In this Issue

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- Meetings
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- Summer Student and Travel Reports

The Genetics Society News is edited by David Hosken and items for future issues can be sent to the editor, by email to d.j.hosken@exeter.ac.uk.

The Newsletter is published twice a year, with copy dates of 1st June and 26th November.

A Tilia cordata tree, the subject of a fieldwork grant. See page 40
Welcome to issue 66.

We have an issue full of interesting reports of various Society meetings and Society funded activity, and I thank all those who continue to contribute these articles. Since the last issue the HE upheaval continues and student applications to Universities are down at present. But rather than focus on this part of Academia, I would like to instead focus on a science career issue that disproportionately impacts women.

A science career is fantastic in many ways and pretty tough in some others. Fantastic partly because of the curiosity driven nature of the job, and tough because of the degree to which one’s ideas are continually, and at times brutally scrutinized. Be that as it may, in most science posts the issues being addressed are not going to have direct life or death consequences in the same way as say a surgeon’s actions. Instead, much of the work conducted in Academia is blue skies and no one is likely to die because an experiment goes wrong, or a paper is published in a low-impact journal.

Why is it then is it so hard to re-enter academic science after a career break? Physiotherapists can re-enter their profession, ditto MDs, dentists, lawyers and so forth, but science is pretty unforgiving in this regard. Take time out and you are out of the game, forever. I use to think this was about falling behind in the publish-or-perish race, but am no longer sure this is the whole picture. I think it may also have something to do with science chauvinism - you clearly do not take the work seriously enough if you have taken time out to raise a family, and science is of course a serious and most noble cause.

The fact that career trajectories are never backward - you cannot be demoted - probably does not help either as it means if you leave at one level you are unlikely to be able to re-enter at a lower level.

Of course there are re-entry schemes for those who do take breaks, but these are few and far between, which make things difficult for most. The flip side of all this is that you cannot have your cake and eat it too, and like all things in biology and life, there are trade-offs. There is some truth to this argument, but if the prevailing ethic disproportionately impacts particular members of the scientific community, perhaps the community needs to have a rethink.

Best wishes

David Hosken
Genetically tractable model organisms have played essential roles in the investigation of complex developmental and cell biological processes, thereby providing a myriad of insights into fundamental biology. These amazing experimental systems continue to open up new areas for investigation as well as enabling powerful practical applications. The Genetics Society 2012 Spring Meeting will showcase model organisms and illustrate how chemical and small molecule screens are enhancing traditional genetic analyses. In addition, the meeting will highlight novel prospects for genetic engineering, as the field moves into uncharted territories through recent advances in synthetic genetics.

Speakers
Dr Tanya Whitfield  Sheffield University
Professor Sean Cutler University of California Riverside
Professor Kevin Eggan  Harvard University
Dr Jason Chin Laboratory of Molecular Biology, Cambridge
Professor Kristala Prather  MIT

Scientific Organisers
Ian Henderson and Patricia Kuwabara

Features
Professor Jonathan Hodgkin  Oxford University
The 2011 Genetics Society Medal recipient
4th International Conference on Quantitative Genetics

17 – 22 June 2012
Edinburgh International Conference Centre, Scotland, UK
www.icqg2012.org.uk

Conference Themes:
1. The Genetic Architecture of Complex Traits
   Current understanding of the genetic control of complex trait variation - Genome-wide association studies and beyond.

2. Evolutionary Quantitative Genetics
   Selective forces on quantitative traits and the maintenance of variation.

3. Variation in the Genome
   Sequence, structural and epigenetic variation and its phenotypic consequences.

4. Advances from New Numerical Methods
   Advances in our understanding of quantitative traits from new statistical, computational and modelling approaches and utilisation of computing power.

5. Opportunities from Technological Advances
   Potential impact of the $1000 genome and other new methods and approaches on our understanding of quantitative variation.

6. Bridging the Genotype-Phenotype Gap
   Networks and pathways connecting DNA variants to trait variation - approaches and models.

7. Interactions among Individuals and with the Environment
   Genetic interactions and covariation with the environment, in social groups and between species.

8. Genomic Information in Prediction
   Prediction of disease risk and performance in humans, plants and animals and use in health care and plant and animal breeding.

9. Emerging Areas
   New frontiers in research and late breaking results.

Key Dates

<table>
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<tr>
<th>Date</th>
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<tr>
<td>Friday 3 February 2012</td>
<td>Abstract Submission Deadline for Oral abstracts only</td>
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<tr>
<td>Friday 6 April 2012</td>
<td>Abstract Submission Deadline for Poster abstracts only</td>
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<tr>
<td>Friday 3 February 2012</td>
<td>Early bird registration deadline</td>
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<tr>
<td>Sunday 10 June 2012</td>
<td>Pre-conference registration closes</td>
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Supported by

Fred van Eeuwijk, Netherlands
Peter Visscher, Australia
Bruce Walsh, USA
Juha Merilä, Finland
Patrick Phillips, USA
Daniel Pomp, USA
Pak Sham, China

Local Organising Committee
Bill Hill (Chair)
Lutz Bünge
Chris Haley
Mike Kearsey
DJ de Koning
Loeske Kruuk
Josephine Pemberton
Alan Wright

International Advisory Committee
David Allison, USA
David Balding, UK
Piter Bijma, Netherlands
Rachel Brem, USA
Ed Buckler, USA
Andrew Clark, USA
Mark Daly, USA
Rebecca Doerge, USA

Marie-Anne Felix, France
Jonathan Flint, UK
Greg Gibson, USA
Mike Goddard, Australia
Ary Hoffman, Australia
Fred Hospital, France
Mark Lathrop, France
Trudy Mackay, USA
Albrecht Melchinger, Germany

Juha Merilä, Finland
Bill Muir, USA
Patrick Phillips, USA
Daniel Pomp, USA
Pak Sham, China
Fred van Eeuwijk, Netherlands
Peter Visscher, Australia
Bruce Walsh, USA
Bruce Weir, USA
Qifa Zhang, China

Supported by
2012 Autumn Meeting

At the cutting edge of molecular biology

25 years of Genes & Development

Thursday 8 – Friday 9 November. The Royal Society, London

Genes & Development has been named one of the Top Five Research Journals in the field of Molecular Biology and Genetics (1997-2007). Genes & Development has a 5 year Impact Factor of 14.198 and is ranked #1 among Developmental Biology research journals. (2009 Thomson Reuters JCR)

Further information and registration will be available via our web site, at www.genetics.org.uk in due course.

