Microbiologist
The magazine of the Society for Applied Microbiology ■ March 2012 ■ Vol 13 No 1 ISSN 1479-2699

Changing environments

INSIDE

Summer Conference 2012

- **Microbial resistance to antibiotics and biocides**
- **Natural and experimental adaptation in bacteria**
- **Bioremediation**

■ Including the Lewis B Perry Memorial Lecture:
Globalization of antimicrobial resistance. *Didier Pittet, University Hospital in Geneva*

The George Hotel, Edinburgh, UK ■ Monday 2 July — Thursday 5 July 2012

CALL FOR ABSTRACTS!

■ We are now accepting abstracts for posters and the student session at the 2012 Summer Conference at The George Hotel in Edinburgh. These can be on any topic in applied microbiology.

■ There are prizes of **£150**, **£100** and **£50** available to winners of first, second and third prize for posters. For the best student oral presentation there is a prize of **£300!**

For more information or to submit your abstract visit:
www.sfam.org.uk/en/events/index.cfm/summer_conference

STUDENTSHIP GRANTS

■ Don't forget that we offer Studentship Grants to enable Student Members to attend Society meetings. The grant covers registration, accommodation, meals (where appropriate) and modest travel expenses.

■ To be considered for a studentship grant please complete the application form at **www.sfam.org.uk/en/grants--awards/conference-studentship.cfm.**

For more information about SfAM grants visit:
www.sfam.org.uk/en/grants--awards/index.cfm

To register online please visit **www.sfam.org.uk/en/events/index.cfm/summer_conference**
or contact Sally Hawkes ■ Email: sally@sfam.org.uk. ■ Telephone: +44 (0) 01933 382191

Full programme and booking form on pages 25 - 27

March 2012 ■ Vol 13 No 1 ■ ISSN 1479-2699

Microbiologist the magazine of the Society for Applied Microbiology

contents

members

publications

news

features

meetings

commercial

Summer Conference 2012

historicalPerspectives

information

Microbiologist is published quarterly by the Society for Applied Microbiology. ISSN 1479-2699. Registered in the UK as a charity and Company limited by guarantee. Registered in England and Wales: 6462427. Registered Charity: 1123044.

Editor: Lucy Harper. lucy@sfam.org.uk

Contributions: These are always welcome and should be addressed to the Editor at: lucy@sfam.org.uk

Advertising: Lucy Harper. Tel: +44 (0)1234 326709. email: lucy@sfam.org.uk

Design and print: Pollard Creativity Limited
Tel: +44 (0)1933 664700.
email: micro@pollardcreativity.co.uk

Cover: Satellite image, Gulf of Mexico

Society for Applied Microbiology, Bedford Heights, Brickhill Drive, Bedford MK41 7PH, UK.
Tel: +44 (0)1234 326661. Fax: +44 (0)1234 326678.

www.sfam.org.uk

editorial

Lucy Harper discusses our changing environment

I think we can all agree that these are changing times and we are living in a constantly changing environment. From new technological developments, to shifts in global climate patterns, we are constantly facing something new.

In this issue of *Microbiologist* we learn about the way microbes change and adapt to their surrounding environment in order to survive. Gayle Ferguson writes: "*In order to survive widely varying conditions, bacterial populations must possess mechanisms for rapid adaptation through the generation of new phenotypes. The basis of phenotypic diversification, and the mechanism upon which traditional adaptation studies have focused, is mutation.*" She continues: "*But what is new and exciting, is a growing understanding of the role of non-mutational mechanisms, to produce phenotypes that are adaptive, but at the same time readily reversible.*" Turn to page 31 to read more.

Conversely, on page 28 we hear about the many and varied ways in which we are using microbes to clean up and change our surrounding environments. Thomas Aspray writes: "*In the UK, there are thousands of hydrocarbon contaminated (brownfield) sites, many of which, through planning and development control, or Part IIA of the Environmental Protection Act 1990 (the Contaminated Land Regime), find themselves in need of remediation to some degree.*"

"*Bioremediation involves the use of microorganisms or plants (the latter usually specifically referred to as phytoremediation), to mitigate risk posed by contaminants in the environment.*"

Having learnt about microbes adapting to changing environments, and us influencing environments using microbes, we continue on the theme of change in the rest of the magazine. The role of science in society is something that seems to be changing. Science is slowly integrating into popular culture and the burgeoning area of public engagement with science is something we highlight in this issue of *Microbiologist*. We look at the work of our members who went to Kenya to talk about applied microbiology with school children there. Turn to page 12 to read Tony Worthington's account of the *World of Microbiology* project on its first international leg.

We continue on the theme of public engagement on page 43 where we hear from Joanna Verran who, with the help of funding from S*f*AM, engaged with a wide variety of audiences on the chilling subjects of zombies, werewolves and vampires for Manchester Science Week. The parallels between the spread of microbiological disease and infection by a vampire, werewolf or zombie are interesting to say the least!

Finally, you may have listened to the new S*f*AM podcast when it launched in early January. We were lucky enough to speak to comedian Robin Ince about science in comedy and the way he has nurtured a culture of curiosity encouraging people to ask questions about the world and to find answers to scientific questions. You can listen to the podcast by visiting: http://www.sfam.org.uk/en/sfam-online/podcasts.cfm/podcast%20robin%20ince. Or you can read about how Robin is making science accessible through his BBC Radio 4 show '*Infinite Monkey Cage*' and his other ventures. You can also learn about his view on mimophants — and if you don't know what a mimophant is, turn to page 18 to find out.

contribute

We are always looking for enthusiastic writers who wish to contribute articles to the magazine on their chosen microbiological subject.

For further information please email the editor, Lucy Harper at: **lucy@sfam.org.uk**

Lucy Harper

Microbiologist is published quarterly by the Society for Applied Microbiology, a registered charity. ISSN 1479-2699.

Copy Dates:

Vol 13 No.2 June 2012
Friday 23 March 2012

Vol 13 No.3 Sept 2012
Friday 22 June 2012

Vol 13 No.4 Dec 2012
Friday 28 Sept 2012

Vol 14 No.1 March 2013
Friday 21 Dec 2012

Subscriptions: A subscription to *Microbiologist* is included in the annual S*f*AM membership fee. For further information about the many benefits of membership please see page 6.

Advertising: Information about advertising in *Microbiologist* and how to submit advertisements can be found on the Society website.

Website: our website **(www.sfam.org.uk)** is a timely source of up-to-date information on all Society matters and maintains a comprehensive archive of articles and reports on a variety of microbiological topics.

contact point

Society for Applied Microbiology
Bedford Heights, Brickhill Drive, Bedford MK41 7PH, UK.

tel: +44 (0)1234 326661
fax: +44 (0)1234 326678
email: communications@sfam.org.uk
www.sfam.org.uk

society office staff

CHIEF EXECUTIVE OFFICER: Philip Wheat
email: pfwheat@sfam.org.uk
tel: +44 (0)1234 326661

COMMUNICATIONS MANAGER: Lucy Harper
email: lucy@sfam.org.uk
tel: +44 (0)1234 326709

COMMUNICATIONS OFFICER: Clare Doggett
email: clare@sfam.org.uk
tel: +44 (0)1234 327679

MEMBERSHIP & FINANCE CO-ORDINATOR:
Julie Wright
email: julie@sfam.org.uk
tel: +44 (0)1234 326846

EVENTS ORGANIZER: Sally Hawkes
email: sally@sfam.org.uk
tel: +44 (0)1933 382191

ADMINISTRATOR: Julie Buchanan
email: julieb@sfam.org.uk
tel: +44(0)1234 326661

proofreader

Liz Rees **email:** liz.rees@lizrees.co.uk
www.lizrees.co.uk

publications subcommittee

FEATURES EDITORS:
Claire Cassar **email:** c.cassar@vla.defra.gsi.gov.uk

Louise Fielding **email:** lfielding@uwic.ac.uk

Clare Taylor **email:** cl.taylor@napier.ac.uk

REGULAR CONTENT EDITOR: Louise Hill-King
email: louise@hill-king.com

executive committee

COMMITTEE MEMBERS

HON PRESIDENT: Professor Martin Adams, School of Biomedical & Molecular Sciences, University of Surrey, Guildford, Surrey GU2 7XH
email: m.adams@surrey.ac.uk

HON GENERAL SECRETARY: Professor Mark Fielder, School of Life Sciences, Kingston University, Penrhyn Road, Kingston upon Thames, Surrey KT1 2EE
email: m.fielder@kingston.ac.uk

HON MEETINGS SECRETARY: Dr Andrew Sails, Health Protection Agency, Newcastle Laboratory, Institute of Pathology, Newcastle General Hospital, Westgate Road, Newcastle NE4 6BE
email: andrew.sails@hpa.org.uk

HON TREASURER: Mr Steve Davies, Microbiology Department, Northern General Hospital, Herries Road, Sheffield S7 5AU
email: steve.davies@sth.nhs.uk

ORDINARY COMMITTEE MEMBERS UNTIL JULY 2012

Mr Mark Reed, Pro-Lab Diagnostics, 7 Westwood Court, Neston Cheshire CH64 3UJ
email: mreed@pro-lab.com

Dr Sally J Cutler, School of Health and Biosciences, University of East London, Stratford Campus, Romford Road, London E15 4LZ
email: s.cutler@uel.ac.uk

Dr Samantha Law, NCIMB, Ferguson Building, Crabstone Estate, Bucksburn, Aberdeen AB21 9YA
email: s.law@ncimb.com

Dr Alison Kelly, School of Life Sciences, Kingston University, Penrhyn Road, Kingston upon Thames, Surrey KT1 2EE
email: a.kelly@kingston.ac.uk

ORDINARY COMMITTEE MEMBERS UNTIL JULY 2013

Dr Louise Fielding, Food Safety and Nutrition Research Group, Cardiff Metropolitan University (UWIC), Llandaff Campus, Western Avenue, Cardiff CF5 2YB
email: lfielding@uwic.ac.uk

Dr Irene Grant, Institute of Agri-Food and Land Use, School of Biological Sciences, Queen's University Belfast, Medical Biology Centre, 97 Lisburn Road, Belfast BT9 7BL
email: i.grant@qub.ac.uk

Dr Katie Laird, De Montfort University, The Leicester School of Pharmacy, Faculty of Health & Life Science, Hawthorn Building, Leicester, LE1 9BH
email: klaird@dmu.ac.uk

ORDINARY COMMITTEE MEMBERS UNTIL JULY 2014

Professor Christine Dodd, Division of Food Sciences, School of Biosciences, University of Nottingham, Sutton Bonington Campus, Loughborough, Leicestershire LE12 5RD
email: christine.dodd@nottingham.ac.uk

Dr Clare Taylor, School of Life, Sport & Social Sciences, Edinburgh Napier University, Sighthill Campus, Sighthill Court, Edinburgh, EH11 4BN
email: cl.taylor@napier.ac.uk

benefits

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

- The opportunity to apply for one of our many grants or funds.
- Eligibility to win any of our awards or nominate a candidate for the SfAM Communications Award.
- Access to our five peer–reviewed Journals: *Journal of Applied Microbiology, Letters in Applied Microbiology*, *Environmental Microbiology, Environmental Microbiology Reports* and *Microbial Biotechnology.*
- Free access to the entire collection of digitized back files for *JAM* and *LAM* dating back to 1938.
- A topical quarterly magazine, *Microbiologist.*
- Substantially reduced rates for attendance at SfAM meetings and conferences.
- Networking with worldwide professionals in over 80 countries.
- Access to private members' area of the SfAM website.
- Monthly email bulletins with the latest news from SfAM.
- Invitation to the annual *Environmental Microbiology* lecture.
- Fostering cross disciplinary research.
- A 25% discount on the extensive Wiley–Blackwell collection of titles.

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

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

Full details of all the Society's grants and awards can be found on the website together with application forms.

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

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

MEETINGS: We hold three annual meetings; the Winter Meeting is a one-day meeting with parallel sessions on topical subjects. The Spring Meeting is a one–day meeting tailored for personnel in clinical microbiology. The Summer Conference is held every July and comprises a main symposium, a poster session, the AGM and a lively social programme. All members are invited to our prestigious annual lecture held to commemorate the success of our *Environmental Microbiology* journal. We also hold joint ventures with other organizations on topics of mutual interest.

WEBSITE: The website is the best source of detailed information on the Society and its many activities. It has fully interactive membership areas where you can find archive issues of *Microbiologist*, exclusive SfAM documentation and much more.

membership options

■ **Full Ordinary Membership** gives access to our many grants and awards, online access to the *Journal of Applied Microbiology*, *Letters in Applied Microbiology*, *Environmental Microbiology, Environmental Microbiology Reports* and *Microbial Biotechnology*, copies of *Microbiologist*, preferential registration rates at Society meetings and access to the members' areas of the website.

■ **Full Student Membership** confers the same benefits as Full Membership at a specially reduced rate for full time students not in receipt of a taxable salary.

■ **Associate Membership** is only open to those with an interest in applied microbiology without it being a prime aspect of their job. For example, school teachers and those taking a career break; on maternity leave, or working temporarily in other areas. It does not provide access to any journals or Society grants and awards.

■ **Honorary Membership** of the Society is by election only and this honour is conferred on persons of distinction in the field of applied microbiology. Honorary Members have access to our online journals.

■ **Retired Membership** is available to Full Members once they have retired from their employment. Retired Members are entitled to all the benefits of Full Membership except grants and access to the Society's journals.

■ **eAffiliate Membership:** This category of membership is open to microbiologists residing in Band I developing countries and is free of charge. It is an online only membership and provides access to the eAffiliate bursary only.

■ **eStudent Membership:** This category of membership is open to undergraduate students only. It is an online only membership and is free of charge. This category of membership does not provide access to the Society's grants or journals.

■ **Corporate Membership** is open to all companies with an interest in microbiology. Corporate Members benefits include:

- Quarter page advertisement in each issue of *Microbiologist* (which can be upgraded to a larger size at discounted rates).
- The opportunity to publish press releases, company news, etc., in each issue of *Microbiologist.*
- FREE banner advert on the Society website with a direct link to your company site.
- Up to three members of company staff attending Society meetings at members' rate (this means a 50% discount on non member registration rate).

JOIN US!

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

BACTERIA

The Benign, the Bad, and the Beautiful

Trudy M. Wassenaar

A comprehensive, reader-friendly introduction to the world of bacteria

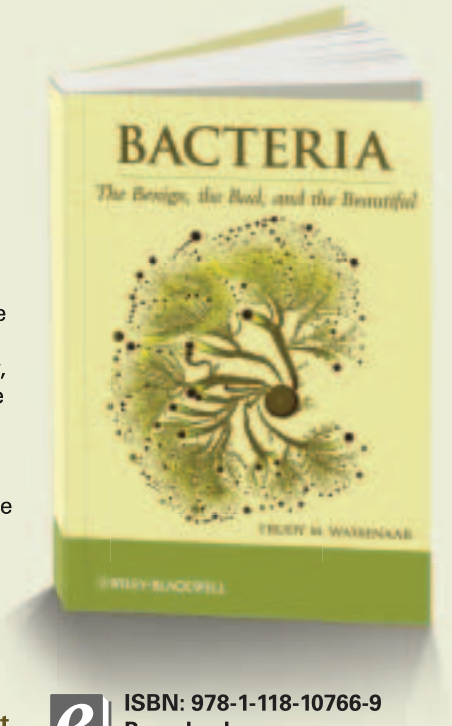
When most people hear the word "bacteria" they think of food poisoning, infections, and acute, debilitating, or fatal diseases. Yet, while bacterial pathogens certainly cause their share of misery in the world, they are only a tiny portion of a vast universe of prokaryotes—the most basic of life forms. Without them, nothing else could live or grow on Planet Earth. *Bacteria: The Benign, the Bad, and the Beautiful* introduces this diverse, microscopic world and explains the fundamental microbiological concepts needed to explore the life and behavior of bacteria. The book's clear, jargon-free language informs the reader, without the need of a background in microbiology, about a wide variety of bacterial subjects such as:

- **The origins and evolution of bacteria**
- **How bacteria have shaped the world**
- **Bacteria commonly found in the healthy human body**
- **Antibiotics and the growing problem of resistance**
- **Marine microbiology, bacterial toxins, and enzymes**
- **Bacterial genetics and genomics**
- **Bacteria that survive in extreme environments**
- **And much more**

This comprehensive guide features custom-drawn, black-and-white illustrations by artist Karoly Farkas, and sixteen color prints of microbial art. The book illuminates its points through real-world examples and engaging stories. A discrete, topic-by-topic structure, text-box summaries of background science, a subject index and a helpful glossary make for quick and easy reference. Whether you are a science professional in need of information on bacteria outside of your specialty, a student in search of an informative introduction, or a curious reader looking for fascinating and reliable stories, *Bacteria: The Benign, the Bad, and the Beautiful* is the resource you need.

Key Features:

- **Concepts are presented in concise, clear language for the non-expert**
- **Illustrated with custom drawn black and white cartoons by artist Karoly Farkas**
- **Includes a glossary of relevant terminology**
- **Chapters cover topics ranging from marine microbiology to bacterial toxins, enzymes, and the future role of bacteria in our world.**
- **Textboxes provide summaries of background science**



ISBN: 978-1-118-10766-9
Paperback
232 pages | November 2011
£26.95/ €32.40/ $39.95

WILEY-BLACKWELL

Find more microbiology news, titles, and discounts at **http://www.facebook.com/microbiologynews**!

The Wiley Life Sciences Blog
Read the latest life science news at **http://wisciblog.com**!

president's column

SfAM President, **Professor Martin Adams** talks about Members' public engagement activities

It is probably the case that most people join SfAM to share a common interest in applied microbiology with like-minded people. They want to have access and contribute to our publications and meetings, to network with fellow professionals and to avail themselves of opportunities to apply for grants and awards. Others though have a rather broader perspective. Rewarding though it is, they are not content to bask in a warm glow of mutual admiration, but are keen to explain and extol the wonders of microbiology to a wider, non-scientific audience. They enjoy enthusiastic and committed support from our excellent communications team and, as a result of their combined efforts, our public engagement activities have burgeoned over the last few years.

SfAM has been a member of the Microbiology in Schools Advisory Committee (MiSAC) (www.misac.org.uk/) for many years and a regular sponsor of their national schools' competition. More recently though, our outreach activities with schools have been expanding, supported through our programme of Public Engagement Grants. The last issue of the *Microbiologist* included an article by Katie Blackett describing her work with schools in Scotland, based around the book '*Germ Wars*' in collaboration with the Dundee Science Centre. In this issue, Tony Worthington tells how another project supported by SfAM and based at Aston University has developed from a local activity with schools in the Birmingham area, to an international one when they took their course to Kenya in November last year. Closer to home, we hope that this project might serve as a template for other SfAM activities with schools in the UK and interested members can access the supporting booklet, '*World of Microbiology*', free of charge on request.

There are obvious paybacks from these and similar activities conducted by us and by our colleagues in SGM. Encouraging an interest in, and understanding of, microbiology in children is of obvious benefit to the individual's personal development, but may also encourage some to go further and become the microbiologists of tomorrow. With adult audiences though, the goal is primarily improved public awareness of the importance of microbiology in our everyday lives. Public engagement events, such as the *Bad Bugs Book Clubs* run by Jo Verran, have been a regular feature of our Summer Conference since 2008. We have a stand, in collaboration with the

British Society for Immunology, at the Big Bang Science Fair at the NEC, Birmingham, later this month and have some other innovative events planned for the future. SfAM members have often contributed to the presentation and discussion of microbiological issues on radio, television and in the press. If we are to expand this area of work and make it more effective, it is important to have some awareness of how the media work and the journalist's perspective on scientific matters. To this end we have supported members, particularly the rising generation of the PECS Group, through sponsored attendance at events such as the Voice of Young Science Workshop run by Sense About Science. The insight this provides is invaluable judging by the excellent feedback we receive.

There are however pitfalls that can await those who follow the public engagement path too successfully. Whilst being a media expert or science popularizer can attract some kudos to the individual, their employer or institution, it is demanding of time and effort and can diminish levels of more conventional grist for the career mill such as income generation, grants and peer-reviewed publications. Sadly it can also attract some disapprobation from one's peers as being an activity unworthy of true scientists. Occasionally this may be prompted by envy. After all, the idea of appearing on television or radio can be appealing, particularly when one reaches the apogee of the field and is transported to exotic locations to record short pieces with some tenuous link to the location. While condemning such a frivolous approach to serious matters I should mention that, on request, I am available to walk purposefully down a tropical beach waxing lyrical on fermented foods, traveller's diarrhoea (or almost anything else for that matter).

Martin Adams
President of the Society

ceo's column

Philip Wheat reports on the latest developments within the Society

As I have stated previously on numerous occasions, as well as being a limited company, SfAM is also a registered charity in England and Wales. By definition, it is necessary for a charity to demonstrate public benefit in their activities. One area through which we benefit the public is discussed by the President in his column where he discusses our burgeoning public engagement activities.

Membership organizations should continually listen to their members. Indeed the raison d'être for a member organization is to meet the needs and exceed the expectations of its members. Our members, who have been with the Society since before 2009, will know that we undertook a comprehensive survey of membership to ensure we understood the requirements and needs of our members. Since then the results have been reviewed and I am pleased to report that the following have been directly implemented:

- An increase in both the financial value and range of grants offered to members. Grants are awarded to appropriate members irrespective of the individual residing within or outside the UK.
- An increase in the award of Studentships enabling more Student Members to attend Society Summer Conferences.
- A significant decrease in the delegate registration fee for members to attend Society Summer Conferences.
- Considerable investment in a total redesign of the Society website. Amongst many improvements the website now enables members to amend their membership profile, change their passwords, search for other members, join and renew membership and apply for grants online.
- No increase in membership fees since 2004. Indeed some membership fees have been reduced e.g. the new 3 for 2 offer for Full Members renewing their membership in 2012.
- The introduction of eStudent membership, which has encouraged undergraduate members to join.
- The introduction of eAffiliate membership for scientists working in developing countries.

These are just a few of the initiatives and changes that have been made as a result of the feedback the member's questionnaire provided in 2009. But as times change, we need to continually monitor the requirements of our members. So during 2012 we will survey our members once again. Please do complete your electronic questionnaire when you receive it, we truly value your opinions.

During 2011 the Executive Committee (EC) agreed to help fund the newly created position of Director of Parliamentary Affairs at the Society of Biology (SB). I am pleased to inform you that the first post holder is Dr Stephen Benn who was appointed in November 2011. Along with the Society and SB the original funders of this position are the: Royal Society of Edinburgh, British Pharmacological Society, Institute of Physics, Royal Society of Chemistry (RSC), Biochemical Society and Society for Experimental Biology. Dr Stephen Benn has held a similar position for over 20 years at the RSC. He has a vast experience of parliamentary affairs not just in the UK parliaments but in other national legislative chambers. Dr Benn's role will be to provide a unified "science" voice and in particular a "life sciences" voice to national and international Governments. On behalf of the Society, in November 2011, I attended the inaugural funders meeting where specific details of Dr Benn's position were discussed and agreed. Regular updates of Dr Benn's activities will be provided to the EC. In addition, we will provide some insight into his work in future issues of the *Microbiologist*.

Once again during 2012 we will be attending a variety of exhibitions and relevant scientific meetings. So far we have agreed to attend the following:

- American Society for Microbiology annual meeting San Francisco, USA, 16 – 20 June.
- International Association for Food Protection annual meeting Providence, Rhode Island, USA, 21 – 26 July.
- Society for Industrial Microbiology, annual meeting, Washington, USA, 11 – 16 August.
- Microbe 2012, Sheffield, UK, 21 – 23 September.

If you are planning to attend any of these meetings please stop by our exhibition stand and say hello.

Finally, don't forget if you would like to attend any of the above meetings and you require some financial assistance, why not apply for one of our grants e.g. President's Fund or Scientific Meeting Attendance Grant? Full details of all our grants including all terms and conditions, as well as online application, are available by visiting www.sfam.org.uk.

Philip Wheat
Chief Executive Officer

Engaging with policy

The Centre for Science and Policy collaborated with the Society of Biology to run a policy seminar for early career biologists, so that young scientists can learn how to engage with policymakers. The seminar was held at the stunning Charles Darwin House in London where delegates arrived for a day full of valuable information, and much interesting discussion.

After coffee and registration, delegates settled into the main room to hear from a panel of academic scientists who had been engaged in the policymaking process. Professor Clive Page (King's College London) shared his experiences and talked about how input from biologists can influence policy. Professor Ajit Lalvani (Imperial College London) told us about how his research papers had influenced policy with regards to tuberculosis screening and Professor Ottoline Leyser (Sainsbury Laboratory Cambridge University, SLCU) discussed her experience in policy. The final speaker, Professor Chris Whitty (Department for International Development) described his experience as a Chief Scientific Advisor with emphasis on the highlights and pitfalls of working outside of his comfort zone.

membership matters

At the end there was a chance for the early career researchers to put questions to these academics regarding what they could do to influence policy. The abundance of questions showed how much interest early career scientists have in science policy.

Lunch was provided enabling delegates to network and offered a great opportunity to gain an insight into the diversity of research currently taking place in the field of biology. It was encouraging to see early career researchers using their skills and applying them to an unfamiliar area; an area that wasn't a lab.

After lunch, delegates were put into small groups to answer the following question: *What three things would you change about the science policymaking process*? The best thing about this discussion was that every member in each of the groups had something to say, and discussions could have continued for the whole afternoon.

After a short break, each group fed back their answers to a panel of policymakers who had previously introduced themselves and explained how they got into policymaking and where they look for scientific information. The main points that were raised by participants included: a committee of experts being readily available, more scientists getting involved and for scientists themselves to become better communicators. Dr Nafees Meah (Department for Energy and Climate Change — DECC) explained that it is important to anticipate issues before they arise (e.g. five years before an event). Dr Miles Parker (Department for the Environment Food and Rural Affairs — DEFRA) explained that he asks for advice from scientific experts to deal with emergencies and to develop policies. Mr Gary Kass (Natural England) explained how science is used to develop a 'what should be' policy, where scientific evidence is used to demonstrate how something should be done 'correctly' or not at all. Finally Dr Helen Dodmer (BIS) described her career and explained that there's an increase in the number of scientists wanting to get involved in policy. Once again, the abundance of questions by early career researchers during the discussion was encouraging and the science policymakers gave delegates some great ideas to take home.

I felt the afternoon session was particularly useful as I didn't know what a policymaker was, or what they did, so it was interesting to have these questions answered and to see that some policymakers were once scientists like us. The entire day had a relaxed, friendly feel with everyone getting involved in the day's activities. The seminar was incredibly useful and I felt I had gained a real understanding of a topic with which I was previously unfamiliar with. The day did exactly what it said — it got everyone engaging with policy.

Samantha Price
PECS Events Organizer

Membership changes

NEW MEMBERS

We would like to warmly welcome the following new members and hope that you will participate fully in the activities of the Society.

