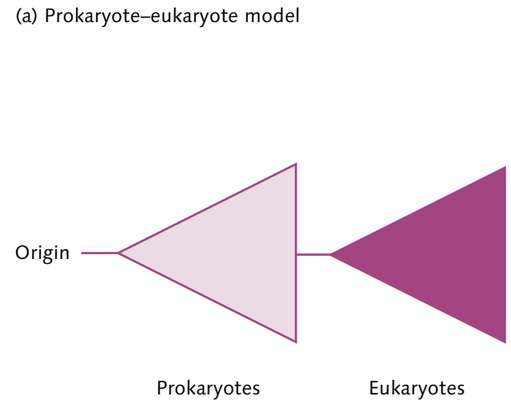

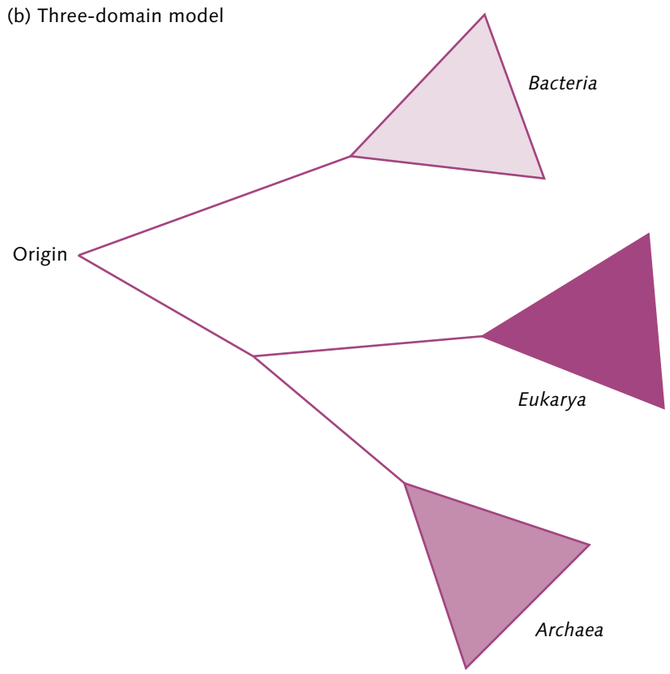

▲ Prokaryote–eukaryote (a) versus three-domain (b) models for biological organization and the course of deep evolution. The wedges indicate radiations within the respective groups.

The three-domain model of relationships and evolution stands in stark contrast to the prokaryote–eukaryote model, as shown in the figure above. The three-domain pattern shows that eukaryotes constitute a phylogenetically coherent group, but there is no specific group to label 'prokaryote'. Both archaea and bacteria would qualify through their lack of a nuclear membrane, but these two groups are not specific relatives. Indeed, archaea are more closely related to eukaryotes than archaea are to bacteria. This relationship is supported not only by molecular phylogeny, but also by many properties of archaeal and eukaryotic cells compared to bacterial cells.

Additionally, the phylogenetic model shows no specific group of organisms that preceded the eukaryotes. The textbook and common wisdom that eukaryotic cells arose late in the history of Earth by fusion of two prokaryotes is incorrect. Mitochondria and chloroplasts were derived from symbiotic bacteria, but the nucleus is far more ancient. The history of the nucleus is seen in the molecular phylogenetic tree as the eukaryal line of descent. The tree shows that the nuclear line is as old as the archaeal line and was derived from neither archaea nor bacteria. The molecular results say nothing at all about whether or not the earliest eukaryotes possessed nuclear membranes. In the light of the sequence comparisons, the presence or absence of the nuclear membrane or other morphological trait is irrelevant for classification or for deduction of the paths of deep evolution.

Some would argue

Some authors defend prokaryote as a useful classification. They argue, for instance, that bacteria and archaea are united by their very small size or their use of coupled transcription and translation. These arguments are not meaningful; rather, they are just other twists on the presence or absence of the nuclear membrane. At the last resort, the proponents of prokaryote insist, '*You have to call them something!*' But that's the problem: there isn't any 'them'. The molecular phylogenetic results, bolstered by decades of biochemical corroboration, show that there is no natural grouping that would correspond to prokaryote.

Proponents of the concept of the prokaryote sometimes argue that the prokaryote terminology is a convenient classification and that historical usage justifies continued usage. But these rationalizations are scientifically inappropriate. A critical point here, one usually missed by proponents of the prokaryote concept, is that scientific classification is not a convenience. As scientists we must observe nature and classify accordingly, so as to promote scientific understanding. As Darwin insisted, '*Our classifications will come to be, as far as they can be so made, genealogies*'. 'Prokaryote' doesn't fit the observed genealogy. It needs to be retired from the language of biology. It has become a distraction.

Why it matters

The legitimacy of prokaryote is more than an issue in terminology. It is also a matter of proper understanding of important biological concepts. Any scientific field rests essentially on two conceptual foundations. One foundation requires understanding of the order, the organization of the subjects of study. The other conceptual foundation is how the subjects of study change. Foundational issues for progress in biology, therefore, are proper perceptions of phylogenetic groups and relationships and, consequently, the path of evolution.

The prokaryote–eukaryote notion fails in both these regards. In contrast, the three-domain pattern of life's organization and large-scale path of evolution is solidly grounded on scientific observations.

What to do about it and how microbiologists are critical

Institutional biology is now heavily invested in the prokaryote concept. The language permeates our literature and thereby distorts understanding of foundational issues. One hurdle that faces efforts to modernize this matter is that most students, biologists and authors of general textbooks don't think very much about microbes. Their world is generally that of large organisms of limited diversity. They, unlike microbiologists, are not faced with trying to make sense of a vast diversity of life with comparatively little observable variation without resort to biochemistry and gene sequences. The three-domain phylogenetic model is beginning to appear in textbooks, but usually as just another method of classification, alongside the five-kingdom scheme. The evolutionary implications of the three-domain pattern of evolution are seldom broached, and the language of prokaryote perseveres. What to do about it?

The retirement of prokaryote from the lexicon of biology will be slow because it is now so deeply entrenched. Consequently, that retirement process needs to be catalysed. Microbiologists are in the best position to understand the issues and to participate in modernization. This is because their organisms span the three domains, and the phylogenetic perspective is referentially necessary and an obvious utility. Modern treatment of issues in classification and evolution by microbiological journals and textbooks eventually will lead to upgraded general texts. One catalytic step that any microbiologist can contribute, however, is simply to stop using the term 'prokaryote'. This may be hard to do because of long conditioning, but it is an important step for educators particularly.

How can teachers broach this issue in the face of the currently pervasive reference to prokaryotes in journals and textbooks? One way to do so is to use the discordance between recently emerging data and the textbooks as a prime example of how science, biology in this case, is an ongoing, living process, evolving in response to new experimental data. Dealing with the prokaryote issue is an opportunity to demonstrate the testing of specific hypotheses with experimental data, with results important for biology. Phylogenetic trees, maps of evolutionary relationships, are straightforward metaphors for the course of evolution and are not hard for students to understand in essence. The three-domain concept poses many questions, to be sure, but it also provides a solid foundation for progress toward answering those questions.

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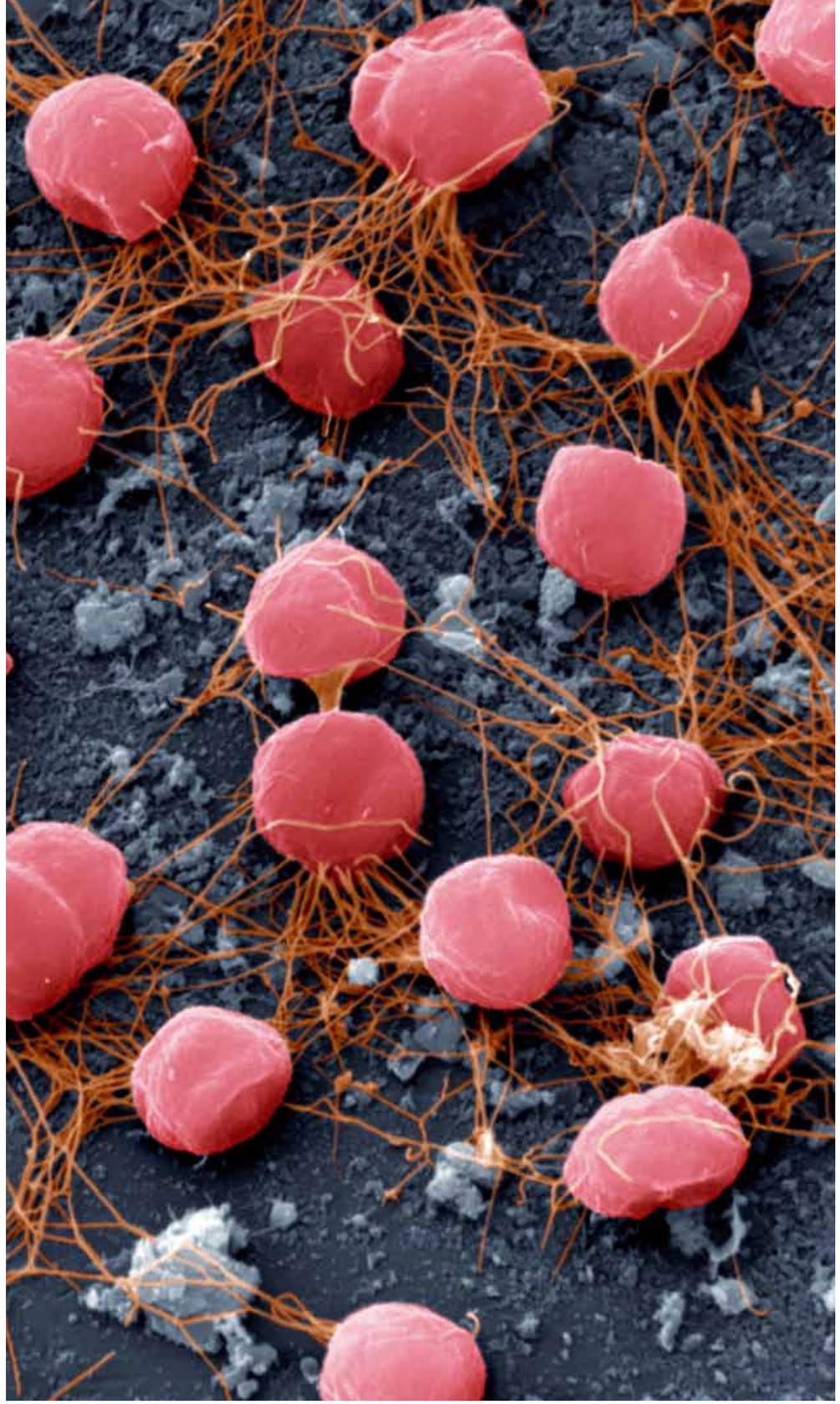
Further reading

Pace, N.R. (1997). A molecular view of microbial diversity and the biosphere. *Science* **276**, 734–740.

Sapp, J. (2005). The prokaryote–eukaryote dichotomy: meanings and mythology. *Microbiol Mol Biol Rev* **69**, 292–305.

Woese, C.R. (1994). There must be a prokaryote somewhere: microbiology's search for itself. *Microbiol Mol Biol Rev* **58**, 1–9.

Woese, C.R. & Goldenfeld, N. (2009). How the microbial world saved evolution from the Scylla of molecular biology and the Charybdis of the Modern Synthesis. *Microbiol Mol Biol Rev* **73**, 14–21.



▶ Scanning electron micrograph of the thermophilic archaeon *Pyrococcus furiosus*. *Eye of Science / Science Photo Library*

A cockatrice was a flamboyant sight at medieval banquets, featuring a roasted chimaera of winged rooster fused to a suckling pig. **Edward L. Bolt** and **Stephane Delmas** take a look at archaea, ancient micro-organisms whose genomes look like chimaeras of apparent bacteria-like and eukaryote-like features and metabolic systems.

Archaea: a microbial cockatrice

Archaea and bacteria are micro-organisms that are similar, yet different. Archaea are evolutionarily ancient organisms that have soaked up diverse ecosystems for at least 2.5 billion years. They are, like bacteria, unencumbered by various complex sub-cellular structures (e.g. mitochondria, a membrane-bound nucleus) and as such have been for most of their long existence, or at least from when microbiologists started looking at them, considered to be bacteria that had evolved to thrive in extreme environments (e.g. at high temperature or salinity). For this reason they were often called archeabacteria.

However, DNA sequencing experiments in the 1970s drove a wedge through the bacteria, splitting it into two separate domains of cellular life: the *Bacteria* and the *Archaea*. The genetic distinction between bacteria and archaea is now generally accepted since its original proposal in 1977, but has its evolutionary root much earlier, probably pre-dating the emergence of oxygen 2.5 billion years ago. Therefore, the classification of cellular organisms is now usually represented in a tree of life consisting of three domains, *Bacteria*, *Archaea* and *Eukarya*. This notion, and the difficulties arising from it, especially with regard to micro-organisms, can be pursued in other articles in this issue of *Microbiology Today*.

Nevertheless, since 1977, detailed whole-genome sequence information has been obtained from many nooks and crannies of bacterial and archaeal life: at the time of writing, according to the NCBI database, there are 1,456 genomes available for bacteria and 69 for archaea. Add to this the substantial number of genomes sequenced from eukaryotes and it is possible to compare the genetic relatedness of any metabolic pathway that takes your fancy.

Comparing archaea to other organisms can make puzzling patterns

The diversity of available DNA sequence information highlights how the same genes are often conserved throughout the three domains of cellular life. These genes, referred to as COGs (conserved orthologous genes), may indicate common descent as some metabolic pathways are conserved in organisms as they diverge through modification during evolutionary time. The *Archaea* contains approximately 7,500 COGs. About 45–55% of these, depending on how strict are the rules of inclusion, are also bacterial. The similarities between some fundamental metabolic pathways in bacteria and archaea are striking and it is apparent from genome sequencing that bacteria and archaea are promiscuous, as they have swapped genetic material with one another in 'lateral gene transfers'. These observations illustrate that although archaea and bacteria are presented as distinct cellular domains they retain the capacity for genetic flux between domains, and the potential for diversity.

Comparative genetics and biochemistry have also illustrated how very different archaea are from bacteria. A topical example of this is how some types of bacteria and archaea derive motility from functionally similar structures called flagella. However, the protein structures of the flagellum in archaea are quite different from those in bacteria. The shape and effect of this cell structure are the same in bacteria and archaea, but are fine-tuned differently. Structural differences between archaea and bacteria are also seen in their genomes, despite the fact that in shape these micro-organisms appear alike because they lack a membrane-covered nucleus. Bacterial cells clone themselves by copying their genetic material (DNA replication) from a single point on the genome (an origin), but archaeal cells are known to copy their DNA from several points (origins) on the genome. This is intriguing because features like having several origins rather than a single origin are commonly ascribed to eukaryotes only. On the other hand, the arrangement of many archaeal genes into operational units where several genes are transcribed together (operons) is a bacterial trait.