Speakers
Sharon Dent
Steve Smale
Jerry Workman
Ken Zaret
Titia de Lange
Steve Elledge
Steve Jackson
Susan Gottesman
Elisa Izaurralde
Narry Kim
Jim Manley

Joan Steitz
Hans Clevers
Elaine Fuchs
Nick Hastie
Rich Losick
Eileen White

Chairs
Terri Grodzicker
Rudi Grosschedl
Winship Herr
Davor Solter

Scientific Organisers
Anne Ferguson-Smith, Terri Grodzicker and Nick Hastie

Features
Steve West
The 2012 Genetics Society Medal recipient

for registration, visit
www.genetics.org.uk
We will happily include any announcements for genetics-based meetings in this section. Please send any items to the editor.

**Molecular Ecology**  
4th – 7th February 2012, Vienna, Austria  
[www.vipca.at/ MOE COL](http://www.vipca.at/MOLECOL/)

**2nd International Conference on Bioscience, Biochemistry and Bioinformatics**  
10th – 11th March 2012, Chennai, India  
[www.icbbb.org/](http://www.icbbb.org/)

**11th European Conference on Fungal Genetics**  
30th March – 4th April 2012, Marburg, Germany  
[www.ecfg.info/](http://www.ecfg.info/)

**Evolution of Caenorhabditis and Other Nematodes**  
3rd – 6th April 2012, Hinxton, UK  
[http://meetings.cshl.edu/meetings/worms12.shtml](http://meetings.cshl.edu/meetings/worms12.shtml)

**Chromosome Biology, Genome Evolution and Speciation**  
23rd – 25th April 2012, Leibniz, Germany  

**Keystone Symposia: Proteomics, Interactomes**  
7th – 12th May 2012, Stockholm, Sweden  
[www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1133](http://www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1133)

**2nd Symposium of Population and Evolutionary Genetics**  
9th – 12th May 2012, Belgrade, Serbia  
[www.peg2012.rs/](http://www.peg2012.rs/)

**The Contribution of Epigenetics in Pediatric Environmental Health**  
30th May – 1st June 2012, San Francisco, USA  
[www.regonline.com/cehn](http://www.regonline.com/cehn)

**European Human Genetics Conference 2012**  
23rd – 26th June 2012, Nürnberg, Germany  
[www.eshg.org/eshg2012.0.html](http://www.eshg.org/eshg2012.0.html)

**Australasian Society of Human Genetics 36th Annual Scientific Meeting**  
22nd – 25th July 2012, Canberra, Australia  
The Genetics Society helps support several sectional interest groups by providing meeting sponsorship. We currently have 11 groups who organise sectional interest meetings with the organizers and dates of any forthcoming meetings are listed below. If you are interested in any of these areas, please contact the relevant organiser. Groups who wish to be considered for sectional interest group status should see the Society website for further details.

**Arabidopsis**
**Organiser:** Ruth Bastow (ruth@arabidopsis.info)
http://garnet.arabidopsis.info/

**Archaea group**
**Organiser:** Peter Lund (lundpa@gmail.com)

**British Yeast Group**
**Organiser:** Alistair Goldman (a.goldman@sheffield.ac.uk)

**C. elegans**
**Organiser:** Stephen Nurrish (s.nurrish@ucl.ac.uk)

**Drosophila**
**Organiser:** Nic Tapon (nicolas.tapon@cancer.org.uk)
Monthly meetings are organised by: Joe Bateman (joseph_matthew.bateman@kcl.ac.uk)

**Ecological Genetics Group**
**Organiser:** Paul Ashton (Genetics@BritishEcologicalSociety.org)

**Genetics Society Pombe Club**
**Organiser:** Jacky Hayles (j.hayles@cancer.org.uk)

**Mammalian Genetics & Development**
**Organisers:** Elizabeth M. Fisher and Nick Greene (mgd.workshop@ich.ucl.ac.uk)

**Mammalian Genes, Development and Disease**
**Organisers:** Rosalind M John and David Tosh (JohnRM@cf.ac.uk)

**Population Genetics Group**
**Organiser:** Lori Lawson Handley (l.lawson-handley@hull.ac.uk)

**The Zebrafish Forum**
**Organiser:** Rachel Ashworth (r.ashworth@ucl.ac.uk),
Caroline Brennan (C.H.Brennan@qmul.ac.uk),
Corinne Houart (corinne.houart@kcl.ac.uk).
There are meetings at 5:30pm-8.00pm on the first Thursday of every other month. Room G12, New Hunt’s House, King’s College - London SE1 1UL
Honorary Secretary’s Notices

Patricia Kuwabara . Honorary Secretary, University of Bristol

The Genetics Society Annual General Meeting

Friday 20 April, 2012

The 2012 Annual General Meeting of the Genetics Society will take place on Friday, the 20th April 2012, in the context of the Society’s Spring Meeting on “Supermodel Organisms: Chemical Genetics and Synthetic Life” at the Royal Society, London. The business includes the election of new members to the Society, and of new members to the Society’s Committee and Exec sub-Committee. A list of new members proposed for election to the Society will be publicised via emails to members, and on the Society’s website www.genetics.org.uk.

Nominations for Committee and Executive sub-Committee vacancies will be proposed by the Society and publicised at a later date by emails to members, and on the Society’s website.

Provisional Agenda

1. Minutes of previous General Meeting (Friday, 1 April 2011); matters arising
2. President’s Report
3. Honorary Treasurer’s Report
4. Honorary Secretary’s Report and Business for Transaction
   (a) Balfour Lecture 2014
   (b) Genetics Society Medal 2014
   (c) JBS Haldane Lecture 2013
   (c) Applications for new membership
   (d) Election of new Exec sub-Committee officers
       Vice-President for Corporate Affairs
       Vice-President for External Affairs
       Honorary Secretary
   (e) Election of new Committee members
       Postgraduate Representative
       Area E (Evolutionary, ecological and population genetics)
       Area F (Corporate genetics and biotechnology)
   (f) Election of new Honorary Members
5. AOB

Important Note

The 2012 AGM will allow advance voting on the Society’s website for those unable to attend in person. Members will be notified by email of the motions to be voted on in this way, and of the mechanisms for online voting. To ensure your involvement in the AGM by this mechanism, please check that the Society has your correct email address. As a check, an email will be sent to all registered members on 14 February, 2012 (Valentine’s Day). If you do not receive this email, please contact theteam@genetics.org.uk and provide an email address update.

A copy of the draft minutes from the 2011 Spring AGM can also be viewed on the Society’s website www.genetics.org.uk
Life Membership in the Genetics Society

Have you reached the age of retirement (65), but wish to continue with your involvement in the Society? If so, and you are an ordinary member who has discharged any arrears the might be due to the Society, then you might consider applying to become a Life Member of the Society. Life members will continue to receive notices and remain eligible to vote in the Society AGM, but will not be required to pay further subscriptions. Recipients of the Genetics Society Medal will also be offered Life Membership. Should you require additional information about becoming a Life Member, please contact The Genetics Society Office (theteam@genetics.org.uk).