Australia

K. Chauhan

Belgium

E. Vandamme

Canada

H. Standing

Ireland

L. Draper; R. Ryan; S. Schuller

Malaysia

H. J. Chua

Nigeria

F. Ade-Ogunnowo; I. Bage; K. T. Eniola; P. Oladele; M. I. Omoruyi; A. O. Osibona; O. D. Oturuhoyi

Syria

M. Y. Hussain

Thailand

N. Aurepatipan; P. Wuttirat; N. Yabueng

UK

C. Adesanno; O. Adeyemi; M. Alkawareek; J-P. Ashton; N. R. Bacasmas; A. Bamber; K. Barnbrook; J. Bass; G. D. Bingley; K. Boagey; L. Broughton; A. Buckley; B. Cass; A. Chambers; G. Clark; H. Cole; L. Coppin; N. J. Donohue; L. Down; J. E. Ebdon; I. V. Emenike; V. Fleming; E. Fletcher; D. J. Fletcher; S. Forrest; P. Fox; D. Gado; C. Gallina-Ramos; A. Graham; M. Graham; K. Gudeleviciute; S. Gupta; J. V. Halawath; C. Harding; J. Hejtmankova; C. Igboanuzue; J. G. Irvine; A. Jakab; A. K. Kheirallah; L. M. Kruitbos; H. Lawtey; L. Licandro Lado; D. V. Lindsay; V. Luang-In; B. Lyinbor; J. MacCallum; P. A. C. Maple; H. Marriott; T. Mathew; B. J. S. McCutcheon; D. Mclean; H. Mkrtchyan; R. Myers; R. O. J. Norman; J. A. Oloya; R. Owen; J. Pattinson; Z. Petrekova; E. Price; Y. N. Price; B. Purchase; G. Raza; R. Rickaby; M. Rogers; C. Rumney; T. Salam; O. Z. Salami; S. Salifu; S. M. Scanlon; C. Shepherd; R. C. Shields; S. Shova; J. Spencer; A. C. Stedman; S. Y. Teo; I. Tsagakis; F. Tucker; K. Turnbull; A. Uddin; F. Ustok; W. Z. Wan Abdullah; A. Ward; H. Wenham; S. Whittle; P. Williams; M. Yavari Ramsheh; L. Young; D. Yunita; A. Zeuner

USA

S. Losing; T. Schmidt

Losses

We were saddened to learn of the death of the following member of the Society: Clive Blackburn

Call for nominations to Committee

There will be up to four vacancies on the S*f*AM Committee in **July 2012.** Nominations are invited from all Full Members of the Society for these vacancies.

Nominations must be made in writing and received by the Society Office by **Friday 4 May 2012.**

Should nominations exceed vacancies, election will be by a system of postal voting arranged by Committee.

Obituary

Emeritus Professor Peter H A Sneath FRS 1923-2011: a personal reflection.

For some of you Peter Sneath will be familiar as one of the authors of the formative text book on microbial systematics, Sneath and Sokal's 'The Principals and Practice of Numerical Taxonomy'. For others you may know him from his involvement in the Bergey's Trust and thus in the production of Bergey's 'Manual of Systematic Bacteriology'. But for some of you the name may mean nothing at all. However, if you have ever used an API strip to identify a bacterium comparing the results against a computer database, frozen your cultures on beads or compared your organisms using a dendrogram, then you are using the legacy of Peter Sneath's work.

I first knew Peter when I joined the Microbiology Department at the University of Leicester as a PhD student in 1975. This was at a transition time when the MRC Microbial Systematics Unit for which Peter was Director was dissolved and he became Head of the new Microbiology Department. It was while I was at Leicester that the development of highly standardized miniaturized tests, which could be used in routine medical testing laboratories, was being undertaken. This was a need which had been highlighted by the work of Johnson and Sneath on test reproducibility, and which also encompassed the polyphasic approach which was central to Peter's approach to taxonomy. This was also the time when the work on freezing strains on beads was developed and published (and I was delighted to get an honourable mention in the paper's acknowledgments section). In my memories of Peter, phrases like 'towering intellect' and 'renaissance man' spring readily to mind; I can recall the delight I felt having listened to a seminar he gave on a new algorithm he had developed to test if groups of a dendrogram were overlapping and realizing that I had actually understood not just the underlying concept, but (mostly) the basis of the maths. More disconcerting was the realization that half the people in the seminar were geologists who were also using the same numerical approaches.

Peter's contribution to science will be a lasting one.

Christine Dodd

Above: Handwashing/infection control practical: Brookhouse International School. Inset: Dr Mohammed Ashraf, Mrs Sudha Rao, Dr Julia Brown, Dr Tony Worthington

The World of Microbiology goes to Kenya: *Hakuna Matata*

In mid-November 2011, the S*f*AM funded '*World of Microbiology*' roadshow presented by four members of staff from Aston University, spent a week in Nairobi, Kenya. This report summarizes the events of the trip which include: a highly successful roadshow with excellent feedback from staff and students of the two superb secondary schools; torrential rain; traffic congestion from hell; gastroenteritis and airport sniffer dogs which were desperate to devour our laboratory consumables and demonstration material. Let me begin by introducing the microbiology roadshow team: **Dr Anthony Hilton** (Food Microbiology), **Dr Julia Brown** (Careers and Business Development), **Dr Mohammed Ashraf** (Molecular Microbiology) and myself, **Dr Tony Worthington** (Clinical Microbiology)

Friday 18 November 2011

Heathrow Airport, 7.30am. The microbiology team waits to check onto flight BA064 destined for Jomo Kenyatta International Airport, Nairobi, Kenya; our mission was to deliver *The World of Microbiology* roadshow. Armed with personal belongings and a mobile microbiology laboratory split over three pelicases, check-in commenced.

Transporting a mobile laboratory 4,500 miles around the world is not an easy task and we encountered our first 'challenge' during check-in, when we were informed that the pelicases far-exceeded the 'legal' weight limit (by approx. 80kg) and the weight would have to be redistributed. Due to the content and nature of the microbiology roadshow, the mobile laboratory comprised: an autoclave, an incubator, 250 blood agar plates, laboratory consumables and glassware, university prospectuses, cuddly microbial toys (MRSA, *Clostridium difficile*, *E. coli*, *Salmonella*); in addition to a plethora of plastic foodstuffs for demonstration purposes including: pizza, raw meat and fish, cheese, cake and a lobster (all will become clear later!). As you can imagine, having to unpack our mobile laboratory in Heathrow Airport attracted some attention; not least that of the Airport Security and their sniffer dogs. After convincing security that we were indeed microbiology professionals and swiftly moving our glassware containing white powder (starch, for practical sessions) and the plastic meat and pizza out of reach of the highly excitable sniffer dogs, we were allowed to continue. With successful redistribution of goods accomplished and an exchange of cash with Airport Officials to soften the blow of the extra weight we were carrying, we boarded the flight and set off for Nairobi.

Exchanging 'bodily fluids': sexually transmitted infection experiment, Nairobi Academy

After a lengthy flight we headed for the arrivals and VISA point at Jomo Kenyatta International. The Kenyan Official within the VISA section eyed us all with a fair amount of suspicion and proceeded to tell us all one by one that "*money talks*"; accentuating his point by frantically rubbing his thumb and forefinger together. After another exchange of cash, he issued our VISAs and we made our way onwards (Fairview Hotel, Bishops Road, Nairobi). On route, the roads were uncluttered and traffic free and we arrived at the hotel in fairly good time; but then again, it was approaching midnight! Upon arrival, we were ready for food. Dr Hilton and I ordered the Murgh Makani (butter chicken) and ate with gusto when it arrived, despite the fact it was fairly lukewarm. Drs Brown and Ashraf ate something far more sensible.

November 21 – 22: Brookhouse International School; the microbiology roadshow commences

The purpose of our visit to Nairobi was to deliver the microbiology roadshow to years 10 to 13 students at two high-ranking schools: Brookhouse International School and Nairobi Academy; both of which offer a very high standard of education in line with the British curriculum to both Kenyan and international students. In previous years, our *World of Microbiology* roadshow was supported by a Wellcome Trust Educational Grant and was delivered to schools within the Birmingham area. However, such was the success of the roadshow that upon cessation of Wellcome Trust funding, S*f*AM have provided further financial support for the team to continue and extend the initiative; the vision is to deliver the project locally, nationally and internationally. For those of you who are unfamiliar with the microbiology roadshow, it comprises four main study sections: *Introduction to Microbiology; Infectious Disease, Superbugs and Infection Control; Sexually Transmitted Infections and Foodborne Infections and Poisoning*. These topics are punctuated with talks on career opportunities within microbiology, student experiences within the field, and the value of current molecular techniques in microbiology research and diagnosis. The topics are delivered through lectures, interactive sessions and practical classes. Existing student knowledge (pre-roadshow) and gain (post-roadshow) are assessed through pre- and post-course questionnaires. Full details of the World of Microbiology roadshow can be found at www.sfam.org.uk /en/public-engagement/index.cfm/worldofmicrobiology.

How different Nairobi looked in the morning light en route to Brookhouse International School; that is if you could see any of Nairobi amid the torrential rain (it was the rainy season after all). Car fumes seemed to create a low-lying, eye-watering smog over the environment and the traffic seemed to occupy every square foot of road (and pavement come to that). Nobody seemed to have the right of way and the traffic system was complete chaos. Fortunately for us, we had a laid-back Kenyan driver for the week; his name was Paul. He knew the roads, the ropes and how to issue constructive criticism to other drivers in Swahili. Dr Hilton and I were fairly quiet on route to Brookhouse School; we both agreed that our gastrointestinal systems didn't feel quite right; perhaps the Murgh Makani on the first night came with added extras.

Upon arrival at Brookhouse, we were greeted by two very enthusiastic and endearing members of staff: the Head of

Brookhouse International School, Nairobi, Kenya

Chemistry, Mr Mohamed Shiekh, and the Head of Biology, Mr Eric Mulindi. We were instantly made to feel very welcome indeed by both staff and pupils. There was a very happy atmosphere at Brookhouse School, which in itself resembled a palace in structure: ornate buildings and lush gardens with free-roaming peacocks and tortoises the size of small suitcases. All pupils wished us "good morning" in passing and referred to us as "Sir". It was very refreshing; if only university students were the same! Dr Hilton and I located the nearest male washroom facilities, which could be accessed with a quick hop and a skip, and the team set up the roadshow which was to be delivered over the next two days.

For those of you unfamiliar with our roadshow, it commenced in usual fashion: pupils were given 'goodie' bags comprising pens, badges, and a *World of Microbiology* roadshow booklet (available for download at www.sfam.org.uk /en/public-engagement/index.cfm/worldofmicrobiology) and a pre-course questionnaire designed to let us know what the students already knew about microbiology.

Following the pre-course questionnaire, it was straight into the first session: *Introductory Microbiology* with Dr Hilton. The students at Brookhouse International loved it. Dr Hilton enthusiastically engaged students in interactive sessions which included a recreation of Antoni van Leeuwenhoek's experiment back in the 1600s, where he first recognized and reported bacteria from his mouth using his home-grown microscope. Participating students from the class were rewarded with 'cuddly' microbe toys including *E. coli* and *C. difficile*. The roadshow then progressed with a lecture from myself on *Infection, Superbugs and Infection Control*. In this component of the roadshow, the risk factors and clinical presentations associated with healthcare and community associated infections were explored, in particular those due to MRSA and *C. difficile*. Prevention of infection was a key theme throughout the roadshow, so in this part of the programme, the students were taught about effective infection control measures in both the community and hospital settings. They also got to practice the six-stage formal handwashing technique which is used in clinical practice and hopefully some of them will go on to use it in everyday life. An important part of the roadshow is to make the students aware of the career opportunities that are available within microbiology, and the importance of establishing links with professional organizations; this was Dr Julia Brown's opportunity to take centre stage and inform the students about Aston University and the degree programmes on offer, hand out prospectuses and tell them about S*f*AM. The importance of molecular techniques in modern day microbiology cannot be underestimated. Dr Mohammed Ashraf undertook his PhD in Molecular Microbiology at Aston University and used his experience in the field to tell the class about gene cloning and restriction enzymes.

Sexually transmitted infections (STIs) are a major cause of morbidity and mortality worldwide; especially in places like sub-Saharan Africa, which is burdened with 70% of the world's HIV/AIDS population. As part of the programme of events, the *World of Microbiology* roadshow took the opportunity to build upon current sex education curricula and reinforce the information already delivered to students in relation to STIs. In this part of the programme I informed students about common STIs including chlamydia, genital warts, gonorrhoea, syphilis and HIV/AIDS, and discussed their

Year 12/13 students enjoying the lectures: Nairobi Academy

associated complications. In addition, they got to see some fairly gruesome images of the clinical presentations associated with common STIs. I then told them about safe sexual practice and the use of condoms for prevention of STIs. Whilst clinical images of STIs drive home an important message, we had designed a very simple, but again very powerful practical exercise in which the students got to have 'unprotected sex with one another'. Each member of the class was issued with a 'bodily fluid' which is basically a milk solution but one student in the group is given a 'bodily fluid' which is 'loaded' with a STI (starch added to the milk solution). Each student then exchanges bodily fluids with three members of the class to represent unprotected sex. Iodine is then added to all bodily fluids: if it turns blue, you're infected, if it remains pale brown, you're not. On most occasions around 75% of the group became infected from the single source. Whilst this is educational fun and the source of the infection always got a thump and a dead-leg from the rest of the class, the message received by students was loud and clear. Day one of the roadshow was a huge success, the staff couldn't offer enough praise and the students wanted us all to sign our photographs in the course booklet: we felt like celebrities.

Day two of the roadshow began with a lecture from Dr Hilton on *Foodborne Infections and Poisoning* and the importance of food storage, preparation and cooking in preventing infections. This session was supported with clips from Dr Hilton's 2006 TV series *Grime Scene Investigation* which not only provided the pupils with appropriate information regarding good food hygiene, but also added a fun element to the session which the class enjoyed. The interactive element of this session allowed willing students to place pieces of 'cooked' and 'uncooked' foodstuffs (hence the plastic pizza, raw meat and fish etc.) in the right parts of a fridge to prevent microbial cross-contamination and subsequent infection. The roadshow concluded at Brookhouse with a whirlwind tour of the School of Life and Health Science at Aston University from Dr Julia Brown and finally a post-course questionnaire. Whilst the pre-course questionnaire showed that students at Brookhouse International School had a good basic knowledge of microbiology from the outset, the post-course questionnaire demonstrated a significant improvement.

23 November: Hillcrest International School

Before commencing the second stage of our roadshow tour at Nairobi Academy, the microbiology team spent a couple of hours at Hillcrest International School, to inform students about the microbiology roadshow, career opportunities within microbiology and the various degree options available to them. The advantages and benefits of joining various societies including S*f*AM were also discussed. The impression we made at Hillcrest was significant and we have been invited to deliver the microbiology roadshow at the school in 2012.

24 – 25 November: Nairobi Academy; the microbiology roadshow concludes

As we approached the final leg of our Kenyan tour, some things were destined never to change: torrential rain; traffic congestion from hell and continued gastroenteritis suffered by Dr Hilton and me. Nairobi Academy is somewhat different yet strangely similar to Brookhouse International: the surroundings are different; it doesn't have the palatial look (or free-roaming peacocks and tortoises come to that), yet the feel of the place is identical: a positive atmosphere and all round good vibe; the pupils treated us like kings and the staff were delighted to have us there and would do anything to help. We were met by the Head of Biology, Mr Edward Ogola, who introduced us to the rest of the staff and helped us get settled. The roadshow was delivered as successfully and with the same vigour and enthusiasm as at Brookhouse International, and the students again showed their appreciation by asking for signatures, handshaking, wishing us well and asking if we would come back again in the future.

Unfortunately, all good things must come to an end. The S*f*AM funded Microbiology roadshow was a success on several levels: strong links were established with excellent schools in Nairobi; students (and staff) benefitted from the lectures and interactive sessions we delivered and this was clearly demonstrated in the post-course feedback; students are now aware of career opportunities within microbiology, Aston University degree programmes, and the importance of joining relevant societies and professional bodies including S*f*AM and the IBMS. Hopefully, our roadshow has inspired many secondary school students in Nairobi to study microbiology at a higher level and eventually consider a career within the discipline. We gave Paul an Aston University T-shirt, packed the remains of our mobile microbiology laboratory, said goodbye to the traffic congestion and headed for home.

Dr Tony Worthington
Aston University

journalWatch

News about the Society's journals

Journal of Applied Microbiology

The following articles were the most downloaded articles from Journal of Applied Microbiology between January and November 2011:

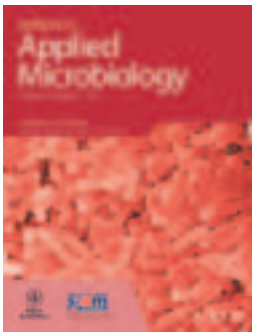
Antimicrobial agents from plants: antibacterial activity of plant volatile oils. H.J.D. Dorman, and S.G. Deans, **Vol. 88,** No. 2.

Antimicrobial activity of essential oils and other plant extracts. K.A. Hammer, C.F. Carson, and T.V. Riley, **Vol. 86,** No. 6.

A study of the minimum inhibitory concentration and mode of action of oregano essential oil, thymol and carvacrol. R.J.W. Lambert, P.N. Skandamis, P.J. Coote, and G.-J.E. Nychas, **Vol. 91,** No. 3.

Editorial. A. Gilmour, **Vol. 107,** No. 2.

A history of influenza. C.W. Potter, **Vol. 91,** No. 4.



Letters in Applied Microbiology

The following articles were the most downloaded articles from Letters in Applied Microbiology between January and November 2011:

Extraction methods and bioautography for evaluation of medicinal plant antimicrobial activity. A. Nostro, M.P. Germanò, V. D'Angelo, A. Marino, and M.A. Cannatelli, **Vol. 30,** No. 5.

Antibacterial activity of selected plant essential oils against *Escherichia coli* O157:H7. S.A. Burt, and R.D. Reinders, **Vol. 36,** No. 3.

Antifungal activity of thyme (*Thymus vulgaris L.*) essential oil and thymol against moulds from damp dwellings. M. Šegvić Klarić, I. Kosalec, J. Mastelić, E. Piecková, and S. Pepeljnak, **Vol. 44,** No. 1.

In vitro antimicrobial activity and chemical composition of Sardinian *Thymus* essential oils. S. Cosentino, C.I.G. Tuberoso, B. Pisano, M. Satta, V. Mascia, E. Arzedi, and F. Palmas, **Vol. 29,** No. 2.

Antibacterial activity of plant extracts on phytopathogenic *Xanthomonas campestris* pathovars. S. Satish, K.A. Raveesha, and G.R. Janardhana, **Vol. 28**, No. 2.

Microbial Biotechnology

The following articles were the most downloaded articles from Microbial Biotechnology between January and November 2011:

Crystal ball – 2011. **Vol. 4**, No. 2.

Marine genomics: at the interface of marine microbial ecology and biodiscovery. K.B. Heidelberg, J.A. Gilbert, and I. Joint, **Vol. 3**, No. 5.

Engineering *Streptomyces coelicolor* for heterologous expression of secondary metabolite gene clusters. J.P. Gomez-Escribano, and M.J. Bibb, **Vol. 4**, No. 2.

Cross-talk of global nutritional regulators in the control of primary and secondary metabolism in *Streptomyces*. J.F. Martín, A. Sola-Landa, F. Santos-Beneit, L.T. Fernández-Martínez, C. Prieto, and A. Rodríguez-García, **Vol. 4**, No. 2.

Genome-wide gene expression changes in an industrial clavulanic acid overproduction strain of *Streptomyces clavuligerus*. M.H. Medema, M.T. Alam, W.H.M. Heijne, M.A. van den Berg, U. Müller, A. Trefzer, R.A.L. Bovenberg, R. Breitling, and E. Takano, **Vol. 4**, No. 2.

Environmental Microbiology

The following articles were the most downloaded articles from Environmental Microbiology between January and November 2011:

Referees' quotes – 2010. **Vol. 12**, No. 12.

Fresh fruit and vegetables as vehicles for the transmission of human pathogens. C.N. Berger, S.V. Sodha, R.K. Shaw, P.M. Griffin, D. Pink, P.

Hand, and G. Frankel, **Vol. 12**, No. 9.

Heavy use of prophylactic antibiotics in aquaculture: a growing problem for human and animal health and for the environment. F.C. Cabello. **Vol. 8**, No. 7.

Global patterns in the biogeography of bacterial taxa. D.R. Nemergut, E.K. Costello, M. Hamady, C. Lozupone, L. Jiang, S.K. Schmidt, N. Fierer, A.R. Townsend, C.C. Cleveland, L. Stanish, and R. Knight, **Vol. 13**, No. 1.

Diversity and ecology of soil fungal communities: increased understanding through the application of molecular techniques. I. C. Anderson, J.W. and G. Cairney, **Vol. 6**, No. 8.

Environmental Microbiology Reports

The following articles were the most downloaded articles from Environmental Microbiology Reports between January and November 2011:

Environmental reservoirs of *Vibrio cholerae* and their role in cholera. L. Vezzulli, C. Pruzzo, A. Huq, and R.R. Colwell, **Vol. 2**, No. 1.

Powering microbes with electricity: direct electron transfer from electrodes to microbes. D.R. Lovley, **Vol. 3**, No. 1.

Alkane degradation under anoxic conditions by a nitrate-reducing bacterium with possible involvement of the electron acceptor in substrate activation. J. Zedelius, R. Rabus, O. Grundmann, I. Werner, D. Brodkorb, F. Schreiber, P. Ehrenreich, A. Behrends, H. Wilkes, M. Kube, R. Reinhardt, and F. Widdel, **Vol. 3**, No. 1.

The global methane cycle: recent advances in understanding the microbial processes involved. R. Conrad, **Vol. 1**, No. 5.

Pyrosequencing reveals a contrasted bacterial diversity between oak rhizosphere and surrounding soil. S. Uroz, M. Buée, C. Murat, P. Frey-Klett, and F. Martin, **Vol. 2**, No. 2.

Read the 2011 special issues from the Society's journals:

Microbial Biotechnology

Chief Editor's Choice Articles Volume 4 — Virtual Special Issue. Chief Editor Kenneth N. Timmis' hand-picked highlights from 2011 — online now! *microbialbiotech.com.*

Extremophiles. Edited by Kenneth N. Timmis, Juan Luis Ramos, Willem M. de Vos, Willy Verstraete and Martin Rosenberg. *Microbial Biotechnology*, **Vol. 4** (4), July 2011.

Lactic Acid Bacteria. Edited by Michiel Kleerebezem and Willem M. de Vos. *Microbial Biotechnology*, **Vol. 4** (3), May 2011.

Crystal Ball and *Streptomyces*. Edited by Hildgund Schrempf, Paul Dyson and Sergey Zotchev. *Microbial Biotechnology*, **Vol. 4** (2), March 2011.

Environmental Microbiology* and *Environmental Microbiology Reports

Chief Editor's Choice Articles Vol. 13 — Virtual Special Issue. Chief Editor Kenneth N. Timmis' hand-picked highlights from 2011 — online now! *env-micro.com.*

Chief Editor's Choice Articles Vols 2 and 3 — Virtual Special Issue. Edited by Kenneth N. Timmis. Chief Editor Kenneth N. Timmis' hand-picked highlights from 2010 and 2011 — online now! *env-micro-reports.com.*

Journal of Applied Microbiology

Campylobacter — Virtual Special Issue. Edited by Frieda Jorgensen and Trudy Wassenaar — online now! *wileyonlinelibrary.com/journal/jam.*

Biodefence — Virtual Special Issue. Edited by Arthur Gilmour — online now! *wileyonlinelibrary.com/journal/jam.*

***Letters in Applied Microbiology* in the Press**

A recent article in *Letters in Applied Microbiology*, 'Cell-penetrating peptides as antifungals towards *Malassezia sympodialis*', looked at potential cures for eczema. The Society publicized this study which attracted much media attention including in the Express, Medical News Today and Medical Daily. Visit the journal's website to read the articles! *wileyonlinelibrary.com/journal/lam.*

Felicity Howlett
Wiley-Blackwell

mediaWatch

microbiology and the media

If you have any views on science in the media which you think should feature in this column, please send them to the Editor at: **lucy@sfam.org.uk**

Robin Ince: science, comedy and mimophants

The new S*f*AM podcast features an interview with the brilliant comedian **Robin Ince** who talks about science and comedy, his fascination in the world around us, and mimophants. I was lucky enough to grab a few minutes with him just before one of his '*Uncaged Monkeys*' shows in Manchester at the end of last year. This series of shows featured Brian Cox, Ben Goldacre, Adam Rutherford, Simon Singh, Helen Arney, and Tim Minchin in a nerd-fest which celebrates all things science and in my opinion is one of the best examples of science communication in action. Here are some highlights from our conversation:

S*f*AM policy on the media

We will:

- always do our best to provide facts, information and explanation.
- if speculation is required, explain the rationale behind that speculation.
- desist from hyping a story—whether it is the journalist or the scientist doing the hyping.

I met Robin at the stage door of the Manchester Apollo Theatre on a very cold December evening. After brief introductions we settled down in a room backstage. I began by asking him about his background and what inspired his interest in science. When asked if he was a scientist by training, his immediate response was: "*No, I'm an idiot*." Anyone who knows anything about Robin will know that is far from the truth and that one of his original inspirations was Carl Sagan's '*Cosmos*' — a television series first screened in the 1980s, from which he's known to quote in many of his stage and radio shows. When he first saw the television series he was…"*11-years-old*..." Robin describes the fact that he became bored of science at school as "*it seemed to have no reflection of what life was about even though* [science] *is everything that it's about...The way I got back into science was I was in a village in Suffolk, Lavenham, where they filmed 'Witchfinder General' and I believe it did also have some witch-hunting trials as well… I found a copy of James Randii's 'Psychic Investigator' book and I read that…and that made me read Carl Sagan's 'Demon Haunted World'… so as usual, as most of my life is, I was skulking around a bookshop, found a thing and then that led me to talk about what I talk about now*." Robin was keen to point out the irony that his return to science took place in a village 'haunted' by the supernatural.

For readers unfamiliar with Robin's work, he began as a stand-up comedian. Since that time he's developed his interest in science and rationalism into a series of shows about science and scepticism — he's become an enabler for what seems to be a burgeoning rationalist/sceptic movement, putting together and leading shows like '*Nine lessons and Carols for a Godless Christmas*' and the BBC Radio 4 show '*Infinite Monkey Cage*' which he presents with Brian Cox.

My most recent contact with Robin came through the Sense About Science 'Standing up for Science' award which he won in November 2011. In his acceptance speech he, typically passionately, discussed his motivations for talking about science and scientific things. These motivations sprung from an innate curiosity and need to answer questions about the world we live in. I asked him what made him want to take this a step further and tell other people about it.

"*I felt that a lot of the media, television had become, to my eyes, very banal. I don't watch that much television anyway and I would occasionally walk into a room and see what was on and I started to think: I'm sure there are lots of people out there who are not really catered for by a lot of the popular media. So I thought: I'm sure people would like to have evenings about interesting things which might not be hilariously funny, but are filled with people who are interesting. So I started to put on shows in cellars of pubs. I asked Simon Singh very early on, I asked Ben Goldacre, people like Stewart Lee came along and talked about some stuff that he'd found and it was…open…a lot of the stand-up that I was seeing, had become cynical or ironic or this kind of bad taste stand-up which was generally sneering all the time. And I thought I'd quite like to put on a show that's celebratory. Friends of mine like Josie Long, who's a wonderful stand-up comedian, she's very good at being enthusiastic and of course the danger of being enthusiastic is that it's much easier to shoot someone down if they're enthusiastic. If you're just doing this sneering cynical making-fun-out-of-everyone-who-is-ultimately-weaker-than-you and then someone takes offence, you go 'it's just a joke'...so that really was what it was driven by — a desire to get across more passionate ideas*."