Archaea are chimaeras in DNA processing

Returning to the distribution of COGs in cellular life, and having pointed out that about 50% of genes in the archaea are also common to bacteria, we see that the other 50% are confined to archaea or conserved with the domain *Eukarya* (which contains fungi and metazoans). A notable example of this dichotomy is in the arena of genetic information processing and genome dynamics (DNA replication, gene transcription, recombination and DNA repair). With some exceptions, proteins in archaea that drive DNA processing are not conserved in bacteria, but about 150 COGs in archaeal DNA processing are conserved in eukaryotes. For example, the complex gene transcription machine (RNA polymerase) of archaea is very similar to the eukaryotic one. However, it was then unearthed that the proteins regulating the running of this machine in archaea are conserved in bacteria, not eukaryotes, highlighting the mixed-up nature of this aspect of gene processing in archaea. How this has arisen during evolution has been tackled in one way by invoking the action of ancient viruses. We now turn to a specific example of DNA processing in archaea that illustrates recently discovered protein functions: homologous recombination.

Two faces of homologous recombination

Homologous recombination is a cellular process used in all organisms and it serves two purposes. In one, homologous recombination promotes genetic stability by repairing broken chromosomes and rescuing DNA replication when it gets blocked as it moves away from origins. On the flip side, homologous recombination facilitates genetic diversity by shuffling genes around inside a cell and allowing integration of foreign DNA into the chromosome.

All these recombination processes need a protein called a recombinase. The recombinase in archaea is similar to eukaryote recombinase, although they have different names (RadA and Rad51), but differs from bacterial recombinase (RecA).

In the cell, the recombinase protein does much to set up recombination events, but other proteins finish them off. One of the finishing events is the forming of an elaborate DNA structure called a Holliday Junction, named after the molecular biologist Robin Holliday. This is a physical manifestation of a recombination event in which two different DNA molecules are co-joined. Another protein, called a resolvase, may be needed to disentangle the co-joined DNA molecules set up by the recombinase. The identities of resolvase proteins are now known in bacteria (e.g. RuvC), archaea (Hjc) and eukaryotes (GEN1/Yen1) and they are all different: there is little similarity between them in sequence or structure, but they do the same job in cells, finishing off homologous recombination. This lack of similarity between resolvase from archaea and eukaryotes indicates that the DNA processing pathway in archaea is not just a mirror of the eukaryotic one.

The machinery that controls the fidelity of homologous recombination, (mismatch repair proteins) also highlights this because it is conserved in bacteria and eukaryotes, but is largely absent from archaea. Perhaps archaea evolved their own protein tools for resolving and monitoring recombination, but have shared tools with eukaryotes for triggering it. The explosion in the number of archaeal genome sequences available and laboratory analyses give a blurred vision of archaea as a kind of cockatrice between bacteria and eukaryotic cells. However, this mixture obviously works very well, to have been around for so long.

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Further reading

Howland, J.L. (2000). *The Surprising Archaea*. Oxford: Oxford University Press.

Blum, P. (editor) (2007). *Archaea: New Models for Prokaryotic Biology*. Norwich: Caister Academic Press.

Doolittle, W.F. & Bapteste, E. (2007). Pattern pluralism and the tree of life hypothesis. *Proc Natl Acad Sci U S A* **104**, 2043–2049.

Forterre, P. (2006). Three RNA cells for ribosomal lineages and three DNA viruses to replicate their genomes: a hypothesis for the origin of cellular domain. *Proc Natl Acad Sci U S A* **103**, 3669–3674.

letters

Antibiotics

Dear Editor

The latest issue was once again very interesting. What I do enjoy most about *Microbiology Today* is that it publishes articles concerning real issues and challenges that we bioscientists have to confront in our daily lives, one of them being the demand for new antibiotics to counteract re-emerging and resistant infections such as XDR tuberculosis and MRSA.

I really enjoyed Flavia Marinelli's article '*Antibiotics and* Streptomyces: *the future of antibiotic discovery*'. I agree that the search for new antibiotics is declining and that microbial product screening particularly for effective *Streptomyces* spp. would be a good start. I believe that research institutes and biopharmaceutical companies should carry out mass isolation and screening of soil microbes as they did in the 'golden age'. I also believe that isolating microbes from other environments might be interesting in discovering a new class of antibiotics as pointed out in Flavia's article.

Articles such as Flavia's help to raise awareness amongst microbiologists about important issues such as these, but I believe we need to convey or channel these strong messages to government and other relevant parties more effectively in order for realistic progress to be made. For instance if this Society can put pressure on the government and research councils that more money is needed to invest in research projects such as antibiotic discovery and mass isolation and screenings of potentially useful microbes, then the sooner these problems and demands can be dealt with more practically. We would find a new class of antibiotics sooner and they would be manufactured by interested biopharmaceutical companies.

Regards

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Sir

The increasing resistance of bacteria to antibiotics is of grave concern, but reversing this trend seems very difficult. The following approach may be of interest.

Consider, as a hypothetical example, a molecule with two antibacterial activities, a penicillin activity and tetracycline activity, but in which the tetracycline is not active until the β-lactam ring of the penicillin is opened. Then the bacterial cell would be killed by tetracycline.

This would in theory select for strains possessing a β-lactamase, and thus for penicillin sensitivity. The approach might be possible with many different pairs of activity, and it may be that fairly small differences in the activities would be sufficient to permit such selection.

Yours sincerely

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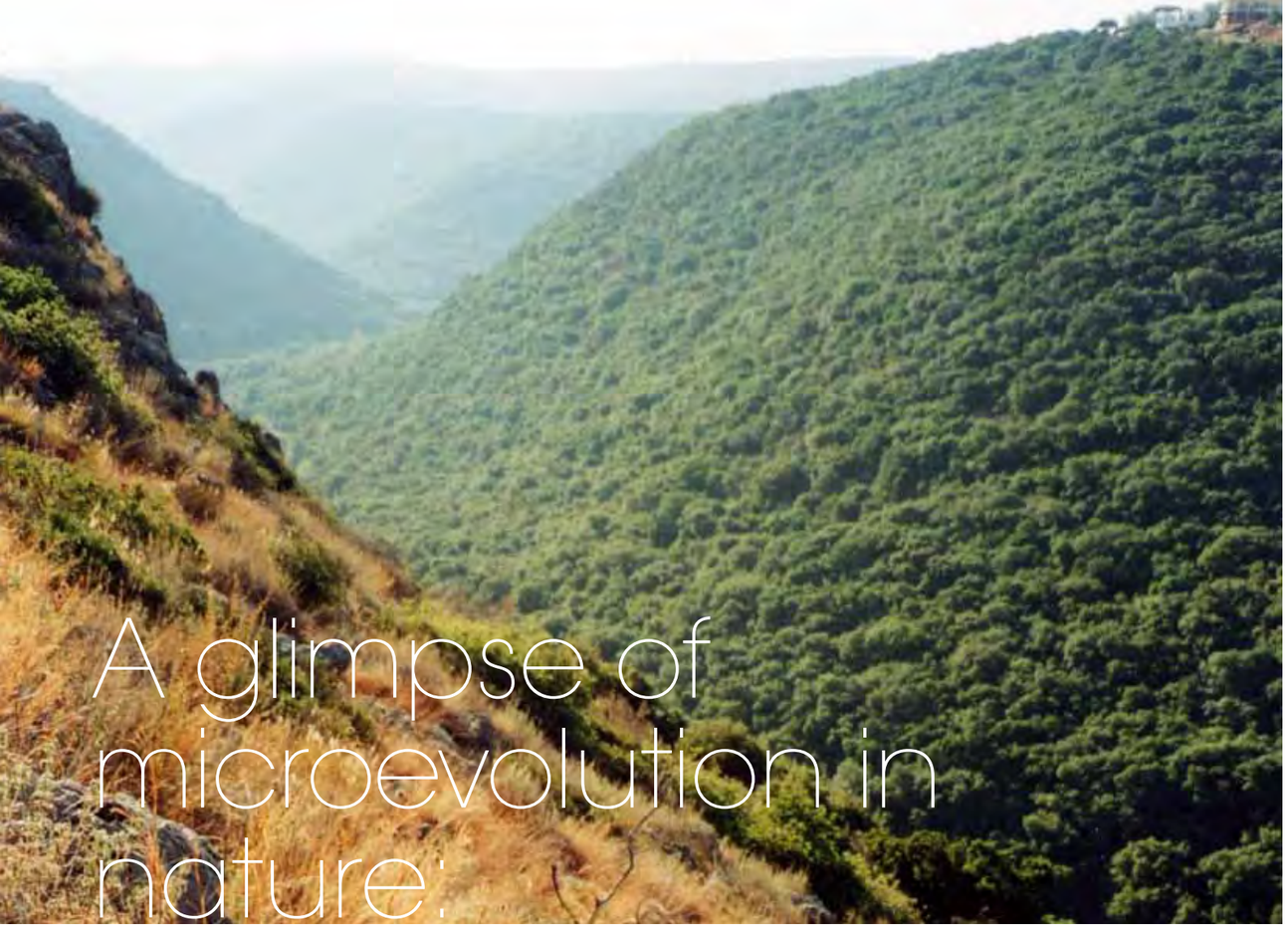


A glimpse of microevolution in nature: bacterial adaptation and speciation in 'Evolution Canyon', Israel

Many of the factors responsible for microbial evolution are becoming well understood, but **Johannes Sikorski** believes that not enough attention is being paid to the effects of the natural environment of organisms.

Bacteria and archaea are genetically, phylogenetically and physiologically very diverse. But how does such diversity start to evolve? How do the first subtle and tender lineages begin to accrue? Oh, you might say, that's trivial. Have a look at the textbooks and you will find everything there about the evolutionary interplay of mutation, recombination, natural selection and genetic drift. The theoretical framework of population genetics is extremely well-developed. Even more, you insist, microbial microevolution has and still is being analysed in very elegant laboratory experiments, where microbes are allowed to mutate, adapt and evolve in test tubes under very stringent and therefore reproducible and adjustable conditions (see the articles in the November 2004 issue of *Microbiology Today*). But may I remind you that the majority of bacteria are neither evolving in a computer, nor are they living in the pencils of mathematicians and theoretical population geneticists, nor in laboratory test tubes, although all these approaches yield tremendous results. Most bacteria live outside in the environment, in water, soil, rocks, plants, etc. Here, where they face a great plethora of biotic and abiotic challenges, they evolve and speciate. Shouldn't we look at how evolution happens in nature, even though as passive observers, we researchers cannot control this process? What are the decisive factors? Is it possible to catch a glimpse of such a natural evolutionary experiment?

'Evolution Canyon', a natural evolutionary laboratory

The 'Evolution Canyon' system in Israel has turned out to be a suitable site for such microevolutionary studies. Eviatar Nevo, the former director of the Institute of Evolution in Haifa, Israel, first realized the beauty and scientific potential of this natural evolutionary laboratory. 'Evolution Canyon' 1 (Fig. 2) at Nahal Oren in the Carmel Mountains close to Haifa is an east–west orientated canyon. The 'African' south-facing slope is constantly irradiated by sun, which makes it hotter and drier – savannah-like – whereas the shady 'European' north-facing slope is a mesic, lush forest. The scientific attraction of 'Evolution Canyon' is obvious. The slopes are separated by just 50–400 metres. Thus, geographical separation cannot account for any slope-specific differences in organisms belonging to the same species.

The canyon system is approximately 3 million–5 million years old. It is a geologically uplifting canyon, not an erosion canyon, and until now relatively undisturbed by humans. Despite having the same macroclimate (overall seasonal temperature, rainfall, etc.), the south- and north-facing slopes have substantially different microclimatic temperatures and drought stress, which allow us to identify natural selective abiotic pressures and to study their effect in nature. For over 20 years, the adaptation and speciation of macro-organisms has been explored in 'Evolution Canyon' using *Drosophila* and wild barley as the main model organisms. Model micro-organisms studied include the cyanobacterium *Nostoc linckia* and the fungi *Sordaria fimicola*, *Penicillium lanosum* and *Aspergillus niger*.

Bacillus simplex from 'Evolution Canyon'

In 2003, during my postdoc, I isolated a population of about 1,000 strains of *Bacillus simplex* bacteria from soils from

◀ Fig. 1. 'Evolution Canyon' 2 at Nahal Keziv, western Upper Galilee, Israel. *Courtesy Michael Margulis*

▼ Fig. 2. Cross-section of 'Evolution Canyon' 1 at Nahal Oren, Mount Carmel, Haifa, Israel, showing the south-facing 'African' slope on the right and the north-facing 'European' slope on the left. *Courtesy Michael Margulis*

'Evolution Canyons' 1 and 2 (Fig. 1), the latter being located in the western Upper Galilee Mountains and separated form 'Evolution Canyon' 1 by about 40 km (Fig. 3). It turned out that strains from the same slope type were very similar, despite the geographical distance, whereas strains from different slope types but in the same canyon were substantially distinct, despite their geographical proximity. This suggested that a distance of 40 km has no effect on genetic differentiation, but that the differential abiotic conditions between the two slope types are probably driving the diversification. Further analysis of genetic diversity, on a reduced set of approximately 130 strains, revealed two major phylogenetic genomic lineages, termed GL1 and GL2. Using Ecotype Simulation, a program developed by Frederick Cohan (Wesleyan University, Connecticut, USA) that models the sequence diversity within a bacterial clade, we identified putative ecotypes within GL1 and GL2 that Ecotype Simulation predicts to be ecologically and evolutionary distinct (see phylogenetic tree in Fig. 4).