2014 Balfour Lecture

The Balfour Lecture, named after the Genetics Society’s first President, is an award to mark the contributions to genetics of an outstanding young investigator. The Balfour Lecturer is elected by the Society’s Committee on the basis of nominations made by any individual member of the Society. The only conditions are that the recipient of the award must normally have less than 10 years’ postdoctoral research experience at the time of nomination, and that any nomination must be made with the consent of the nominee. Those making nominations must be members of the Genetics Society, but there is no requirement for the nominee to be a member, nor is there any restriction on nationality or residence. Örjan Carlberg (Uppsala University) will present the Balfour Lecture for 2012.

A call for nominations for the 2014 Balfour Lecturer will be made in the 2012 summer Newsletter and by email; the Lecture is normally delivered at the Society’s annual spring meeting. Note that there is no restriction on the subject matter of the Balfour Lecture. To make a nomination, you will be asked to confirm that your candidate is willing to be nominated and to provide a two-page CV of the candidate, together with a list of his or her ten most important publications, plus a one-page letter of recommendation outlining why you feel their contributions to the field have been outstanding.

2013 The JBS Haldane Lecture

The JBS Haldane Lecture will recognise an individual for outstanding ability to communicate topical subjects in genetics research, widely interpreted, to an interested lay audience. This speaker will have a flair for conveying the relevance and excitement of recent advances in genetics in an informative and engaging way.

The annual open lecture will be delivered on a topic, and in a place, agreed with the Genetics Society. The recipient will be selected by a committee chaired by the Genetics Society’s Vice President for the Public Understanding of Genetics (Dr Christopher Smith) from nominations made by Society members.

Nominees need not be members of the Society, but should be active researchers working in the UK. To make a nomination, please confirm that your candidate is willing to be nominated, then submit both a two-page CV and a short explanation of how the candidate meets these criteria.

In addition to delivering the Lecture, the nominee will receive an honorarium of £1,000 and a three-year membership of the Society. Nominations should be sent to the Honorary Secretary of the Society, Patricia Kuwabara (p.kuwabara@bristol.ac.uk) by January 16th 2012.
2014 Genetics Society Medal

The Genetics Society Medal is an award that recognizes outstanding research contributions to genetics. The Medal recipient, who should still be active in research at the time the Medal is awarded, will be elected annually by the Committee on the basis of nominations made by any individual member of the Society.

Those making nominations must be members of the Genetics Society, but there is no requirement for the nominee to be a member, nor any restriction on nationality or residence. Neither current members of the Committee nor those who have retired from office in the past four years may be nominated for the award.

The recipient will be invited to deliver a lecture at a Genetics Society meeting, where the medal will be awarded, in the year following his/her election. Stephen West (LRI, CRUK) will present the Genetics Society Medal lecture for 2012.

A call for nominations for the 2014 Genetics Society Medal will be made in the 2012 summer Newsletter and by email. To make a nomination, you will be asked to confirm that your candidate is willing to be nominated and to provide a two-page CV of the candidate, together with a list of his or her ten most important publications, plus a one-page letter of recommendation outlining why you feel their contributions to the field have been outstanding.

The Sir Kenneth Mather Prize 2011

The Sir Kenneth Mather prize, of £150, is awarded to recognise a BSc, MSc or PhD student of any UK University or Research Institution who has shown outstanding performance in the area of quantitative or population genetics.

There was an exceptionally strong field of candidates for the Sir Kenneth Mather Prize in 2011, and the judges were unable to resolve between the merits of the two strongest candidates. The outcome has been that, in 2011, there will be two Sir Kenneth Mather Prizes awarded, to Gibran Hemani and Ben Longdon.

The first recipient of the Sir Kenneth Mather Prize 2011 is Gibran Hemani, a PhD student at the Roslin Institute, University of Edinburgh. His project has been on dissecting interactions in quantitative traits. The identification of genetic interactions is a famously difficult problem in quantitative genetics, in that the numbers of possible two-way interactions increases with the square of the numbers of genetic markers, and the threshold for significance has to be scaled to allow for this. Gibran Hemani has created software resources, and identified computing power, necessary for the task. In addition to these developments, he has also developed population genetics theory predicting the timescale of the maintenance of epistatic interactions in populations.

The second winner is Dr. Ben Longdon, who recently completed his PhD in the Institute of Evolutionary Biology, University of Edinburgh. Ben’s work has been on the vertically, and bipaternally, transmitted viruses of insects. His PhD work has been extraordinarily productive and has already resulted in seven first-author publications. Notwithstanding their vertical transmission, the spread of these viruses through Drosophila populations can be remarkably rapid, and can be investigated using sequence variation in a coalescent context. Similarly, Ben has been able to demonstrate the patterns of cross-species transfer of these viruses, and the impact of host phylogeny on viral persistence.

The Mather Prize 2012

We are seeking nominations for this annual prize, of £150, to reward a BSc, MSc or PhD student of any UK University or Research Institution who has shown outstanding performance in the area of quantitative or population genetics.

Nominations should be made between July 1st and November 1st 2012 through the local Head of Department or School of the nominee. Nominations should consist of no more than one page of A4, setting out the case for the nomination, including relevant comparison with other students where possible. Nominations should be sent to the Head of School, School of Biosciences, The University of Birmingham, Birmingham, B15 2TT, clearly labelled as a nomination for “The Sir Kenneth Mather Memorial Prize”. Kay Boulton (University of Edinburgh) was awarded the Mather Prize for 2011.

Nominations will be assessed by a panel of two people with experience in the area of quantitative/population genetics, one from the University of Birmingham and the other nominated by the UK Genetics Society. Decisions will be announced in December 2012.
Local Representatives

The Local Representative acts as a key liaison between the membership and the Society’s Office and Committee by helping to recruit new members, publicising the Society’s scientific meetings and other activities, and in providing feedback from the membership on matters of professional concern. The Society normally appoints only one local representative per company, institution or department, but exceptions can be made when there are semi-autonomous sub-divisions containing a substantial number of members or potential members.

We seek to fill vacancies and to update our database of Local Representatives on a yearly basis. Should you wish to volunteer as a local representative or if existing representatives wish to update their contact details, please contact the Honorary Secretary, Patricia Kuwabara by Email at p.kuwabara@bristol.ac.uk.