I asked Robin if he thinks that it's important that people who aren't scientists or interested in science know about science. "*The moment you mention the term science, people read lots of different things into it, and some people see it as just a subject at school…science is really, to me anyway, a method of looking at the world, of trying to understand the world…and you can find answers, or even if you can't find the answers, at least have your mind open enough to look at things and ask: I wonder why that did that?*

"*Also, the internet is a wonderful place…it has inspired things like the Skeptic movement, the science movement…the internet is a great resource for getting people together who are like-minded from across the world. Also it's a great resource for new-age bamboozlement, for selling miracle cures, and for getting across all manner of strange propaganda…people are starting to respect some quite devious and nefarious ideas and so to me one of the most important things is to try and be able to look at the world rationally. To try and be able to ask why someone has written something and why you should believe what they've written. I think we're at lucky times because of things like CERN, it's wonderful…you look at the LHC* [Large Hadron Collider] *and what goes on underground — it's quite phenomenal, we have the human genome being mapped, we have things like the child mortality rate which in the last 50 or 60 years you can watch that curve just suddenly plummet. But then you see things like the anti-vaccination lobby, and you see things like some of the extremists in climate change scepticism, and you realize that it's very, very, important for us to be able to think critically about the world*."

With shows like Robin's *Infinite Monkey Cage* and *Uncaged Monkeys*, as well as the apparent rise of things like Skeptics in the Pub and Cafe Scientifique, and the other ways in which organizations and people are trying to engage with each other about science and scientific ideas, I asked Robin whether he thinks rationalism is building momentum.

"*Well I think it's…lost some of its threat… all of these things, whether it's this, whether it's the Bright Club, whether it's Skeptics in the Pub, whether it's Festival of Spoken Nerd, all of them are quite accessible…you're going to leave with lots of questions and you're going to want to try and find out your own answers and yes, some of it you may not understand but don't feel that you're stupid... There have always been great communicators of science, and there have always been those who have snottily looked down on the great communicators of science. Brian Cox, obviously I work with quite a lot and I'm endlessly amused by those people who say things like: 'Oh, he's dumbing down science'...putting on a show about the heat death of the universe at 9pm on a Sunday night, talking about entropy isn't dumbing down...it's not a be-all and end-all; it's a starting point. All the shows I've just been talking about are starting points for people, then they have to do their own work*."

When talking about the *Uncaged Monkeys* show which took place the previous evening, Robin says: "*At the moment it's fascinating to look at the cross-section of the audience, like last night there were a lot of teenagers. It's also great in terms of the gender mix — it's 50/50 men and women…that's greatly helped by the fact that Tim Minchin and Brian are on, ultimately from an evolutionary point of view it is helpful if you're not too dowdy...but it's great because the people...whatever reasons they're coming to science, are leaving*

enthused and interested and I love the fact that I often have people come up to me and go 'I think you're wrong about this.' Brilliant, as long as the discussion is open."

Robin continues on the subject of open discussion and describes "*certain people in what I would really count as the anti-science lobby who are threatening legal action and trying to close down debate. We have this wonderful word that Steve Jones used on Infinite Monkey Cage the other day which I love: it's mimophant. A mimophant is someone who when they're criticizing someone they see as their opposition they are an elephant. They trample on everyone, they don't care about what anyone else feels, but should you return fire they become a mimosa plant* [saying] *'Oh it's so unfair, I'm only a little flower'...again I think this kind of open forum where someone is going to see Simon Singh talking about an enigma machine and Brian Cox talking about how he's suddenly excited by biology after all these years, because he's seen that there may well be some quantum behaviour in photosynthesis...all of these things will hopefully inspire people.*"

There's an element of comedy to the *Uncaged Monkeys* shows and having noticed a rise in science in comedy, and comedians talking about science, I asked Robin whether he agrees that comedy and science make great bedfellows: "*I think they go well because a lot of stand-up is observational comedy, looking at the world and sometimes asking why you do things. At the same time science is going 'Why does that behave like that?' So that's why I think they work well together.*"

Prior to interviewing Robin (and because I love his podcasts and radio shows) I listened to an episode of the *Infinite Monkey Cage*, on the subject of balance. This was very interesting to me as a science communicator, because it was talking about the role of balance in the media and science reporting, and the fact that if you're having a scientific debate, both sides of the debate need to be playing by the same rules. Often, when science is reported in the media, this isn't necessarily the case. We discussed the role of balance in science reporting and the fact that science is uncertain. Robin said: "*Science is not based around 100% certainties, then it becomes dogma. The wonderful end to one of the episodes of 'Ascent of Man' this beautiful moment where Jacob Bronowski talks about the difference between science and dogma particularly talking about fascism in Germany and he's standing in…as far as I remember it's in Auschwitz…and he talks there as he walks into just a pool of water that would still contain the ashes of human beings who had been burnt there and he says: 'This is not science, this is when you believe something 100%.'*"

We talk about homeopathy: "*Homeopathy I think has been very interesting because there have been various campaigns about this in the last few years. I would say that most people used to believe that homeopathic remedies were just herbal remedies. They didn't question them…and they weren't being stupid taking homeopathic remedies, they presumed arnica contained some arnica. The moment you explain to someone about Samuel Hahnemann and how he came up with the idea of homeopathy and what it actually involves, and you talk about these lovely facts about the* [homeopathic] *cure for flu using duck's liver* [that] *would actually require more water than…exists in the entire universe…people go 'Oh I didn't really know that, I just thought it was a thing that was alright for you because it's sold in shops.' And that's also been a good way in to persuade people more about rationalism because it affects them financially...and then that's a doorway through an actual personal experience into* [them] *questioning more...it's never about the answers to me, it's always about just questioning things.*"

I asked Robin about microbiology: "*Well, it gets more and more exciting, the more I read books by Carl Zimmer. I've got his recent book which has some lovely pictures of various different types of virus, it's very interesting. Even that alone has opened people's eyes once they find out that wonderful thing that Walt Whitman mentioned in a poem and Carl Sagan also used: 'We are a multitudes'…the fact that there is life around us and within us all the time…and we are basically citadels filled with other living creatures. When you get down to some of those levels you can see evolution in action...so that's one of the reasons I find microbiology quite exciting, is because you can see in action certain ideas which people believe they cannot see examples of.*"

I finished by asking Robin what his favourite fact was and of course his answer was far from simple: "*Do you know what, it changes so…I mean…today it's the fact that when you're looking at the size of superstrings if…I'm not going to do this by numbers...but the size of the knowable universe compared to the earth is the same as the size of an electron compared to the size of a superstring.*"

Here there was a long pause while my head exploded, then Robin continued: "*So that's my favourite thing 'cos it makes you a bit dizzy. But every single day the fact will change. That's one of the things I enjoy...oh and I was just reading Richard Feynman's piece about seeing all of science in a glass of wine.*"

Upon probing about this, Robin goes on to explain that he was considering reading it out in

the show later, so we left the interview at that brief description. Robin then dashed off to do a sound-check for the show, leaving me inspired and a little shell-shocked from a fascinating interview and Robin's seemingly unending enthusiasm.

To end the article, here is Richard Feynman's piece: "*If we look at a glass of wine closely enough we see the entire universe. There are the things of physics: the twisting liquid which evaporates depending on the wind and weather, the reflections in the glass, and our imagination adds the atoms. The glass is a distillation of the Earth's rocks, and in its composition we see the secrets of the universe's age, and the evolution of stars. What strange arrays of chemicals are in the wine? How did they come to be? There are the ferments, the enzymes, the substrates, and the products. There in wine is found the great generalization: all life is fermentation. Nobody can discover the chemistry of wine without discovering, as did Louis Pasteur, the cause of much disease. How vivid is the claret, pressing its existence into the consciousness that watches it! If our small minds, for some convenience, divide this glass of wine, this universe, into parts — physics, biology, geology, astronomy, psychology, and so on — remember that Nature does not know it! So let us put it all back together, not forgetting ultimately what it is for. Let it give us one more final pleasure: drink it and forget it all!*"

further information

- To hear the full interview, listen to the new SfAM podcast and visit: www.sfam.org.uk/en/sfam-online/podcasts.cfm/podcast%20robin%20ince.

More about Robin Ince

- From Nine Lessons and Carols for Godless People 2009: www.youtube.com/watch?v=50UAdIRzlts&feature=related — Boring science.

http://www.youtube.com/watch?v=xBAEh9McMHo&feature=related — Richard Feynman.

- www.robinince.com.

who's who

- **Brian Cox** OBE – British particle physicist, Royal Society Fellow and Professor at the University of Manchester. Brian is best known for presenting the award-winning series' '*Wonders of the Solar System*' and '*Wonders of the Universe*'.
- **Ben Goldacre** – British medic and author of the regular Guardian column, blog and book '*Bad Science*'.
- **Adam Rutherford** – British scientist in evolutionary biology and molecular genetics, author and broadcaster. He is an editor at the science journal '*Nature*' and is a presenter on television and radio.
- **Simon Singh** – British particle physicist, author, journalist and TV producer, specializing in science and mathematics.
- **Helen Arney** – British musical comedian based in London, performing original and unusually funny songs on the ukulele or piano.
- **Tim Minchin** – Australian musician, composer, songwriter, actor, comedian and writer based in London.
- **James Randi** – American magician and escape artist, who is now best known as an investigator and demystifier of paranormal and pseudoscientific claims.
- **Carl Sagan** – American astronomer, astrophysicist, cosmologist, author, science popularizer and science communicator in astronomy and natural sciences.
- **Stewart Lee** – British television, radio, newspaper and magazine writer and comedian.
- **Josie Long** – British comedian.
- **Steve Jones** – British geneticist, broadcaster and writer.
- **Jacob Bronowski** – Polish-Jewish British mathematician, biologist, historian of science, theatre author, poet and inventor. He is best remembered as the presenter and writer of the 1973 BBC television documentary series, '*The Ascent of Man*', and the accompanying book.
- **Carl Zimmer** – American science writer. Members may know his book: 'Microcosm – *E. coli* and the new science of life.'
- **Richard Feynman** – American Nobel Prize winning physicist for contributions to the development of quantum electrodynamics, popularizer of physics, writer and lecturer.

Lucy Harper
Communications Manager

bioFocus

Mark Downs reports on science and education policies

The Society of Biology is a single unified voice for biology:

- advising Government and influencing policy.
- advancing education and professional development.
- supporting our members.
- engaging and encouraging public interest in the life sciences.

For further information visit:

www.societyofbiology.org

Have the science and education policies of 2011 set the right agenda for a vibrant science base?
By anyone's standards 2011 was a challenging policy year for education and research in the UK. Schools were challenged to change their governance structures to grow the academy cadre, whilst local business and community groups have been actively encouraged to help schools develop down this particular ideological pathway, or even to set up brand new "Free Schools". Yet, the schools policy debate has largely been about the National Curriculum review in England and Wales and "Curriculum for Excellence" in Scotland.

The Society of Biology, along with many sister organizations, has placed considerable importance on trying to help the Department for Education improve the current Programme of Study for science — all well and good. But, the elephant in the room is Government's current policy allowing academies and free schools to opt out of the national curriculum. With a target of 90% of schools going down these semi-independent routes, all the current work may be for little return. All this really does matter. Whilst some schools may specialize in science, and most will offer some science, there will be pressures for a wider curriculum and lower costs in free schools and academies and single or double science options may well become the norm. That would be a disaster. Biology, chemistry and physics backed by solid maths are all needed for an ever integrated approach to university level science and, ultimately, for the development of sufficient and appropriately skilled, biologists to underpin services, policy, education, manufacturing and research.

To add to the confusion the university landscape is little better. The focus of science policy over the last year has inevitably been research funding. Whilst it is undoubtedly important that debate has masked the real concern — the fact that policymakers are still decoupling teaching and research in universities. The truth is that they go hand in hand. The new student fee structure and research funding have to be considered together. Inevitably the potential impacts are greater for some universities than others but there are already signs that some are "re-balancing" their teaching portfolio to reduce costs. And, as we know, practical biology is never cheap. If these pressures are then coupled with a schools agenda that does not provide wide enough 16 to 18 science teaching across the country, the cost of teaching "remedial science" to raise standards on entry to university is surely another disincentive to offer fully experiential (practical) life science courses. It may be that the market solution does deliver what the UK needs but it is certainly accompanied by risk, and we will be trying hard to spot trends and consult our expert Member Organizations and Fellows to ensure policymakers are alerted to our concerns.

In many ways the life sciences have fared better than was feared with additional funding announcements made during the course of last year. The money is welcome but the Coalition's commitment to the life sciences is equally important. David Cameron described the life sciences as the "jewel in our crown" whilst Cabinet Office Minister Oliver Letwin said of the environment and the National Ecosystem Assessment process:

"*…until now, nobody in Britain (and, for that matter, nobody else in the world) has attempted to draw on this treasure trove of detail to produce a coherent picture of what is happening to nature…*"

"*…all in all, this unseen, but brilliant and assiduous work should provide us with a basis for policies that will preserve our natural environment and its contribution to humanity's well-being for decades to come".*

This made the commitment clear until in his Autumn Statement, George Osbourne said: *"If we burden* [British businesses] *with endless social and environmental goals – however worthy in their own right — then not only will we not achieve those goals, but the businesses will fail, jobs will be lost, and our country will be poorer."*

"We will make sure that gold-plating of EU rules on things like habitats aren't placing ridiculous costs on British businesses."

The Chancellor's lack of recognition of the contribution of the environment to our social and economic well-being has to be addressed. As does the general ignorance of the vast array of activity that the definition encompasses including high and low technology employment and intellectual leadership. As *Sf*AM members know all too well, knowledge of microbiology is critical within environmental science offering stable ecosystems for food supply, nitrogen rich soils and pollution control. Yet, how many within Westminster or Holyrood recognize that? Collectively we need to ensure that these issues are regularly part of the environmental debate.

Dr Mark Downs, PhD, FSB
Chief Executive, Society of Biology

Wednesday 18 April 2012

Spring Meeting

6th broadening microbiology horizons in biomedical science meeting

■ Including the Procter and Gamble Applied Healthcare Microbiology Award Lecture presented by Professor Anne Glover, Chief Scientific Advisor to the European Commission

The Stratford Q Hotel, Stratford-upon-Avon, UK

IBMS CPD ACCREDITATION 6 POINTS

Programme

09.15-10.15 **Tea, coffee, trade exhibition and registration**

10.15-10.20 **Chairman's welcome**

Chair: Phil Wheat

10.20-11.00 **Procter & Gamble Applied Healthcare Microbiology Award Lecture**
Anne Glover, Chief Scientific Advisor to the European Commission

Morning session: A centenary of microbiology

Chair: Ron Dixon

11.05-11.35 **Influenza — future and past**
Jonathan Nguyen van Tam, Nottingham City Hospital

11.35-12.05 **The Mediterranean Fever Commission — what, why, where? (*Brucella*)**
Kevin Brown, St Mary's NHS London

12.05-12.35 **The birth of the Group A *streptococcus*: a case of retarded development?**
David Petts, retired biomedical scientist

12.35-14.00 **Lunch and trade exhibition**

Afternoon parallel sessions
Session A: Sepsis and implants

Chair: Steve Davies

14.00-14.30 ***Proteus mirabilis* catheter associated UTI**
Brian Jones, University of Brighton

14.30-15.00 **Infections and shunts**
John Hartley, Great Ormond Street Hospital

15.00-15.30 **Artificial devices and the intensive care patient**
Paul Dark, Salford Royal NHS Foundation Trust

15.30-16.00 **Orthopaedic implants**
David Partridge, Sheffield Teaching Hospitals Foundation Trust

Session B: Virology

Chair: Laura Ryall

14.00-14.30 **Molecular typing methodologies**
Saheer Gharbia, Health Protection Agency, Colindale, London

14.30-15.00 **Clinical applications of HIV genotyping**
Pat Cane, Health Protection Agency, Colindale, London

15.00-15.30 **Cutting edge technology: applications in respiratory virology**
Paul Kellam, Sanger Institute

15.30-16.00 **Bioinformatics: value to virology**
Steven Riley, Imperial College, London

16.00 **Finish, tea and coffee**

To register online for the Spring Meeting please visit www.sfam.org.uk/spring_meetings.php or contact Sally Hawkes ■ Email: sally@sfam.org.uk ■ Telephone +44 (0)1933 382191

2012 SPRING MEETING BOOKING FORM and INVOICE

SfAM SPRING MEETING WEDNESDAY 18 APRIL 2012

Only ONE person per form please. CLOSING DATE FOR REGISTRATIONS: Wednesday 11 April 2012
EARLY BIRD DISCOUNT of £30.00 is applied to all bookings made before **Wednesday 21 March 2012**

Cancellation policy: Up to 30 days prior to the event all cancellations will be subject to a 10% cancellation fee, up to 14 days prior to the event there will be a 50% cancellation fee, and no refunds will be given on cancellations made within 7 days of the event.

***Non-members: You can add 1 year's membership to your event booking using this form, then register at the member rate and spend the same amount of money or less!**

FEES	Before 21/03/2012	Between 22/03/2012 and 11/04/2012
Full member	£50 ☐	£80 ☐
Student member	£30 ☐	£60 ☐
Honorary member	£30 ☐	£60 ☐
Associate member	£30 ☐	£60 ☐
Retired member	£30 ☐	£60 ☐
Student non member	£60 ☐	£90 ☐
IBMS member	£50 ☐	£80 ☐
Non-member	£100 ☐	£130 ☐

YOUR INTERESTS

Please indicate which of the two afternoon parallel sessions you wish to attend

Session A: Sepsis and implants ☐ **Session B:** Virology ☐

*ADD MEMBERSHIP TO YOUR BOOKING

Add Student membership (£25.00): ☐ **Add Full membership (£50.00):** ☐

YOUR DETAILS

Title:_____ **First Name:**_____ **Family Name:**_____

Organization/Affiliation:_____

Address:_____

_____ **Postcode:**_____

Tel No:_____ **Fax No:**_____ **Email:**_____

Please indicate any special dietary or other requirements (such as disabled access):_____

YOUR NAME BADGE

Please enter the information below in **BLOCK CAPITALS** as you would like it to appear on your name badge

First Name:_____ **Family Name:**_____

Organization/Affiliation:_____

YOUR PAYMENT

● For all participants: **The Society DOES NOT INVOICE for conference fees. Please treat your completed booking form as an invoice. Cheques must be in £ STERLING ONLY and made payable to 'The Society for Applied Microbiology'. Foreign cheques/ drafts MUST be negotiable for the full amount due.** We accept payment **ONLY** by the following credit and debit cards: VISA, Mastercard, Eurocard, Delta, Electron, JCB and Maestro.

☐ **Cheque enclosed** ☐ **Please charge my *Mastercard/Visa card /Debit card*** *(please delete inapplicable items)*

TOTAL amount enclosed/ to be charged: £_____

Card number: ☐☐☐☐ ☐☐☐☐ ☐☐☐☐ ☐☐☐☐

Issue No. ☐☐☐ Expiry Date: ☐☐☐☐ Start Date: (*Debit cards only*) ☐☐☐☐

Security Code (last 3 digits on reverse of card): ☐☐☐

Cardholder's address to which credit card statement is sent:

_____

_____

Signature:_____ Date:_____

Please return the completed form by fax (post if you are enclosing a cheque) to: **The Society for Applied Microbiology, Bedford Heights, Brickhill Drive, Bedford MK41 7PH, UK. Tel: +44(0)1933 382191. Fax: +44(0)1234 326678. Email: sally@sfam.org.uk**

SUMMER CONFERENCE 2012 BOOKING FORM and INVOICE

SfAM SUMMER CONFERENCE 2 — 5 July 2012

CLOSING DATE FOR REGISTRATIONS: Friday 22 June 2012. EARLY BIRD DISCOUNT of £50.00 is applied to all bookings made before 8 June 2012

Cancellation policy: Up to 30 days prior to the event all cancellations will be subject to a 10% cancellation fee, up to 14 days prior to the event there will be a 50% cancellation fee, and no refunds will be given on cancellations made within 7 days of the event.

FEES BEFORE 8 JUNE 2012	Full Member	Student, Honorary, Associate & Retired Member	Student Non–Member	Non–Member
Full Conference Rate: (inc accommodation)	£250.00 ☐	£200.00 ☐	£400.00 ☐	£600.00 ☐
Conference Rate: (no accommodation)	£100.00 ☐	£50.00 ☐	£100.00 ☐	£200.00 ☐
Conference Day Rate:	£50.00 ☐	£25.00 ☐	£50.00 ☐	£100.00 ☐

FEES BETWEEN 9 JUNE and 22 JUNE 2012	Full Member	Student, Honorary, Associate & Retired Member	Student Non–Member	Non–Member
Full Conference Rate: (inc accommodation)	£300.00 ☐	£250.00 ☐	£450.00 ☐	£650.00 ☐
Conference Rate: (no accommodation)	£150.00 ☐	£100.00 ☐	£150.00 ☐	£250.00 ☐
Conference Day Rate:	£100.00 ☐	£75.00 ☐	£100.00 ☐	£150.00 ☐

Conference Day Rate delegates please tick the day you wish to attend: Mon 2nd ☐ Tue 3rd ☐ Wed 4th ☐ Thur 5th ☐

INTELLECTUAL PROPERTY WORKSHOP: please tick this box if you would like to attend the workshop taking place on Monday 2 July 11.00 – 17.00 ☐

LEWIS B PERRY MEMORIAL LECTURE: please tick this box if you would like to attend the lecture on Monday 2 July ☐

QUIZ NIGHT: please tick this box if you would like to attend the quiz on Monday 2 July ☐

CONFERENCE DINNER: please tick this box if you would like to attend the dinner at The Hub on Wednesday 4 July (extra fee applies) **£50.00** ☐

***Non–Members please note: You can add 1 year's membership to your event booking using this form, then register at the member rate and spend the same amount of money or less!**

*ADD MEMBERSHIP TO YOUR BOOKING

Add Student membership (£25.00): ☐ **Add Full membership (£50.00):** ☐

YOUR DETAILS

Title:_____ **First Name:**_____ **Family Name:**_____

Address:_____

Postcode:_____ **Tel No:**_____ **Email:**_____

Special dietary or other requirements:_____

YOUR NAME BADGE

Please enter the information below in **BLOCK CAPITALS** as you would like it to appear on your name badge

First Name:_____ **Family name:**_____

Organization/Affiliation:_____

YOUR PAYMENT

● **For all participants: The Society DOES NOT INVOICE for conference fees. Please treat your completed booking form as an invoice. Cheques must be in £ STERLING ONLY and made payable to 'The Society for Applied Microbiology'. Foreign cheques/ drafts MUST be negotiable for the full amount due.** We accept payment **ONLY** by the following credit and debit cards: VISA, Mastercard, Eurocard, Delta, Electron, JCB and Maestro.

☐ **Cheque enclosed** ☐ **Please charge my *Mastercard/Visa card /Debit card*** *(please delete inapplicable items)*

TOTAL Amount enclosed/ to be charged: £_____

Card number: ☐☐☐☐ ☐☐☐☐ ☐☐☐☐ ☐☐☐☐

Issue No. ☐☐☐ Expiry Date: ☐☐☐☐ Start Date: (*Debit cards only*) ☐☐☐☐

Security Code (last 3 digits on reverse of card): ☐☐☐ Cardholder's address to which credit card statement is sent:

_____

Signature:_____ Date:_____

Please return the completed form by fax (post if you are enclosing a cheque) to: **The Society for Applied Microbiology, Bedford Heights, Brickhill Drive, Bedford MK41 7PH, UK. Tel: +44(0)1933 382191. Fax: +44(0)1234 326678. Email: sally@sfam.org.uk**

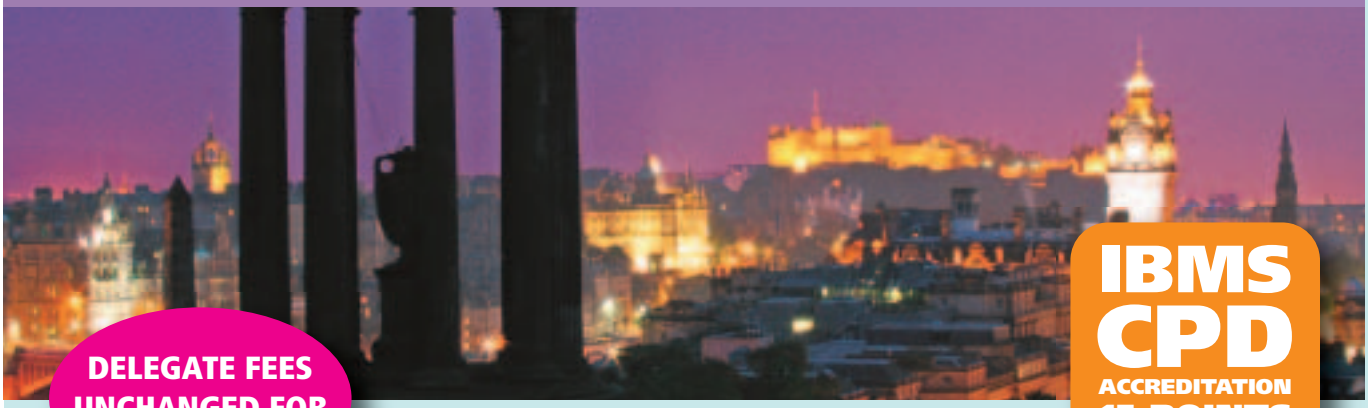
2 - 5 July 2012

Summer Conference 2012

- **Microbial resistance to antibiotics and biocides**
- **Natural and experimental adaptation in bacteria**
- **Bioremediation**

■ Including the Lewis B Perry Memorial Lecture:
Globalization of antimicrobial resistance. *Didier Pittet, University Hospital in Geneva*

The George Hotel, Edinburgh, UK ■ Monday 2 July — Thursday 5 July 2012



DELEGATE FEES UNCHANGED FOR 2012!

IBMS CPD ACCREDITATION 15 POINTS

Programme

Monday 2 July 2012

11.00-17.00 **Intellectual property workshop**

18.00-19.00 **Lewis B Perry Memorial Lecture**
Globalization of antimicrobial resistance
Didier Pittet, University Hospital in Geneva, Switzerland

19.00-20.00 **Drinks reception and buffet**

20.30-22.30 **Quiz night**

Tuesday 3 July 2012

Session 1: Microbial resistance to antibiotics and biocides

09.00-09.35 **Impact of bacterial resistance to biocides in the healthcare industry**
W. Rutala, University of North Carolina School of Medicine, USA

09.35-10.00 **Bacterial resistance and cross-resistance: overrated story or real concern?**
Jean-Yves Maillard, Cardiff University, UK

10.10-10.45 **Recent advances in antibiotic resistance in *Ps. aeruginosa***
Keith Poole, Queen's University, Kingston Ontario, Canada

10.45-11.15 **Tea, coffee and trade show**

11.15-11.50 **Evolution and dissemination of vancomycin resistance in Gram-positive cocci**
Patrice Courvalin, Institut Pasteur, France

11.50-12.25 **β lactamase resistance in Enterobacteriaceae**
Neil Woodford, Health Protection Agency, Colindale, London, UK

These preliminary programme times and titles were correct at the time of going to press.