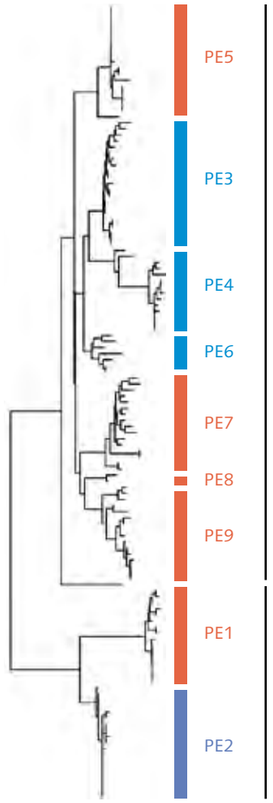
But, are these putative ecotypes really ecologically distinct, as one would assume from their preference for slope type? Indeed, at the upper temperature limit of growth, the 'African' strains generally grow faster than the 'European' strains. Apparently, 'African' strains are still metabolically active at the very high temperatures at which 'European' strains start to capitulate. This was a first indication of the high-temperature adaptation of the 'African' strains. Further support came from fatty acid analysis of the cell membranes. Compared with proteins and genomes, the cell membrane is hardly a focus of mainstream research. Yet a functioning cell membrane is crucial for microbial life. Just imagine a bottle of your favourite wine. Obviously, you are only interested in the wine, not in the bottle itself, but once the disregarded bottle gets damaged, all the precious wine spills out. This illustrates the substantial importance of an intact cell membrane. The cell membrane reacts very flexibly to changing environments, for example by changing its fatty acid composition. Under cold conditions, to ensure

◀ Fig. 3. Geographical locations of 'Evolution Canyons' 1 and 2 in Israel. *Satellite image – Earth Satellite Corporation / Science Photo Library*

▶ Fig. 4. Phylogenetic tree demonstrating the genetic similarity of 131 *Bacillus simplex* strains isolated from 'Evolution Canyons' 1 and 2. The orange clades are from the 'African' south-facing slope, whereas the blue clades are from the 'European' north-facing slope. Each clade consists of strains from 'Evolution Canyons' 1 and 2. *J. Sikorski*

the fluidity of the membrane, bacilli incorporate predominantly anteiso-branched fatty acids. In contrast, iso-branched fatty acids are favoured at higher temperatures. Interestingly, the 'African' strains generally produce more iso-branched fatty acids than the 'European' strains, irrespective of the lab temperature at which the strains are grown. This strongly suggests a genetically fixed difference between 'African' and 'European' strains, with respect to fatty acid branching, most probably as a result of long-term exposure to different environmental temperatures.

However, not all traits follow the south-/north-facing slope dichotomy. Although the soil on both slopes is classified as 'Terra rossa', small but significant differences exist, for example in the organic carbon content. This prompted us to test for quantitative differences in the utilization of a variety of different carbon sources. Interestingly, the observed differences were not associated with the different habitats, but rather with the phylogenetic split into GL1 and GL2.



Future research

Many questions remain. For example, do 'African' and 'European' strains differ in their drought resistance, since the south-facing slope soil is significantly drier? Do the spores of 'African' and 'European' strains differ in their heat resistance? Do the strains contain plasmids, and if so, does the abundance or diversity of plasmids correlate with either the phylogenetic structure or the ecological origin of the host strains? The possibilities are endless. Finally, how do these diverse traits relate to each other among the wealth of the 131 *B. simplex* strains analysed in this study? We are currently addressing some of these issues. Once we have enough phenotypic characterizations, genome sequence comparisons will help us to understand how these evolutionary changes are implemented at the molecular level.

Despite the paucity of information, we do already understand that the observed evolutionary lineages (putative ecotypes) represent speciation events. These putative ecotypes are genetically different, reside preferentially in different habitats and show characteristic physiological traits related to the habitats in which they live. In fact, from a biological and evolutionary perspective, they probably already represent different species, though this proposal is currently not supported by the current pragmatic but rather artificial taxonomic rules of microbial species delineation.

It is perhaps too naïve to expect that the traits observed have evolved precisely in those sites from where the *B. simplex* bacteria were isolated, taking into account that there are probably thousands of such east–west-directed canyons on the globe and that sporulating bacteria like bacilli easily migrate with the wind from continent to continent. But most probably, such marked microclimatic contrasts in close proximity reinforce within-species evolutionary splits, and thereby 'Evolution Canyon' represents a beautiful site in which to study microevolution in natural habitats.

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Further reading

Koeppel, A., Perry, E.B., Sikorski, J. & other authors (2008). Identifying the fundamental units of bacterial diversity: a paradigm shift to incorporate ecology into bacterial systematics. *Proc Natl Acad Sci U S A* **105**, 2504–2509.

Sikorski, J., Brambilla, E., Kroppenstedt, R.M. & Tindall, B.J. (2008). The temperature adaptive fatty acid content in *Bacillus simplex* strains from 'Evolution Canyon', Israel. *Microbiology* **154**, 2416–2426.

Sikorski, J., Pukall, R. & Stackebrandt, E. (2008). Carbon source utilization patterns of *Bacillus simplex* ecotypes do not reflect their adaptation to ecologically divergent slopes in 'Evolution Canyon', Israel. *FEMS Microbiol Ecol* **66**, 38–44.

Virus evolution

As new mass sequencing techniques reveal that the diversity of viruses is much greater than ever imagined, **Peter Simmonds** shows that the latest discoveries of new viruses are providing some clues to how viruses evolved.

In the spirit of Darwin 200, which marks the bicentenary of Charles Darwin's birth, I will describe a little of what we know about the evolution of viruses and their ultimate origins. One of the immediate problems facing such studies is the evident fact that viruses are hugely diverse in size, appearance, even the nature of their genetic material (DNA or RNA). From this, it is reasonably clear that they are a not a single evolutionary group, and cannot be easily added as a single unit to the tree of life with its three main divisions (*Bacteria*, *Archaea* and *Eukarya*). By the same token, it seems likely that different virus groups (e.g. animal RNA viruses, retroviruses, large DNA viruses, bacteriophages) may indeed have entirely separate evolutionary origins.

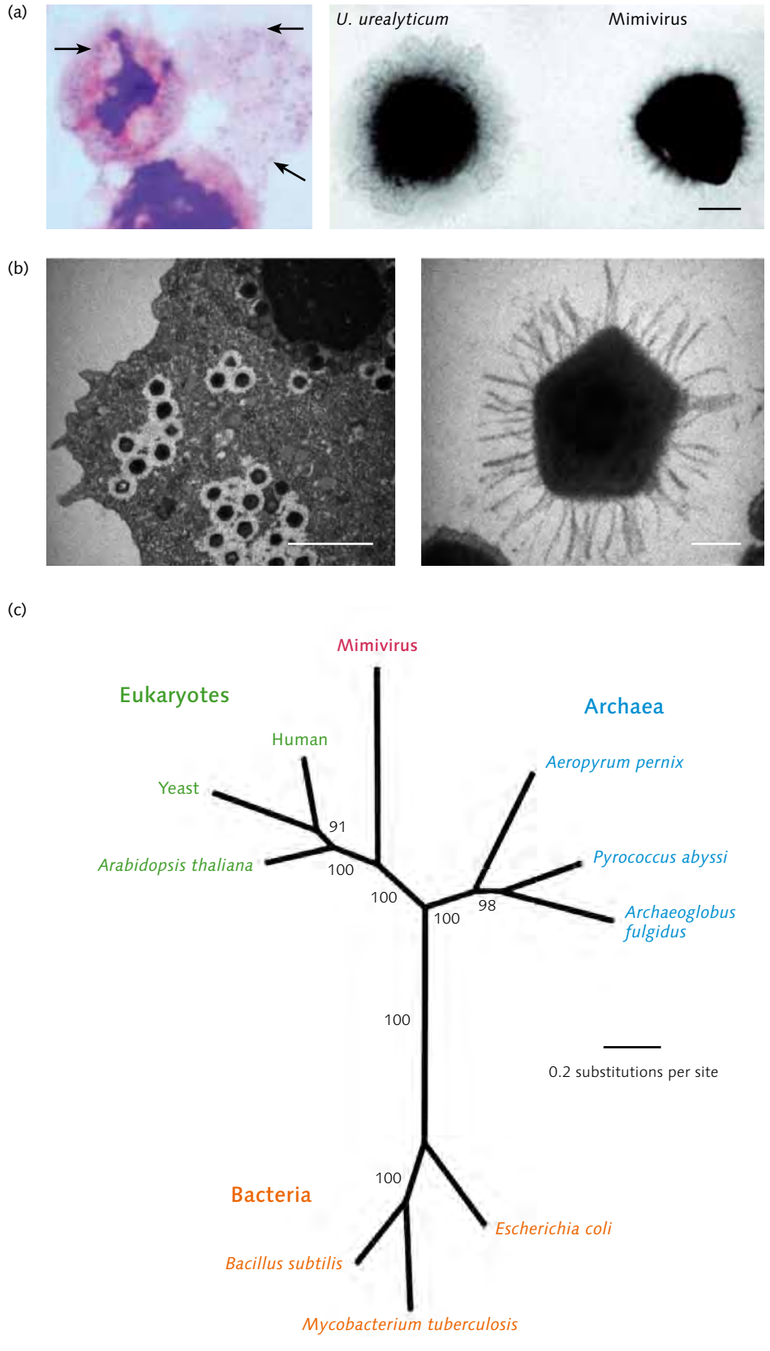
In this short article I will describe two areas where recent discoveries have produced tantalizing new insights into the origin and ubiquity of some of these groups. Through the application of new, mass-sequencing techniques and scope for large-scale environmental sampling for virus genomic sequences, we may finally be able to understand the extent and complexity of the 'virosphere' in which we live, and the extraordinary diversity of viruses that infect us.

The tale of a 'Gram-positive' virus

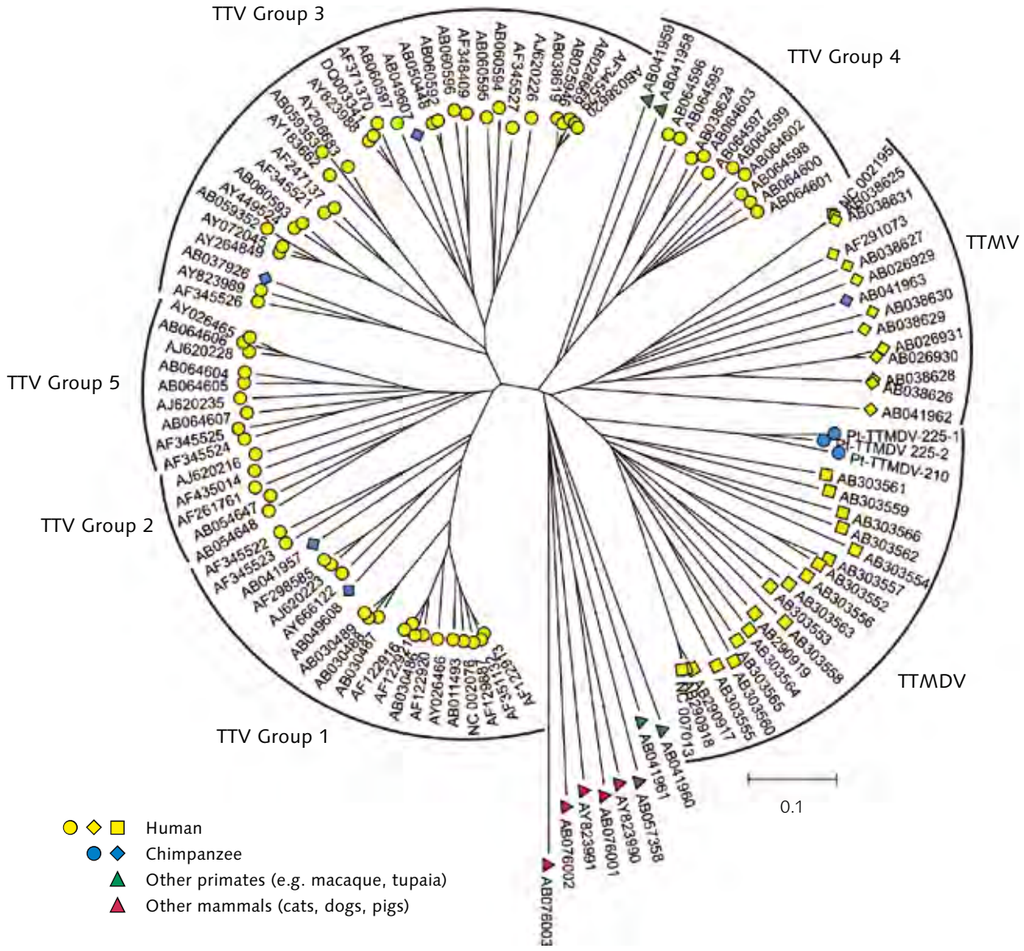
Amoebae growing in a water-cooling tower during the investigation of an outbreak of pneumonia in Bradford, UK, were found to harbour a number of intracellular *Legionella*-like organisms. There the issue might have been forgotten were it not for a attempt several years later by La Scola and colleagues in Marseilles to catalogue the bacteria in these and other environmental samples collected worldwide by ribosomal RNA (rRNA) sequencing. Puzzlingly, one of the Gram-positive amoeba-infecting bacteria with a diameter of around 500–700 nm (Fig. 1a) proved resistant to attempts to amplify the rRNA genes. Fortunately for future studies, the decision to sequence its genome revealed the presence of an entirely novel, large virus-like genome, 1.2 Mb in size and containing over 900 genes, far larger than many parasitic bacteria such as *Rickettsia*, *Ureaplasma* and some *Legionella* species with which it was first confused (Fig. 1a). Remarkably, the genome of what is now called mimivirus ('microbe-mimicking' virus) contained many genes involved in translation, such as amino acyl-tRNA synthetases, translation initiation, elongation and peptide release factors not found in other viruses, as well as a huge complement of genes (76%) encoding proteins with no identifiable homology and unknown function.

What are mimiviruses? While they breach the size and complexity barrier that traditionally separates viruses and bacteria (Fig. 1a, b), they clearly aren't bacteria. Mimiviruses contain only seven genes homologous to a set of 61 core genes shared among bacteria, archaea and eukaryotes, and of these three, mimiviruses are actually most similar to those of eukaryotes (Fig. 1c). Remarkably though, they adopt a phylogenetic position ancestral to the split of the animal, plant and other component kingdoms of eukaryotes, implying an extraordinarily long evolutionary existence, possibly reaching back as far as the origin of life. Mimiviruses additionally lack ribosomal genes, an absence universal to viruses and which confine them to their obligate parasitic life cycle. Their genomes are linear with covalently closed ends, comparable to other large DNA viruses, such as asfarviruses (e.g. *African swine fever virus*) and poxviruses (e.g. smallpox virus), and distinct from the circular genomes of most bacteria and archaea. Finally, they replicate in the infected cell through construction of multiple virus assembly structures rather than by binary fission. This latter feature seems to preclude the existence of free-living mimiviruses in nature that might retain a greater proportion of ribosomal and other core genes required for autonomous replication.