SEE FULL LIST ON PAGE 13
## Genetics Society Local Representatives

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<thead>
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<th>Location</th>
<th>Local representative</th>
<th>Institute</th>
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<td>Aberystwyth</td>
<td>Dr Glyn Jenkins</td>
<td>University of Wales</td>
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<tr>
<td>Bath</td>
<td>Dr Steve Dorus</td>
<td>University of Bath</td>
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<tr>
<td>Birmingham</td>
<td>Prof FCH Franklin</td>
<td>University of Birmingham</td>
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<tr>
<td>Brighton</td>
<td>Dr Felicity Z Watts</td>
<td>University of Sussex</td>
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<tr>
<td>Bristol</td>
<td>Prof Patty Kuwabara</td>
<td>University of Bristol (SOMs)</td>
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<td>Bristol</td>
<td>Dr Colin M Lazarus</td>
<td>University of Bristol (Biol. Sci)</td>
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<td>Dr Timothy Bowen</td>
<td>University of Wales College of Medicine</td>
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<td>Coventry</td>
<td>Dr Peter Glen Vallely</td>
<td>University of Warwick</td>
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<td>Prof Micahel JR Stark</td>
<td>University of Dundee</td>
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<td>Edinburgh</td>
<td>Dr David Burt</td>
<td>Roslin Institute</td>
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<td>Exeter</td>
<td>Sarah E. Flanagan PhD</td>
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<td>Glasgow</td>
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<td>University of Surrey</td>
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<td>Heather Sealy-Lewis</td>
<td>University of Hull</td>
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<td>Kent</td>
<td>Prof Mick F Tutte</td>
<td>University of Kent</td>
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<td>Leeds</td>
<td>Elizabeth Valleeley</td>
<td>University of Leeds, St. James’s University Hospital</td>
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<td>Dr Ed Holloxy</td>
<td>University of Leicester</td>
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<td>London</td>
<td>Prof EMC Fisher</td>
<td>Nat’l Hosp for Neurology &amp; Neurosurgery</td>
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<td>London</td>
<td>Dr Kevin M O’Hare</td>
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<td>London</td>
<td>Dr Richard A Nichols</td>
<td>Queen Mary and Westfield College</td>
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<td>London</td>
<td>Dr Stephen Ansell</td>
<td>The Natural History Museum</td>
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<td>London</td>
<td>Dr Francesca Mackenzie</td>
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<td>Dr John FY Brookfield</td>
<td>University of Nottingham (University Park campus)</td>
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<td>Dr Richard D. Ems</td>
<td>University of Nottingham (Sutton Bonnington)</td>
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<td>Oxford</td>
<td>Dr SE Kearsey</td>
<td>University of Oxford (Zoology)</td>
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<td>Prof Liam Dolan</td>
<td>Dept of plant sciences</td>
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<td>Prof Andrew OM Wilkie</td>
<td>University of Oxford (John Radcliffe Hosp)</td>
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<td>Plymouth</td>
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<td>Dr Louise Johnson</td>
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<td>Dr George E Johnson</td>
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<td>University of Ulster</td>
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<td>Royal Botanic Gardens Kew</td>
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**IMPORTANT ANNOUNCEMENT**

**Action required by all members**

We would like to bring to your attention a significant change in operation of the Genetics Society. As of 1st September 2011, Portland Customer Services (PCS) has been designated the office service provider for the Society and the office in Roslin has been closed.

This change will not affect the remit of the Genetics Society; however, it does mean that services such as membership applications and Direct Debit collections, meeting organization, web hosting and secretariat services have been transferred to PCS.

As part of the handover, PCS will be contacting all members during the coming renewal periods. Those members who used to pay their membership fees by Direct Debit will be required to complete a new Direct Debit mandate form as we will no longer be using the previous collection bureau for this. In addition this will be the opportunity for those members who pay by other means to set up a Direct Debit payment, a saving of £5.00 off all categories of membership.

A copy of the new Direct Debit Mandate form can be found on the Genetics Society website under the Membership tab.

Veronica van Heyningen, President, said, “The Genetics Society is pleased to appoint Portland Customer Services who are able to provide a high level of services to our members and committees. As part of Portland Press, a wholly owned subsidiary of the Biochemical Society, Portland Customer Services has a unique insight into the needs of membership based organizations and a thorough understanding of the requirements of a specialist scientific society.”

Members are the life-blood of the Society and active participation by members in the Society will help to continue to make the Society a modern, relevant, lively, vibrant community of professionals as it moves towards the centenary in 2019.

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**New rates for Genetics Society meetings**

The Genetics Society organizes two annual meetings on which it spends a considerable part of its annual budget.

This means that attendance fees, especially those for members, are very cheap and do not cover the full cost of the meeting.

However, the executive committee has recently agreed an increase of the attendance fee to better reflect the actual attendee cost of the meeting.

This means that overall venue costs and speaker costs are still fully met by the Genetics Society.

**The new rates will take effect for the Spring meeting in 2012 and will be as follows:**

- Full Member: £65
- Non Member (non academic): £180
- Non Member (academic): £120
- Charity: £40
- Retired: £30

The autumn meeting will be a two-day meeting and this will also be reflected in the attendance fees.

Please find announcements for these meetings elsewhere in the Newsletter.

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**Dryad and Data**

The 1,000th data package has been entered into the Dryad Data Repository. It is associated with an article to appear soon in the journal Heredity: Hager R, Cheverud JM, Wolf JB (2011) Data from: Genotype dependent responses to levels of sibling competition over maternal resources in mice. Dryad Digital Repository. doi:10.5061/dryad.qqqp07d8

For more information please see: http://blog.datadryad.org/2011/10/07/1e3/
This year’s Autumn Meeting brought together a diverse and dynamic set of speakers, whose contributions have helped shape the field of epigenetics and the directions of current research. The theme running throughout the day was the importance of epigenetic processes in development and disease, and to this end, the meeting was a huge success. The range of talks included those focused on genomic imprinting, the study of which gave rise to the ever-expanding field of epigenetics, to those addressing the importance of epigenetic marks in cancers and in mediating long-term memory of early life experiences. The programme also included the 2011 Balfour Lecture which explored gene regulatory networks, providing an additional perspective on how genetic systems respond to environmental challenges.

There was no better way to open proceedings and capture the interest of the audience than with a talk by Azim Surani (University of Cambridge), whose early studies were crucial in the discovery of genomic imprinting. Azim’s current work addresses how primordial germ cells, arising from cells that have already embarked on the process of differentiation, are reprogrammed to achieve a more stem cell-like state. This includes erasure of epigenetic marks to adopt a profile more similar to ES cells. Azim discussed key germ cell determining factors, including Prdm1 and Prdm14, that repress the somatic programme and initiate epigenetic reprogramming.