12.25-13.00 **Controlling antibiotic resistance through stewardship**
Rob Townsend, Sheffield Teaching Hospitals Foundation Trust, UK

13.00-14.00 **Lunch, trade show and posters**

Session 2: Natural and experimental adaptation in bacteria

14.00-14.35 **The various lifestyles of the *Burkholderia cepacia* complex species: a tribute to adaptation**
Eric Deziel, Centre INRS, Canada

14.35-15.10 **Adaptive evolution in Geobacter**
Pier-Luc Tremblay, University of Massachusetts, USA

15.10-15.45 **Extremophiles and halophiles: adaptation to high salinity environments**
Terry McGenity, University of Essex, UK

15.45-16.00 **Tea, coffee and trade show**

16.00-17.00 **Attended poster session 1**

17.00-18.00 **Student session**

17.00-19.30 **Trade show and competition**

Wednesday 4 July 2012

Session 2 continued: Natural and experimental adaptation in bacteria

09.00-09.35 **Studying and designing systems: towards orthogonal biochemical reaction networks**
Sven Panke, ETH-Zurich, Switzerland

09.35-10.10 **Engineered bacteria as pollution bioreporters**
Jan Roelof van der Meer, University of Lausanne, Switzerland

10.10-10.40 **Tea, coffee and posters**

10.45-12.00 **Attended poster session 2**

12.00-13.00 **Lunch and posters**

Session 3: Bioremediation

13.00-13.35 **Microbial resource management and environmental biotechnology**
Willy Verstraete, University of Gent, Belgium

13.35-14.10 **Selection and manipulation of bacteria for rhizoremediation**
Juan Luis Ramos, EEZ, Granada, Spain

14.10-15.10 **Student presentations**

15.10-15.30 **Tea, coffee and posters**

SfAM Award Lectures

15.30-15.35 **Introduction to the New Lecturer Research Grant**
Martin Adams, President of the Society

15.35-16:10 **SfAM New Lecturer Research Grant Lecture**
To be confirmed

16.10-16.15 **Introduction to the WH Pierce Prize**
Martin Adams, President of the Society

16.15-16.45 **W H Pierce Prize Lecture**
To be confirmed

16.45-17.15 **Annual General Meeting**

19.00 onwards **Drinks reception and conference dinner at The Hub**

Thursday 5 July 2012

Session 3 continued: Bioremediation

09.00-09.35 **Bioremediation of petroleum hydrocarbon contaminants in marine environments**
Ian Head, University of Newcastle, UK

09.35-10.10 **Exploiting fungi in bioremediation of hazardous chemicals**
Hauke Harms, Helmholtz Centre for Environmental Research, Germany

10.10-10.45 **Tea, coffee and posters**

10.45-11.20 **Geomicrobiology and bioremediation**
Geoffrey Gadd, University of Dundee, UK

11.20-11.55 **Bioremediation of uranium from minewaters**
Lynne Macaskie, University of Birmingham, UK

12.00-13.00 **Lunch and close**

For the latest programme please visit: www.sfam.org.uk/en/events/index.cfm/summer_conference

Bioremediation of hydrocarbon contaminants: an industry perspective

As a result of media coverage, many of us have witnessed the environmental impact of petroleum hydrocarbon spills such as those seen from the Exxon Valdez oil spill of 1989 and the more recent BP Deep Horizon spill of 2010. As a reminder, Atlas and Hazen (2011) reviewed these two important environmental events. Thankfully hydrocarbon spill events of this magnitude don't happen every day, however hydrocarbon contamination is widespread. Numerous sites are contaminated by hydrocarbons as a result of a history of industrial use. Such industries or sites include metal works, gasworks, oil refineries, and fuel depots to name but a few. In the UK, there are thousands of hydrocarbon contaminated (brownfield) sites, many of which, through planning and development control, or Part IIA of the Environmental Protection Act 1990 (the Contaminated Land Regime), find themselves in need of remediation to some degree.

Traditionally, disposal to landfill (dig and dump) has been the main approach for dealing with contaminated waste material arising from brownfield sites, however, legislative and financial drivers (such as the annually-rising landfill tax) are making this an increasingly less desirable option. This short article gives an overview of the current status on the use of bioremediation for treating hydrocarbon contamination in soil (and to a lesser extent groundwater) and some future research directions. I am sure many more aspects will be covered at the *Sf*AM Summer Conference this year (see pages 26-27 for details).

Bioremediation

Bioremediation involves the use of microorganisms or plants (the latter usually specifically referred to as phytoremediation), to mitigate risk posed by contaminants in the environment. When compared to chemical and physical based remediation techniques such as chemical oxidation, thermal desorption or traditional 'dig and dump' to landfill, bioremediation represents a cost-effective and relatively efficient technique. Microorganisms, such as *Rhodococcus* spp. (Bouchez, Blanchet & Vandecasteele, 1995) and *Dechloromonas* spp. (Meckenstock & Moutakki, 2011), can treat a wide range of hydrocarbon contaminants through biodegradation; either mineralization where the contaminant is used as a primary food source or, cometabolism where contaminant biodegradation is a beneficial side-effect of other metabolic processes. Hydrocarbon contaminants, treatable by bioremediation include not only crude oils and refined petroleum products, but solvents, phenols, glycols, surfactants, pesticides and explosives.

Bioremediation approaches

Although bioremediation processes occur naturally in the environment, they can be slow and uncontrolled. As such, human intervention in the form of engineered approaches is more often than not required to accelerate these processes in a controlled manner.

The two engineered approaches to remediate contaminated soil and groundwater are to either (1) treat it '*in situ*' in the ground or, (2) '*ex situ*' following excavation (soil) or pumping (groundwater). *In situ* remediation can address both unsaturated (above groundwater level) and saturated (below groundwater level) environments. A summary of *in situ* and *ex situ* soil and groundwater approaches is shown in Table 1. These engineering approaches are primarily designed to introduce air (oxygen) into the contaminated matrix to promote aerobic biodegradation. Although many organic contaminants can be degraded anaerobically, the rates of reaction are far less favourable. For example, the half-life of benzene under aerobic conditions is a few days rather than years as is the case under anaerobic conditions.

Although *in situ* remediation is concerned solely with mitigating risk, and the protection of human or environmental receptors, there are several options available once soil is excavated, or groundwater pumped, using *ex situ* remediation. For soil, if not treated for re-use on-site to specific risk assessment criteria, it can be treated off-site at a soil treatment centre (or hub site). This can lead to site re-use, or treatment for waste reclassification (due to the soil becoming classified as a waste following removal from the ground) prior to disposal. Options for groundwater include treatment for disposal to foul sewer, or tankering off-site for treatment and subsequent disposal.

Factors limiting biodegradation

In addition to oxygen, various factors may limit the rate of biodegradation (Table 2). For example, although hydrocarbon contamination results in an influx of carbon, nitrogen is usually the limiting essential nutrient. Therefore, the addition of nitrogen rich nutrients is an effective approach to enhance the bioremediation process (Hollender *et al.*, 2003). However, while nutrient limitation can be determined theoretically, recent work has resulted in the development of assays based on monitoring respiration under differential nutritional loading to determine optimum requirement for soil bioremediation (Aspray, Gluszek & Carvalho, 2008). The latter approach avoids uncertainty in the composition of carbon and the bioavailability of nutrients already present in the soil.

Table 1. Summary of bioremediation approaches for soils and groundwater

	Soil	Groundwater
in situ	Bioventing (unsaturated) Biosparging (saturated)	Biosparging
ex situ	Land farming Windrow Biopile Soil slurry bioreactor	Bioreactor

Table 2. Optimal conditions for biodegradation

Parameter	Optimal conditions for hydrocarbon bioremediation
Soil pH	≥ 6 pH ≤ 8
Soil moisture content	40 – 85 % field capacity
Nutrient content (C:N:P)	100:10:1
Temperature	10 – 45°C
Organic contaminants	< 50,000 ppm
Heavy metals	< 2,500 ppm
Soil texture	Minimal clay content

To enhance *ex situ* soil bioremediation, exogenous nitrogen can be added as an inorganic nutrient in the form of agricultural fertilizers, or organic materials such as poultry litter, spent mushroom compost, horse manure or green and food waste composts (Atagana, 2004; Semple, Reid & Fermor, 2001) or even digestate. There are numerous potential advantages of using organic nutrients over inorganic fertilizers, besides being cheap sources of nitrogen, in many cases they can enhance porosity and oxygen diffusion. In addition, as slow-release nutrient sources the possibility of external ecosystem contamination from nutrient leaching is minimal (Sarkar *et al.*, 2005). Finally, composts have enormous potential for bioremediation (sometimes referred to as compost bioremediation), as they are capable of sustaining diverse populations of microorganisms, which themselves have the potential to degrade hydrocarbon contaminants. Although organic materials have been successfully applied for bioremediation of hydrocarbon contaminated soils, further research is needed to optimize the approach and understand the benefits of the introduced microorganisms.

Biostimulation and bioaugmentation

As discussed, biodegradation of hydrocarbon contaminants in soil and groundwater can usually be enhanced by the addition of nutrients, a process termed biostimulation. If the indigenous microorganisms do not have the appropriate metabolic capability, then microbial cultures can be added. This is known as bioaugmentation and examples of microorganisms that can be used for this purpose are shown in Table 3. Although there have been many studies comparing biostimulation and bioaugmentation for petroleum hydrocarbon contaminated soils (Margesin & Schinner, 2001; Evans *et al.*, 2004; Bento *et al.*, 2005), many bioremediation

Table 3. Microorganisms which are considered for bioaugmentation of chlorinated solvent, pesticide and explosive bioremediation

Microorganism	Contaminant type	Example
Pseudomonas sp. strain ADP	Nitroaromatic	Atrazine
Ralstonia eutropha JMP134 (pJP4)	Chloroaromatic	2,4-dichlorophenoxyacetic acid (2,4-D)
Dehalococcoides sp. strain BAV1	Chlorinated solvent	Tetrachloroethene (PCE)
Phanerochaete chrysosporium	Nitroaromatic	2,4,6-trinitrotoluene (TNT)
Rhodococcus sp. NJUST16	Nitroaromatic	2,4,6-trinitrophenol

practitioners would argue that bioaugmentation is not needed with petroleum hydrocarbon contamination, because metabolic capability is ubiquitously present. Furthermore, the culture of microorganisms on such a large-scale may become cost prohibitive for clean-up of petroleum hydrocarbon contaminants, making this a less attractive option. However, there is good evidence for continuing research on bioaugmentation strategies in other areas such as for the bioremediation of xenobiotic contaminants (those synthesized by humans) including (chlorinated) solvents, pesticides and explosives, where metabolic capability may be lacking in the environment. Crucially the nature of contaminants such as these is that they are generally bioavailable, in contrast to contaminants such as polyaromatic hydrocarbons (PAHs) (Vogel, 1996), and hence bioaugmentation in such cases would enhance bioremediation.

Contaminant bioavailability in soils

Bioavailability is a term becoming increasingly important for bioremediation practitioners, as it relates to the ability to predict soil bioremediation endpoints. For example, if hydrocarbon contaminants are not bioavailable, microorganisms (whether indigenous or introduced) will not be able to degrade them. Therefore the development of assays which can determine the bioavailable fraction of particular contaminants, rather than the total amount present (exhaustively extracted with harsh solvents), are potentially valuable. To this end, significant research into PAH contaminants using cyclodextrin based (non-exhaustive) extraction assays, has been undertaken. Results of this work have been shown to correlate with biodegradable fractions (Hickman *et al.*, 2008). However, although suited to specific compounds, in most sites contamination is a complex mixture of compounds and as such further work is needed in this area.

Conclusions

Although there remains a degree of uncertainty for remediation practitioners in the decision to adopt bioremediation over traditional dig and dump, fundamental research on hydrocarbon biodegradation and more recent development of bespoke assays (respiration and bioavailability) has helped in managing the risk. With alternatives requiring the use of harsh and costly chemicals (chemical oxidation), energy (thermal desorption) or generating waste residue (soil washing) the future remains bright for bioremediation. The main challenge going forward will be to apply these processes to increasingly complex contaminants, as well as higher concentrations and mixed contaminant scenarios.

references

- Aspray, T.J., Gluszek, A., and Carvalho, D. (2008). Effect of nitrogen amendment on respiration and respiratory quotient (RQ) in three hydrocarbon contaminated soils of different type. *Chemosphere*, **Vol. 72**, pp947–951.
- Atagana, H.I. (2004). Co-composting of PAH-contaminated soil with poultry manure. *Letters in Applied Microbiology*, **Vol. 39**, pp163–168.
- Atlas, R.M., and Hazen, T.C. (2011). Oil biodegradation and bioremediation: a tale of the two worst spills in U.S. history. *Environmental Science and Technology*, **Vol. 45**, pp6709–6715.
- Bento, F.M., Camargo, F.A.O., Okeke, B.C., and Frankenberger, W.T. (2005). Comparative bioremediation of soils contaminated with diesel oil by natural attenuation, biostimulation and bioaugmentation. *Bioresource Technology*, **Vol. 96**, pp1049–1055.
- Bouchez, M., Blanchet, D., and Vandecasteele, J.P. (1995). Degradation of polycyclic aromatic hydrocarbons by pure strains and by defined strain associations: inhibition phenomena and cometabolism. *Applied Microbiology and Biotechnology*, **Vol. 43**, No.1, pp156–164.
- Evans, F.F., Alexandre, S., Rosado, A.S., Sebasti, G.V., Casella, R., Machado, P.L.O.A., Holmstrom, C., Kjelleberg, S., van Elsas, J.D., and Seldin, L. (2004). Impact of oil contamination and biostimulation on the diversity of indigenous bacterial communities in soil microcosms. *FEMS Microbiology Ecology*, **Vol. 49**, pp295–305.
- Hickman, Z.A., Swindell, A.L., Allan, I.J., Rhodes, A.H., Hare, R., Semple K.T., and Reid, B.J. (2008). Assessing biodegradation potential of PAHs in complex multi-contaminant matrices. *Environmental Pollution*, **Vol. 156**, No.3, pp1041–1045.
- Hollender, J., Althoff, K., Mundt, M., and Dott, W. (2003). Assessing the microbial activity of soil samples, its nutrient limitation and toxic effects on contaminants using a simple respiration test. *Chemosphere*, **Vol. 53**, pp269–275.
- Margesin, R., and Schinner, F. (2001). Bioremediation (natural attenuation and biostimulation) of diesel-oil-contaminated soil in an alpine glacier skiing area. *Applied and Environmental Microbiology*, **Vol. 67**, No.7, pp3127–3133.
- Meckenstock, R.U., and Mouttaki, H. (2011). Anaerobic degradation of non-substituted aromatic hydrocarbons. *Current Opinion in Biotechnology*, **Vol. 22**, pp406–414.
- Sarkar, D., Ferguson, M., Datta, R., and Birnbaum, S. (2005). Bioremediation of petroleum hydrocarbons in contaminated soils: comparison of biosolids addition, carbon supplementation, and monitored natural attenuation. *Environmental Pollution*, **Vol. 136**, pp187–195.
- Semple, K.T., Reid, B.J., and Fermor, T.R. (2001). Impact of composting strategies on the treatment of soils contaminated with organic pollutants. *Environmental Pollution*, **Vol. 112**, pp269–283.
- Vogel, T.M. (1996). Bioaugmentation as a soil bioremediation approach. *Current Opinion in Biotechnology*, **Vol. 7**, pp311–316.

Thomas Aspray

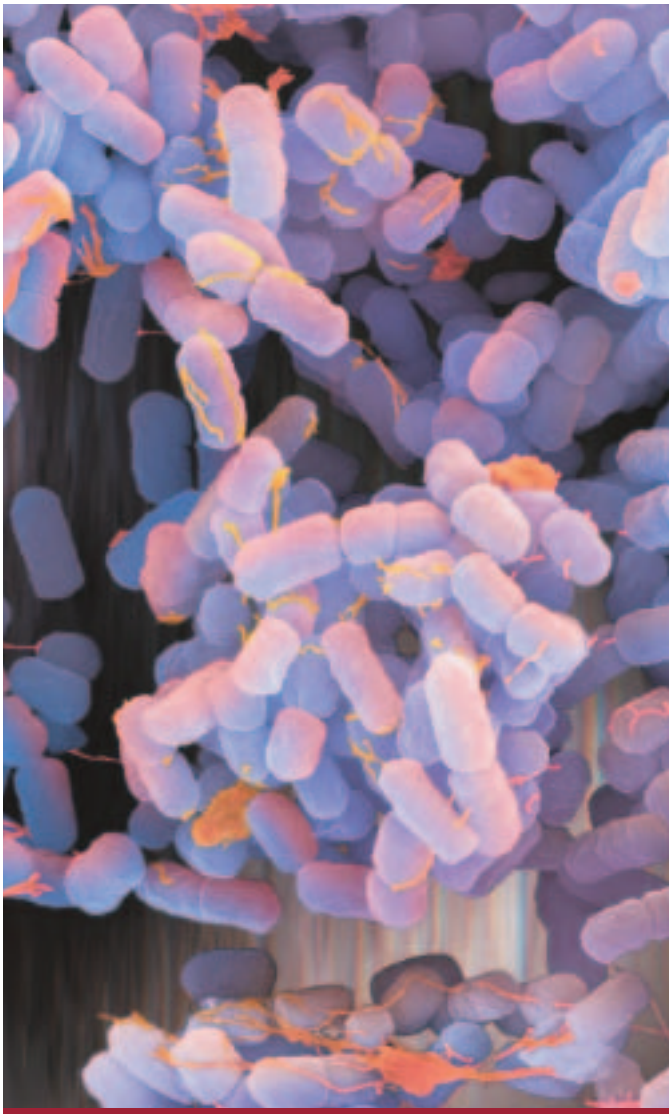
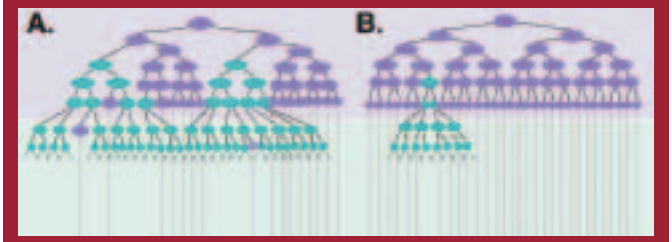


Figure 1. *Bet-hedging as an evolutionary stable strategy*



Population A switches stochastically between two bistable states (purple and green), each of which confers a fitness benefit in the environment of corresponding colour but is maladaptive in the alternative environment. Upon environmental change, population A is primed for rapid growth and recovery. Population A trades off optimal fitness in each environment (by continually generating a proportion of maladaptive types) with the ability to adapt rapidly to environmental change. Population B generates random variation by a mutation. By chance, a small number of individuals may carry mutations enabling growth in the alternative environment. Upon environmental change, population B recovers effective population size more slowly; if environmental fluctuations were to occur rapidly, population B may lack adaptive variants and could face extinction

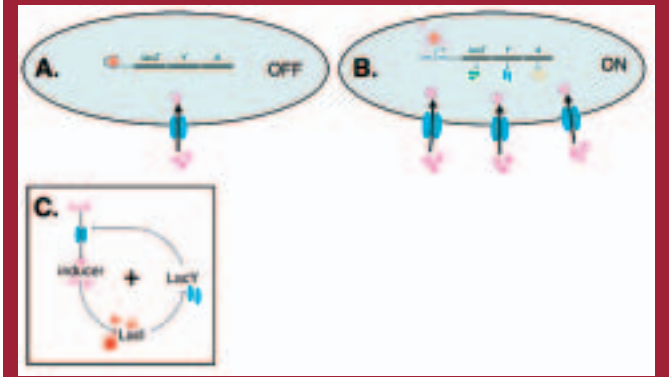
Hedging bets for survival – how bacteria adapt to changing environments

The natural environments that bacteria encounter, from soil microcosms to the human gut, are diverse and stressful. In order to survive widely varying conditions, bacterial populations must possess mechanisms for rapid adaptation through the generation of new phenotypes. The basis of phenotypic diversification, and the mechanism upon which traditional adaptation studies have focused, is mutation. Mutational mechanisms of adaptation to changing environments, including the evolution of 'contingency loci' for locus-specific hypermutation in pathogens, have been well-characterized and reviewed extensively (Arber, 2011). But what is new and exciting, is a growing understanding of the role of non-mutational mechanisms, to produce phenotypes that are adaptive, but at the same time readily reversible. 'Bistability' or 'stochastic switching' is an epigenetic phenomenon whereby cells can switch between two distinct physiological states without mutation or DNA rearrangement (Dubnau & Losick, 2006). The adaptive benefit, is that it enables a population to 'hedge its bets' in the environmental change stakes, without a genetically-encoded commitment, maintaining a proportion of individuals maladapted for the current regime but primed and ready for growth should the environment change (Figure 1). 'Bet-hedging' is predicted to be the diversification strategy of choice when environments fluctuate unpredictably, whereas regular, predictably changing environments, and those with strong cues, have been shown to promote more deterministic (sensor-based) diversification strategies (Jablonka *et al.*, 1995; and other reviewed in Libby & Rainey, 2011).

Bet-hedging as a strategy

Until recently, evolutionary thinking about bet-hedging as an adaptive strategy has focused on plants and animals with complex life-cycles (Simons, 2011). The relevance to microorganisms was revealed only with the revolution in the way we think about populations. Where once we thought of populations of bacteria as identical clones, each individual exhibiting the same genotype, patterns of gene expression and, subsequently, phenotype as its neighbours, we now know that heterogeneity is everywhere and that, even fleeting

Figure 2. *Bistable expression of the E. coli lac operon*



(A) Normally, LacI repressor binds cooperatively to two operator sites upstream of the *lac* promoter, inhibiting transcription of *lacZYA*. (B) Repression is lifted when sufficient inducer accumulates intracellularly, removing LacI from the operator sites. Once on, expression of the lac operon is stably maintained, even when inducer concentrations are reduced to levels below that required for induction, by virtue of the LacY permease — the key determinant of bistability. (C) Expression of *lacY* leads to accumulation of more permease molecules in the cell membrane, which in turn leads to further import of inducer, stimulating continued expression of *lacZYA*. In essence, the circuit creates a positive feedback loop. Fluorescence microscopy has revealed that the threshold concentration above which lac operon expression flips into the ON state is ~375 permease molecules (Choi *et al.*, 2008). Individual cells cross the threshold into the ON state stochastically, as a consequence of 'noise': rare instances of complete dissociation of the the LacI tetramer from both operator sites leads to 'bursts' of transcription sufficient to push LacY concentrations above the threshold

heterogeneity, is crucial for adaptation by natural selection. The realization of the true extent of phenotypic heterogeneity in 'clonal' populations has come about in the last decade, riding on the back of vastly improved resolution in microscopy. Now, technology allows tracking of individual cells as they divide within the constraints of microscopic growth chambers, and the development of sophisticated fluorescence tools enables the visualization of gene expression at the level of the single molecule (Choi *et al.*, 2008; Elowitz *et al.*, 2002). In many cases, gene expression is found to be inherently 'noisy' (Elowitz *et al.*, 2002). Furthermore, we now know that certain regulatory circuit 'architectures' have the capacity to generate and 'capture' useful stochastic noise and translate it into phenotype. What we see is that some individuals within a population display one phenotype and others another; individuals are not clones, but have different 'histories', encode the ability to 'memorize' their history, and - where different phenotypes translate into different fitnesses in the face of environmental change - may have very different futures.

An understanding of the capacity for stable maintenance of 'all-or-none' gene expression simultaneously within populations experiencing the same environmental conditions is not new. Novick and Weiner described the canonical example of bistability — the *lac* operon in *E. coli* — back in 1957 (Figure 2) (Novick & Weiner, 1957). As early as 1961, Jacob and Monod had theorized the underlying regulatory architecture that would permit the bifurcation of populations into bistable states (Monod & Jacob, 1961); a phenomenon that even then was understood to underlie cellular differentiation during development. What is new is the ability to get at the crux of the issue: how does noisy gene expression arise and how is it regulated? How do gene and protein regulatory networks (aka 'architectures') evolve to either minimize the impact of gene expression noise (where faithful expression of a trait is essential for optimal population fitness in the short-term) or harness it (where stochastic variation in expression of a trait, and resultant population heterogeneity — 'bet-hedging' — optimizes population fitness in the long-term)?

The influence of 'noise'

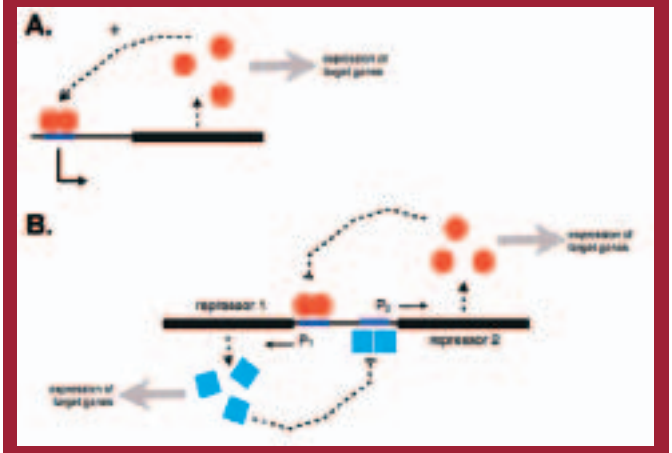
Noise can be 'intrinsic' or 'extrinsic'. 'Intrinsic' noise results from fluctuations in expression of the same genes, within the same cell, over time, as a consequence of the stochastic nature of DNA-protein and protein-protein binding reactions. Whereas 'extrinsic' noise results from stochastic cell-to-cell differences in the concentrations and ratios of protein regulators and effectors (Eldar & Elowitz, 2010; Elowitz *et al.*, 2002; Locke *et al.*, 2011). For an excellent review of 'noise', how it arises, how it is amplified, and how it affects heterogeneity within populations, see Eldar and Elowitz (2010). More to the point, how does circuit architecture translate expression noise into heritable bistable phenotypes? To cut a long story short, the majority of bistable expression phenomena are underpinned by one or a combination of two circuit designs: a positive feedback loop enabling the auto-regulatory production of a key player in the switch, or a double-negative feedback loop whereby a pair of antagonistic regulators inhibit each other's production (Figure 3) (Dubnau & Losick, 2006). Additional features include the need for non-linearity. So the system is only ON when the concentration of a key player rises above a crucial threshold required to flip the switch into the alternative expression state. When the key player drops below the threshold, the switch flips to OFF. Key players are typically expressed at low levels, such that higher than usual transcription due to stochastic events at the promoter, result in significant upwards deviation from mean protein concentrations. Some degree of cooperative binding of key players at the promoters they regulate is usually also involved — hence the non-linearity of response.

The question for the evolutionary biologist is whether levels of noise are evolvable and tunable to environmental fluctuations, and whether noise can lead to adaptation. Systems biologists now believe that they can predict which genes in a global network are subject to stochastic expression from their organization in the protein interaction network, and their position in the gene regulatory network – rudimentary evidence of 'design' (Li *et al.*, 2010). Expression noise may well be an evolvable genetic trait (Cağatay *et al.*, 2009; Locke *et al.*, 2011). Certainly, noise-based stochastic switching is the basis of many bacterial phenotypes that are intuitively highly adaptive. These include: competence, sporulation, and swimming vs biofilm formation in *Bacillus subtilis* (Dubnau & Losick, 2006), persistence of a non-dividing subpopulation in the face of antibiotic challenge (Balaban *et al.*, 2004; Rotem *et al.*, 2010), and a growing list of similarly intriguing adaptations.