A final remarkable feature of mimiviruses is their pervasive presence in the environment. Large-scale metagenomic sampling has revealed a plethora of viruses related to mimiviruses in seawater at frequencies that rival bacteriophages in detection frequency. What these viruses infect and whether there are indeed free-



▶ Fig. 1. (a) Left: mimiviruses (arrows) infecting the amoeba *Acanthamoeba polyphaga*, resembling Gram-positive particles. Right: comparison of the size of mimivirus with the intracellular bacteria *Ureaplasma urealyticum*. *Reproduced from Suzan-Monti* et al. *(2006) (see 'Further reading' for details) with permission from Elsevier.* (b) Left: appearance of mimiviruses in the cytoplasm of infected amoebae cells (bar, 2 μm. Right: electron micrograph of the non-enveloped icosahedral mimivirus virion surrounded by fibrils (bar, 100 nm). (c) Phylogenetic relationship of core genes of representative eukaryotes, bacteria and archaea with homologues in mimiviruses, showing their ancestral position relative to eukaryotes. *(b, c) Reproduced with permission from La Scola* et al. *(2003) (see 'Further reading' for details) with permission from AAAS*



▲ Fig. 2. Diversity of human and other mammalian TTV-like viruses (family *Anelloviridae*). The phylogenetic tree of ORF1 sequences reveals a large number of divergent types and groups (e.g. TTV, TTMDV, TTMV) as well as more divergent viruses infecting other primates and mammalian species. The greater number and diversity of TTV-like viruses found in humans (yellow circles) compared to other primates (blue) and other mammals (red) is undoubtedly the simple outcome of the greater attention being paid to human samples. Similar or probably greater diversity of TTV-like viruses certainly exists in these other species. *Adapted from Ninomiya* et al. *(2009) in* J Gen Virol *(see 'Further reading' for full details)*

living relatives built on the same structural plan are vital research questions for the future, as is the nature of the huge complement of unidentifiable gene sequences in the sea that probably belong to further uncharacterised virus groups and families. Because of their large size, filtering seawater for bacteria in metagenomic analyses doesn't produce only bacterial sequences.

The transition of the mimivirus from its humble, unsuspected origin in a water tank in the Midlands to one of the most abundant life-forms on the planet in the space of 4 years is a stark demonstration of how little we really know of viral diversity and evolution.

Unsuspected human viruses

The development and recent spectacular success of metagenomics and methodologically related molecular-based virus discovery methods has also greatly expanded the number and pace of discovery of human and veterinary viruses. The wealth of data emerging about the diversity of viruses and the unsuspected existence of a range of newly discovered parvoviruses (human bocavirus, PARV4), picornaviruses, paramyxoviruses, coronaviruses (including SARS virus), three new polyomaviruses and several new anelloviruses again highlights our current ignorance of the true size of the 'virosphere' infecting humans and animals.

One of the remarkable characteristics of these newly discovered viruses is their frequent wide distribution in human and animal populations. In the picornavirus family, past or current infection with Saffold virus (SAFV), a newly discovered member of the genus *Cardiovirus*, was detected in >95% of children by the age of two, even though the virus itself has remained undetectable by conventional virus isolation methods applied over the last 50 years and whose actual existence was entirely unsuspected until 2 years ago. *Cosavirus*, a newly discovered genus of human picornaviruses, with dozens of serotypes and several species, which is likely to be as diverse genetically and clinically as human enteroviruses, has been detected in 50% or more of faecal samples from young children in locations all over the world (Pakistan, Nigeria, Egypt). Similarly, infections with TTV and related small DNA viruses, collectively termed anelloviruses, are ubiquitous in human, primate and probably all mammalian species, a finding more surprising for their persistence and ongoing lifelong replication in the lymphoreticular system (including bone marrow), and multiple infection in each person with a plethora of different types and species (Fig. 2). A wealth of further small, persistent and ubiquitous DNA viruses undoubtedly await to be discovered in the coming years.

The frequent ubiquity and non-pathogenicity of many of the recently discovered viruses may indeed be a particular attribute that has hindered their identification in the past. Most virus isolation and detection attempts have been necessarily clinically driven, aimed at identifying causes of various diseases with a suspected or demonstrated infectious aetiology, SARS and AIDS being two recent examples. Secondly, and particularly for DNA viruses, tight control of replication is a commonly used strategy to avoid immune recognition and elimination, but also one that hinders their detection and diagnosis. In the future, virus discovery programmes, such as those based on massively parallel sequencing of RNA and DNA in samples and tissues will reveal much more about the viruses that infect humans, their ecology and host adaptation, and, for some, their role in currently unexplained human and veterinary diseases.

These examples of the very large and the very small viruses give a flavour of their unexpected pervasiveness in the environment and their diversity. Viruses are numerically the most abundant and the most genetically diverse organisms on earth. With their short generation times, often huge population sizes and rapid sequence change over time, viruses additionally provide us with the opportunity to directly study evolution in action as they colonize diverse environments and adapt to new hosts.

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Further reading

Claverie, J.M., Ogata, H., Audic, S., Abergel, C., Suhre, K. & Fournier, P.E. (2006). Mimivirus and the emerging concept of 'giant' virus. *Virus Res* 117, 133–144.

Ghedin, E. & Claverie, J.M. (2005). Mimivirus relatives in the Sargasso sea. *Virol J* 2, 62.

Jones, M.S., Lukashov, V.V., Ganac, R.D. & Schnurr, D.P. (2007). Discovery of a novel human picornavirus in a stool sample from a pediatric patient presenting with fever of unknown origin. *J Clin Microbiol* 45, 2144–2150.

Kapoor, A., Victoria, J., Simmonds, P., Slikas, E., Chieochansin, T., Naeem, A., Shaukat, S., Sharif, S., Alam, M.M., Angez, M., Wang, C., Zaidi, S., Shafer, R.W., Zaidi, S. & Delwart, E. (2008). A highly prevalent and genetically diversified *Picornaviridae* genus in South Asian children. *Proc Natl Acad Sci U S A* 105, 20482–20487.

La Scola, B., Audic, S., Robert, C., Jungang, L., De Lamballerie, X., Drancourt, M., Birtles, R., Claverie, J. M. & Raoult, D. (2003). A giant virus in amoebae. *Science* 299, 2033.

Ninomiya, M., Takahashi, M., Hoshino, Y., Ichiyama, K., Simmonds, P. & Okamoto, H. (2009). Analysis of the entire genomes of torque teno midi virus variants in chimpanzees: infrequent cross-species infection between humans and chimpanzees. *J Gen Virol* 90, 347–358.

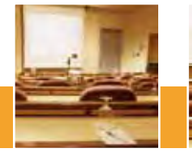
Raoult, D., Audic, S., Robert, C., Abergel, C., Renesto, P., Ogata, H., La Scola, B., Suzan, M. & Claverie, J.M. (2004). The 1.2-megabase genome sequence of mimivirus. *Science* 306, 1344–1350.

Simmonds, P. (2002). TT virus infection: a novel virus–host relationship. *J Med Microbiol* 51, 455–458.

Suzan-Monti, M., La Scola, B. & Raoult, D. (2006). Genomic and evolutionary aspects of *Mimivirus*. *Virus Res* 117, 145–155.

Venter, J.C., Remington, K., Heidelberg, J.F., Halpern, A.L., Rusch, D., Eisen, J.A., Wu, D., Paulsen, I., Nelson, K.E., Nelson, W., Fouts, D.E., Levy, S., Knap, A.H., Lomas, M.W., Nealson, K., White, O., Peterson, J., Hoffman, J., Parsons, R., Baden-Tillson, H., Pfannkoch, C., Rogers, Y.H. & Smith, H.O. (2004). Environmental genome shotgun sequencing of the Sargasso Sea. *Science* 304, 66–74.

Zoll, J., Erkens Hulshof, S., Lanke, K., Verdyn Lunel, F., Melchers, W.J.G., Schoondermark-van de Ven, E., Roivainen, M., Galama, J.M. & Kuppeveld, F.J.M. (2009). Saffold virus, a human Theiler's-like cardiovirus, is ubiquitous and causes infection early in life. *PLoS Pathog* 5, doi:10.1371/journal.ppat.1000416.



Autumn**09** | Heriot-Watt University Edinburgh

7–10 September 2009 www.sgmheriot-watt2009.org.uk

Putting microbes to work – the latest in translational and applied microbial science

Top international speakers will consider current challenges and developments in translational microbiology. Sessions will cover wide-ranging applications of micro-organisms in food and drug production, disease diagnosis and prevention, environmental clean-up, as microbial factories and as model organisms.

Who should attend?

Anyone who wants to keep up to date with modern microbial science, no matter what their field or stage of their career. The conference will also provide a great opportunity for networking.

Where is it?

Located on a pleasant rural campus on the outskirts of Scotland's capital city, Edinburgh Conference Centre has excellent facilities, including the purpose-designed James Watt Centre. High quality en-suite overnight accommodation is available on-site. Situated next to the city bypass and central to Scotland's motorway network, the Centre is only ten minutes from Edinburgh's International Airport and has good public transport links.

Grants

Conference grants are available to SGM Postgraduate Student Associate Members.

Deadlines

Abstract submission	29 May 2009
Earlybird registration	7 August 2009

- Putting microbes to work
- Microbial polysaccharides
- Microbial factories
- Alternative models to study mammalian pathogens
- Cultivating and sensing microbes in micro-scale devices (industry session)
- Glycoengineering
- Conjugate vaccines
- Microbial stress and food production: coping with the work environment
- Bioenergy fuel sources
- Bacterial cell walls
- Contribution of the global N cycle to global processes
- Meningitis (clinical microbiology)
- Polar microbiology

Darwin's tree of life

A symposium on microbial evolution to mark the 200th anniversary of the birth of Charles Darwin

Fred Griffith Prize Lecture

From spores to antibiotics via the cell cycle – Jeff Errington FRS

Other highlights

- Young Microbiologist of the Year
- Microbial genomics (hands-on workshop)
- CV skills (workshop for early career microbiologists)
- Trade exhibition/Poster sessions
- Gala dinner and ceilidh

Spring**10** | Edinburgh International Conference Centre

29 March–1 April 2010

www.sgmeicc2010.org.uk

Systems microbiology

Other**Events**

FEMS 2009 – 3rd Congress of European Microbiologists

Gothenburg, Sweden
28 June –2 July 2009

Microbes and man – interdependence and future challenges

www.kenes.com/fems-microbiology

ASM/SGM Joint Meetings

Cambridge MA, USA, 1–4 July 2009
Prokaryotic Development

Aix-en-Provence, France
5–9 October 2009
3rd International Conference on Salmonella

www.asm.org/meetings

Irish**Division**

Spring 2010

University of Cork, Ireland

Recombinant protein synthesis

Organizer Gerard Wall

Autumn 2010

University of Maynooth, Ireland

Joint meeting with Irish Society for Clinical Microbiology

Organizer Kevin Kavanagh

For details of all Irish Division activities, contact Evelyn Doyle (e evelyn.doyle@ucd.ie).

Harrogate Meeting Abstract Book

The legacy of Fleming: diagnosing, preventing, controlling and treating infectious diseases in the modern world

The full text of the abstracts book is available online at:
www.sgm.ac.uk/meetings/pdfabstracts/harrogate2009abs.pdf

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Abstracts

Titles and abstracts for all presentations must be submitted through the SGM website by the advertised deadlines. For further information contact the Administrator.

www.sgm.ac.uk/meetings

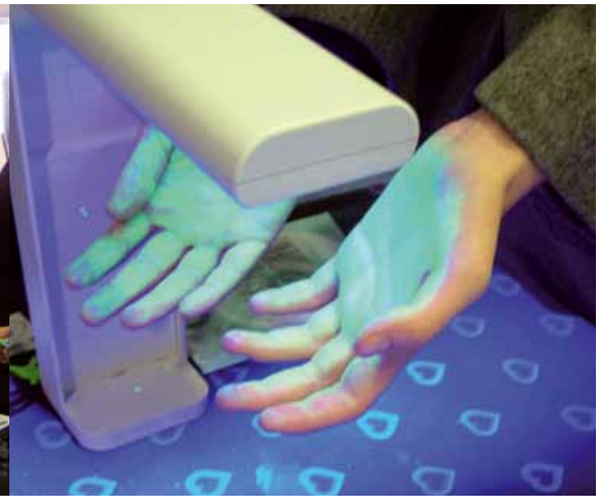
delivering modern microbial science

society for general microbiology
sgmconferences

Schools Membership costs only £10 a year. Benefits include *Microbiology Today*, advance copies of new teaching resources and discounted fees on SGM INSET courses. To join see **www.sgm.ac.uk/membership**. Enquiries: **education@sgm.ac.uk** or go to **www.microbiologyonline.org.uk** for full details of resources and activities.

The *Big Bang*

4–6 March, 2009
QE2 Centre, London



The *Big Bang* was an exciting event that brought together the science and engineering communities to celebrate and promote the very best of UK science and engineering to school students of all ages. Nearly 5,000 young people and more than 1,500 teachers, politicians, exhibitors, sponsors, scientists and engineers were there.

Sir Anthony Cleaver, Chair of the Engineering Training Board (ETB), Co-patron of The Big Bang, said:

> '*The* Big Bang *lived up to its name. To have been able to give nearly 5,000 young people the opportunity to look at science and engineering with fresh eyes and explore the exciting opportunities on offer in the sector, is a tremendous achievement. I thank the nearly 50 organizations from the public and private sectors for coming together to give so many young people a boost towards something that might just change their lives.*'

Hand hygiene can be fun!

The Science Council co-ordinated a cross-disciplinary themed exhibition area under the banner 'Fusion'. Three areas relevant to students' lives were addressed: 'Your Health', 'Your Planet' and 'Your Environment'. The SGM exhibited in the Health zone with a display that focused on 'Microbes and Us'.

Dariel Burdass, Janet Hurst, Yvonne Taylor and Jane Westwell demonstrated to over 600 students how hand washing is one of the easiest ways to prevent the transmission of infection. With a kit that makes use of Starglow UV germ technology, we were able to reveal through a simulation how, for example, cold and 'flu viruses are spread and how correct hand washing can reduce the risk of becoming infected. A harmless cream that shows up under UV light is used to mimic the virus.

The students, who ranged in age from 5 to 18 and came from schools in both the public and private sector, were all amazed at how far the 'germs', a tiny blob of the cream on their hands, could spread. After hand washing, finger nails and the cracks between fingers often gave off an unearthly green glow under UV light, highlighting the fact that during cleaning, some areas are frequently missed.

We also showed how pathogens can be spread in the home – on remote controls, door handles and mobile phones. Just touching a light switch sprayed with invisible 'Starglow' was enough to make a student's finger turn green under UV!

At the end of the activity the students were given some SGM goodies to remind them of the importance of 'when and how to wash their hands'.

The feedback from both the teachers and the students was very positive as all enjoyed the 'yuk' factor of the activity. However, there was a serious point to get across and the comment below, made by one of the participant's reflects the overall feedback that we received during the 3 days.

> '*I hadn't realized the huge difference that washing my hands could make to the spread of colds. Next time I sneeze I won't be wiping my hands down my jumper!*'

In 2010 the *Big Bang* will be in Manchester and the organizers anticipate that over 10,000 young people will witness the UK's biggest celebration of science and engineering. The SGM hopes to be there to raise the profile of microbiology in an engaging and informative manner.