The theme of epigenetic signatures and stem cells was continued by Myriam Hemberger (The Babraham Institute), who demonstrated how epigenetic marks can impose lineage restriction. The earliest post-fertilisation differentiation event distinguishes cells that will give rise to the trophoblast lineage (trophoblast stem (TS) cells), critical for placental development, from those that will form the embryo proper (ES cells). DNA methylation is necessary for these two cell lineages to be defined. Myriam discussed her work identifying Elf5 as a gene differentially-expressed between the two cell types. The Elf5 promoter is densely methylated and inactive in ES cells but methylation is erased in TS cells, allowing Elf5 to be expressed. Elf5 functions as a gatekeeper, reinforcing commitment to the TS cell lineage. Myriam is now investigating other components of the TS/ES cell epigenetic signatures, including differences in global levels of hydroxymethylation. These epigenetic lineage boundaries define distinct stem cell populations and this mechanism is likely to be relevant in other developmental contexts.

After coffee, the president of the Genetics Society, Veronica van Heyningen, presented the Balfour Award to Madan Babu (MRC Laboratory of Molecular Biology). Madan delivered an inspiring guest lecture on gene regulatory networks, discussing the mechanisms by which such networks have evolved, and how this enables appropriate responses to environmental cues.

The President of the Genetics Society Veronica van Heyningen presents the award to the Balfour Lecture winner for 2011, M Madan Babu.
Regulatory networks are composed of motifs, such as single input motifs in which one master regulator directly influences expression of a number of targets, and multiple input motifs in which more than one input signal is required to elicit a response. Madan has demonstrated that a sudden environmental stress, such as heat shock, induces gene expression changes mostly through single input motifs, where the effect is fast-acting and direct. Other physiological processes, such as cell cycle progression, utilise multiple input motifs to enable tighter control over gene expression changes. This enlightening work is changing our view on how genomes and gene networks evolve.

After a splendid lunch networking, with views over The Mall and St James’s Park, we reconvened to hear two captivating talks on the importance of epigenetics in cancer. Andrew Feinberg (Johns Hopkins University) described how a sightseeing trip to Westminster Abbey sparked an idea that random epigenetic variation might act as a driving force in development and evolution. He presented some compelling evidence for this theory, and has recently extended this idea to studies of the cancer epigenome, identifying the sites of methylation that vary the most between cancers. The theme was continued by Alan Clarke (Cardiff University), who proposed that tumour progression could be suppressed by interfering with DNA methylation. Alan has shown that deficiency for a methyl binding protein, MBD2, is highly protective against colorectal cancer and presented recent work elucidating the mechanism of this tumour suppression. MBD2 and other epigenetic regulators provide a range of potential novel therapeutic targets.

Next, Dietmar Spengler (Max Planck Institute of Psychiatry) turned our attention to how early life stress can influence behaviour and health in adulthood. Epigenetic marks represent an important component of this long-term memory. DNA methylation profiles at specific loci differ between mice exposed to early life stress and control animals, and these differences persist at least one year later. This results in gene expression differences that are likely to influence adult physiology. In line with the meeting aim, Dietmar provided an exciting and additional perspective on the importance of epigenetics in health and disease.

The final session focussed on genomic imprinting, a classic example of a biological process regulated by epigenetic mechanisms. Anne Ferguson-Smith (University of Cambridge) discussed the functional significance of loss of imprinting in normal in vivo situations. As a model, Anne explored the loss of imprinting of Dlk1 in adult neural stem cells and niche astrocytes. In this stem cell niche, expression of both copies of Dlk1 is required for postnatal neurogenesis. This study raises provocative questions about the importance of genomic imprinting as a dosage control mechanism, where loss of imprinting, and thus a ‘double dose’ of gene expression, may be required for specific functions and developmental contexts.

The function of genomic imprinting was further explored in the final two talks. While Dlk1 shows loss of imprinting in some cells, Andrew Ward (University of Bath) described how Grb10 exhibits a complete switch of its imprint between the brain and other tissues. Expression of the maternally-inherited copy of Grb10 in tissues such as liver and skeletal muscle influences growth, size and metabolism. In the brain, it is the paternally-inherited copy that is expressed, and Andrew showed how this influences social behaviour. The concept that two parental copies of the same gene could influence distinct physiological processes is intriguing and raises questions about how and why imprinting may have evolved.

Expanding on these questions, Barry Keverne (University of Cambridge) explored how imprinted genes may mediate coadaptive development of the brain and placenta. Imprinted Peg3, for example, is expressed in the foetal placenta where it primes the maternal hypothalamus to ensure correct maternal care and milk production after birth. At the same time, Peg3 in the placenta primes the hypothalamus of the developing foetus itself, ensuring that these animals in turn become ‘good mothers’. This interaction between the maternal and foetal genomes means they are coadapted, with benefits for both mother and offspring.

A drinks reception concluded the day, and the conversation was buzzing with discussion of the truly excellent set of talks. Ros John and Anthony Isles organised a terrific line-up that opened our minds to the dynamic roles that epigenetics plays in development and disease.
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Telomeres are the tandem repetitive sequences (TTAGGG motif) that occur at the end of all chromosome arms in most eukaryotes and which are thought to protect chromosomes through life. Individuals are born with different average telomere length, and while telomeres may lengthen or shorten over time, in humans and some other species there is emerging evidence that in general they shorten quickly over development and slowly over adult life. There is a considerable amount of research effort directed at understanding the relationships between telomere dynamics, ageing and health, mostly in humans and model organism, with much of the work being in vitro. We know much less about the diversity of telomere dynamics across species and how this relates to variation in life histories. Recently however, telomeres are being investigated outside of the biomedical context, but there are a number of challenges in working with non model species and in asking questions at ecological and evolutionary levels.

This workshop, organised by Pat Monaghan (Glasgow), Dan Nussey (Edinburgh) and Neil Gemmell (Otago, New Zealand) brought together evolutionary biologists (who to varying degrees had started work on telomeres) and selected experts from the biomedical field to discuss how telomeres can be measured in different species. Given that there are a number of methods of measuring telomere length, different organisms have varying telomere lengths, some have telomeric sequences other than at the chromosome ends, large sample sizes and longitudinal sampling is required in some studies, and that working in field conditions can pose particular challenges for sample storage, there were many issues to be discussed.