Bistable switching

The last few years have seen a plethora of studies in which simple, artificial bistable switch systems were constructed and their performance monitored in the face of environmental perturbation (Acar *et al.*, 2008; Lou *et al.*, 2010; Cağatay *et al.*, 2009). These reductionist approaches have demonstrated how the molecular circuitry underlying 'bistability' is achievable, robust and selectable, and how a simple gene-regulation circuit may convert a triggering stimulus into an 'all-or-nothing' cellular response (Nandagopal & Elowitz, 2011). But can natural bistable switches evolve from existing circuitry in response to selection for bet-hedging strategies? To date, only one study has shed light on the ecological conditions that provoke the *de novo* emergence of bistable switching. An evolutionary experiment that explored the ability of bacteria to repeatedly adapt to alternating environments saw the emergence of genotypes that switch rapidly, without mutation, between two phenotypic states (Figure 4) (Beaumont *et al.*, 2009). As with so many remarkable findings, the evolution of 'switchers' was an unexpected and surprising outcome of efforts to address a different question. Beaumont *et al.* (2009) were exploring the capacity of simple experimental bacterial populations to adapt to repeated bouts of selection in two different environments (A and B) by traditional mutational mechanisms. The question was one of 'reverse evolution': how many times can a genome recreate an adaptive state before all available genetic routes to realization of that state are exhausted? Bacterial populations were required to genetically adapt, by natural selection, to environment A. Once achieved, a single colony of the most dominant novel type to emerge from selection in environment A was transferred to environment B (where it is now maladaptive) and asked to adapt to this new environment. Once this was achieved, a single colony of the newly emergent most dominant novel type was returned to environment A (thus completing a single cycle of 'reverse evolution') and the process continued. In this way, an evolutionary series of genotypes was built up, where each mutant genotype contained the genetic complement of its immediate ancestor and a single additional mutation. Surprisingly, in 3 out of 12 replicate lines, genotypes displaying high frequency phenotypic switching between two distinct colony morphologies evolved. Emergence of 'switching' is an interesting experimental outcome as, intuitively, this type of 'bet-hedging' strategy circumvents the problems posed by 'reverse evolution'. Of the nine experimental lines in which 'switchers' did not evolve, one lost the capacity for further adaptation after three cycles through environments A and B, most likely due to mutational exhaustion of all genetic routes to realization of the adaptive phenotype. Unlike a random mutational mechanism, a locus-specific switch allows the organism to switch (indefinitely) between two beneficial phenotypic states without the need for additional (potentially detrimental) mutations. Interestingly, a mathematical exploration of the parameters that led to emergence of switching types, revealed that switching emerged less as an adaptive response to changing ecological conditions than as an adaptive strategy to satisfy the 'rules' of selection imposed by the experimenter. The most potent selective agents were, in fact, the combination of an 'exclusion rule' and a severe population bottleneck (Libby & Rainey, 2011). Our story can thus be likened to the strong selection imposed on microbial

Figure 3. *Circuit architectures that actuate bistable gene expression (Dubnau & Losick 2006)*

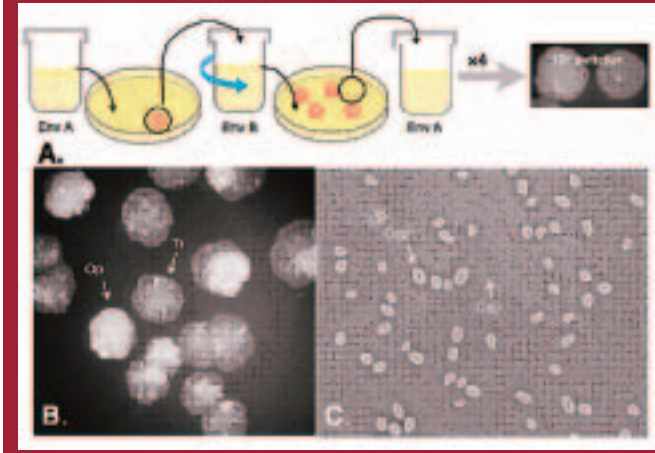


(A) Bistable gene expression may derive from positive transcriptional auto-regulatory loops, where a key regulator stimulates further transcription at its own promoter. Since cooperative (hence non-linear) binding of the regulator to its promoter is required for activation, a threshold protein concentration is typically required before the positive feedback loop kicks in. The loop may be triggered by stochastic overproduction of the regulator, either as a consequence of 'leaky' expression, or by the action of an upstream inducer. (B) An alternative network configuration leading to bistability is a pair of mutually repressing repressors. Each repressor inhibits the expression of its 'rival'. Inhibition may be lifted, pushing the switch in one or the other direction, when one or the other repressor drops below a crucial threshold concentration or is prevented from carrying out its repressive duties by the presence of an inducer. An example is the cI/cro determinants of lysogeny and lysis pathways in *E. coli* phage λ

populations by the immune system: 'winners' win not because of their superior fitness *per se*, but by virtue of being different; a genotype with the capacity to repeatedly generate novel (but not necessarily fitter) variants would consequently beat a genotype without this capacity.

How does the bistable switch manifest at the molecular level? What we know of the parameters for bistability predict a pinch of molecular 'noise', a dash of non-linearity, and the amplification and maintenance of a key regulator above a certain threshold by a combination of positive auto-regulation and negative feedback loops. However, the complexity of the architecture of cellular metabolism means that feedback loops may be indirect, extensive and not at all obvious - we do not anticipate a simple answer (Kotte, Zaugg & Heinemann, 2010)! Subsequent work has focused mainly on the 'switcher' that evolved in 'line 1'–1B^4. 1B^4 has been extensively characterized, and the sequence of mutations comprising its genotype are known (Beaumont *et al.*, 2009). 1B^4 exhibits bistable switching between capsulated (Cap$^+$) and non-capsulated (Cap$^-$) cellular states, the molecular basis of which appears to be altered flux through a pathway deeply embedded in central metabolism which is key to the synthesis of purines, pyrimidines and arginine (Figure 4C). A feasible epigenetic model — supported by empirical studies and mathematical modelling — has been formulated: a simple single nucleotide polymorphism (SNP) in *carB* (a gene both necessary and sufficient for phenotypic switching, but not

Figure 4. *Evolution of a 'phenotypic switcher' during repeated, cyclic selection in alternate environments*



(A) Twelve isogenic populations of *Pseudomonas fluorescens* SBW25 were subjected to bouts of 'reverse' evolution by repeated, cyclic selection in alternate environments: EnvA, a spatially structured environment that selects for the evolution of genotypes able to colonize the air-liquid interface, and EnvB, a spatially non-structured environment that selects for the evolution of genotypes able to colonize the broth phase (Beaumont *et al*., 2009). (B) In line one, during the 5th cycle of 'reverse evolution' a genotype ($1B^4$) evolved that switches rapidly and heritably between two phenotypic states — an 'opaque' (Op) colony form and a 'translucent' (Tr) colony form. (C) These colony phenotypes correlate with phenotypic differences at the cellular level: Tr colonies are largely composed of motile, cellulose-synthesizing cells (Cap^-) capable of colonizing the air-liquid interface, while Op colonies are largely composed of non-motile, capsule-synthesizing cells (Cap^+) that colonize the broth phase. Transposon (Tn) mutagenesis has revealed the structural component of the opaque cell capsule to be a colanic acid-like polymer (CA)

likely part of the switch itself) is believed to generate a degree of instability in a set of biochemical feedback loops. This leads to a frequent drop in intracellular levels of metabolites below a particular threshold, triggering self-sustaining capsule formation in a subset of the isogenic population. However, the fine details of the switch mechanism, namely the full spectrum of genes, gene products and metabolites involved in modulating the switch, remain unknown.

Conclusions

The overarching goal of this research is to reach an understanding of how 'molecular noise' can be crudely 'harnessed' then refined and adapted to purpose, within the constraints of pre-existing cellular networks responsible for modulating a great many phenotypic responses. We have recently sequenced and compared the transcriptomes of the Cap^+ and Cap^- cell fractions, along with the ancestral genomes and from preliminary analysis of the data, we can report that it is starting to make sense. Watch this space!

Gayle C Ferguson
Institute of Natural Sciences, Auckland
New Zealand

references

- Acar, M., Mettetal, J.T., and van Oudenaarden, A. (2008). Stochastic switching as a survival strategy in fluctuating environments. *Nature Genetics*, **Vol. 40**, No. 4, pp471–475.
- Arber, W. (2011). Molecular Darwinism: the contingency of spontaneous genetic variation. *Genome Biology and Evolution*, **Vol. 3**, pp1090–1092.
- Balaban, N.Q. *et al*., (2004). Bacterial persistence as a phenotypic switch. *Science*, **Vol. 305**, No. 5690, pp1622–1625.
- Beaumont, H.J.E. *et al*., (2009). Experimental evolution of bet-hedging. *Nature*, **Vol. 462**, No. 7269, pp90–93.
- Cağatay, T. *et al*., (2009). Architecture-dependent noise discriminates functionally analogous differentiation circuits. *Cell*, **Vol. 139**, No. 3, pp512–522.
- Choi, P.J. *et al*., (2008). A stochastic single-molecule event triggers phenotype switching of a bacterial cell. *Science*, **Vol. 322**, No. 5900, pp442–446.
- Dubnau, D., and Losick, R. (2006). Bistability in bacteria. *Molecular Microbiology*, **Vol. 61**, No. 3, pp564–572.
- Eldar, A., and Elowitz, M.B. (2010). Functional roles for noise in genetic circuits. *Nature*, **Vol. 467**, No. 7312, pp167–173.
- Elowitz, M.B. *et al*., (2002). Stochastic gene expression in a single cell. *Science*, **Vol. 297**, No. 5584, pp1183–1186.
- Jablonka, E. *et al*., (1995). The adaptive advantage of phenotypic memory in changing environments. *Philosophical Transactions of the Royal Society of London. Series B: Biological Sciences*, **Vol. 350**, No. 1332, pp133–141.
- Kotte, O., Zaugg, J.B., and Heinemann, M. (2010). Bacterial adaptation through distributed sensing of metabolic fluxes. *Molecular Systems Biology*, **Vol. 6**, p355.
- Li, J. *et al*., (2010). Exploiting the determinants of stochastic gene expression in *Saccharomyces cerevisiae* for genome-wide prediction of expression noise. *Proceedings of the National Academy of Sciences of the United States of America*, **Vol. 107**, No.23, p10472.
- Libby, E., and Rainey, P.B. (2011). Exclusion rules, bottlenecks and the evolution of stochastic phenotype switching. *Proceedings Biological Sciences/The Royal Society*, **Vol. 278**, No. 1724, pp3574–3583.
- Locke, J.C.W. *et al*., (2011). Stochastic pulse regulation in bacterial stress response. *Science*, **Vol. 334**, No. 6054, pp366–369.
- Lou, C. *et al*., (2010). Synthesizing a novel genetic sequential logic circuit: a push-on push-off switch. *Molecular Systems Biology*, **Vol. 6**, No. 1, p350.
- Monod, J., and Jacob, F. (1961). General conclusions: teleonomic mechanisms in cellular metabolism, growth, and differentiation. *Cold Spring Harbor Symposia on Quantitative Biology*, **Vol. 26**, pp389–401. Available online at: http://symposium.cshlp.org/content/26/389.extract.
- Nandagopal, N., and Elowitz, M.B. (2011). Synthetic biology: integrated gene circuits. *Science*, **Vol. 333**, No. 6047, pp1244–1248.
- Novick, A., and Weiner, M. (1957). Enzyme induction as an all-or-none phenomenon. *Proceedings of the National Academy of Sciences of the United States of America*, **Vol. 43**, No. 7, p553.
- Rotem, E. *et al*., (2010). Regulation of phenotypic variability by a threshold-based mechanism underlies bacterial persistence. *Proceedings of the National Academy of Sciences*, **Vol. 107**, No. 28, p12541.
- Simons, A.M., (2011). Modes of response to environmental change and the elusive empirical evidence for bet-hedging. *Proceedings Biological Sciences / The Royal Society*, **Vol. 278**, No. 1712, pp1601–1609.

historical**Perspectives**

Ancient tuberculosis and leprosy

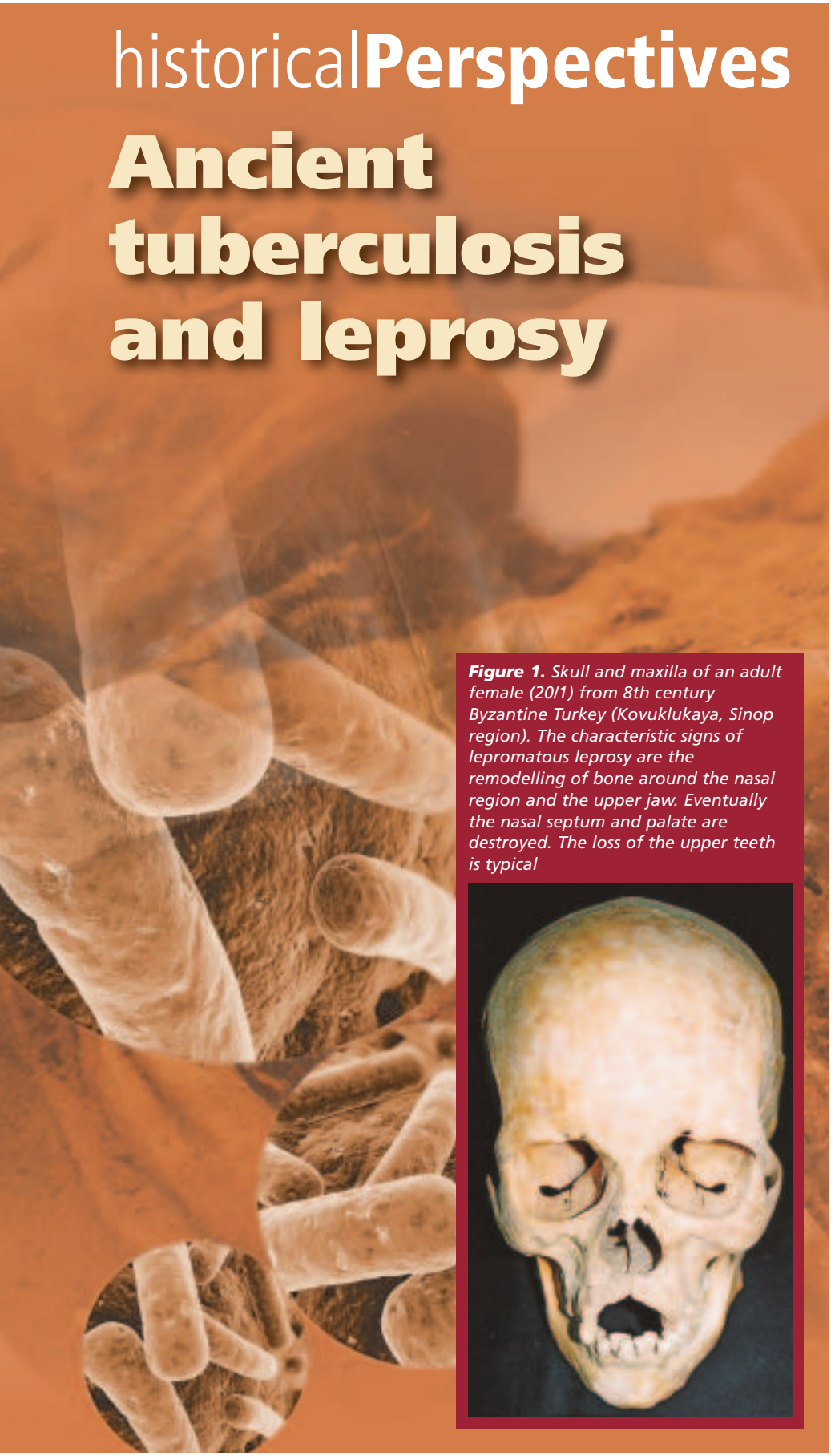


Figure 1. *Skull and maxilla of an adult female (20/1) from 8th century Byzantine Turkey (Kovuklukaya, Sinop region). The characteristic signs of lepromatous leprosy are the remodelling of bone around the nasal region and the upper jaw. Eventually the nasal septum and palate are destroyed. The loss of the upper teeth is typical*

How old are these human infectious diseases? There are several strands of evidence we can use to attempt to answer this question. Many historical texts contain recognizable descriptions of tuberculosis, where it is named as consumption, King's Evil, lupus vulgaris, phthisis or scrofula. The Greek physician Hippocrates (460 to 370 BC) clearly described the vertebral changes associated with Pott's disease — the formation of a gibbus due to tuberculosis of the spine, while leprosy is described in ancient Chinese medical texts of a similar date but based on older material (Skinsnes & Chang, 1985). However, written descriptions alone can be misleading. For example, there has been much debate over the actual disease described as leprosy in the Bible.

Skeletal remains from past populations are the most obvious sources of scientific information. Many diseases leave traces on bones and teeth: some are non-specific — such as abscesses, others are so specific that a diagnosis is possible. Both tuberculosis and leprosy (Figure 1) can be recognized in archaeological skeletal remains, based on very characteristic combinations of changes, some of which are visible to the naked eye, others are disclosed by imaging and histology. Palaeopathology has emerged from physical anthropology, biomedical science and forensic science as a distinct discipline. Diagnostic criteria have been agreed, based on skeletal changes verified by archived patient records.

A totally different way to estimate the age of infectious diseases is that of genomics and ancestral sequence inference. Molecular sequences from different strains and species of modern pathogenic microorganisms are compared and bioinformatics lead to a calculation of 'the most recent common ancestor'.

Examination of human remains for molecular traces of past pathogens is a direct way to study ancient infections. Early studies tackled the host response and sought specific proteins or antibodies. The development of PCR led to much over-enthusiastic research on ancient animal and plant remains until the problems of contamination with modern DNA were appreciated. It was after this phase that the first attempt was made, in our department at University College London (UCL), to

detect ancient pathogenic bacterial DNA in human skeletal specimens (Spigelman & Lemma, 1993). Tuberculosis was the targeted disease due to a fortuitous combination of circumstances. There was consensus on the diagnostic criteria based on skeletal changes, and the molecular diagnosis of tuberculosis had been driven by the extremely slow growth of the causative organism and the need for speedier results. Also, there is no environmental reservoir of the pathogen. We published the first report of ancient PCR-confirmed leprosy a year after that of tuberculosis (Rafi *et al.*, 1994).

Mycobacterium tuberculosis and *Mycobacterium leprae* have GC-rich DNA enclosed in a resistant hydrophobic lipid-rich cell wall, both traits which are believed to contribute to the persistence of their ancient DNA (aDNA). This enables the molecular typing of both pathogens and characterization of individual members of the closely related *Myco. tuberculosis* complex. The aDNA findings are supported by parallel developments in organic chemistry, enabling the direct detection of protein and lipid biomolecules using techniques such as fluorescence high-performance liquid chromatography and negative ion chemical ionization gas chromatography mass spectrometry (Gernaey *et al.*, 2001; Redman *et al.*, 2009; Donoghue *et al.*, 2010). As a result the new field of palaeo-microbiology has emerged during the past 18 years (Table 1).

Tuberculosis is still a major global cause of death and disease, even though antimicrobial therapy has been available for over half a century. Around two billion people, about one third of the world's total population, are infected with tubercle bacilli (http://www.who.int/tb/publications/factsheets/en/index.html, accessed 7th September 2011) and in 2009 1.7 million people died from the disease. It is primarily a respiratory infection spread by infectious aerosols. Swallowing infected sputum or ingestion of infected animal products can cause gastrointestinal tuberculosis. Skeletal tuberculosis is rare as these are disseminated infections yet the host needs to survive for sufficient time for lesions to develop. Even in the pre-antibiotic era it is estimated that only 3 to 5% of tuberculosis infections were associated with bony changes. The great majority of human infections are caused by *Myco. tuberculosis sensu strictu*. *Mycobacterium bovis* is responsible for about 6% of human deaths from tuberculosis.

Table 1. How palaeomicrobiology has increased our understanding of ancient human infectious diseases

- Confirmation of visible palaeopathology of specific diseases
- Detection of disease in the absence of specific bony changes, or even of any skeletal or other morphological changes
- Detection of past co-infections, such as tuberculosis with leprosy, leishmaniasis, or intestinal parasites
- Insights into the social context of past human infections
- Evidence of the epidemiology and past geographical range of ancient infections
- Provision of real-time markers of genetic changes, thus enabling better understanding of the evolution of human pathogens
- Potential to increase our understanding of evolution of the host/pathogen relationship

Leprosy continues to be an ongoing problem in many parts of the world. It can be cured with multi-drug therapy but it is often under-reported due to social stigma and is therefore not treated. More than 213,000 people mainly in Asia and Africa are infected (http://www.who.int/wer/2011/wer8636/en/index.html, accessed 7th September 2011), with 228,474 new cases of leprosy detected during 2010. *Myco. leprae* targets Schwann cells and causes nerve damage. The clinical presentation can range from multi-bacillary or lepromatous leprosy, where there is a minimal host response and extremely high numbers of *Myco. leprae* in tissues, to the pauci-bacillary or tuberculoid form, with a good cell-mediated response and very low bacterial load. If left untreated, leprosy causes progressive and permanent damage to the skin, nerves, limbs and eyes in about 10 to 30% of cases, resulting in severe disability.

The very high level of latent tuberculosis, the slow rate of progression and low infectivity of leprosy suggest a long period of co-evolution of the pathogen with its human host. It is believed the long hunter-gatherer stage of human evolution, with small population sizes, selected symbionts or pathogens that could persist until transmitted (Blaser & Kirschner, 2007). In tuberculosis, active disease and transmission generally occurs in those with a less effective immune system such as the very young and old, or who suffer from malnourishment, other diseases, physical or mental stress. The development of agriculture and animal

Figure 2. *Real-time PCR using a 6-carboxyfluorescein (FAM) specific fluorescent probe for an 80 base pair locus in the RLEP region of extinct Myco. leprae strains obtained from European archaeological samples, which span over 1,000 years. The cycle threshold is unrelated to the chronological age of samples but depends upon the local burial conditions and preservation of the aDNA*

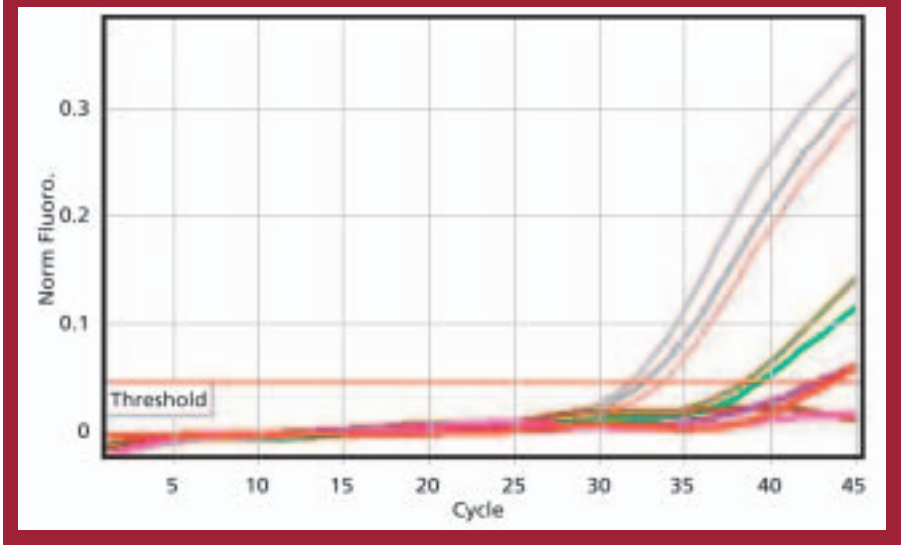
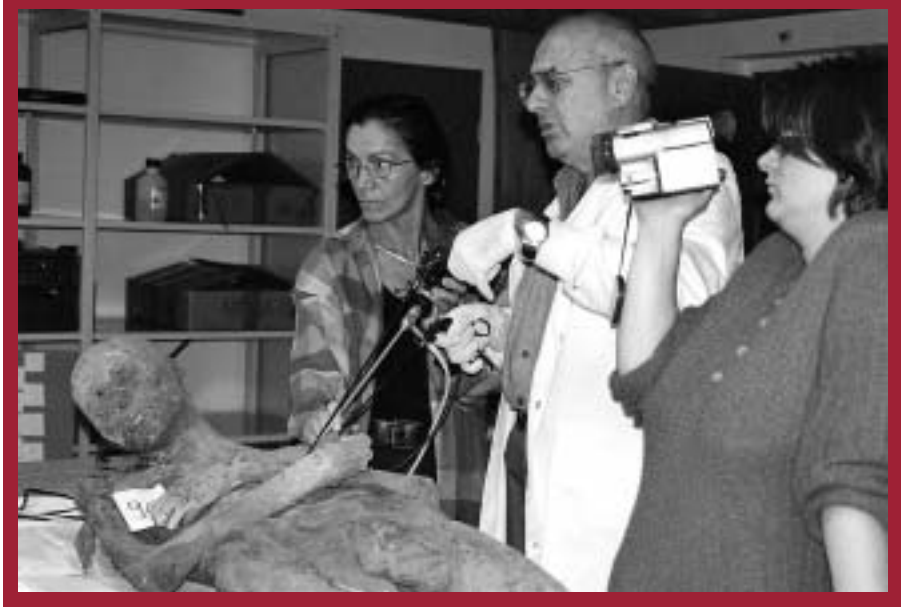


Figure 3. *A naturally mummified body of a 33 year-old man from 18th century Vác, Hungary, one of 263 found in a church crypt during renovation. Chest X-rays suggested that several individuals had tuberculosis, which led to aDNA studies*

domestication in the Neolithic period had a profound impact on human society. There was a switch from foraging and hunting to settled communities, a sedentary lifestyle, less varied diet and pronounced differences in social status. According to the archaeological record tuberculosis is one of several diseases that appeared at this time. This led to the suggestion that humans acquired the infection from domesticated animals and that *Myco. bovis* was the ancestor of *Myco. tuberculosis*. This has now been disproved (see below) but it is certainly true that infectious diseases such as tuberculosis are associated with larger, denser populations.

Figure 4. *Sampling one of the naturally mummified bodies from 18th century Vác, Hungary, using a surgical endoscope. This shows the team working in the Anthropology Department of the Natural History Museum, Budapest, in 1999. Left to right, Ildikó Pap — Head of Department, Mark Spigelman — the pioneer surgeon turned archaeologist who started work in this field, and Ildikó Szikossy — anthropologist in the Budapest department*



The first primers used to detect ancient tuberculosis were based on a specific locus found in all members of the *Myco. tuberculosis* complex, located in the insertion sequence IS6110, usually present in multiple copies in *Myco. tuberculosis*. Early studies confirmed tuberculosis in ancient Egypt, pre-European contact Borneo, China and pre-Columbian South America (Donoghue, 2011). *Mycobacterium africanum* was reported from ancient Egypt (Zink *et al.*, 2003), but the only reported case of ancient *Myco. bovis* infection is of a group of Iron Age pastoralists in Siberia (Taylor *et al.*, 2007). Single nucleotide polymorphisms (SNPs), deletion analysis and other specific loci have confirmed an extant lineage of *Myco. tuberculosis* in a Pre-Pottery Neolithic village in the Eastern Mediterranean from 9,000 years ago (Hershkovitz *et al.*, 2008).