Dariel Burdass, SGM

Teachers! Students! Have your say

Makeover for www.microbiologyonline.org.uk

The SGM microbiology education website is going to be completely redesigned. The new version of **www.microbiologyonline.org.uk** will be launched late in 2009 and will reflect the needs of both teachers and students.

We want to know who uses the site and what they hope to gain from it both now and in the future.

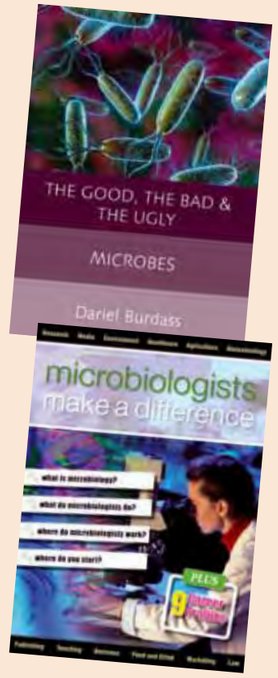
The SGM is looking for a group of 10 teachers and students either working or studying in institutions across the secondary education sector to comment on the content and design of the new website.

We hope that the first focus group meeting will take place on Friday 26 June Refreshments and lunch will be provided. The SGM will reimburse reasonable travel costs.

If you would like to join our focus group and be involved in this exciting new project please contact Dariel Burdass (d.burdass@sgm.ac.uk)

New SGM resources

The Good, The Bad and The Ugly: Microbes is aimed at the 11–16 age group and comprises a well-illustrated book and CD-ROM covering all aspects of microbiology in the UK school specifications. Copies have already been sent to all School Corporate Members of the Society, but single copies are also free to UK-based SGM Ordinary and Associate members who engage in outreach work in schools. Otherwise the cost is £10 including postage and packaging. Special prices apply for bulk purchases by schools. Contact **education@sgm.ac.uk** for details.



Microbiologists Make a Difference is a colourful 12-page booklet for 16- to 18-year-olds, packed with information on careers in microbiology. It includes details of how to train and profiles of nine young microbiologists. Copies are free from **careers@sgm.ac.uk**

New editions of existing resources

Cold Wars, *Hand Hygiene*, *TB* and *MRSA* have all been revised and redesigned. For copies, contact education@sgm.ac.uk

Science Photo Library

Darwin and antimicrobial resistance

2009 is Darwin Year and **Dariel Burdass** explains how antimicrobial resistance demonstrates some of Darwin's ideas in practice.

Darwin – the father of evolution

Charles Darwin was born 200 years ago on 12 February 1809, and 2009 is also the 150th anniversary of the publication of *On the Origin of Species*. In this book, Darwin introduced the term 'natural selection' – the process that forms the basis of evolution:

> '*As many more individuals of each species are born than can possibly survive; and as, consequently, there is a frequently recurring struggle for existence, it follows that any being, if it vary however slightly in any manner profitable to itself, under the complex and sometimes varying conditions of life, will have a better chance of surviving, and thus be naturally selected.*'

Evolution of antibiotic resistance

Antibiotics are chemical compounds produced by soil fungi and bacteria. Antibiotics kill or inhibit the growth of other micro-organisms in the natural environment where they live. Microbes that secrete antibiotics are more successful as they reduce competition for limited resources such as nutrients by preventing the growth of other micro-organisms around them. Antibiotic-producing microbes are resistant to their own antibiotic, so there has probably always been a gene in nature for resistance to antibiotics.

Doctors prescribe antibiotics to treat bacterial infections. Giving a patient antibiotics causes the harmful microbes to adapt or die; this is known as 'selective pressure'.

If a strain of a bacterial species acquires resistance to an antibiotic, it will survive the treatment. As the bacterial cell with acquired resistance multiplies, this resistance is passed to its offspring. In ideal conditions some bacterial cells can divide every 20 minutes; this means that after only 8 hours in excess of 16 million bacterial cells carrying resistance to that antibiotic could exist.

One of the main ways that resistance genes can be spread is through bacterial conjugation.

Bacterial conjugation

Bacterial conjugation is the transfer of genetic material between bacteria through direct cell-to-cell contact. It was discovered in 1946 by Joshua Lederberg and Edward Tatum and is a mechanism of horizontal gene transfer. It mainly occurs in Gram-negative bacteria.

Conjugation involves a donor cell (F+) which contains a conjugative plasmid (F plasmid) and a recipient cell (F–) which does not (F = fertility).

Conjugation is initiated when a pilus (encoded by the F plasmid) grows from the F+ donor cell, attaches to a specific receptor on the F– recipient cell and draws the two cells together. One strand of the F plasmid DNA is nicked, by an enzyme, and a single strand of DNA is transferred to the recipient cell. A strand complementary to the single-stranded plasmid in the F+ cell is synthesized. Then synthesis of a complementary strand begins in the F– recipient cell, forming a new plasmid. The recipient cell is now an F+ donor cell. The cells then separate.

Antibiotic resistance is transferred on conjugative resistance (R) plasmids that carry genes for resistance to antibiotics and other drugs.

Dariel Burdass, SGM

Darwin-related free resources for secondary schools

The Wellcome Trust has sponsored *Survival Rivals*, a set of Darwin-inspired experiments. The kits are available free to all state secondary schools across the UK.

Survival Rivals aims to provide opportunities for young people to undertake practical science. The series comprises three kits: *I'm a Worm, Get Me Out of Here* (11–14); *Brine Date* (14–16); and *The X-Bacteria* (post-16), which is about antibiotic resistance.

In *The X-bacteria* students learn how antibiotic resistance spreads between bacteria by 'mating' two strains of *E. coli* that are resistant to different antibiotics and testing to see if resistance has been transferred from one to the other by conjugation. Students will learn practical skills required for culturing micro-organisms, practice aseptic techniques and consider experimental design.

Each experiment will illustrate the link between Darwin's ideas, modern evolutionary principles and contemporary biomedicine and will help teachers to deliver the relevant parts of the UK curricula. *The X-Bacteria* in particular may be used to introduce discussions around topical issues such as MRSA.

The kits provide everything required to carry out the experiments in school, including notes for teachers, technicians and students, and online videos will demonstrate how to successfully deliver these practicals.

Clare Matterson, Director of Medicine, Society and History at The Wellcome Trust, said: "*2009 is going to be a fantastic year celebrating the life and science of Charles Darwin, one of the world's most famous and influential scientists. The Wellcome Trust is funding a range of national projects throughout the year to engage people of all ages with the scientific legacy of Darwin's ideas.*"

Survival Rivals kits are available to pre-order now, see **www.survivalrivals.org**

Nuffield Science Bursaries

The Nuffield Science Bursary scheme offers first-year post-16 science students throughout the UK a chance to work alongside practising scientists in science-, technology-, engineering- and maths-based projects. Unlike work experience schemes, students carry out a project of their own that will make a contribution to the work of the host organization. Projects last between 4 and 6 weeks, and students complete them during their summer holiday.

The SGM has provided bursaries for microbiology projects for several years. In 2008 we funded 10 bursaries, which took place in a range of institutions and on a broad variety of topics, some of which are shown in the table below.

Project provider	Project title	Supervisor
Food Microbiology, Agriculture & Food Science Dept, Queen's University Belfast	Evaluation of the efficiency of probiotic bacteria to inhibit the growth of *Mycobacterium smegmatis* used as a surrogate for *M. paratuberculosis* implicated as a cause of Crohn's disease in humans	Michael Rowe
Marine Biological Association	Growth of microalgae, relating algal pigments to wavelength of light	Dr Richard Pipe
University College London	The effect of Epstein–Barr virus on membrane trafficking in B lymphocytes, using microscopy and some biochemical techniques.	Professor Theresa Ward
Royal Free Hospital	The molecular epidemiology of the penicillin-binding (*pbp*) genes of *Streptococcus pneumoniae* (affect sensitivity to penicillin-like antibiotics).	Dr B. Charalambos
National Institute of Medical Research	Characterization of promoters of genes that play a part in the pathogenicity of *Mycobacterium tuberculosis*	Yvonne Braun Roger Buxton
Health Protection Agency	Microbiology of air	Katy-Anne Thompson
University of Glasgow	Studies on cell division in the trypanosome parasitic protozoan	Tansy Hammarton
Royal Holloway, University of London	How endophytic fungi, *Cladosporium* and *Trichoderma* affect the creeping thistle	Professor Alan Gange

This year the Nuffield Foundation is offering up to 1,000 bursaries for enthusiastic students. As the scheme is expanding, they are looking for more project providers for this summer and are always keen to hear from anyone who is interested in hosting a student. If you would like further information, please contact Sarah Saunders at The Nuffield Foundation on **020 7681 9626** who will put you in touch with your local Co-ordinator.

For more information, see the Bursary website: **www.nuffieldfoundation.org/scb**

Gradline aims to inform and entertain early-career microbiologists. If you have any news or stories, or would like to see any topics featured, contact **Jane Westwell** (**e** j.westwell@sgm.ac.uk).

Planned happenstance: an alternative approach to career development

Thinkstock / Jupiter Images

A common approach to career planning is to identify your 'ideal job' and work out a route to get there. However, for many of us, life can get in the way of the grand plan. Maybe you are forced to move by a partner's career change or perhaps you have family commitments that restrict your job mobility. Sometimes, people are indecisive about their careers and don't really have any long-term aims. A traditional, fairly rigid approach to career-planning can make it difficult to respond to imposed changes. Also, people who are racked by indecision can feel overwhelmed when faced with the task of identifying their perfect job.

As a researcher, there are likely to be several factors (professional and personal) influencing your career decision-making:

- Difficulties in finding a suitable postdoc or academic position
- Dilemma over leaving academic research – is it the right time? Would it be judged a sign of failure? What job can I actually do outside the lab?
- Family commitments
- Financial concerns.

Planned happenstance – an approach to career development based on chaos theory – has gained popularity in recent years. It recognizes that people can be indecisive or that outside factors influence our work and it offers a different perspective to the more traditional approach. It abandons the idea of mapping-out a perfect career and instead views a career as something that will gradually unfold and encourages you to make the most of opportunities as they arise.

Table 1. Planned happenstance vs the traditional approach to career planning

Traditional approach	Planned happenstance
Makes clear decisions	Embraces indecision
Process is logical and systematic	Recognizes that the future is unpredictable and uncertain
Identifies an ideal job	Unexpected events offer opportunities
Matches skills and interests to job	Curiosity-driven
Narrows down choices	Adopts a flexible attitude to changes in circumstances

Planned happenstance means following your curiosity or 'tuning into' those activities that you feel naturally drawn to. The happenstance part is all about noticing situations that you could not have anticipated and recognizing the potential opportunities they might offer. The planned part is about being prepared to take advantage of the situations – knowing what your interests are, being receptive to unfolding events and being ready to act on them.

Planned happenstance in action

At a recent workshop I attended, almost every participant was in their current job due to chance events. Take my own career for instance. As a PhD student I was ambivalent about research. At the end of my studentship I was looking for postdoc positions and administrative posts with an equal lack of success (probably due to a very unfocused CV). However, fate took me to Reading where my partner had recently been appointed to a lectureship. I was resigned to doing temporary shop-work until a second chance event led to a part-time junior technician post at the university. It was not the most exciting job, but it was a 1 year contract so I took it. The job put me in the right position to apply successfully for a research administration position (again part-time) at the end of the year. So much for the 'happenstance', now for the 'planned' part. Whilst working in the department I had the opportunity to get involved with outreach activities. I discovered that I really enjoyed communicating science and organizing events, and gave up quite a lot of my free time to help run open days and hands-on exhibitions. It was this experience combined with the administrative work that gave me the skills needed to obtain an interesting post in the External Relations Office at SGM.

Equip yourself to embrace change

There are things you can do to take advantage of the opportunities brought by chance events:

- Become more self-aware – think about what interests you and follow up on it
- Don't dismiss apparently off-the-wall jobs – are they really that crazy? Consider how you might be able to develop them
- Be positive and don't dismiss an idea before you have had a chance to think about it
- If things don't go to plan, look for new opportunities as they crop up
- Make good contacts and network as widely as possible
- Don't be afraid to approach people for advice
- Look for opportunities to learn and develop new skills
- Don't be held back by stereotypical views of how things should happen – there is often not a right way (or a direct route) into a job
- Follow up on your curiosity. Don't worry about whether you will be successful or where it will lead – if you don't try new ideas you'll never know where they might have led.

Which approach is best?

On the face of it, the traditional approach to career planning and planned happenstance seem poles apart. The former is fairly structured and systematic, and works well if you know what you want to do. Planned happenstance allows for indecision and unpredictability (Table 1).

Most people are likely to use a mixture of both approaches in their working lifetime. Whatever approach you adopt in your next career step, to ensure success there are several key features common to both: learning and developing new skills, networking, being proactive. Not to mention an excellent CV!

Further information

career.berkeley.edu/Article/ 040910 a-dm.stm
Career development via planned happenstance

www.careers.salford.ac.uk/students/phd/blog/?p=105
Why you should leave your career plans to luck? by Fiona Christie

career.berkeley.edu/Article/020809a.stm
Serendipity and the job search

Myers–Briggs Type Indicator: personality at work

It is not the purpose of a psychological typology to classify human beings into categories – this in itself would be pretty pointless – Carl Jung

At the recent SGM Harrogate Meeting, a group of early-career microbiologists enjoyed a fascinating and interactive workshop led by Sarah Blackford, an experienced careers advisor and qualified MBTI practitioner.

Sarah outlined how the MBTI (Myers–Briggs Type Indicator) classifies personality in terms of an individual's preferred way of gathering information and making decisions. The scheme measures only preferences, not abilities, values or skills. She stressed that there is no right or wrong way to be and made comparison to left or right handedness – you have a preferred hand, but with a lot of effort you can write with the other. However by recognizing your MBTI personality type you gain self-awareness and understanding of others.

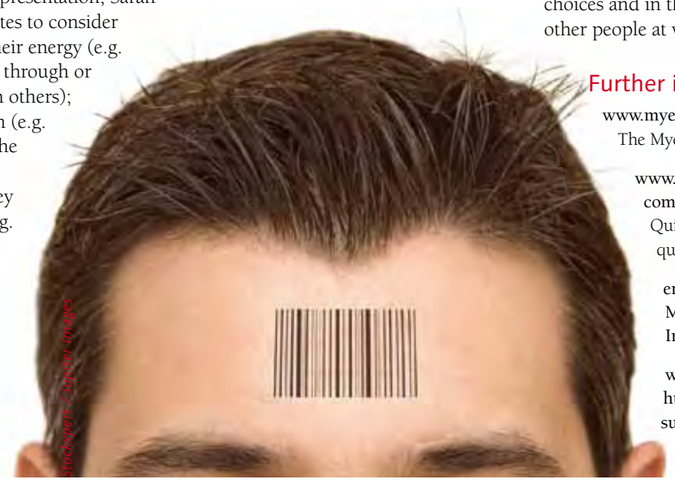
In an entertaining presentation, Sarah encouraged delegates to consider how they derive their energy (e.g. by thinking things through or talking it over with others); take in information (e.g. concentrating on the factual or seeing concepts), how they make decisions (e.g. thinking with the head or feeling with the heart), how they organize their lifestyles (e.g. using lists and filing systems or taking a less structured approach).