The first session was devoted to the Telomere Restriction Fragment (TRF) method of measuring telomere length. This technique uses a Southern blot approach and probing with the telomere repeat yields a smear which is then analysed for position and intensity using image analysis software. Abraham Aviv (New Jersey Medical School) and Mark Haussmann (Bucknell University, Pennsylvania) outlined some of the issues involved in this technique when applied to human and bird blood cells respectively. Thorsten Horn (University of Otago) studying the rare long-lived parrot, the kakapo, Nils Hartmann (Leibniz Institute for Ageing Research) studying the world’s shortest-lived fish and Mats Olsson and Emily Miller (University of Sydney) studying a wild lizard population, provided examples of applications to a variety of study organisms. Some clear points from this session were that this technique requires quite a large amount (2-3ug) of high quality DNA, and it is relatively time-consuming and low throughput. Professor Aviv also drew our attention to a dot blot technique, which shows great promise, but expressed frustration at the fact that Invitrogen has stopped manufacturing the SybrDX reagent required to measure the DNA quantity loaded onto each dot. Since the workshop concluded, some delegates (led heroically by Aviv and Monaghan) have managed to arrange for some of the reagent to be produced and shipped by Invitrogen. It is hoped a wider assessment of the utility of this new method in a variety of different species and context should follow shortly.

The next session was devoted to qPCR approaches. Here, the total quantity of telomere repeats per genome is measured. Length is not given in absolute terms, but relative to a ‘golden sample’. The attraction of this approach over the TRF method is considerable, since there is potential for high throughput and much less DNA is required. David Howells (Agilent Technologies) gave an overview of qPCR and then Thomas von Zglinicki (University of Newcastle) described its application in large human cohorts. Technical issues were discussed by Emma Barrett (University of East Anglia) working on a large Seychelles warbler sample set, Thorsten Horn (University of Otago) on kakapo and Chris Turbill (University of Vienna) on hamsters. A major talking point of the workshop was how best to run qPCR and what software to use. Telomere length, measured by TRF and qPCR in the same samples, are generally correlated, and Aviv discussed a recent double blind study of samples measured by the two methods. The successful use of either
method clearly hinges on it being deployed with suitable care and skill, and appropriate information being reported in publications to allow readers to fully assess the accuracy and repeatability of the assay conducted.

The third session saw a review of workshop progress so far by Neil Gemmell (University of Otago) followed by a talk by Duncan Baird (University of Cardiff) which touched on QFISH but really concentrated on STELA. QFISH is the staining of chromosome spreads with telomere probes and given that it requires live cells in metaphase, it may have limited utility in natural population studies. STELA (Single Telomere Length Analysis) uses sequence information adjacent to the telomere to design primers that amplify a specific telomere – for example the one on the p arm of the X and Y chromosome in humans. Remembering that a sample of tissue contains cells from many clonal lineages, the technique reveals variation between cells in the length of the target telomere. The screening process is complex: amplification is followed by running on a gel that is 40cm long but only 0.5% agarose (in order to reveal fragments between 0.1 and 40kb) which is then hybridised to the telomere repeat. The level of detail revealed is high, but getting accurate sequence data for subtelomeric regions in order to design primers for non-model organisms may prove difficult. Most vertebrate studies investigate telomere length in blood cells (white cells in mammals and the nucleated red cells in birds). There has been much emphasis on the need for longitudinal studies of telomere dynamics in order to discriminate sources of variation, notably individual effects and age effects. In a second presentation, Aviv also showed results of within-individual comparisons of telomere length in proliferative and non-proliferative tissues in dogs, suggesting that this approach might give an index of lifetime loss. This might be useful for ecologists where suitable post mortem tissues are available.

Simon Verhulst (University of Groningen) and Dan Nussey (University of Edinburgh) ended the presentations with talks about statistical analysis issues, particularly the need to take into account regression to the mean effects when looking at loss rate in relation to starting length, and issues around how best to analyses longitudinal data when survival information is not complete, as if often the case with field studies. Analyses need to be able to partition out variation which is due to three separate effects: (i) individuals have different telomere length at the start of life, (ii) telomere length changes over time, at different rates in different individuals, and (iii) biases introduced by selective death – i.e. whether death removes individuals of particular telomere length from the population. The latter process can introduce very serious artefacts in cross-sectional studies. Verhulst pointed to two relatively recent approaches using mixed models. Nussey followed up with a review of the literature on studies of the inheritance of telomere length. Many human studies have conducted parent-offspring regressions of telomere length, but the results have been conflicting – suggesting both stronger mother-offspring and stronger father-offspring correlations in different data sets.

Interspersed through the talks, and on both evenings, the workshop had many discussion sessions with the aim of consolidating ideas on how those studying telomere dynamics in different species and settings should proceed. On the first evening, discussion was enhanced by a selection of TRF gel pictures from bird studies by Ellis Mulder (University of Groningen). In particular, these discussions focussed on the best methods for sample collection and storage, DNA extraction, DNA quality checks, telomere length measurement and data analysis. Workshop members plan to put together a journal article from these discussions outlining the different methodological issues and how these might or might not be resolved for different study systems. Altogether it was a wonderfully well-organised and thoroughly stimulating and constructive meeting, and sponsorship by the Genetics Society, BBSRC and Agilent was much appreciated by all attendees.

For more information see: www.gla.ac.uk/researchinstitutes/bahcm/news/telomereworkshop
Genetic Aspects of Male Infertility

A Genetics Society Sponsored lecture by Prof. Csilla Krausz at the Reproductive Function and Dysfunction conference September. Edinburgh, Scotland.

Ian Adams . University of Edinburgh

The Reproductive Function and Dysfunction conference in Edinburgh brought together a range of world-renowned experts in the field of reproductive biology to discuss the latest research and developments. The conference included sessions on the development of artificial reproductive systems, mathematical modeling of reproductive function, reproduction and disease, and a Festschrift to honour Prof. Roger Gosden on his retirement. The Genetics Society-Sponsored lecture by Prof. Csilla Krausz from the University of Florence in Italy on Genetic Aspects of Male Infertility was a timely and informative account of progress that is being made to identify the genetic causes of male infertility. Around 7% of men in the general population are affected by infertility, but very few genetic mutations other than Y chromosome microdeletions and abnormal karyotypes have been established as recurrent causes of male infertility in human populations. Prof. Krausz’s lecture highlighted important unanswered questions in the field, and described how mapping genes affected by azoospermia factor (AZF) Y-chromosome microdeletions, and sequencing patient families for genes in the AZF region converged on the Y-linked USP9Y gene. Prof. Krausz also described how high resolution comparative genomic hybridisation was providing new insights into the genetics of male infertility by identifying X-linked and autosomal infertility-associated copy number variations (CNVs). In particular, Prof. Krausz showed that there is an increased X-linked CNV burden in men with idiopathic severe spermatogenic failure, and suggested that this infertility phenotype may be associated with genomic instability. Ongoing genome-wide association studies may yet identify more genes associated with male infertility in human populations, but Prof. Krausz’s work suggests that after so much research has been done on the role of Y-linked CNVs in male infertility, perhaps it is time to consider the role of X-linked and autosomal CNVs in male infertility too.