The *Myco. leprae* genome shows evidence of widespread deletions and the organism is uncultivable. Ancient DNA studies have focused on repetitive elements such as RLEP, which has 37 copies per cell, thereby increasing the sensitivity of detection. Leprosy has been confirmed by aDNA in 1st century Palestine, Roman Egypt and the early Byzantine Empire (Donoghue *et al.*, 2005; Monot *et al.*, 2009). Some *Myco. leprae* aDNA is remarkably well preserved (Figure 2) enabling both SNP analysis, and identification of individual strains by microsatellite analysis (Taylor & Donoghue, 2011). In several cases of lepromatous leprosy, the individuals were shown by aDNA analysis to be co-infected with tuberculosis (Donoghue *et al.*, 2005). Reports of this phenomenon were found subsequently in historical accounts of the disease from the pre-antibiotic era.

In both *Myco. tuberculosis* and *Myco. leprae* there is a virtual lack of horizontal gene exchange, reducing the likelihood of SNPs. Therefore SNPs are phylogenetically informative and have enabled the identification of lineages in both species. It also appears that genomic regions lost by deletions are not re-acquired. Therefore the global population structure of both the *Myco. tuberculosis* complex and of *Myco. leprae* can be defined by these lineages. Because the sequence of deletion events is one-way, the evolutionary pathway and possible timescale can be inferred. This has clearly demonstrated that the

Myco. tuberculosis lineage is more ancestral than that of *Myco. bovis* (Gordon *et al.*, 2009). The discrimination between SNPs or principal genetic groups 1 to 3 in the *Myco. tuberculosis* complex is based on functionally neutral base changes in the catalase-peroxidase encoding gene *katG* and a subunit of the DNA gyrase gene *gyrA*. Little work has been done on the timescale of the emergence of these SNPs, but a study on naturally mummified bodies from 18th century Hungary, with exceptionally good preservation (Figures 3 and 4), showed that the population was infected with *Myco. tuberculosis* SNP types 2 and 3, thus demonstrating that these had emerged before the antibiotic era (Fletcher *et al.*, 2003).

It appears that both *Myco. tuberculosis* and *Myco. leprae* have undergone an evolutionary bottleneck and have a clonal relationship with their human host. Different human lineages have an association with a particular lineage of these pathogens, even in the modern world and in second-generation or third-generation inhabitants of ethnically diverse cities. In the case of the *Myco. tuberculosis* complex, one estimate based on bioinformatics is that the major lineages emerged 10,000 to 20,000 years ago (Wirth *et al.*, 2008). Therefore, direct detection of *Myco. tuberculosis* lineages from ancient human remains of known date, such as the detection of a lineage from 9,000 years ago which lacks the TbD1 deletion (Hershkovitz *et al.*, 2008) provides a marker in real-time.

Palaeomicrobiology has been especially helpful in elucidating the phylogeography of leprosy as it has enabled the genetic analysis of European indigenous strains of *Myco. leprae* from around 1,500 years ago that are now extinct (Monot *et al.*, 2009). Sub-genotyping of both extant and extinct strains of *Myco. leprae* from around the world showed a strong geographical association, suggesting migration patterns of early humans and trade routes. One conclusion of this study was that leprosy originated in Europe or the Middle East and then spread to the Far East.

Improvements in PCR procedures have increased the sensitivity and detection rate of aDNA from microbial pathogens. One example is that of specific DNA probes, which incorporate a fluorescent reporter that is quenched unless the probe has bound to the specific target sequence. This enables the design of primers with a far smaller target sequence, which is needed as strand separation during PCR leads to fragmentation of aDNA. The norm now is a target fragment size of around 70 base pairs. Next generation technologies that incorporate direct sequence capture to surface-bound primers or aptomers should facilitate the enrichment and detection of aDNA in this challenging field.

Until now most work has been centred on the microorganism. However, the characteristics of the host are of equal importance. In this regard, the exceptionally well-preserved human remains from 18th century Hungary, with a contemporary archive giving details of family members, suggest a possible strategy for the future, as it appears possible to discriminate between individuals with active and latent tuberculosis infections. A study based on material such as this may enable us to address the question of the changing nature of the interactions between host and pathogen over time.

references

- Blaser, M.J., and Kirschner, D. (2007). The equilibria that allow bacterial persistence in human hosts. *Nature*, **Vol. 449**, pp843–849.
- Donoghue, H. D. (2011). Insights gained from palaeomicrobiology into ancient and modern tuberculosis. *Clin. Microbiol. Infect.*, **Vol. 17**, pp821–829.
- Donoghue, H. D., Lee, O. Y.-C., Minnikin, D. E., Besra, G. S., Taylor, J. H., and Spigelman, M. (2010). Tuberculosis in Dr Granville's Mummy: a molecular re-examination of the first Egyptian mummy to be scientifically examined and given a medical diagnosis. *Proc. Roy. Soc. London Ser. B*, **Vol. 277**, pp51–56.
- Donoghue, H. D., Marcsik, A., Matheson, C., Vernon, K., Nuorala, E., Molto, J. E., Greenblatt, C. L., and Spigelman, M. (2005). Co-infection of *Mycobacterium tuberculosis* and *Mycobacterium leprae* in human archaeological samples: a possible explanation for the historical decline of leprosy. *Proc. Roy. Soc. London Ser., B,* **Vol. 272**, pp389–394.
- Fletcher, H. A., Donoghue, H. D., Holton, J., Pap, I., and Spigelman, M. (2003). Widespread occurrence of *Mycobacterium tuberculosis* DNA from 18th-19th century Hungarians. *Am. J. Phys. Anthropol.*, **Vol. 120**, pp144–152.
- Gernaey, A.M., Minnikin, D., Copley, M., Dixon, R., Middleton, J., and Roberts, C. A. (2001). Mycolic acids and ancient DNA confirm an osteological diagnosis of tuberculosis. *Tuberculosis (Edinburgh)*, **Vol. 81**, pp259–265.
- Gordon, S.V., Bottai, D., Simeone, R., Stinear, T. P., and Brosch, R. (2009). Pathogenicity in the tubercle bacillus: molecular and evolutionary determinants. *Bioessays*, **Vol. 31**, pp378–388.
- Hershkovitz, I., Donoghue, H. D., Minnikin,. D. E., Besra, G. S., Lee, O.Y.-C., Gernaey, A. M., Galili, E., Eshed, V., Greenblatt, C. L., Lemma, E., Bar-Gal, G. K., and Spigelman, M. (2008). Detection and molecular characterization of 9,000-year-old *Mycobacterium tuberculosis* from a Neolithic settlement in the Eastern Mediterranean. *PLoS One*, **Vol. 3**, e3426.
- Monot, M. *et al*., (2009). Comparative genomic and phylogeographic analysis of *Mycobacterium leprae*. *Nat. Genet.*, **Vol. 41**, pp1282–1288.
- Rafi, A., Spigelman, M., Stanford, J., Lemma, E., Donoghue, H. D., and Zias, J. (1994). *Mycobacterium leprae* DNA from ancient bone detected by PCR. *The Lancet*, **Vol. 343**, No. 8909, pp1360–1361.
- Redman, J.E., Shaw, M. J., Mallet, A. I., Santos, A. L., Roberts, C. A., Gernaey, A. M., and Minnikin, D. E. (2009). Mycocerosic acid biomarkers for the diagnosis of tuberculosis in the Coimbra skeletal collection. *Tuberculosis (Edinburgh)*, **Vol. 89**, pp267–277.
- Skinsnes, O.K., and Chang, P. H. C. (1985). Understanding of leprosy in ancient China. *Int. J. Leprosy*, **Vol. 52**, No. 2, pp289–307.
- Spigelman, M., and Lemma, E. (1993). The use of the polymerase chain reaction (PCR) to detect *Mycobacterium tuberculosis* in ancient skeletons. *Int. J. Osteoarchaeol.*, **Vol. 3**, pp137–143.
- Taylor, G. M., and Donoghue, H. D. (2011). Multiple loci variable number tandem repeat (VNTR) analysis (MLVA) of *Mycobacterium leprae* isolates amplified from European archaeological human remains with lepromatous leprosy. *Microb. Infect.*, **Vol. 13**, pp923–929.
- Taylor, G. M., Murphy, E., Hopkins, R., Rutland, P., and Chistov, Y. (2007). First report of *Mycobacterium bovis* DNA in human remains from the Iron Age. *Microbiology*, **Vol. 153**, pp1243–1249.
- Wirth, T., Hildebrand, F., Allix-Béguec, C., Wölbeling, F., Kubica, T., Kremer. K., van Soolingen, D., Rüsch-Gerdes, S., Locht, C., Brisse, S., Meyer, A., Supply, P., and Niemann, S. (2008). Origin, spread and demography of the *Mycobacterium tuberculosis* complex. *PLoS Pathog.*, **Vol. 4**, e1000160.
- Zink, A. R., Sola, C., Reischl, U., Grabner, W., Rastogi, N., Wolf, H., and Nerlich, A. G. (2003). Characterization of *Mycobacterium tuberculosis* complex DNAs from Egyptian mummies by spoligotyping. *J. Clin. Microbiol.*, **Vol. 41**, pp359–367.

Helen Donoghue
University College London

StatNote 28

In the 28th of a series of articles about statistics for biologists, **Anthony Hilton** & **Richard Armstrong** discuss: **Canonical Variate Analysis** (CVA)

Introduction

To test the degree of correlation between a single dependent (Y) variable and an independent (X) variable, one can use Pearson's correlation coefficient ('r') (StatNote 14, Hilton & Armstrong, 2008). Similarly, to test the degree of correlation between a single Y variable and several X variables, one can use the methods of multiple linear regression (StatNote 24, Hilton & Armstrong, 2011a). However, the question arises as to how one would test the correlation between two sets of variables, i.e., multiple Y and X variables? Testing each combination of variables sequentially using Pearson's 'r' would not be satisfactory, as it would involve a large number of individual correlations, and the likelihood that some correlations would arise by chance.

The pattern of correlation between two sets of variables can be tested using canonical variate analysis (CVA). CVA, like principal components analysis (PCA) and factor analysis (FA) (StatNote 27, Hilton & Armstrong, 2011b), is a multivariate analysis. Essentially, as in PCA/FA, the objective is to determine whether the correlations between two sets of variables can be explained by a smaller number of 'axes of correlation' or 'canonical roots'. CVA can be used in a wide variety of circumstances. First, the objective might be to examine the relationships between the abundance of different species of soil bacteria (Y variables) in a number of soil samples and a variety of determining environmental factors such as temperature, moisture, pH etc. (X variables). In this example, it is clear which variables constitute the Y set and which the X set. In some circumstances, however, variables cannot be identified as dependent or independent and both sets of variables are simply labelled as the 'left or first set' and 'right or second set'. For example, the relationships between the DNA profiles of two sets of strains of bacteria might be examined to determine whether they comprised one or two distinct species. This StatNote describes the use of CVA in the analysis of the correlation between the pathological changes in two areas of the brain in the prion disease Creutzfeldt-Jakob disease (CJD).

Scenario

Background

CJD is caused by unusual proteinaceous infectious agents called 'prions'. Prions are protein particles, lacking DNA, and made up of 'prion protein' together with attached carbohydrate chains. Characteristic of the brain pathology caused by prions are first, the development of vacuolation within the brain resulting from the death of neurons and second, the deposition of prions in the form of distinct deposits or 'plaques'. Degeneration of an area of brain called the cerebellum is a particular feature of CJD and may be a factor in the development of several of the clinical symptoms of the disease including myoclonus, ataxia, dysarthria, and nystagmus.

The cerebellum has a layered structure comprising the molecular layer (ML), Purkinje cells (PC), and the granule cell layer (GL) (Figure 1). Atrophy of the GL, vacuolation of the ML, and gliosis (proliferation of glial cells) of white matter have all been reported in CJD (Schulz-Schaeffer *et al.*, 1996; Kirk & Ang, 1994; Costa, Brucher & Laterre, 1998). In addition, prion deposits, in the form of diffuse and florid plaques, occur in the cerebellum (Schulz-Schaeffer *et al.*, 1996; Muramoto *et al.*, 1992). Hence, an investigator wished to investigate whether there were correlations between the densities of pathological changes that develop within the ML and GL in the variant form of CJD (vCJD) (Armstrong *et al.*, 2009), in which order the laminae were likely to have been affected by the disease, and therefore, how prions may have spread into the cerebellum (Armstrong & Cairns, 2003; Armstrong *et al.*, 2009).

Methodology

A block of the right cerebellar cortex was taken from each of 15 vCJD cases at the level of the superior cerebellar peduncle. Tissue was fixed in 10% phosphate buffered formal-saline and embedded in paraffin wax. For quantitative analysis, sequential coronal 7μm sections were then immunolabelled using the monoclonal antibody 12F10 (dilution 1:250) which binds to a region of human PrP downstream of the neurotoxic domain adjacent to helix region 2: residues 142 to 160 (Krasemann *et al.*, 1996) (kindly provided by Professor G. Hunsmann, The German Primate Centre, Göttingen, Germany). Immunoreactivity was enhanced by formic acid (98% for 50 minutes) and autoclaving (121°C for 10 minutes) pretreatment (Hashimoto, Mannen & Nukina, 1992). Sections were treated with Dako Biotinylated Rabbit anti-Mouse (RAM) (dilution 1:100) and Dako ABComplex HRP kit for 45 minutes (Amersham, UK). Diaminobenzidine tetrahydrochloride was used as the chromogen. Immunolabelled sections were also stained with haematoxylin for one minute.

The densities of the vacuoles and diffuse and florid prion plaques were measured along a randomly selected folium of

Figure 1. *Pathology in the cerebellar cortex in a case of variant Creutzfeldt-Jakob disease (vCJD) showing florid prion deposits (FP) in the granule cell layer (GL), diffuse prion deposits (DP) in the molecular layer, and loss of Purkinje cells (PC) (Antibody 12F10), magnification bar = 30μm*

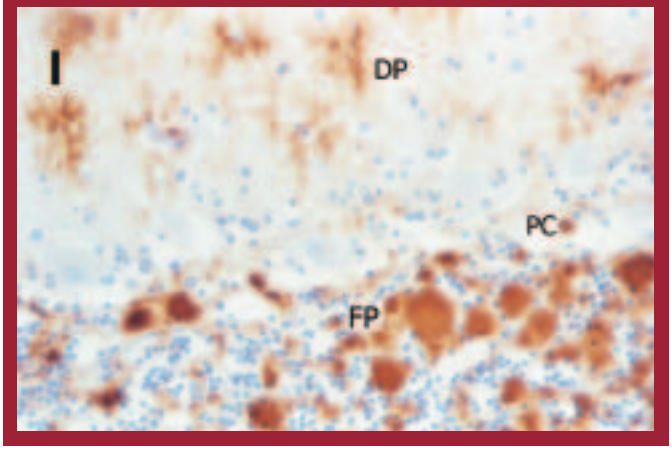


Table 1. Densities (per 50 x 250μm field) of the vacuoles and prion protein deposits (Vac. = Vacuolation, DP = Diffuse plaques, FP = Florid plaques), and surviving Purkinje cells (PC) in the cerebellar cortex in each of the 15 cases of variant Creutzfeldt-Jakob disease (vCJD)

Left set of variables — Molecular layer (ML)					**Right set of variables** — Granule cell layer (GL)		
Case	Vac.	DP	FP	PC	Vac.	DP	FP
A	4.41	4.98	0.04	0.22	15.05	8.66	4.74
B	7.00	3.92	0.12	0.31	34.92	10.75	3.05
C	9.45	5.93	0.49	0.17	31.27	13.68	3.34
D	7.26	4.93	0.30	0.14	36.99	11.94	3.81
E	10.23	4.88	0.78	0.18	30.70	10.31	1.80
F	3.26	5.17	0.25	0.30	14.64	12.11	3.14
G	4.57	2.33	0.32	0.38	44.83	18.70	2.05
H	4.30	4.01	0.19	0.41	31.40	18.33	2.78
I	7.13	0.05	0	0.39	60.30	0.11	0.15
J	2.78	2.43	0.14	0.17	35.25	8.47	2.12
K	3.19	2.79	0.59	0.27	36.70	21.13	3.01
L	4.29	2.84	0.89	0.28	43.51	2.71	2.56
M	6.67	0.95	0.20	0.20	48.98	6.84	1.12
N	4.98	5.59	0.42	0.15	31.43	10.42	5.06
O	9.91	1.90	0.31	0.39	56.98	8.23	1.90

the cerebellum from each vCJD case. Within each folium, a strip of cerebellar cortex 3,200 to 4,800μm in length, starting at a randomly determined position, was studied using between 64 and 96, 50 x 250μm sample fields arranged contiguously and parallel to the surface of the folium. First, the sample field was positioned with the shorter dimension aligned along the edge of the GL at the base of the Purkinje cells to quantify the density of Purkinje cells and the pathology of the inner region of the ML (Armstrong & Cairns, 2003). In each of these fields, the number of surviving Purkinje cells, distinct vacuoles greater than 5μm in diameter, and discrete prion plaques were counted. The florid plaques consist of a condensed core of prions surrounded by a peripheral ring of small vacuoles, while the diffuse plaques are more irregular shaped and lightly stained (Figure 1). Second, at the same position, the field was moved to sample the GL with the short edge of the field aligned with the edge of the granule cells. Within this layer, the number of vacuoles and the florid and diffuse prion deposits were counted in each sample field.

Data

The data comprise the densities of the various pathological features and PC in the ML and GL and are shown in Table 1. In this example, there are no clear dependent and independent variables, and hence the two sets of variables are simply referred to as the 'left set' comprising the ML (four variables: vacuoles, diffuse deposits, florid deposits, Purkinje cells) and 'right set' comprising the GL (three variables: vacuoles, diffuse deposits, florid deposits).

How is the analysis carried out?

The first step of the analysis is to examine the distribution of each variable, together with its mean and standard deviation (SD) (or median and quartile range) to provide a check against non-normality, as CVA is a parametric analysis. There was no evidence of non-normality in the present data.

Several CVA statistics are then calculated. CVA calculates 'canonical roots' which are axes of correlation of decreasing statistical significance. Hence, the first root expresses the greatest degree of correlation between the left and right set of variables and subsequent roots decreasing amounts of correlation. First, canonical 'R' relates to the first and most significant canonical root and is an estimate of the overall degree of correlation between the left and right sets of variables. Hence, R^2 expresses the proportion of the variance accounted for by the canonical variates. Second, the 'variance extracted' indicates the average amount of variance extracted in each set of variables by all the canonical roots. Hence, there are three variables in the right (smaller) set of variables and the three roots account for 100% of the variance because for one of the variables there will always be as many independent canonical variates as there are variables present. For the larger left set of four variables, the variance extracted will always be less than 100%. Third, the 'redundancy' describes the amount of the variance that, given the right set of variables, accounts for the variance of the left set of variables. Similarly, the left set of variables will account for a certain proportion of the variance in the right set. If these proportions are large, e.g., greater than 50% then there is a strong overall relationship between the densities of the pathological features in the ML and GL.

The statistical significance of the canonical roots can now be examined. Canonical 'R' represents only the first root, i.e., the strongest and most significant correlation present. The maximum number of roots that can be extracted is equal to the smallest number of variables in either set of variables, i.e., three in this example. Testing the significance of all roots is carried out using a series of chi-square (χ^2) tests. First, all canonical roots are examined together, i.e., without any roots removed. If this test is highly significant, the first and most significant root is removed and the remaining roots tested. If this test is not significant, the analysis is terminated and it can be concluded that only the first root is statistically significant. If the second test is significant, then the analysis can be extended to the third root. If only the first root is significant, then the correlations between the variables in each list with

Table 2. Average amount of the variance extracted in each set of variables by all canonical roots. As many roots are extracted as the minimum number of variables in either set. The variance of one set (the smaller) will always by 100%

Set of variables	No. of variables	Variance extracted	Total redundancy
Left set	4	82.40	31.26
Right set	3	100	56.195

this canonical root can be calculated and comprise the canonical factor 'loadings'. Hence, those variables in the respective lists that correlate with the first canonical root comprise the most important individual correlations between the variables comprising the two sets.

Interpretation

The results of the CVA are shown in Tables 2 to 4. Canonical 'R' was 0.934 (χ^2 = 26.92, P < 0.01) suggesting the presence of at least one significant canonical root. The average amount of the variance extracted from the variables in each set by all canonical roots is shown in Table 2. Hence, the right set 'explains' 56.195% of the variance in the left set but the left set only explains 31.26% of the variance in the right set. The statistical significance of the canonical roots is shown in Table 3. When all roots are tested (0 removed), χ^2 is highly significant (χ^2 = 26.92, P = 0.007). Removal of this root (root 1 removed) results in a non-significant χ^2 (χ^2 = 8.32, P = 0.22). Hence, removal of successive canonical roots suggests that only the first root is statistically significant (R = 0.934, P < 0.01). Examination of the factor structure (Table 4) suggests that the density of vacuoles in the GL is negatively correlated (R = -0.90) and the density of diffuse prion plaques in the ML is positively correlated with the first root (R = 0.84), i.e., the first canonical root can be explained largely by the correlation between the vacuoles in the GL and the diffuse prion plaques in the ML.

Hence, in the cerebellum of those cases with a significant level of vacuolation in the GL, there are fewer diffuse prion deposits in the ML and *vice versa*. Furthermore, density of vacuoles in the GL was negatively correlated with duration of the disease in different patients, which may reflect the loss of vacuoles as the disease develops. This result together with the CVA suggests that vacuolation may be an early feature of the pathology of the GL, and that diffuse prion deposits are a later development in the ML. Furthermore, the pathology may have spread into the cerebellum via anatomical pathways that initially affect the GL, the pathology then spreading to affect the ML.

Conclusions

CVA is a method of examining the pattern of correlations between two sets of variables. CVA calculates 'canonical roots' which are axes of correlation of decreasing statistical significance. Hence, the first root expresses the greatest degree of correlation between the variables and subsequent roots decreasing amounts of correlation. Canonical 'R' relates to the first and most significant canonical root and is an estimate of the overall degree of correlation between the two sets of variables. Factor loadings of each variable onto the significant canonical roots enables a more detailed analysis of the pattern of correlation between the two sets of variables to be carried out.

Table 3. Statistical significance of the canonical roots. Only the first root is statistically significant in the present example

Root removed	R	R^2	χ^2	DF	P
0	0.934	0.873	26.92	12	0.007
1	0.775	0.60	8.32	6	0.22
2	0.072	0.005	0.047	2	0.976

'R' = Canonical R, DF = Degrees of freedom, P = Probability

Table 4. Correlations between the individual variables and the canonical roots. Only the first root is significant and that is explained by the correlations between the vacuolation in the GL and the diffuse prion deposits in the ML

Region	Pathology	1	2	3
Granule cell layer (GL)	Vacuolation	-0.90*	-0.43	-0.07
	Diffuse prion deposits	0.54	0.19	-0.82
	Florid prion deposits	-0.37	-0.88	-0.30
Molecular layer (ML)	Vacuolation	-0.29	0.12	0.65
	Diffuse prion deposits	0.84*	-0.32	0.39
	Florid prion deposits	0.17	0.44	0.81
	Purkinje cells	-0.03	0.74	-0.61

Canonical 'R' = 0.934 (χ^2 = 26.92, P <0.01), only first canonical root was significant

references

- Armstrong, R.A., and Cairns, N.J. (2003). Spatial patterns of the pathological changes in the cerebellar cortex in sporadic Creutzfeldt-Jakob disease (sCJD). *Folia Neuropathol.*, **Vol. 41**, pp183–189.
- Armstrong, R.A., Ironside, J.W., Lantos, P.L., and Cairns, N.J. (2009). A quantitative study of the pathological changes in the cerebellum in 15 cases of variant Creutzfeldt-Jakob disease (vCJD). *Neuropathol. Appl. Neurobiol.*, **Vol. 35**, pp36–45.
- Costa, C.M.D., Brucher, J.M., and Laterre, C. (1998). Sporadic Creutzfeldt-Jakob disease: a clinico-neuropathological analysis of nine definite cases. *Arquivos de Neuro-Psiquiatria*, **Vol. 56**, pp356–365.
- Hashimoto, K., Mannen, T., and Nukina, N. (1992). Immunohistochemical study of kuru plaques using antibodies against synthetic prion protein peptides. *Acta Neuropathol.*, **Vol. 83**, pp613–617.
- Hilton, A., and Armstrong, R.A. (2008). StatNote 14: The correlation of two variables (Pearson's 'r'). *Microbiologist*, **Vol. 9**, No. 3, pp34–36.
- Hilton, A., and Armstrong, R.A. (2011a). StatNote 24: Multiple linear regression. *Microbiologist*, **Vol. 12**, No. 1, pp40–43.
- Hilton, A., and Armstrong, R.A. (2011b). StatNote 27: Principal components analysis (PCA). *Microbiologist*, **Vol. 12**, No. 4, pp37–40.
- Kirk, A., and Ang, L.C. (1994). Unilateral Creutzfeldt-Jakob disease presenting as rapidly progressive aphasia. *Can. J. Neurol. Sci.*, **Vol. 21**, pp350–352.
- Krasemann, S., Groschup, M.H., Harmeyer, S., Hunsmann, G., and Bodemer, W. (1996). Generation of monoclonal antibodies against human prion proteins in PrPO/O mice. *Mole. Med.*, **Vol. 2**, pp725–734.
- Muramoto, T., Kitamoto, T., Koga, H., and Tateishi, J. (1992). The coexistence of Alzheimer's disease and Creutzfeldt-Jakob disease in a patient with dementia of long duration. *Acta Neuropathol.*, **Vol. 84**, pp686–689.
- Schulz-Schaeffer, W.J., Giese, A., Windl, O., and Kretzschmar, H.A. (1996). Polymorphism at codon 129 of the prion protein gene determines cerebellar pathology in Creutzfeldt-Jakob disease. *Clin. Neuropath.*, **Vol. 15**, pp353–357.

Dr Anthony Hilton[1] and Dr Richard Armstrong[2]
[1]Biology & Biomedical Sciences and [2]Vision Sciences, Aston University, Birmingham, UK

Enhance your career prospects; learn to teach

In this PECS column **Emmanuel** and **Amara** discuss their experience of the Postgraduate Certificate for Teaching in Higher Education (PGCTHE). How the course was structured, what they learnt from it and what prompted the decision to embark on the course in the first place

In the loop pecs

News from the S*f*AM Postgraduate and Early Career Scientist Committee

"Hooray, I have completed the first part of the PGCTHE course. I have now embarked on the second module, a wise choice? Well, ask me again this time next year!" Emmanuel.

At some point during your PhD, you will have to ask yourself the question, 'what next?' For those considering a career in academia, obtaining a teaching qualification can improve your chances of finding a job in higher education (HE) after you complete your degree. The PGCTHE qualification was created to better equip both new lecturers and non-academic staff, affiliated with teaching and learning activities, with the tools needed to provide students with an environment that facilitates learning. Attending this course enables participants to gain a better understanding of theories and frameworks that underpin teaching and learning in HE including different learning styles used by students.

I (Amara) decided to start this course during my PhD to equip me with the skills I needed to carry out my teaching and demonstrating responsibilities effectively. Most HE institutions have made the completion of postgraduate teaching qualifications compulsory during the probationary period of lectureships. Postdoctoral researchers and PhD students are also encouraged to undertake the course and support is usually provided to enable them to successfully meet the required learning outcomes.