Combining all these preferences leads to 16 personality types made up of a combination of 4 binary dimensions:

- Extroversion (E) or Introversion (I) – where you derive your energy
- Sensing (S) or Intuition (N) – how you take in information
- Thinking (T) or Feeling (F) – how you make decisions
- Judging (J) or Perceiving (P) – how you organize your life

ISTJ Systematic	ISFJ Sympathetic	INFJ Insightful	INTJ Visionary
ISTP Pragmatic	ISFP Considerate	INFP Idealistic	INTP Logical
ESTP Action-oriented	ESFP Friendly	ENFP Enthusiastic	ENTP Innovative
ESTJ Decisive	ESFJ Helpful	ENFJ Appreciative	ENTJ Enterprising

By the end of the session most delegates had a feel for what their preferences were and could probably recognize features of friends, colleagues and family members. Although the workshop could only give a taste of MBTI (an accurate profile requires completion of a questionnaire and a discussion with a qualified practitioner), delegates had an understanding of how personality can play a part in making career choices and in their interactions with other people at work and at home.



Further information

www.myersbriggs.org
The Myers & Briggs Foundation

www.personalitypathways.com/type_inventory.html
Quick informal MBTI quiz

en.wikipedia.org/wiki/Myers-Briggs_Type_Indicator

www.bbc.co.uk/science/humanbody/mind/surveys/whatamilike/index.shtml
Quick informal quiz

council08–09

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SGM aims to promote microbiology to a whole range of audiences. In this issue we feature an initiative by academics to promote microbiology to schools, the inside story behind The Wellcome Window and a way to use a departmental website to disseminate free educational resources.

Getting the bug in schools

Rising to the challenge of getting school students enthused about microbiology can be done, as **Karen Moss** and **Gina Manning** describe.

▲ Plates prepared to welcome students to the lab session. *CELS*

Since 2003, there has been a 28% drop in the number of students in the UK applying for degrees with microbiology somewhere in their award title, according to the recent Higher Education Academy Centre for Bioscience report. This is an alarming statistic given that microbiology impacts on human lives in so many ways, both positive and negative. One major factor is ignorance – students do not know what sort of careers they can go into with a microbiology degree, and the study of microbiology in schools is often theoretical rather than hands-on.

Recently, the university sector has been charged with re-engaging the next generation in the thrill and challenge of scientific discovery.

What more can the education community do to develop scientific literacy in young people? More hands-on science and good teaching of practical skills by enthusiastic, specialist teachers are needed … Creativity in science needs to be encouraged along with more cross-curricular links to help enthuse pupils, make science relevant and encourage innovation. Sharing of resources and improved outreach work by universities would help many educational establishments further develop their work (Biosciences Federation, 2008).

With this in mind, staff from the School of Science and Technology at Nottingham Trent University (NTU) have tackled the problem head-on, specifically developing a programme of science outreach activities in microbiology for schools and colleges.

This is part of a wider programme of science outreach work here at NTU where CELS – the Centre for Effective Learning in Science – is based. CELS aims to teach science more effectively and inspire the next generation of scientists. In our strategy to attract more young people into science careers, we offer a wide portfolio of practical sessions with a strong emphasis on practical scientific enquiry, for ages 5–18, covering a range of science curriculum areas.

Through CELS, academic staff undertake sabbatical projects in teaching, learning and outreach. Sabbatical cover is provided by our novel CELS Lectureship scheme, and projects are supported by the CELS team with its teacher fellow. (For more information see **www.ntu.ac.uk/cels**) As a result of her CELS sabbatical, SGM member Gina Manning developed her role as Bioscience Outreach Coordinator. She identified a number of key staff who could give relevant and interesting talks to school students, and equally importantly, help to develop and enhance practical bioscience activities for schools.

As Gina is a microbiologist, she and microbiology colleagues have come up with a number of specific microbiology talks and taster sessions for schools to try to encourage students to become interested in microbiology as a subject in its own right, as well as in its potential as a future career path.

> '*It is encouraging that these pupils are interested in science which goes against the prevalent view from the media.*' (Michael Loughlin).
>
> '*It is rewarding to think we might have triggered a few people's interest to become a biologist.*' (Alan McNally)

Activities

Our seminars are designed to fit any age group from 11 to 18, and can be tailor-made to fit with the delivery of a school's timetable. Teachers tell us time is their most precious commodity. Given practical or economic restrictions on taking a class out of school, having talks and events that can be taken into the schools is a big advantage. It also allows maximum exposure to students of all abilities, some of whom may have never considered microbiology as a subject worth studying further.

The focus of our talks is carefully chosen to catch the attention of the teen audience with titles such as '*Flesh-eating bugs and other friendly bacteria*' and '*Dead long ago…diseases from history*' (a look at infectious diseases at different times in the past, including the Egyptians and the black death), through to the more topical '*Bird 'flu*', as well as careers-related seminars such as the general '*w.w.w.bioscience – a why, what & where guide to the biosciences*', which can cover any discipline within the biosciences, or the more focused '*A cultured career – a career in microbiology*'.

Getting careers information into the right hands is always a challenge. We've been developing some new approaches, e.g. web pages on '*50 reasons to study science*', Science graduate profiles and links to careers sites, as well as posters for classrooms ('*Where can I go with biology?*') and pocket-sized 'biology careers' leaflets.

At the bench

Building upon the evidence that practical work is very effective at engaging young people with science, we have developed some laboratory-based sessions to demonstrate our point about the relevance of microbiology to everyday life. These sessions are inquiry-based and allow students the opportunity to work within the university's microbiology teaching labs to carry out their practical investigations.

The most popular of these sessions is '*Forensic microbiology*' in which the students investigate an outbreak of dysentery on a housing estate, suspected of being associated with a local school with poor toilet facilities. The students are told that various samples have been taken from patients and sent to the lab for analysis. The students try to work out the source of the outbreak using bacteriological and DNA fingerprinting techniques. The session can also be expanded to include a consideration of what happens in the patient's blood in response to an infection. Students get an insight into a biomedical science environment and how specimens are handled, e.g. streaking out from a mock sample and examining pre-inoculated selective media and pre-prepared Gram films of these bacteria. They use these to try to identify the source of the outbreak. The DNA fingerprinting is used to introduce the students to molecular analysis, and they get the chance to perform restriction enzyme digests and gel

▼ Students preparing to load DNA digests on an agarose gel. *CELS*

electrophoresis with data analysis to confirm their suspicions. A general discussion as to how easy infection is spread and good hygiene concludes the session.

Another popular activity is the bird 'flu taster session. This is a dry-lab activity which can be run in a seminar room. The students are guided through the biology of the avian 'flu virus and the latest molecular techniques used in tracking infections. The students then take part in a detective activity where, through the analysis of clues and deduction, they track the likely path of an international outbreak, suggesting how it could have been contained.

Outcomes

Feedback from the students attending these sessions has been very positive with comments such as:

'*The hands-on approach! It was one amazing experience*.'

'*The practical experience was quite fascinating.*'

'*Learned something new*.'

'*The practical side. Getting hands-on experience really helped me to understand the subject.*'

Obviously, you can't always win – in response to 'what did you like the least about the session', one student wrote '*The germs*', and another '*The microscopes made my eyes go funny*'! We are constantly seeking to improve our communication with schools through active consultation with teachers. For example, teachers invited to a twilight information session, were able to discuss areas in which they need help, e.g. with aspects of the curriculum, whilst at the same time allowing us opportunities to update them on recent developments in university research, teaching and outreach activities.

If you'd like to discuss any of these activities further please contact us.

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Acknowledgements

The activities mentioned were developed by Alan McNally, Gina Manning, Phil Cheetham, Michael Loughlin and Steve Forsythe. Special thanks go to Mike Brice, Pam Horne and the rest of the Microbiology Technical Support Team. CELS is funded by HEFCE as a Centre for Excellence in Teaching and Learning.

Further reading

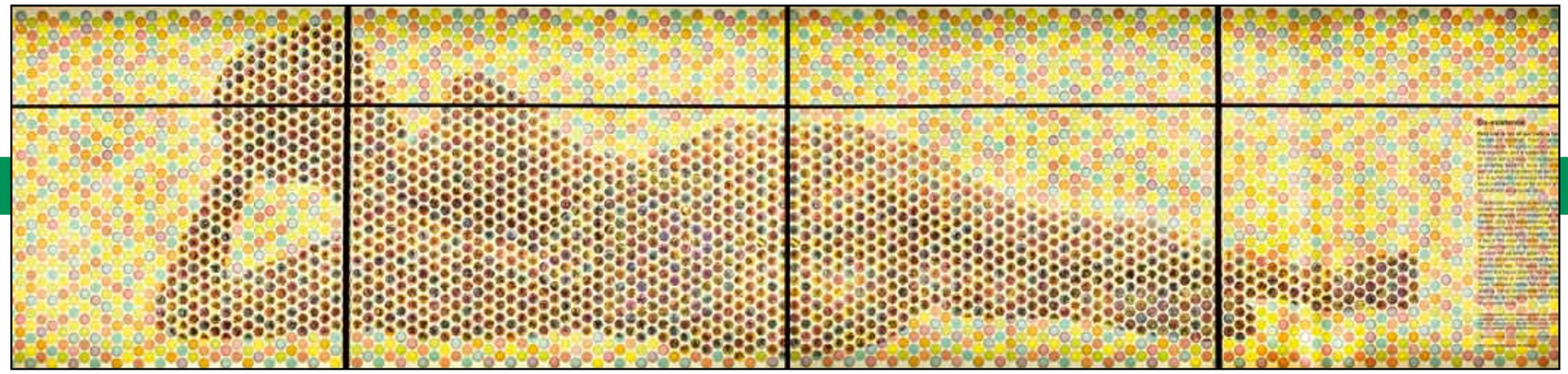
Biosciences Federation (2008). Independent Review of '*A Vision for Science and Society*'. A response to the Department for Innovation, Universities and Skills, available at **www.bsf.ac.uk/responses/ScienceAndSocietyOct08.pdf**

www.ntu.ac.uk/cels
The CELS website

The Higher Education Academy Centre for Bioscience (2008). *National Subject Profile for Higher Education Programmes in Microbiology* available at **www.bioscience.heacademy.ac.uk**

In the Loop – www.sci-eng.mmu.ac.uk/intheloop

Chair of the SGM Education Division, Jo Verran, has recently launched her website *In the Loop*. Whilst this aims to promote microbiology services at MMU, it also provides a valuable resource of information for teachers, both in schools and of undergraduates, and outreach activities for the general public. Going to the section 'Education and Communication' leads to a whole range of activities, services and links. You can also download free chapters from an audio-visual aid, an *Introduction to Practical Microbiology*, which was filmed with undergraduate students and shows all the basic techniques necessary to carry out microbiology investigations.



Co-existence – The Wellcome window display

When **Mike Wilson** and **Derren Ready** were invited to work with an artist to produce a window display on bacteria, much ingenuity was required.

In September 2008 we were invited to collaborate with the artist Julia Lohmann to produce a display that would show the distribution of bacteria on and in a healthy human. Julia already had the idea of using Petri dishes with backlighting as a framework for the display and she wanted to place in these microscopic images of the various members of the indigenous microbiota. However, we explained to her that these images would not be particularly exciting as bacteria came in only three basic shapes and that there was much more variation in the size, shape and colour of colonies – especially when selective and elective media were used. After showing her some of the beautiful colony shapes and colours she became convinced that this was the way to go.

As a guide to which bacteria were to be found at which body site we used a book recently published by one of us: *Bacteriology of humans: an ecological perspective* (Michael Wilson, Blackwell Publishing, 2008). Because of the enormous complexity of the microbiota at certain body sites, we obviously had to compromise with regard to the number of different microbes that could be included at a particular one. Also, we used one body image to display the composition of the various bacterial communities that reside on the skin and the other image to represent the communities to be found 'internally', i.e. in the respiratory, gastrointestinal and genital tracts.

Culturing and photographing images of the colonies of members of our indigenous microbiota was a great opportunity that we're sure any microbiologist would enjoy. We used a number of different selective and elective culture media and needed to use several different atmospheric conditions to allow us to grow a diverse group of micro-organisms. Fortunately, we already work with a large number of different genera and species, so we were able to readily obtain images of streptococci, staphylococci, micrococci, clostridia, *Prevotella* spp., *Campylobacter* and, of course, working in a dental institute culturing members of the oral microbiota wasn't a challenge for us. However, we were less experienced with a few of the organisms, making it necessary not only to buy in several strains such as *Helicobacter* and mollicutes, but also to get out the text books for recipes of culture media. We also tried to collect images of the same bacterial species on a selection of different culture media, to allow the artist to have a range of images and colours to choose from.

In many ways collecting the images was more challenging than the microbiological aspects of the work. We decided to photograph the colonies using a light microscope with a digital camera attached. The magnification of the objective needed to be altered from isolate to isolate as some colonies were very small (mollicutes), whereas other were much larger (clostridia), and we had been asked to collect images of discrete colonies and also groups of colonies. The lighting made a tremendous difference to the final image and for the majority of the images we illuminated the colonies from above. However, if there were interesting internal structures, such as the star-like structures seen in *Aggregatibacter actinomycetemcomitans* colonies then we also needed to illuminate from below the colony. We finally obtained in excess of 750 digital images from 32 different genera. More than 9,000 glass Petri dishes were used to construct the two figures.

One of the problems that Julia faced was conveying a three-dimensional effect using only the petri dishes and colonial images. Shading of some kind was essential for this purpose so Julia decided to superimpose on the images some black line drawings depicting what she had imagined bacteria to look like before learning more about their true nature from us. The two images went on display in January 2009 and Julia and one of us (MW) gave talks at the Wellcome Collection explaining the artistic and scientific background to the project.