Genetics Society Sponsored Events

The Genetics Society is keen to promote the study of genetics to senior school pupils. One way to do this is for Universities to run conferences for local schools. If you are a GS member and would like to run such an event in your University or institute, please contact the society’s office with an outline plan and costing.
Celebrating the life of Noreen Murray

Noreen Murray was President of the Genetics Society from 1987 to 1990. She was an internationally renowned pioneer in the development of recombinant DNA technology using bacteriophage lambda as a cloning vehicle. Her work from the early 1970’s, carried out partly in collaboration with her husband Ken Murray and her colleague Bill Brammar, provided many of the underlying concepts and the practical tools for what used to be called genetic engineering, and it laid the foundation for the phenomenal expansion of molecular biology. In 2010 Noreen was diagnosed with a type of motor neurone disease. She dealt with the disease with quiet dignity and grace and died peacefully on 12 May 2011, with Ken at her side.

Noreen was born in Lancashire into a family that valued education – her father was a headmaster. Around the age of 15 she switched her ambitions from becoming a domestic science teacher to studying biology. She read botany at Kings College London and then decided to undertake a PhD in Neurospora genetics in the new microbiology department Birmingham, with David Catcheside (GS President 1961-1964). Her work required the isolation of different methionine-dependent mutants, and the need to map these led to an interest in mechanisms of recombination. Noreen showed that recombination occurred at hotspots and was not evenly spaced along the chromosomes. It was during this time that she met, and in 1958 married, a fellow PhD student working on the chemistry of DNA, Ken Murray.

David Catcheside warned Noreen that marriage would ruin her career prospects and certainly for many years, despite loving support from Ken, she had a difficult time gaining proper independence or recognition for her work.

In 1959 Ken and Noreen went to Stanford as postdocs for a year and stayed for five. Noreen worked in the lab of David Perkins who also had a strong interest in meiosis in Neurospora and in ascospore generation involving chromosomal crossing over. Perkins, who later served as President of the Genetics Society of America, collaborated with high-profile and inspiring scientists such as Lederberg (bacterial transformation) and Tatum (one-gene-one enzyme), so Noreen had many opportunities to engage in exciting scientific discussions. Frank Stahl (of semi-conservative replication fame) was another colleague there. In 1964 on
their return to the UK, to Cambridge, Noreen was working with the geneticist Harold Whitehouse, when Frank Stahl arrived as a visiting scientist at the MRC Laboratory of Molecular Biology. Noreen collaborated with him on exploring recombination in bacteriophage.

Experience with this simple organism led Noreen to switch the full focus of her own studies to exploring recombination in bacteriophage lambda from 1968, when Ken accepted a post as Senior Lecturer in the newly formed Molecular Biology department in Edinburgh. Noreen was soon able to join the new MRC Molecular Genetics Unit led by Bill Hayes (GS President 1971-1973), although she was expected to take on menial tasks that were considered women’s work. Nevertheless, it was in Edinburgh that the very fruitful collaboration with Ken began. As a biochemist, Ken was working on the specificity of DNA sequence recognition by proteins such as restriction endonucleases. There was great excitement when it was realised that some of these enzymes made staggered cuts at the recognition site, leading to sticky ends which could be used to promote site-specific annealing. Noreen’s deep understanding of the bacteriophage system, with the judicious use of its complex genetics, led to the realisation that with the aid of these specific restriction endonucleases lambda phage could be engineered to function as a cloning vector for the site-specific insertion of defined DNA fragments. The inserted DNA could even encode toxic proteins in the lysogenic state, which could be expressed and purified in large quantities after induction of the lysogen.

Noreen’s skills in creating and selecting many new strains of lambda phage with appropriate packaging strains now came to the fore. The work was meticulously carried out and documented, mostly by Noreen herself, with clones carefully stored. Although she did much of the labwork herself, she also spent a lot of time teaching and mentoring her students and postdocs in all aspects of the work, from the theoretical background and historical provenance to the need for careful strain preservation and documentation. To crown all these important contributions, Noreen was generous to a fault, sharing with many requestors her knowledge and the carefully designed innovative combinations of vector and packaging systems, designated NM### – not many Material Transfer Agreements were sent out for signature in those days! The methods devised for lambda cloning still constitute one of the few ways of amplifying relatively large DNA fragments, and many of the concepts introduced by Noreen have been used to develop other specific purpose vectors, some for commercial use, for example to make DNA vaccines. With much of this substantial contribution under her belt, Noreen was finally given MRC tenure in 1973. Now at last she had the first opportunity to submit a grant in her own name (she had previously written several for others to submit), and following its successful funding, was able to set up her own group. However, in 1977, when Ken was offered the opportunity to go to the EMBL labs Noreen had to choose between continuing her group in Edinburgh or accompanying Ken to Heidelberg. Of course she chose the latter and spent further productive years there in fruitful collaboration with Ken and others.

The development of cloning technology brought fantastic advances to the academic science of molecular genetics, but the potential for expressing proteins for biomedical use as therapeutic agents was immediately identified. The new approach soon led to a most important result: Ken cloned the hepatitis B virus surface antigen which could be used as a vaccine and still is to this day. This work provided the opportunity for Ken to become a founding member of the scientific board of the pioneering biotech company Biogen. The company took out patents to safeguard the technology for itself and for the University of Edinburgh. Royalties from this benefited the University greatly and also led to the setting up of the Darwin Trust which has supported molecular biology at Edinburgh and elsewhere.

Noreen’s deep understanding of the bacteriophage system, with the judicious use of its complex genetics, led to the realisation that with the aid of these specific restriction endonucleases lambda phage could be engineered to function as a cloning vector for the site-specific insertion of defined DNA fragments.
Ken and Noreen, both Trustees of the Darwin Trust, have been great benefactors for the University of Edinburgh.

1982, at the end of the EMBL period, turned out to be the auspicious year that Noreen was elected a Fellow of the Royal Society. This finally gave her the proper recognition she deserved. Soon she was back in Edinburgh, a member of University staff, following the dissolution of the MRC Molecular Genetics Unit a few years earlier when Bill Hayes retired. It was 1988 before Noreen was appointed to a personal Chair of Molecular Genetics, despite strong support earlier from several people, including John Fincham (GS President 1978-1981).