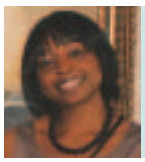
PhD students and early career scientists undertaking this course should expect to undergo certain adjustments, as the language and structure used is very different from what is common place and expected in science. Anyone who has embarked on the PGCTHE course would have experienced the emphasis given to critical reflection and this ultimately means some deconstruction of writing style from third person to first person language using words such as 'I', 'feel', 'believe', 'think' etc. That does take some getting used to! Depending on the institution, the course is broken down into modules which are studied on a part-time basis.

On a personal note, although I (Emmanuel) felt confident in leading teaching and learning activities, I learnt there were other important factors involved in facilitating lectures such as preparing lecture plans and providing formative/summative feedback. In addition to this, I was also able to critically analyse how teaching methods can create an environment that can enhance or limit the learning strategies of the students in teaching sessions.

During the course I had to complete two main assessments. Firstly, during my teaching and assessment activities I had to develop a detailed and structured portfolio. This had to demonstrate that specific learning objectives had been achieved and obtained through teaching and assessment activities, mentoring, feedback and the university quality assurance processes. The portfolio was supported by a critical reflective analysis of the process of teaching and learning based on individual experience. The second assessment was for an enquiry based project focused on any area of the learning and teaching process that could serve as a means of enhancing or developing the student learning experience.

Successful completion not only provides the PGCTHE qualification but participants also become eligible to apply for professional recognition from the Higher Education Authority (HEA) either as an Associate Fellow or Fellow. A word of warning though, if you are considering undertaking this qualification — it is not an easy option. The PGCTHE is a postgraduate qualification and seeking to obtain it will place a considerable demand on your time and other resources, therefore embarking on it during your PhD should only be done after serious consideration and discussion with your supervisors.

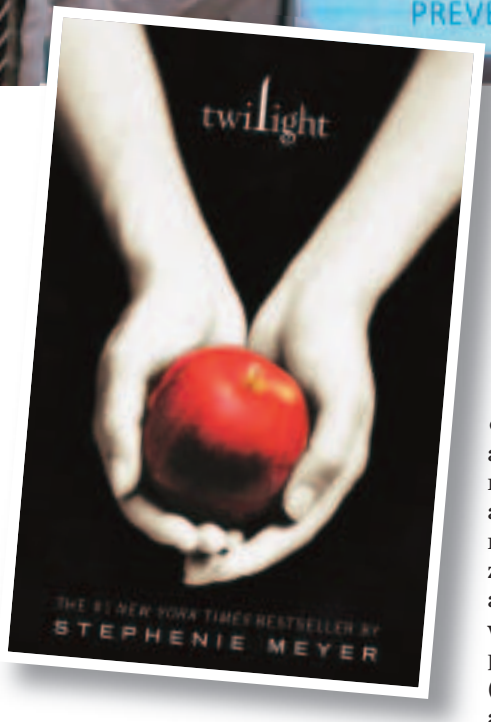
Nonetheless we would definitely recommend this course to any PhD students who have an interest in teaching, well, at least the first module in any case! The programme will serve to ensure that as a lecturer, you are better equipped to deal with the changing demands of working in HE, ensure continuous development of student learning, as well as making the journey into academia a pleasant one.



Amara Anyogu
PECS Secretary

Emmanuel Adukwu
PECS Chairman

Public Engagement Grant: **Monsters, Maths...and Microbiology**



As a microbiologist, I can see no reason why the public should not be as enchanted with my subject as I am. But, to encourage engagement, perhaps scientists should be using activities that are not obviously relevant: to engineer 'science by stealth' into the public domain.

So the Monsters, Maths and Microbiology group was formed at Manchester Metropolitan University (MMU). I had previously set up the Bad Bugs Book Club (with several previous meetings supported by S*f*AM), and had managed — successfully — to use the *Twilight* vampire novel by Stephenie Meyer to encourage discussion on the transmission of infectious disease at the 2010 Manchester Children's Book Festival. As Director of the Science and Engineering Graduate School, I met Matt Crossley, a new PhD student in the School of Computing, Maths and Digital Technology, during his induction. He was working on 'Sim-Zombie', a programme which could theoretically model a zombie epidemic, and we decided to develop our interest in the undead together. Joined by Naomi Jacobs, Manager of the MMU EPSRC Bridging the Gap project 'NanoinfoBio' and Charlotte Jones, undergraduate biology project student, we planned a range of public engagement activities to bring monsters, maths and microbiology together, harmoniously and with educational aims.

Our first task was to differentiate between our monsters of choice — vampires, zombies and werewolves — in terms of the parameters affecting outbreaks. Obvious differences included activity (vampires are only active at night, zombies are active all the time, and werewolves are active once a month) and speed (the traditional zombie is rather slow moving, vampires and werewolves somewhat faster — when active). Other aspects such as prevention (garlic anyone?), treatment (irreversible and generally gory) were also explored. Eventually we created an 'activity mat', which was provided to participants along with a brief scenario. They were then asked to identify the different parameters we required and write the information on the mat. The

data could then be taken from the mat and entered into the 'Sim-Zombie' programme, which presented the spread of the outbreak via 2,000 individuals (dots) converting from green to red on the screen over time (this took a considerable time for werewolves!). There was no correct or incorrect answer, but it was immediately apparent that different 'diseases' spread at different rates.

We trialled the activity twice within the university, the first time in the Faculty of Science and Engineering, the second time across the institution, with all staff and students being invited to participate. It was such fun getting people interested in monsters, maths or microbiology together — I am sure everyone learnt a lot. I especially enjoyed the contributions from our Professor of Gothic Literature, and an academic expert in the horror film genre! I am pretty sure they picked up some useful microbiology too.

Now that we had an activity and a lot of ideas, we needed some funding. So, many, many thanks to S*f*AM for supporting this venture! We developed an ambitious series of events across September and October of last year, intending to engage with a range of different audiences.

In September, for our 'trailblazer' events, the Bad Bugs Book Club linked up with the MMU 'trauma' screenings group, which show movies throughout the year, and accompany the screenings with discussion. We picked Richard Matheson's *I am Legend* (1954) to read, and embarked on a movie marathon of three movies based on the novel, screened on three consecutive nights. We were joined by the Manchester Science Fiction Book Club, and the Manchester Graphic Novel Club, and held discussions on the first and final evening after the screenings. Chronologically, we watched *The Last Man on Earth*, starring Vincent Price (1964); *The Omega Man* (1971), starring Charlton Heston, and *I am Legend* (2007), starring Will Smith. The book is short, but surprisingly scientific, as the hero tries to identify the cause and nature of the infectious agent. There is plenty of microbiology to discuss, and it is also interesting to see how the different films reflect the paranoia (and fashions!) of their time. Notes from the meeting and a reading guide are posted on our website (www.hsri.mmu.ac.uk/microbiology/education_and_communication/bad_bugs_book_club.asp).

The Manchester Science Festival extends across the school half-term in October, and attracts significant numbers of participants. The Monsters, Maths and Microbiology group's 'Science of the Undead' theme was highlighted throughout the festival by the organizers. We started with a book club meeting, reading *World War Z* by Max Brooks. We attracted an interesting range of readers, including members of the Greater Manchester Skeptics — all with a fascination for zombies. Soon to be a movie starring Brad Pitt, the book narrates the interviews carried out by a journalist with survivors of a global zombie plague. The individual stories, when put together, provide a really good epidemiological study, so there is plenty of microbiology to be gleaned (see the meeting report and reading guide on the website). The following day we utilized the skills of Dr Austen from the Zombie Institute of Theoretical Studies (ZITS!) based at the University of Glasgow. He has perfected a hugely entertaining family-friendly public lecture (Wellcome Trust supported) where he investigates the science underpinning the nature of zombies, and suggests some possible physiological rationale, and aetiological agents. That evening, we hosted a sell-out pub quiz, where participants worked on the activity mat prior to being tested on their knowledge of…yes, monsters, maths and microbes (with movie rounds and a microbiology picture quiz that even included Cheryl Cole)!

Overall, almost 300 people came to the different events. Feedback was always really positive – particularly for the zombie lecture (despite one adult fainting at the sight of blood…!!). We were able to do more in-depth evaluation for the pub quiz, since we retained the activity sheets and the quiz responses as well as evaluation sheets. On a 1 to 5 scale, enjoyment was rated 5 virtually across the board. In terms of 'did you learn any new science?', the activities were rated 4. We found this interesting, because the entire event was based on science, but since we had not hammered home that fact, perceptions were perhaps skewed…was this truly 'science by stealth'?

These activities will be developed further. We intend to adapt the activity mat for the 2012 Manchester Children's Book Festival, accompanied by a mini-Bad Bugs Book Club meeting. We will also make the 'Sim-Zombie' resource available online, and develop some simulations for outbreaks caused by real microorganisms.

Thanks again to S*f*AM for helping our ideas to materialize. I think we have developed some really novel activities, with plenty of potential for the future, as we infect more of the public with our passion for microbiology, and watch it spread!

Joanna Verran

W H Pierce Prize report

The human gut mobile metagenome

Dr Brian Jones was the 2011 Winner of the W H Pierce Prize. In this article he outlines his research interests. If you know a young microbiologist (under the age of 40) who has made a substantial contribution to the science of applied microbiology you could nominate them for this year's award. For further information see the box at the end of this article or visit the S*f*AM website at: www.sfam.org.uk/en/grants--awards/w-h-pierce-prize.cfm

The human intestinal tract is home to a dense population of microorganisms which form a complex microbial ecosystem that interacts extensively with the human host (1-6) (Table 1). Collectively these microbes are referred to as the gut microbiota, and owing to a long co-evolutionary relationship with the human host, this community undertakes a wealth of functions important to our health and well-being (1-6). However, these microbes also play host to their own 'hitch-hikers' in the form of mobile genetic elements (MGEs) such as plasmids, transposons, integrons and bacteriophages. Collectively the pool of MGEs associated with a microbial community may be referred to as its mobile metagenome (7-10), and there is currently increasing interest in the role this flexible gene pool plays in the development of the gut microbiota, as well as its interaction with the human host.

MGEs promote horizontal gene transfer (HGT) between bacterial species, facilitating the formation of new functional pathways and dissemination of adaptive traits (8-10). There is already evidence for a large human-associated network of gene exchange in the human microbiome as a whole, with the human gut indicated as possessing one of the highest rates of transfer of all body sites analysed (11). Furthermore, MGEs comprising the mobile metagenome appear to reflect some aspects of host-microbe co-evolution in this community (12) (Table 2). As such, functions encoded by the gut mobile metagenome are likely to be shaped according to key environmental stresses, and host-microbe interactions important to life in the human gastrointestinal (GI) tract (8-12).

In keeping with these hypotheses are the observations that some MGEs appear to be enriched or potentially unique to this community, and encode functions that are prevalent within the human gut microbiota as a whole (Table 2). Particular examples of such MGEs come from recent studies of plasmids resident in this ecosystem (7-9, 26). Sequences with high homology to several of these plasmids could be detected in the gut microbiomes of geographically isolated individuals distributed across the globe (America, Europe, and Japan) (8). This indicates that certain plasmids or plasmid families exhibit a distinct association with the human gut microbiota, and suggests a long-term relationship with human gut bacteria (Figure 1) (8, 9). Analysis of the functions encoded by these plasmids further supported this hypothesis and revealed that several of these functions were more prevalent in the human gut microbiome, compared with other microbial ecosystems examined (Figure 1) (8). These include activities with the potential to influence many facets of community development (including interaction with the human host) (8, 9), and confirmed that MGEs comprising the mobile metagenome may encode functions prevalent in the community as a whole (8, 9). Similar observations have also been made for other MGEs including conjugative transposons and bacteriophages (Table 2).

In essence these studies emphasize the novelty represented in the mobile metagenomes of microbial communities, such as the human gut microbiota, as well as the significant amount of 'biological dark matter' that is likely to be comprised of MGEs in this

Dr Brian Jones receiving the W H Pierce Prize from Richard Marsh of Oxoid

Table 1. Features of the human gut microbiota and impact on human health

Feature	Summary
Population density	In adults, levels of microbes increase with progression along the human GI tract. The stomach and small intestine are relatively sparsely populated (~10^6cells/ml luminal contents), with the distal colon harbouring the greatest concentration of microbes at 10^{13} - 10^{14} cells (1; reviewed in references 5 and 6).
Population structure and diversity	Comprised predominantly of bacteria, with methanogenic archaea forming major components in some individuals. Viruses, particularly bacteriophages, are also thought to be prominent members of this community. Eukaryotic microorganisms are present though less well characterized and thought to constitute relatively minor components. **Bacteria:** Low diversity at higher taxonomic levels with only 8 of the 55 known bacterial phylogenetic divisions well represented. Species derived from the Bacteroidetes and Firmicutes co-dominate with Actinobacteria and Proteobacteria forming comparably minor but significant fractions. Fusobacteria, Spirochaetes, Verrucomicrobi, and the candidate division VadinBE97 comprise the vast majority of the remainder. However, considerable diversity at the strain and species level is apparent with the adult gut microbiota estimated to contain ~150 to 800 distinct species. (References 2-5, 27). **Archaea:** Represented by only two species in the human gut microbiota: *Methanobrevibacter smithii* and *Methanosphera stadmanae*. However, in some individuals archaeal species, particularly *M. smithii* [L1], can account for a significant proportion of the total population (up to 10%). (References 2-5). **Viruses:** Initial metagenomic surveys indicated high viral diversity in this community, predominantly derived from bacteriophages, and detected ~1,200 viral genotypes (28). More recent surveys indicate much person to person variation and a potential dominance of a low number of high abundance virotypes (14).
Cultivability	Estimated that ~70 to 80% of bacterial species present in this community remain uncultured (5, 6, 27).
Stability and Inter-individual variation	Gut microbiota of healthy adults is generally considered both functionally and phylogenetically stable over time. However, considerable inter-individual variation is apparent, with each person believed to harbour their own distinct gut microbial community, both in terms of species present and the relative abundance of different bacteria. (2-4, 27, 29).
Gene-content	Due to the high gene density of prokaryotic genomes, the human gut microbiome is estimated to encompass a significantly greater gene complement than the human genome. Recent large scale metagenomic surveys identified 3.3 million unique genes from the gut microbiomes of 124 individuals, ~150 times larger than the gene set encoded by the human genome (3).

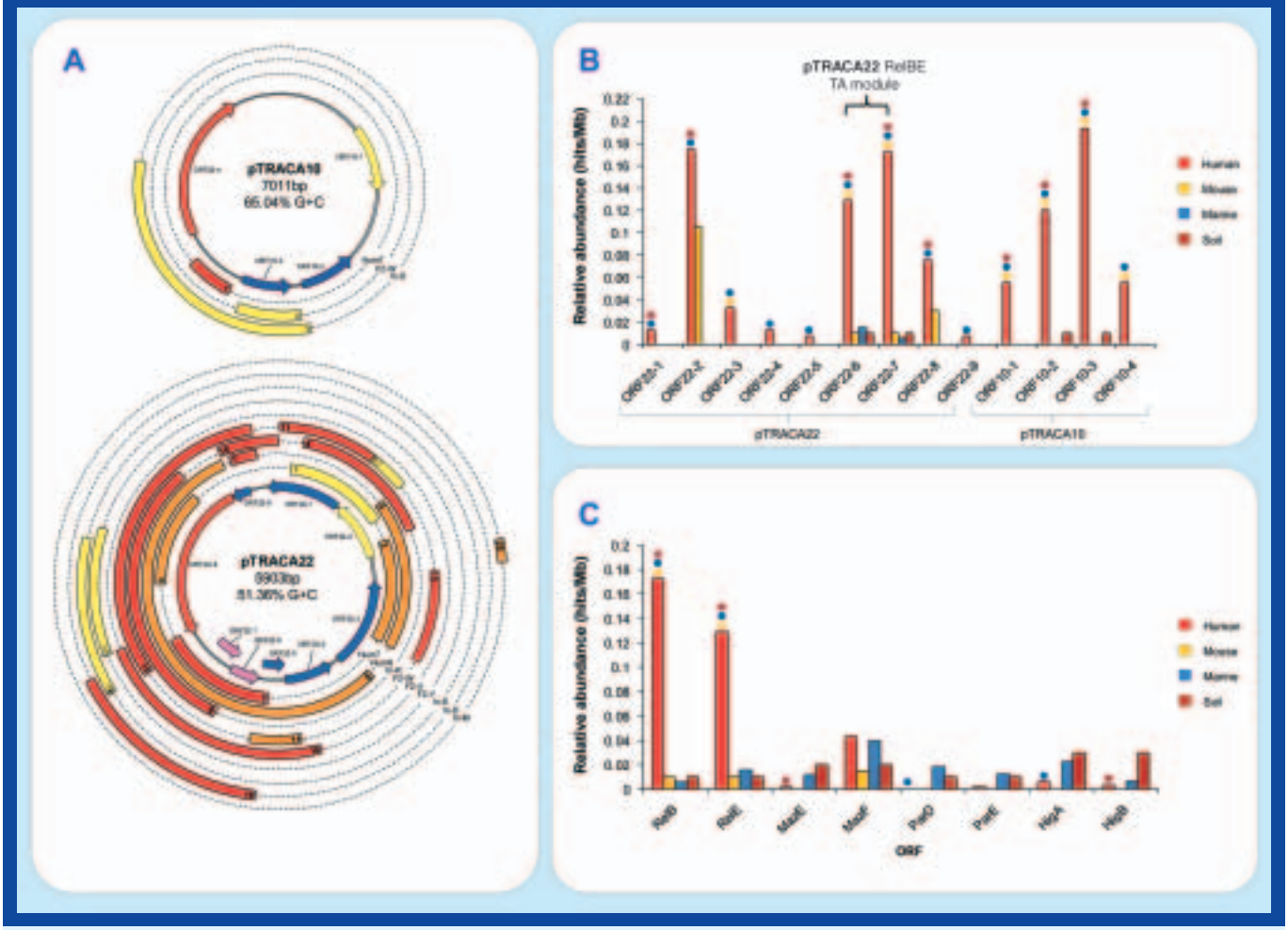
ecosystem. This naturally leads to questions regarding the activities encoded by the mobile metagenome, and how attributes of this flexible gene pool are involved in community development and function. A particular aspect of the gut microbiota that has been closely linked with HGT is the relative functional stability of this community over time in healthy adults (5, 6). Although this may be achieved through recruitment of member species with overlapping metabolic and functional profiles, HGT in the gut microbiota has been implicated as an important factor contributing to the development of a functionally stable community (15-18). In this case MGEs are thought to aid the dissemination of genes encoding core activities to a wide range of species in this ecosystem. This is thought to generate functional redundancy among community members, which guards against loss of key activities, and ensures continuity of important community functions (6, 9, 15).

A key example of functional stability, achieved through HGT generated redundancy in this community, comes from studies of genes involved in carbohydrate utilization, a major activity of gut microbes which salvages energy from the host diet (15) (Table 2). It has been estimated that up to 10% of our daily calories are derived from microbial fermentation of plant polysaccharides resistant to host digestive mechanisms (19), which recovers energy from the diet that is otherwise inaccessible to the human host. The ability of gut microbes to ferment such carbohydrates and release energy to the host in the form of short chain fatty acids, is distributed among a diverse array of species spanning the main bacterial divisions of the human gut microbiota (Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria) (3, 5, 6, 13, 15, 16). While it is likely that some of this redundancy is the result of early events in the development of the gut microbiota, reflecting the recruitment of species capable of colonizing and utilizing available nutrients without harming the host, recent studies have also highlighted the role of HGT in the convergence and expansion of the required gene sets (15).

Alternatively, studies of the Japanese gut microbiome have demonstrated how MGEs can facilitate the acquisition of new abilities by the gut microbiota, which can benefit both host and microbe (13). Hehemann and co-workers recently demonstrated the acquisition of porphyranse and agarase degrading ability by the gut microbiomes of Japanese individuals (13). This was linked to the horizontal transfer of these genes from marine bacteria naturally colonizing dietary seaweeds (which are consumed without cooking), to members of the Japanese gut microbiota (13). Acquisition of these genes by gut commensals should permit the Japanese gut microbiota to utilize this dietary energy source, unlocking additional calories from the diet to the benefit of both host and microbe (13) (Table 2).

In light of the potential for functional upgrades to this community that may be accessed through the mobile metagenome, it has also been proposed that a major role of this mobile gene pool may be as a conduit to the vast reservoir of genetic information extant in the wider prokaryotic world (9). Commensal and symbiotic microbes comprising the human gut microbiota are already becoming widely accepted as

***Figure 1**. Comparative metagenomic analysis of plasmids resident in the human gut microbiome (After Jones et al. 2010, BMC Genomics 11:46)*



A) The complete nucleotide sequence of plasmids was used to search 15 human gut metagenomes, the combined gut metagenome of lean and obese mice, Sargasso Sea, and soil metagenomes. The central ring shows the physical plasmid map with encoded ORFs. Concentric rings represent the nine human gut metagenomes in which homologous sequences were identified, and bars indicate regions of homology between sequences retrieved from human gut metagenomes and corresponding regions of the pTRACA10 or pTRACA22 plasmids. Colours of bars indicate the % identity at the nucleotide level for each metagenomic sequence: ■ = 80 to 85% identity, ■ = 85 to 90% identity, ■ = 90 to 96% identity. Only sequences >100bp in length are shown.

B) Relative abundance of pTRACA22 ORFs, expressed as hits/Mb, in the combined human gut metagenomes of 15 individuals compared to the combined murine gut metagenome, Sargasso Sea, and soil metagenomes. The observed differences between human and non-human metagenomes were explored using the χ^2 distribution. Symbols above bars indicate approximate significance of differences between combined human metagenomes and each non-human metagenomes (P = 0.01 or less): ● Significant difference between human and murine metagenomes; ● Significant difference between human and marine metagenomes; ● Significant difference between human and soil metagenomes. ORF22-6 and ORF22-7 comprise the pTRACA22 RelBE toxin anti-toxin (TA) module and are among the most enriched functions encoded by this plasmid.

C) Relative abundance (as hits/Mb) of the pTRACA22 RelBE TA module (ORF22-6 and ORF22-7 in part A and B) in human gut, murine gut and environmental metagenomes, compared to relative abundance of MazEF, ParDE and HigBA TA modules. The observed differences between human and non-human metagenomes were explored using the χ^2 distribution. Symbols above bars indicate approximate significance of differences between combined human metagenomes and each non-human metagenome (P = 0.01 or less), as in Figure 1B.

true components of the human 'superorganism' with the genetic content of our microbial partners often referred to as the second human genome (5, 6, 9, 20). Many researchers now consider complex metazoans such as mammals to be amalgams of both eukaryotic cells and their prokaryotic symbionts, rather than being exclusively eukaryotic (5, 6, 9, 20, 21). This has given rise to new ecological and evolutionary theories, which integrate host-associated communities into the development of the higher organisms they colonize (5, 6, 9, 21, 22). In this context, the mobile metagenome may constitute a key resource in the adaptation of both host and microbe, by providing access to an immense genetic resource through which community function, and fitness of both host and microbe may be augmented (9).

Although the study of the mobile metagenome, and the theories surrounding this concept are of significant interest and importance from a fundamental standpoint alone, there is

Table 2. (After Ogilvie *et al*., 2011, reference 10): Evidence for co-evolution of gut associated MGEs with human host and the role of the gut mobile metagenome in community function, development and host-microbe interaction

MGE type/process	Summary	Study(s)
Conjugative transposons	CTn-1549 like family of elements designated CTnRINT observed to be enriched in the gut microbiomes of Japanese and American individuals examined. In conjunction a high level of recombinases and integrases also observed in gut microbiomes.	Kurokawa *et al*., *DNA Res* 2007; 14: pp169-181.
Plasmids	Plasmids or plasmid families enriched and potentially unique to the human gut microbiome identified, with homologous sequences detected in gut microbiomes of geographically isolated hosts (America, Europe, and Japan). Enrichment of some functions encoded by plasmids also observed. In particular plasmid pTRACA22 was noted as widely distributed and potentially unique to the human gut microbiome, with RelBE type toxin-antitoxin addiction modules (TAMs) enriched in terms of relative abundance in human gut microbiomes compared to other datasets examined. Plasmids infecting gut associated bacteria exhibit the same patterns of habitat-associated gene convergence observed for bacterial chromosomes. *Lactobacilli* commonly harbour large megaplasmids encoding genes proposed to be involved in adaptation to the gut environment. Genes associated with the probiotic or protective effect of some species also appear to be encoded by megaplasmids.	Jones, B.V., *Gut Microbes* 2010; 1: pp415-431. Jones *et al*., *BMC Genomics* 2010; 11: pp46. Zaneveld *et al*., *Nucleic Acids Res* 2010; 38: pp3869-3879. Claesson et al., *Proc Natl Acad Sci USA* 2006; 103: pp6718-6728. Li *et al*., *Appl Environ Microbiol* 2007; 189: pp6128-6139. Corr *et al*., *Proc. Natl. Acad. Sci. USA*. 2007; 104(18): pp7617-7621.
Bacteriophage, Virus like particles	Isolation and characterization of bacteriophages infecting *Bacteroides* spp GB-124, indicated these phages were specific to the human gut, and carriage in the general population is high A large inter-individual variation in gut virome composition has been documented, but viromes have been found to be relatively stable over time within an individual. Functions associated with a wide range of processes in anaerobic gut bacteria found to also be encoded by gut viromes. A dominance of temperate phages observed and a general lack of predator-prey dynamics in host-virus interactions suggested, which is in contrast to other microbial ecosystems.	Ebdon *et al*., *Water Res* 2007; 41: pp3683-3690. Reyes *et al*., *Nature* 2010; 466: pp334-338.
General HGT	Gain of functional capacity in the Japanese gut microbiome attributed to plasmid mediated HGT of genes conferring ability to utilize seaweed glycans, from marine *Bacteroides* spp. to gut commensal *Bacteroides* spp. Habitat associated gene convergence of glycoside hydrolases and glycosyltransferases in gut associated bacteria and archaea largely generated through HGT. Evidence that the human microbiome is connected by a large network of gene exchange with rates of HGT up to 25-fold higher between human associated bacteria than non-human associated isolates.	Hehemann *et al*., *Nature* 2010; 464: pp908-912. Lozupone *et al*., *Proc Natl Acad Sci USA* 2008; 105: pp15076-15081. Smillie *et al*., *Nature* 2011; doi:10.1038/nature10571.

also much potential for translational research and 'bio-prospecting' of this sphere of the human gut microbiome (as well as other microbial communities) (10). As our understanding of the human microbiome in general grows, we will increasingly move towards strategies to manipulate this community for therapeutic or prophylactic purposes. In order to realize these goals, a detailed characterization of many important species comprising the gut microbiome will be required, including their genetic dissection and manipulation. For many species the appropriate molecular genetic systems are yet to be established, and the mobile metagenome may provide the raw genetic material to develop many of these tools (9). In addition, a greater understanding of the forces that govern gene flow in this community will also be required to develop effective methods to limit the appearance and spread of undesirable traits, such as antibiotic resistance (10). In this context it is notable that the human gut microbiome is considered a reservoir for such genes, which may subsequently be acquired by more problematic pathogens and be disseminated to the wider environment.