Microbes and Me

Related to this window display is another project we are currently engaged in – *Microbes and Me*. This is a travelling exhibition, financed by a People Award from The Wellcome Trust, which aims to inform the general public about the microbial communities that inhabit healthy humans. As well as describing the composition of the microbial communities inhabiting the various body sites, it will emphasize the many benefits that we derive from our indigenous microbiota. It will also describe important concepts. such as symbiosis, antibiotic resistance, superbugs, biofilms, probiotics, competitive exclusion, disease transmission, etc. One of the main objectives of the exhibition is to rehabilitate microbes to the general public by making them aware that, as well as causing disease, microbes are essential to human well-being. The first exhibition venue will be the Cheltenham Science Festival, 3–7 June and the website (currently under construction) is **www.ucl.ac.uk/microbesandme/**

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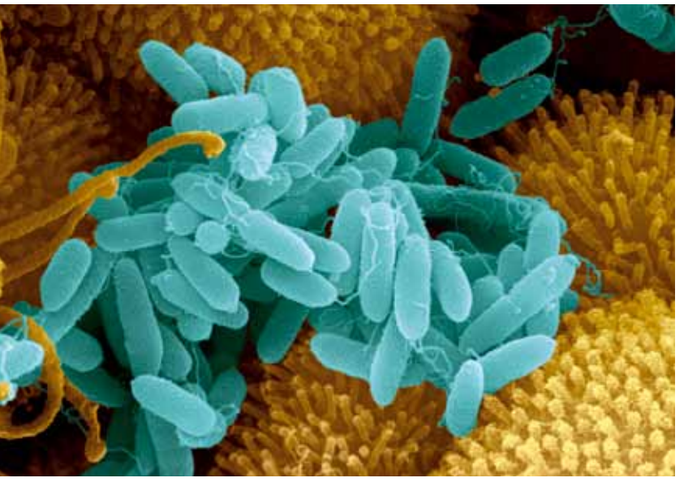
hotoffthepress

Science writer **Meriel Jones** takes a look at some recent papers in SGM journals which highlight new and exciting developments in microbiological research.



◀ Coloured SEM of *Pseudomonas aeruginosa* bacteria on ciliated human nasal epithelium. *Juergen Berger / Science Photo Library*

Sense and respond

Gooderham, W.J., Gellatly, S.L., Sanschagrin, F., McPhee, J.B., Bains, M., Cosseau, C., Levesque, R. & Hancock, R.E.W. (2009). The sensor kinase PhoQ mediates virulence in *Pseudomonas aeruginosa*. *Microbiology* **155**, 699–711.

Pseudomonas aeruginosa is an intriguing bacterium. It is a normal inhabitant of soil, but is also a pathogen of plants, insects and animals. It rarely infects healthy people, but exploits opportunities offered by other illnesses – it is the most common cause of acute hospital-acquired pneumonia and causes chronic lung infections in patients with cystic fibrosis. How does *P. aeruginosa*, amongst all the bacteria in the air, manage this when, despite inhaling over 10,000 litres of air a day, healthy people have few bacteria in their lower lungs?

Bacteria have to sense and respond to their environment, and one way is via two-component regulatory systems that consist of two proteins. One is a sensor protein embedded in the cell membrane. Once this picks up a signal from outside the cell, it can interact with a second, response regulator protein in the cytoplasm which will alter the cell's metabolism to fit the new circumstances. The PhoQ sensor with its associated PhoP response regulator is important for virulence of several bacterial species, but its role in *P. aeruginosa* was unknown until researchers in Canada took a closer look.

For initial tests, lettuce leaves were used to test whether mutant bacterial strains without the PhoQ protein could still cause infections. Several *P. aeruginosa* infection processes are the same in plants and animals, so plant leaves provide a more humane test. Bacterial strains lacking PhoQ consistently caused a less-severe soft rot. Taken together with other laboratory tests showing impaired characteristics that usually correlate with bacterial pathogenicity, the researchers felt confident that PhoQ was important in infections.

Further tests, using cultures of human cells from the surface of the lung, showed that *P. aeruginosa* cells containing the PhoQ protein were at least twice as effective at damaging these cells than bacteria without PhoQ. To discover whether these pathogenic effects were mediated by PhoQ within a living lung, and following recommendations from the ethics committee for animal treatment at their university, the researchers infected rats with mutant and normal *P. aeruginosa* cells. Although these colleagues had studied lung infections for many years, they had never seen such a dramatic difference between two strains of *P. aeruginosa* before. In a group of seven rats, four managed to remove all the mutant bacteria from their lungs within 4 days, and the overall level of the infection was reduced by more than 10,000-fold. PhoQ therefore appears to be essential for *P. aeruginosa* to set up a lung infection.

To find out what PhoQ was doing to make the bacteria virulent, the researchers turned to transcriptomics. These are methods to determine which genes are in use. Over 5,500 genes have been identified in *P. aeruginosa* and the Institute for Genomic Research Pathogenic Functional Genomics Resource Center in the USA supplies microscope slides containing DNA from each of them for scientific research. The researchers used these slides to test which genes were in use when *P. aeruginosa* was grown under different circumstances, both with and without a functional version of PhoQ. Lack of PhoQ affected the use of 474 genes. Many of these were already known to be regulated by PhoQ, but others were new. These included genes for proteins involved in transporting materials into or out of the cell, and some for scavenging iron, which is well known to be an important activity for pathogens. Others that were used less in the mutant were involved in providing energy for the cell, and in controlling the function of other genes.

The outcome of this study is new confidence that PhoQ is essential for success of *P. aeruginosa* as an opportunist extracellular pathogen. Researchers already knew about some of the virulence-related processes in *P. aeruginosa*. However, this new, complex control-system for around 12% of the genes in *P. aeruginosa* provides more targets for researchers working towards treatments for these infections.

Routine arbovirus surveillance reveals a novel animal virus

Cowled, C., Palacios, G., Melville, L., Weir, R., Walsh, S., Davis, S., Gubala, A., Lipkin, W.I., Briese, T. & Boyle, D. (2009). Genetic and epidemiological characterization of Stretch Lagoon orbivirus, a novel orbivirus isolated from *Culex* and *Aedes* mosquitoes in northern Australia. *J Gen Virol* **90**, 1433–1439.

Animals are important to the Australian economy. Export of live cattle, sheep and goats as breeding stock and for their meat provides a significant income for the country. For this global trade, it is important that disease-causing viruses are not exported along with the animals. Unfortunately, viruses do not respect national boundaries, especially the arboviruses which are transmitted to animals by insects. These can cause serious animal diseases such as bluetongue. Australia therefore has a national arbovirus-monitoring programme.

Northern Australia is an important location for arbovirus surveillance. Its geographical location means that cyclones make landfall in the region and these strong winds can bring new insects from the tropics. As well as insect traps, herds of young cattle that have not previously been exposed to arboviruses are used as sentinel animals to see if the new insects carry any new viruses. Many well-known, insect-borne viruses are regularly identified, but a key problem is to detect previously unknown viruses that could be the cause of new diseases. Hundreds of unidentified viruses have been collected since the start of the monitoring programme, waiting for attention.

Researchers in Australia and the USA have been working on this problem. The results of tests suggested that most of the unidentified virus collection was from the family *Reoviridae*, and more specifically the genus *Orbivirus*. They focused their attention on the only virus isolated in 2002 from a homogenized pool of 25 *Culex* mosquitoes collected at Stretch Lagoon in the Kimberly region of Western Australia. The tests showed that it was not among the 11 orbivirus species that had previously been recognized in Australia.

The criteria for defining orbivirus species relate to the genes for several of the viral proteins. When the researchers worked out the sequences from the Stretch Lagoon isolate, they confirmed that it was definitely an orbivirus, but only distantly related to all known species. The obvious name for it was Stretch Lagoon orbivirus (SLOV). They developed and used a rapid diagnostic test to identify six further isolates among the collection of unidentified isolates. When the researchers tested stored blood for a reaction to SLOV, the results indicated that some horses, donkeys and goats had potentially been infected with SLOV as far back as 1984. Animal samples from before 2000 need to be tested to confirm this hypothesis. However, several important questions remain unanswered. These include whether SLOV causes a disease, and whether it is really transmitted by mosquitoes. Horses, donkeys and goats are not routinely tested for arboviruses in Australia so the researchers do not yet know the real distribution of SLOV within Australia. Putting a name to the unknown isolate is clearly only the beginning.

A novel bacterium from deep glacial ice

Loveland-Curtze, J., Miteva, V.I. & Brenchley, J.E. (2009). *Herminiimonas glaciei* sp. nov., a novel ultramicrobacterium from 3042 m deep Greenland glacial ice. *Int J Syst Evol Microbiol* **59**, 1272–1277.

Is there life on other planets? The answer requires us to be able to recognize living creatures when we see them. This is not always easy to do, especially for bacterial life. Bacteria may be recognized by the consequences of their activities, which range from soured milk, corroded metal and concrete to glowing water, but these can also have chemical, rather than biological causes. Most life on our planet has always consisted of bacteria, so it is certainly reasonable to consider that this might be true on other planets as well. With this in mind, the NASA Astrobiology Institute in the USA has funded several projects to study bacteria that live in extreme conditions on Earth.

The authors have cultivated very small bacteria from 3,042 m below the Greenland ice cap, collected during the Greenland Ice Sheet Project Until the drill brought it to the surface, this ice had lain undisturbed for over 120,000 years. It was discovered that there are many living bacteria in this ice, although patience is required to coax them back to activity. The authors' strategy is to incubate water from the ice core in anaerobic conditions at 2°C and, after several months, spread it over special oxygen-free culture medium to see what grows.

The authors' most recent discovery is a novel species with very small cells that they have called *Herminiimonas glaciei*. Its small, initially brown–purple colonies of thin, mobile cells could actually grow in air, although seemed to enjoy oxygen levels below that of the current atmosphere. The researchers carried out a battery of tests, leading to identification of the novel species. They were intrigued to discover that it was resistant to three-quarters of the antibiotics used in the tests, even though it came from long before the era of modern medicine. Projects like this extend our knowledge of life on Earth as well as providing ideas about life on other planets.

Greenland. Stockxpert / Jupiter Images

Management of antibiotic side-effects using probiotics

Engelbrektson, A., Korzenik, J.R., Pittler, A., Sanders, M.E., Klaenhammer, T.R., Leyer, G. & Kitts, C.L. (2009). Probiotics to minimize the disruption of faecal microbiota in healthy subjects undergoing antibiotic therapy. *J Med Microbiol* **58**, 663–670.

Probiotics are marketed as food supplements that can confer health benefits. They come in the forms of capsules, powders, yoghurt or other fermented foods that contain live bacteria similar to some of those known to reside in the gut. Knowledge of benefits conferred by probiotics is of both medical and commercial importance. One situation where researchers think probiotics could be of real value is for patients undergoing antibiotic treatment.

Antibiotics are life savers from bacterial diseases, but they can also cause problems. One of these is disruption to the normal, beneficial bacterial inhabitants of the gastrointestinal tract through the killing of some of them as well as the bacteria causing the infection. The consequences can range from mild discomfort to diarrhoea to inflammation and serious illness. Managing antibiotic therapy to have fewer of these unwanted impacts is obviously desirable, but not easy to do.

Studying bacteria from the human gut means analysing faeces. Although clinicians have grown bacteria from this source for over a century, real appreciation of their numbers and diversity is only now starting to become apparent. Estimates of the total number in each person's gut range up to 100 trillion (10^{14}) and the vast majority of these bacteria have never been grown in a laboratory culture. To identify these uncultured bacteria, researchers use the latest DNA technologies so that the diversity of bacterial genes is a measure of the diversity of the bacteria.

A collaboration between microbiologists in the USA working in medical gastroenterology, genome sequencing and the dairy technology and food industries has studied the effects of probiotics on the intestinal flora of 40 healthy volunteers in their 30s after they were giving a 7-day course of antibiotics. The antibiotic used was Augmentin because it is in common medical use and has a reputation for causing diarrhoea. The volunteers took capsules that contained a carbohydrate either with or without probiotics along with the antibiotics. As well as keeping a diary of their eating and toilet experiences over this time, the volunteers delivered faeces to the study co-ordinator on several days before and after taking the antibiotics. These were analysed for both their diversity of bacterial DNA and contents of living bacteria.

There were some very clear results from the study. The level of diarrhoea and vaginal yeast infections in the volunteers, whether they were taking the probiotic or the placebo, was similar to that reported in other clinical trials involving Augmentin. It was also very obvious that the antibiotic altered the gut bacterial flora. The researchers monitored the molecular signals of over 200 types of bacteria as well as the diversity of species that grew on five distinct culture media. Comparing the bacterial profiles of each individual before and after taking Augmentin showed that the probiotic minimized any disturbance, which was presumably beneficial. Although the researchers did not specifically test a mechanism for this effect, they speculated that the additional *Bifidobacterium* and *Lactobacillus* bacteria from the probiotic could act on the contents of the gut to make it a more suitable habitat for bacteria, so providing extra stability to the normal population.

Two other interesting features came out of this study because it was based on quite a large group of healthy people. The researchers analysed three faecal samples from volunteers during the 2 weeks before they took the antibiotics. Surprisingly, the volunteers differed in how similar the results were for these three samples. They were similar from some people, but distinctly different from others. Since this is the first detailed and repeated analysis of healthy people supplied with probiotics, it is not clear whether this diversity is a real picture of the variety of human gut flora, or whether it is an artefact caused by the way the samples were processed, despite efforts to use a standardized procedure. This is obviously an important subject for future studies.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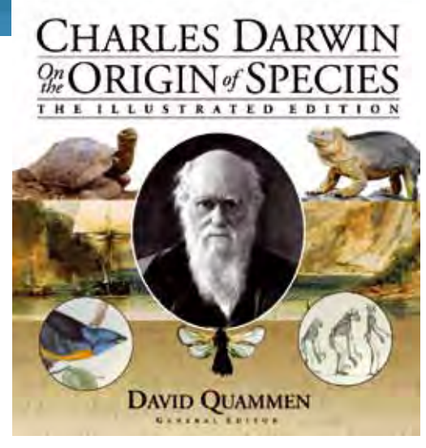
Charles Darwin: On the Origin of Species – The Illustrated Edition

Edited and with an introduction by David Quammen
Published by Sterling Publishing (2008)
£20.00 pp. 560
ISBN 1-40275-639-9

On the Origin of Species would be my desert island book – and with luck, the island would be as fascinating as the Galapagos. But would I take this edition? Probably not. I would prefer a first edition, plain and unadorned. This one is a coffee table book, lavishly illustrated, and interspersed with extracts from the 'Beagle' letters and other documents. This seems to suggest that the *Origin* text might need sweetening for a new, and perhaps reluctant, reader. But if that is the case, the insertions break up the text of *Origin* in a way that actually makes reading it more difficult. You either have to read the *Origin* text and try to ignore the other material – all of which is available in other publications – or look at the insets and bypass *Origin*. Though it is pretty, this book doesn't really offer anything new in a very crowded market. Surely there's a little evolutionary tale here?



***Hilary Fraser**, Berkshire*

Horizontal Gene Transfer in the Evolution of Pathogenesis

Edited by M. Hensel & H. Schmidt
Published by Cambridge University Press (2008)
£75.00 pp. 355
ISBN 0-52186-297-4

This is a very interesting book which presents an up-to-date overview of the current understanding of this field of research. The book includes lively discussions of both philosophical and theoretical aspects of evolution due to HGT in addition to chapters on 'paradigms of bacterial evolution' which explore both human and plant pathogens. The inclusion of eukaryotic examples of HGT provides a well-rounded account of the subject. It would have been more comprehensive to include one or more examples of HGT-mediated evolution in animal pathogens as these are often adapted to conditions in a host-specific niche; however, this could be included in any future edition. The chapters are well-edited, extremely well-referenced and mostly up to date. The book is aimed at graduate students and researchers in the field and is a must for relevant institutional libraries and laboratories alike.

***Adam P. Roberts**, UCL Eastman Dental Institute*

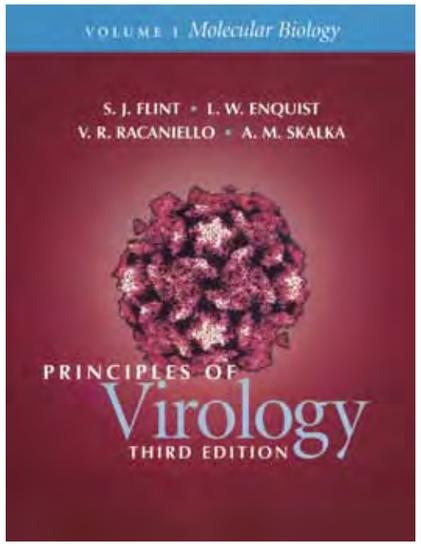
Cellular Signaling and Innate Immune Responses to RNA Virus Infections

Edited by A.R. Brasier, A. Garcia-Sastre & S.M. Lemon
Published by American Society for Microbiology (2008)
US$139.95 pp. 454
ISBN 1-55581-436-6

This is an excellent and authoritative collection of detailed chapters from some of the worlds leading scientists working on the nature of RNA virus interactions with the host innate immune system. Usefully, the book is organized both by topic area and then separately by RNA virus family, providing a systematic and cross-referenced approach invaluable to those who are interested in specific viruses as well as those interested in the detailed biochemistry of host response to virus infection. Each chapter provides a stand-alone review; inevitably, this approach does lead to some repetition, but this is a minor criticism for what is overall a very timely state-of-the-art specialist review text book suited to a postgraduate and professional virology and cell biology audience.

The cost of the book indicates that it is unlikely to be a personal purchase, but is highly recommended for laboratories and institutes working on viral pathogenesis, and innate immune responses. It should also have a place in university biological science libraries for reference purposes during those final year essay crises. Highly recommended.

***Maria Zambon**, Health Protection Agency*



Principles of Virology, 3rd edn: Vols I and II

By S.J. Flint, L.W. Enquist, V.R. Racaniello & A.M. Skalka
Published by American Society for Microbiology (2009)
US$169.95 pp. 1,032
ISBN 1-55581-443-4

Over a period of only 9 years this book has now reached its third edition. Declared to be a textbook for students, it aims for the highest standards. Compared to the second edition (2004), a number of changes have taken place. One novelty is that the book is now published in two volumes, with principles of the molecular biology of animal viruses being presented in Vol. I, and aspects of pathogenesis, treatment and prevention, and evolution reviewed in Vol. II. Whilst *Field's Virology*, fifth edition (2007), is recommended as all-inclusive and for detailed information on specific virus families, it is evident that plenty of special and novel information is contained in these two volumes too. The books gain strength from explaining the basic molecular principles of animal virology with examples from different virus families, constantly comparing them. Students were instrumental to increase clarity, and many internationally recognized virologists with special expertise have reviewed different parts of the books. The outcome is splendid: basic information is presented in a succinct and refreshing manner, interspersed by original and unexpected observations and short reports on research highlights. Compared to the second edition, many very recent research data are reported, allowing witness to the excitement of good contemporary science. Original photographs, illustrations and diagrams are of excellent quality. The text is further complemented by information boxes on background, terminology, methods, particular experiments and items for discussion, and the perspectives of relevant research are outlined at the end of each chapter. The content of different chapters has been carefully cross-referenced. The references are very up-to-date, reaching from 'classics' in the 1930's to journal publications in early 2009, with particular emphasis on publications of 2005–2008.

The basics of the viral infectious cycle are described in a very short chapter, followed by hundreds of pages reviewing details of the underlying molecular biology. Viral genomes and the various viral structures are introduced in close correlation with their functions. Transcriptional strategies of viral DNA are extensively discussed. Good coverage is given to various techniques of manipulating viral RNA genomes and to the potential for reversion analysis 'to order'. The possibilities for gene therapy using mutated DNA and RNA viruses as vectors are outlined. Various aspects of viral messenger RNA synthesis and mechanisms of translation control are discussed in detail. The relatively novel but very active research area of cellular and viral small interfering RNAs is introduced. Mechanisms of intracellular trafficking of viral components are recognized as critical for proper virus particle assembly.

The chapters on viral pathogenesis deal with the molecular mechanisms of intrinsic, innate and adaptive immune responses. Factors determining the outcome of persistent or latent viral infection are described. A separate chapter is dedicated to the pathogenesis of HIV infections. Mechanisms of viral transformation and oncogenesis are described in their full diversity. The chapter on vaccines touches many important issues, e.g. the controversy over the MMR vaccine as a possible cause of autism (now solidly refuted) and the difficulties encountered in developing an AIDS vaccine. The development of antivirals is described as being guided by rational design according to viral targets and molecular mechanisms of action. A final chapter introduces the various factors influencing viral evolution.

Detailed replication strategies for particular virus families, diagrams of the pathogenesis and epidemiology of selected animal viruses and an introduction to unusual infectious agents (viroids, satellites, prions) are found in appendices to both volumes.

The collated information in the two volumes represents the state-of-the-art of many topics and is of interest for students and teachers of virology alike. In addition, the books are strongly recommended to an interested readership of molecular biologists, cell biologists and general microbiologists, and their wide distribution is highly desirable.

***Ulrich Desselberger**, Cambridge*

Superbugs and Superdrugs: A History of MRSA

Edited by L.A. Reynolds & E.M. Tansey
Published by The Wellcome Trust Centre for the History of Medicine at UCL (2008)
£6.00 pp. 144
ISBN 0-85484-114-1

This is a transcript of a Witness Seminar held in 2006 involving many eminent researchers, past and present, concerned with staphylococci, infection control, and the pharmaceutical industry in the UK covering the era from the late 1950s until today. Amongst other topics, the history and discovery of MRSA, its epidemiology and spread, resistance mechanisms, changing attitudes to infection and infection control, pharmaceutical responses and new drugs are discussed. Most compellingly it is revealed that similar epidemics of (then) multidrug-resistant *Staphylococcus aureus* had occurred in the 50s and early 60s, generating an understanding of the mechanisms of spread and transmission of epidemic *S. aureus* and measures to curtail its spread, which has been forgotten or overshadowed by other priorities in dealing with the current MRSA problem. There are also concise biographical sketches of key figures of the field and instructive illustrations.

This is a must read for every microbiologist, which is also fascinating and accessible to the layman.

***Dietrick Mack**, University of Swansea*

Bad Science

By B. Goldacre
Published by Fourth Estate Ltd (2008)
£12.99 pp. 338
ISBN 0-00724-019-7

It is difficult to explain just how engaging and entertaining this book is. Much of the content is aimed at doctors and people who want to defend good science, but I would go as far as to say this is essential reading for anyone who has ever read a scare story in the tabloids, picked up a book by Gillian McKeith or bought a homeopathic remedy.

Ben Goldacre starts with ear candles, detox patches and the Brain Gym, which is '*riddled with transparent, shameful and embarrassing nonsense*'. (p. 13)

Cosmetics are up next, and ingredients like Regenium XY Technology, Nutrileum Complex and Covabeads are all tools of an '*utterly defensible pseudoscience*'. (p. 21)

Homeopathy is given a lot of attention, because it '*has an elaborate and sciencey-sounding framework for how it works, without scientific evidence to demonstrate its veracity*'. (pp. 28–29)

As any reader of his column in *The Guardian* might expect, an entire chapter is devoted to the life and work of Dr Gillian McKeith PhD. Fascinating, shocking and written fairly, this is my favourite bit.

We hear numerous reports about magic pills that can cure behavioural problems, or even improve intelligence in children. Goldacre refers to this as '*medicalization*' and, in some depth, discusses its problems. From pills to pharmaceuticals, where companies crunch numbers to make their products look good.

Despite all the pitfalls of some of the research he cites, we still read incorrect interpretations in the papers. Why? '*My basic hypothesis is this: the people who run the media are humanities graduates with little understanding of science, who wear their ignorance as a badge of honour … in their choice of stories, and the way they cover them, the media create a parody of science.*' (pp. 207–208)

Statistics, he says, are often misreported, or interpreted in an irresponsible way. And then there's the health scares, like the '*MRSA hoax*' and the '*MMR hoax*', which dominated the headlines for a decade.

This book is intelligent, well-researched and funny. Goldacre has a talent for explaining complex ideas without being patronizing, so, in my opinion, *Bad Science* will be a great read for anyone. He has a tendency to slip off into a rant occasionally, but he pulls himself back to the point. (To be honest, I agreed with almost every word, so even the long tangents were appreciated.)

***Lucy Goodchild**, Imperial College London*

Reviews on the web

Reviews of the following books are available on the website at **www.sgm.ac.uk/pubs/micro_today/reviews.cfm**

Filoviruses: A Compendium of 40 years of Epidemiological, Clinical and Laboratory Studies

Emerging Infections 8

Gene Therapy Protocols Vol. 2: Design and Characterization of Gene Transfer Vectors, 3rd edn

Stem Cell and Gene-based Therapy

Clostridia Molecular Biology in the Post-genomic Era

Mycobacterium*: Genomics and Molecular Biology*

Dictionary of the Fungi, 10th edn

Wound Care: A Collaborative Practice Manual for Health Professionals, 3rd edn

Handbook of Plant-based Biofuels

The Septins

Medical Product Regulatory Affairs: Pharmaceuticals, Diagnostics, Medical Devices

Mycoplasma Diseases of Ruminants

Real-time PCR Current Technology and Applications

Microbial Ecology of the Oceans, 2nd edn

Geomicrobiology, 5th edn

Practical Handbook of Microbiology, 2nd edn

Changing Trends in Managing Aquatic Animal Disease Emergencies, Vol. 27 (1)

Biotechnology, 5th edn

Insect Symbiosis, Volume 3

OIE Quality Standard and Guidelines for Veterinary Laboratories: Infectious Diseases

An Introduction to Genetic Engineering, 3rd edn

Mushrooms as Functional Foods

Bluetongue in Northern Europe

Biotechnological Approaches for Pest Management and Ecological Sustainability

Handbook of Nucleic Acid Purification

HIV Protocols, 2nd edn

Handbook of Probiotics and Prebiotics, 2nd edn

MicrobeLibrary Atlas CD-ROM, 2nd edn

Clinical and Diagnostic Virology

comment

an april diary

The SGM President, **Robin Weiss**, reflects on a busy month, not only for himself, but for microbiologists worldwide.

I have never quite fathomed why T.S. Eliot began *The Waste Land* with '*April is the cruellest month*' although April 2009 has certainly ended cruelly with the unseasonable emergence of Mexican 'flu.

1 April. In Harrogate for the Spring Meeting of the SGM. It was my privilege to introduce the first recipient of the SGM Prize Medal Lecture, Stanley Prusiner from the University of California, San Francisco. In 1982, Stan isolated prion proteins that induce spongiform encephalopathy and was awarded the Nobel Prize in 1997 (see *Microbiology Today*, February 2009). Stan's fascinating story ended with his current research on inhibitors of the protein conversion process. The day included a mini-symposium on prion diseases with British contributors. The UK is at the forefront of research in this field, as well we should be, having generated mad cow disease and its human form, variant Creutzfeldt–Jakob disease. The notion that 'infectious' proteins lacking nucleic acids cause scrapie seemed preposterous when Tikvah Alper *et al.* first postulated it in 1967 and had it been published in *Nature* on April 1st rather than May 20th it might well have been regarded as an April Fool prank.

3 April. In Liverpool to give the Keynote Talk at the Annual Meeting of the British HIV Association. The reason why I had been invited to speak to 500 AIDS physicians was that my laboratory had collaborated with Sunil Ahuja's in Texas on Duffy antigen receptor for chemokines (DARC) as a risk factor for HIV. Our paper last year claimed that people who lack DARC on red blood cells are more likely to become infected by HIV. As 90% of sub-Saharan Africans are DARC-negative (it confers resistance to vivax malaria) we attributed 11% of the African AIDS burden (some 2.6 million HIV-infected Africans) to this genetic risk. In other words, prehistoric selection for resistance to malaria appeared to make Africans more susceptible to HIV today. My problem was that other groups cannot confirm our results. I presented our data but announced that the findings had become controversial.

19 April. Lago d'Iseo, Italy, for a small workshop on HIV infection of macrophages. It is the best kind of specialist meeting, intense yet friendly, lubricated with excellent Francia Corte wine. It is 101 years since Ilya Mechnikov was awarded the Nobel Prize for discovering phagocytosis, and we now know that macrophages are antigen-presenting cells in addition to mopping up opsonized microbes. HIV is not cytopathic in macrophages, but it does adversely affect their various functions. Amongst all the elegant microarray data and cytokine signalling presented by others, I suggested that the wasting syndrome in AIDS is due to infection of macrophages, not CD4+ lymphocytes, by invoking Maedi–Visna disease in sheep.

22 April. Istituto San Raffaello, Milano. I joined two avuncular Italian scientists to conduct a viva voce examination of a student who had written a thesis (in English) on a novel method for isolating immortalized B-memory cells secreting monoclonal antibodies that neutralize H3N2 influenza virus. The student wished to gain her doctorate before the birth of her baby, a mission satisfactorily accomplished.

24 April. In Rome for the formal inauguration of the European Society for Virology. Ron Desrosiers (Harvard), Ab Osterhaus (Rotterdam) and I were the speakers in the scientific session. Shortly after Ab's talk, his mobile phone rang. It was the WHO calling about the outbreak of H1N1 influenza in Mexico. Thus I gained inside knowledge 3 hours before the public announcement, and Ab had to leave hurriedly.

27 April. My phone rings frequently with journalists asking for comments on the new 'flu outbreak. Not being a genuine expert, I give the media the names of four SGM members who really are, and who can explain the situation authoritatively and clearly.

30 April. I'm clearing out old files and piles. Can I dump 3 years of SGM Council papers straight into the recycling box or should I shred them first? The first Londoner is confirmed to have Mexican 'flu. Was it just imagination, or were more people than usual coughing and sneezing on the Northern Line Underground this morning? I rationalize the situation by telling myself that it might be smart to catch the 'flu early, before it becomes more virulent, and gains resistance to Tamiflu. But then again, I'm not an expert.

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Please note that views expressed in Comment do not necessarily reflect official policy of the SGM Council.