Furthermore, MGEs typically encode functions advantageous to their bacterial hosts, often permitting them to deal with pervading environmental stresses and maintain a competitive advantage over other microbes. Coupled with the observation that some MGEs in this community encode functions relevant to host-microbe interaction (Table 2), the mobile metagenome may also constitute a reservoir of genes useful in a variety of biotechnological or pharmaceutical applications (10). The development of novel probiotics and bacterial drug delivery systems are areas that would particularly benefit from access to a library of genes that facilitate survival and persistence in the GI tract (10). Studies demonstrating that MGEs can facilitate the transfer of genetic material across kingdom boundaries (23, 24), including transfer from bacteria to mammalian cells (25), add an additional dimension to the study of MGEs resident in host-associated microbial ecosystems, and also has obvious biotechnological potential. Finally, the novelty of many of the MGEs associated with the human gut may in itself lend such elements to biotechnological applications (10). A prime example comes from the use of bacteriophage specific to the human gut as microbial source tracking tools, to monitor water quality and identify sources of contamination (26).

Overall, the high level of novel gene content typical of MGEs, coupled with their predicted high level of diversity, suggests that the mobile metagenome constitutes an immense genetic resource likely to encode many novel activities relevant to development and functioning of the gut microbiota, and with potential biotechnological or pharmaceutical value (10). Despite this, we remain relatively ignorant of the true diversity, abundance and functions encoded by MGEs associated with the gut microbiome, and bacterial ecosystems in general (9, 10). A greater understanding

References

■ 1. Savage, D. C. (1977). Microbial ecology of the gastrointestinal tract. *Ann. Rev. Microbiol.*, **Vol. 31**, pp107–133.

■ 2. Turnbaugh, P. J., Quince, C., Faith, J. J., McHardy, A. C., Yatsunenko, T., Niazi, F., Affourtit, J., Egholm, M., Henrissat, B., Knight, R., and Gordon, J. I. (2010). Organismal, genetic, and transcriptional variation in the deeply sequenced gut microbiomes of identical twins. *Proc. Natl. Acad. Sci. USA*, **Vol. 107**, pp7503–7508.

■ 3. Qin, J., Li, R., Raes, J., Arumugaum, M., Burgdorf, K. S., Manichanh, C., *et al.*, (2010). A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*, **Vol. 464**, pp59–65.

■ 4. Tap, J., Mondot, S., Levenez, F., Pelletier, E., Caron, C., Furet, J.-P., Ugarte, E., Muñoz-Tamayo, R., Paslier, D. L. E., Nalin, R., Dore, J., and Leclerc, M. (2009). Towards the human intestinal microbiota phylogenetic core. *Environmental Microbiology*, **Vol. 11**, pp2574–2584.

■ 5. Bäckhed, F., Ley, R. E., Sonnenburg, J.L., Peterson, D. A., and Gordon, J. I. (2005). Host-bacterial mutualism in the human intestine. *Science*, **Vol. 307**, pp1915–1920.

■ 6. Ley, R. E., Peterson, D. A., and Gordon, J. I. (2006). Ecological and evolutionary forces shaping microbial diversity in the human intestine. *Cell*, **Vol. 124**, pp837–848.

■ 7. Jones, B. V., and Marchesi, J. R. (2007). Transposon-aided capture (TRACA) of plasmids resident in the human gut mobile metagenome. *Nat. Methods*, **Vol. 4**, pp55–61.

■ 8. Jones, B. V., Sun, F., and Marchesi, J. R. (2010). Comparative metagenomic analysis of plasmid encoded functions in the human gut microbiome. *BMC Genomics*, **Vol. 11**, p46.

■ 9. Jones, B. V. (2010). The human gut mobile metagenome: a metazoan perspective. *Gut Microbes*, **Vol. 1**, pp415–431.

■ 10. Ogilvie, L. A., Firouzmand, S., and Jones, B. V. (2011). Evolutionary, ecological, and biotechnological perspectives on plasmids resident in the human gut mobile metagenome. *Bioengineered Bugs (In Press)*.

■ 11. Smillie, C. S., Smith, M. B., Friedman, J., Cordero, O. X., David, L. A., and Alm, E. J. (2011). Ecology drives a global network of gene exchange connecting the human microbiome. *Nature*, **Vol. 480**, pp241–244.

■ 12. Zaneveld, J. R., Lozupone, C., Gordon, J. I., and Knight, R. (2010). Ribosomal RNA diversity predicts genome diversity in gut bacteria and their relatives. *Nucleic Acids Res.*, **Vol. 38**, pp3869–3879.

■ 13. Hehemann, J.-H., Correc, G., Barbeyron, T., Helbert, W., Czjzek, M., and Michel, G. (2010). Transfer of carbohydrate-active enzymes from marine bacteria to Japanese gut microbiota. *Nature*, **Vol. 464**, pp908–912.

■ 14. Reyes, A., Haynes, M., Hanson, N., Angly, F.E., Heath, A.C., Rohwer, F., and Gordon, J. I. (2010). Viruses in the faecal microbiota of monozygotic twins and their mothers. *Nature*, **Vol. 466**, pp334–338.

■ 15. Luzopone, C. A., Hamady, M., Cantral, B. L., Coutinho, P. M., Henrissat, B., Gordon, J. I., and Knight, R. (2008). The convergence of carbohydrate active gene repertoires in human gut microbes. *Proc. Natl. Acad. Sci. USA*, **Vol. 105**, pp15076–15081.

■ 16. Xu, J., Mahowals, M. A., Ley, R. E., Lozupone, C. A., Hamady, M., Martens, E. C., *et al.*, (2007). Evolution of symbiotic bacteria in the distal human intestine. *PLoS Biol.*, **Vol. 5**, No. 7, pp1574–1586.

■ 17. Jones, B. V., Begley, M., Hill, C., Gahan, C. G. M., and Marchesi, J. R. (2008). Functional and comparative metagenomic analysis of bile salt hydrolase activity in the human gut microbiome. *Proc. Natl. Acad. Sci. USA*, **Vol. 105**, pp13580–13585.

■ 18. Jones, B. V., and Marchesi, J. R. (2007). Accessing the mobile metagenome of the human gut microbiota. *Mol. Biosyst.*, **Vol. 3**, pp749–758.

■ 19. McNiel, N. I. (1984). The contribution of the large intestine to energy supplies in man. *Am. J. Clin. Nutr.*, **Vol. 39**, pp338–342.

■ 20. Nelson, K. E., Weinstock, G. M., Highlander, S. K., Worley, K. C., *et al.*, (2010). A catalog of reference genomes from the human microbiome. *Science*, **Vol. 328**, pp994–999.

■ 21. Zilber-Rosenberg, I., and Rosenberg, E. (2008). Role of microorganisms in the evolution of animals and plants: the hologenome theory of evolution. *FEMS Microbiol. Rev.*, **Vol. 32**, pp723–735.

■ 22. Dethlefsen, L., McFall-Ngai, M., and Relman, D. A. (2007). An ecological and evolutionary perspective on human-microbe mutualism and disease. *Nature*, **Vol. 449**, pp811–818.

■ 23. Zambryski, P. (1988). Basic processes underlying Agrobacterium-mediated DNA transfer to plant cells. *Annu. Rev. Genet.*, **Vol. 22**, pp1–30.

■ 24. Heinemann, J. A., and Sprague, G. F. Jr. (1989). Bacterial conjugative plasmids mobilize DNA transfer between bacteria and yeast. *Nature*, **Vol. 340**, pp205–209.

■ 25. Waters, V. L. (2001). Conjugation between bacterial and mammalian cells. *Nat. Genet.*, **Vol. 29**, No.4, pp375–376.

■ 26. Ebdon, J., Muniesa, M., and Taylor, H. (2007). The application of a recently isolated strain of *Bacteroides* (GB-124) to identify human sources of faecal pollution in a temperate river catchment. *Water Res.*, **Vol. 41**, pp3683–3690.

■ 27. Eckburg, P. B., Bik, E. M., Bernstein, C. N., Purdom, E., Dethlefsen, L., Sargent, M., Gill, S. R., Nelson, K. E., and Relman, D. A. (2005). Diversity of the human intestinal microbial flora. *Science*, **Vol. 308**, pp1635–1638.

■ 28. Breitbart, M., Hewson, I., Felts, B., Mahaffy, J. M., Nulton, J., Salamon, P., and Rohwer, F. (2003). Metagenomic analyses of an uncultured viral community from human feces. *J. Bacteriol.*, **Vol. 185**, pp6220–6223.

■ 29. Zoetendal, E. G., Akkermans, D. L., and de Vos, W. M. (1998). Temperature gradient gel electrophoresis analysis of 16S rRNA from human faecal samples reveals stable and host-specific communities of active bacteria. *Appl. Environ. Microbiol.*, **Vol. 64**, pp3854–3859.

of the contribution of the mobile metagenome to evolution and function of the human gut microbiome in particular, will be important in the development of strategies to manipulate this community for the benefit of human health, as well as harnessing its full biotechnological potential.

Brian Jones
University of Brighton

Call for nominations for W H Pierce Prize

Do you know a young microbiologist (under 40 years of age) who has made a substantial contribution to microbiology? If so, why not nominate them for this prestigious and substantial award which is now worth £3000.

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

The prize is presented annually at the Summer Conference. Full Members wishing to make a nomination for the 2012 prize should write in confidence to the Honorary General Secretary, Professor Mark Fielder, at the Society Office in Bedford, including a full CV of the nominee and a letter of support.

Please note that application is through nomination by Full Members of *Sf*AM only and that there are no official forms for this award.

Closing date for nominations is Thursday 19 April 2012

corporate news

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

Specific *Salmonella* detection with Lab M's new XLT4 Agar for effective monitoring in the presence of competing organisms

It's often a challenge to identify *Salmonella* species in samples heavily contaminated with competing microbiological flora, so Lab M has added new Xylose Lysine Tergitol-4 (XLT4) Agar to its extensive range of products for salmonella isolation and identification.

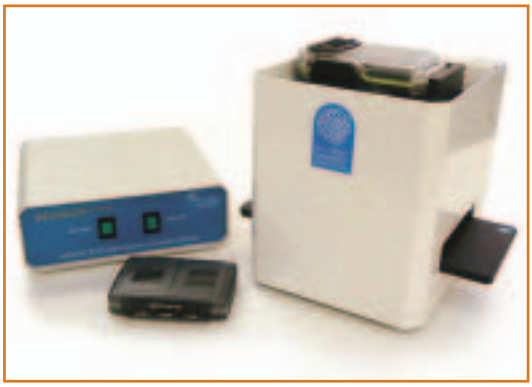
Lab M's new XLT4 is a highly selective and very cost-effective medium for the specific detection and enhanced recovery of non-typhi *Salmonella* spp. from environmental, food and clinical samples. It enables labs to rapidly determine whether or not these pathogenic organisms are present, for effective monitoring even when faced with difficult materials such as faecally contaminated agricultural samples.

XLT4 Agar is part of Lab M's comprehensive and proven range of media for the isolation and culture of salmonellae. Offering a convenient choice of methodologies to fit individual laboratory testing requirements, the Lab M range supports the need to rapidly screen, isolate and identify salmonellae from a variety of sample types.

Lab M is known for the development and manufacture of culture media that meet the rigorous demands of microbiological testing. Through an ongoing programme of product development, the company continues to introduce new formulations, thereby helping users achieve their specific requirements..

further information

Visit: www.labm.com
Tel: +44 (0)161 797 5729
Email: info@labm.com



New Whitley Petrifoto System

Don Whitley Scientific has launched a fantastic new accessory for their range of workstations — the Whitley Petrifoto System. The product fits inside a workstation and enables you to take detailed photographs of organisms growing on Petri dishes during incubation. This is ideal when colony development needs capturing throughout the incubation cycle.

The system uses a quality Canon compact digital camera with auto focus, a wide angle zoom lens and a 12.1 megapixel high resolution sensor, all designed to elicit a good quality image from even the most amateur of photographers. The camera can also be used independently of the imaging system, either inside or outside the workstation.

The robust unit is small enough to pass through the airlock on the Whitley A35 Workstation but is large enough to feature an innovative lighting system. The 3D LED light box has underside and side lighting that can be controlled independently to accommodate all agar and colony types. The Petrifoto System comes with an SD memory card and is compatible with Eye-Fi wireless memory cards to allow automatic image transmission to an external PC or MAC.

This product can be retrofitted providing there is a spare cable gland available on the workstation.

further information

Visit: www.dwscientific.co.uk
Tel: + 44 (0)1274 595728
Email: sales@dwscientific.co.uk

Comprehensive bio-imaging service

AHVLA Scientific offers a unique and comprehensive bio-imaging service for research and diagnostic purposes to customers in both the public and animal health sectors. This includes sample preparation, image production and identification as well as training, support and equipment rental options.

The AHVLA bio-imaging unit has state of the art modern equipment that includes Transmission & Scanning Electron Microscopes and Confocal Laser Scanning Microscopes. AHVLA has over 40 years experience in complex bio-imaging and has high level containment facilities for pathogens and extensive diagnostic capabilities across a wide range of microorganisms. Services include:

- cell ultrastructure
- bacteria, virus and fungal examinations
- Negative staining from fresh field isolates
- Non-invasive live cell examination
- X-Ray microanalysis
- Examination of hydrated and dehydrated samples
- Examination of non-biological samples

further information

Visit: www.vlascientific.com
Tel: +44 (0)1932 357641
Email: salesdesk@ahvla.gsi.gov.uk

Leatherhead Food Research

Food microbiology at Leatherhead provides a broad range of microbiological food analyses covering food spoilage and pathogenic micro-organisms for our customers.

We are able to determine the levels of microorganisms in foods, predict their ability to grow/survive in your products and verify their behaviour through real-time analysis. Leatherhead can evaluate and confirm the shelf life of your products, and advise you on the necessary recipe alterations, packaging and process conditions that will help you achieve a safe shelf life or even allow you to extend your product's shelf life.

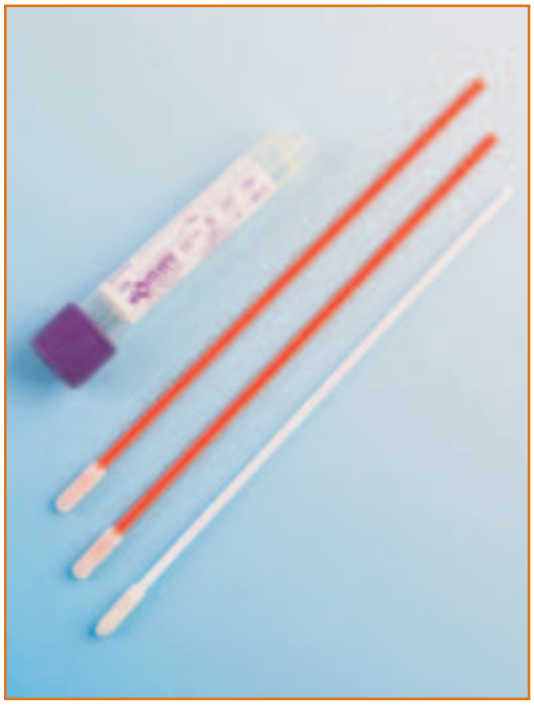
Using our expertise in microbial recovery from complex matrices, we are able to help you validate your heat process and provide you with data on microbial susceptibility to the application of that heat.

If you are looking to reduce the level of heat applied to your products, make energy savings and/or enhance the sensory characteristics of your products, we are able to advise you on the use of alternative preservation technologies that will ensure the safety of your products.

Leatherhead's Food Safety services are supported by expertise in Food Innovation, Sensory and Consumer Science, Nutrition, Global Regulatory Services and Market Intelligence.

further information

Visit: www.leatherheadfood.com
Tel: +44 (0)1372 822298
Email: help@leatherheadfood.com



Liquid Amies medium for automated processing

There are now a number of automated processing platforms for routine microbiology. All of these require a liquid transport medium for processing. Medical Wire's Σ-Transwab® (Sigma Transwab®) has emerged as one of the leading collection devices compatible with all current platforms.

Key to Σ-Transwab® is the liquid Amies medium which can recover and maintain all the organisms in the CLSI M40 panels for aerobes, anaerobes and fastidious organisms. The swabs have a bud of cellular (open cell) flow through polyurethane foam with superb pick up and release of microorganisms from all body sites.

A choice of standard and fine-tip swabs are available, and multi-swab versions are available with two or three swabs, suitable for sampling multiple body sites, for example for MRSA. All swabs have a convenient breakpoint to allow snapping into the transport tubes. In versions with a single standard swab, the swab is "captured" by the cap when it is screwed onto the tube. With double and triple swab versions, one swab has a white shaft which is captured, while the other swabs have red shafts and are not captured. The screw cap is fully compatible with automatic capping and decapping mechanisms.

further information

Visit: www.mwe.co.uk
Tel: +44 (0) 1225 810361
Email: sales@mwe.co.uk

New Sterilin 30mL Universals with quick start cap and improved leak-free performance

A range of new, improved Thermo Scientific Sterilin 30mL Universal Containers with easier handling and improved leak-free performance is now available. The improved containers benefit from a 'QuickStart' cap which is based on a three start thread, requiring fewer turns to open and close.

The containers' new multi-seal design has been independently validated when it was shown to give unrivalled leak-free performance. For ease of use in the laboratory, containers are supplied in eight handy bags of 50 (400 containers to a carton) and to aid traceability the lot number is printed on each container.

"*We are always looking for ways to improve performance of our products and the improvements to the 30mL Universal Containers will make a big difference in labs across all industry sectors from healthcare to university research*", said Rachel Adams, marketing manager, Thermo Scientific Sterilin products. "*Our new cap design is easier to use. Requiring less effort than conventional designs this new cap should benefit those who handle large numbers of containers. The improved leak-free performance also helps protect valuable and potentially hazardous samples — another great benefit for laboratories of all types.*"

Many variants of the new containers are available including unlabelled, labelled, irradiated and non-pyrogenic.

further information

Visit: www.sterilin.co.uk
Tel: +44 (0) 844 844 3737
Email: info@sterilin.co.uk

TCS Biosciences

Here at TCS Biosciences we have over 40 years experience in supplying the needs of microbiologists worldwide. As Europe's leading supplier of donor animal blood and sera for inclusion in plated media, we have built a reputation for quality, versatility and outstanding customer service.

Selectrol® discs are first generation microorganisms that are manufactured under licence from the Health Protection Agency Culture Collections (HPACC). Selectrol® strains are fully traceable and guaranteed to be first generation derivatives of the original NCTC or NCPF strain. Presented as a water soluble freeze-dried disc, Selectrol® is versatile in its application for use with

either plated or liquid media.

Our in-house Selectrol® quality control testing laboratory is UKAS accredited and our growing range encompasses nearly 70 strains, many of which have been added as a direct result of customer requests.

As Selectrol® organisms are guaranteed to be first generation microorganisms, they are ideal for use in accredited laboratories. Selectrol® batches are tested for a range of identification and characterization attributes and certificates of analysis for each batch can be accessed via our website: www.tcsbiosciences.co.uk.

further information

Visit: www.tcsbiosciences.co.uk
Tel: +44 (0)1296 714222
Email: sales@tcsgroup.co.uk

Cherwell Laboratories — the complete validation solution

Cherwell Laboratories have been manufacturing prepared microbiological media under the Redipor name since the early 1980's and have built a strong reputation within the pharmaceutical industry for high quality products and a flexible, effcient service. The extensive Redipor range includes petri dishes, contact plates, gamma irradiated media, injection vials, broth in bags and ampoules. They also specialise in supplying bespoke prepared media solutions and low volume requirements.

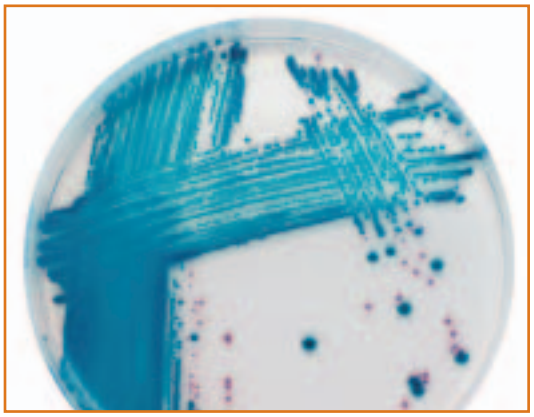
As the newly appointed UK distributor for Raven Laboratories and Apex Laboratories, Cherwell now also supply a comprehensive range of biological indicators, chemical integrators and process indicators for industrial and healthcare applications.

The biological indicator range, from Cherwell Laboratoriesincludes spore strips, spore suspensions, self-contained biological indicators, industrial use biological indicators and chemical indicators. The range is ideal for developing, monitoring and validating a range of sterilisation processes including steam, dry heat, hydrogen peroxide vapour, ethylene oxide and gamma irradiation.

The addition of biological indicators to the product range, which also includes data loggers and microbial air samplers means Cherwell can now offer a fully integrated range of high quality products for environmental monitoring and validation of sterilisation processes.

further information

Visit: www.cherwell-labs.co.uk
Tel: +44 (0)1869 355500
Email: sales@cherwell-labs.co.uk



A unique chromogenic medium for the isolation of both O157 and non-O157 STEC

An increasing and worrisome number of studies have lately shown that, non-O157 Shiga-Toxinproducing *E.coli* (STEC) have been responsible for foodborne poisoning outbreaks. The CDC has also reported warnings about this potential risk:

"60 STEC serotypes have been implicated in diarrheal disease, and several non-O157:H7 serotypes have been implicated as the cause of foodborne outbreaks and HUS in the United States, Europe, and Australia. Studies from Canada, Europe, Argentina, and Australia suggest that non-O157:H7 STEC infections are as prevalent, or more so, than O157:H7 infection."

In many cases, laboratories have limited their search for pathogenic *E.coli* to the common O157 serotype. This is due, among other reasons, to the fact that there were no available selective culture media for non-O157 *E.coli*. CHROMagar STEC is designed to fill this gap: detection, as mauve colonies, of not only the classical STEC O157, but also many other serotypes.

An outbreak of STEC O104:H4 was reported in Europe during 2011, this media was used to screen large numbers of samples and successfully isolate the STEC that would not have been routinely identified. In addition CHROMagar developed a selective supplement for addition to this media rendering it highlyselective for the specific strain causing the outbreak.

CHROMagar manufacture a large range of chromogenic media that have applications in both clinical and industrial microbiology. These media are now available in the UK through BioConnections.

further information

Visit: www.bioconnections.co.uk
Tel: +44 (0)1937 541717
Email: welcome@bcnx.co.uk

Report from the conference: *Advances in microbial and mammalian cell phenotyping; linking phenotype to genotype,* held at the University of Surrey, Guildford, UK.

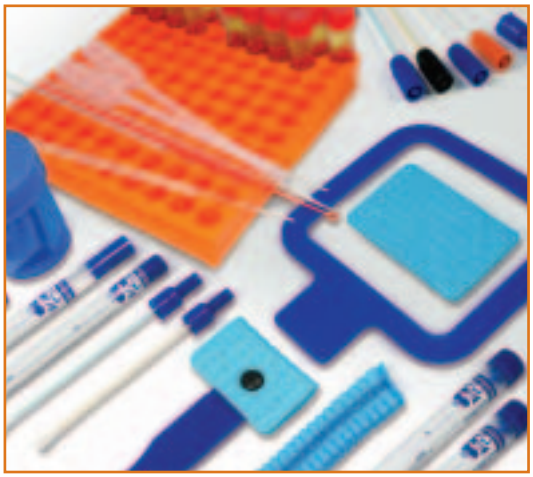
The two day conference focused on recent advancements in the application of the microbial and mammalian Biolog Phenotype Microarrays to study cell metabolism in relation to genotype. In total eleven internationally recognised speakers presented at the conference and a number of posters were also displayed.

Dr Barry Bochner, CEO of Biolog opened the meeting with an overview of the diverse Biolog applications. This was followed by oral presentations on the application of Biolog Phenotype Microarrays to human, animal and plant pathogens with a particular emphasis on new and emerging pathogens and zoonoses. Other topic areas covered included antimicrobial resistance, mammalian cell phenotyping, bioinformatics and modelling to interrogate large Phenotype Microarray data sets. All presentations were very well received with lively discussion sessions and a number of new collaborative links forged.

The conference was attended by over 80 delegates many of which attended the wine reception and conference dinner in the Lakeside restaurant at the University. The organisers wish to thank S*f*AM, the commercial sponsors and in particular Professor Roberto Marcello La Ragione of the University of Surrey.

further information

Visit: www.techno-path.com
Tel: +44 (0)28 3083 3808
Email: info@techno-path.com



Protect has recently celebrated its 30th birthday

The *original* low temperature bead storage system is ideal for long term maintenance of stock and quality control microorganisms. Protects colour coded cap, beads and slimline vial provides 20 subcultures, dramatically reducing the cost per test versus other techniques. Using TSC's customised accessories simplifies the process even further, providing a reliable long term cryopreservation method for a wide range of standard and fastidious microorganisms.

Preserving in Protect also sustains the exact strain, permitting consistent results every time. The specially designed cryopreservative solution prevents damage whilst frozen. Available in Red, Blue, White, Green and Yellow.

- **Protect Select** offers the end user a specialised range, created to optimise recovery without extra workload.
- **Protect Select Anaerobe** improves viability and performance with problematic microorganisms.
- **Protect Select Dairy** is based on BSI/ISO formulation and recommendations and is for the dedicated storage of microorganisms isolated from milk and dairy products.
- **Protect Select Yeast and Mould** offers easier suspension of fungal spores with spore grab formulation and is suitable for preservation of yeast cells.
- **Protect Select Meat Free** provides the biotechnological and pharmaceutical sector with a guaranteed BSE/TSE (Bovine/Transmissible Spongiform Encephalopathy) free alternative.

further information

Visit: www.tscswabs.co.uk/
Tel: +44 (0)1706 620600
Email: sales@tscswabs.co.uk

information

Are you a Corporate Member of the Society? If so, this section of *Microbiologist* is for you. Here you can publish short press releases, acquisition notices, news of new staff appointments, technical developments and much more.

Each Corporate Member of the society may publish ***up to*** 200 words on a topic related to their field of activity in each issue of *Microbiologist*. For further information please contact Lucy Harper by email at: **lucy@sfam.org.uk**

Both Corporate Members and Ordinary Members of the Society will find a wealth of useful information and resources in this section.

society for applied sfam microbiology

SfAM events in 2012
Save the dates!

Wednesday 18 April 2012

Spring Meeting

6th broadening microbiology horizons in biomedical science meeting

- Including the Procter and Gamble Applied Healthcare Microbiology Award Lecture presented by Professor Anne Glover, Chief Scientific Advisor to the European Commission

The Stratford Q Hotel, Stratford-upon-Avon, UK

2 - 5 July 2012

Summer Conference

● Microbial resistance to antibiotics and biocides ● Natural and experimental adaptation in bacteria ● Bioremediation

- Including the Lewis B Perry Memorial Lecture: Globalization of antimicrobial resistance. *Didier Pittet, University Hospital in Geneva*

The George Hotel, Edinburgh, UK

For further information on these events please visit sfam.org.uk or contact Sally Hawkes
■ Email: sally@sfam.org.uk ■ Telephone +44 (0)1933 382191

Society for Applied Microbiology
Bedford Heights, Brickhill Drive, Bedford MK41 7PH, UK.

tel: +44 (0)1234 326661
fax: +44 (0)1234 326678
email: communications@sfam.org.uk
www.sfam.org.uk