With the fellowship of the Royal Society came new roles and demands on Noreen’s time. She was now asked to sit on many committees and advisory bodies. She served on several different Royal Society committees including as Chairman of the RS Working Party on GMOs (Genetically Modified Organisms) which explored, in a balanced and rational way, the possible hazards of genetically modified food crops (after the claims of Dr Pusztai about GM potatoes) and made recommendations on how evidence should be gathered, reviewed and published. A little later, in 2002, Noreen acted as Advisor to an EU Consortium on the development of highly specific enzymes for genome manipulation. Around this time she was elected again to RS Council, this time as Vice-President. In 2002, just after her official retirement date, she was awarded a CBE. There were many other honours, including several honorary doctorates; she was the inaugural recipient Gabor medal of the Royal Society and the Royal Medal of the Royal Society of Edinburgh. Despite her eminence and great achievements Noreen remained quiet and modest. All the extra committee work did not displace her efforts in the lab, she just worked harder. She never shirked her lecture allocation and although she found public speaking stressful, she always delivered clear and well thought-out lectures and was an excellent teacher.

On 26 November 2011, Ken, with help from friends and colleagues, organised a splendid Symposium in Edinburgh as a celebration of Noreen’s life. It was a moving and educational event – a slice of immortality. Contributors talked about Noreen’s scientific achievement but also about her as a person. Several remarked how Noreen always had time in her 70-hour working week to talk to students and colleagues about their work and she was an excellent listener. Despite her “niceness”, she was a tough critic of her colleagues’ science. She had a way of looking at people to convey if the concepts or experimental approaches presented were not up to the rigorous standards she expected of herself and of them. She followed this up with knowledgeable advice and help wherever possible.

Several participants commented on Noreen’s incredible work ethic, but then it was suggested that for Noreen science was life and the rest of life had to be fitted in around that. And there was a lot to the “rest of life”. Ken and Noreen loved hill walking and climbing from their earliest days of courtship. They travelled widely for work and pleasure – Noreen’s 60th birthday present was a trip to the Galapagos. Having started as a botanist, Noreen was very knowledgeable about plants, and gardening was one of her passions. She was most exacting about the design and maintenance of the garden at their large house, within walking distance of the lab at Kings’ Buildings. She did most of the upkeep work herself and was always very happy there, as reflected in the photograph. Ken and Noreen also enjoyed art and there is a wonderful collection in their house, about which they were both extremely knowledgeable. They entertained often and generously, inviting students and postdocs to meet their eminent friends and visitors, plying all with delicious food and wine, as Noreen was also an excellent cook. It will be a lasting memory to many to picture Noreen, always trim and elegant, smiling to greet her guests, with Ken at her side.

Noreen Elizabeth Parker (Lady Murray), molecular geneticist: born Read, Lancashire 26 February 1935; Professor of Molecular Genetics, Institute of Cell and Molecular Biology, University of Edinburgh 1988-2001, then Emeritus; CBE 2002; married 1958 Sir Kenneth Murray; died Edinburgh 12 May 2011.
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A wide range of research topics were extensively covered during the conference, with particular emphasis on development, stress responses, computational biology, cell metabolism and signalling networks. Many of the sessions were concurrent due to the high number of contributors, and were followed by after-dinner workshops and evening poster sessions containing over 600 poster presentations. I presented a poster in these sessions on the transcriptional regulation of LHY, a gene central to the plant circadian clock. I have summarised a few of the presentations that I found the most interesting below.

Leaf morphology is highly conserved within species, yet extremely divergent across species. Przemyslaw Prusinkiewicz (University of Calgary) described the creation of a computational model to explain the regulation of leaf shape development. It was known that PIN1 polarises to areas on the leaf margin known as convergence points and promotes the influx of Auxin, causing localised serration of the margin. The model therefore contained Auxin nodes at intervals, however the convergence points fluctuated. The addition of a stabilising factor in the form of CUC2, which is known to inhibit growth and be suppressed by Auxin, concentrated between the Auxin nodes enabled the model to correctly predict leaf shape in CUC2 and PIN mutant plants.

Post-transcriptional regulation operates via mRNA sequence motifs, and ~90% of plant genes have at least one additional AUG codon upstream of the main transcriptional start site. These 5’ uAUGs produce short protein coding uORFs, which will usually suppress translation of the main ORF due to loss of the reinitiation competence of ribosomes. The question of whether uAUGs may be conserved in some genes was considered in a comparative transcriptome study. Justin Vaughn (von Arnim lab, University of Tennessee) explained that in a small subset of genes, AUG was the most conserved triplet in the 5’UTR in all plant lineages examined. A combination of modelling and experimental studies were used to show that if the uORF is short enough, the usual inhibitory effect on the gene can be compensated for by eIF3, a component of the basal translation machinery, remaining at the DNA and re-initiating translation at the major ORF.

The majority of roots grown on agar will preferentially disregard gravitropism in favour of hydrotropism, i.e. they will grow towards moisture rather than gravity. Local moisture influences the growth and development of the root through hydropatterning. José Dinneny (TLL Singapore) presented findings that reporter constructs under the control of the promoter of NCED2, the product of which is an enzyme performing the rate-limiting step in ABA biosynthesis, are expressed on the dryside and not wetside of agar-grown roots, suggesting that NCED2 expression, and hence ABA biosynthesis, is activated by dryness. The role of ABA and NCED2 in inhibiting the root gravity response under locally dry conditions was confirmed using null and overexpression NCED2 lines. In addition, this and other pathways have been identified using FACS (Fluorescence Activated Cell Sorting) as having their activity within roots regulated locally by moisture.

Finally, Siobhan Braybrook (University of Bern) detailed the new application of Atomic Force Microscopy (AFM) as a micro-force sensor to extrapolate the structure of cell walls of living plant tissue and cells from their surface elasticity. In particular, this technique was used to investigate organogenesis, showing that growth is associated with increased elasticity and that, for example, the application of Auxin caused an increase in elasticity of the meristem, which can be correlated to organ formation.

I would like to thank the Genetics Society for awarding me a Junior Scientist Grant to attend this, my first international conference, and also the ICAR organisers for making it such a success.
This summer I attended the 8th European Meeting on Mitochondrial Pathology in Zaragoza, Spain. This meeting is held every three years and being able to attend one of them during third year of my PhD was invaluable. I want to thank to the organizing committee (Jose Antonio Enriques, Patricio Fernandez-Silva, Asiclo Perez-Martos and Antonio L. Andreu) for organizing such a beautiful meeting. The kick-off of the conference has been made by J. A. Enriquez by welcome and introduction talk. Then he surprised all of us by inviting the traditional Spanish folk dancers to the stage. After this warm welcome, the first keynote lecture was given by Prof. Douglas Turnbull entitled “From mitochondrial diseases to mitochondria in disease”.

There were two sessions in the first day. First one was, “Mitochondrial Diseases”, in which I particularly enjoyed Massimo Zeviani’s talk on finding new genes and treatments for mitochondrial diseases. Then we have moved on to the second session entitled “Mitochondria in Cardiovascular and Metabolic diseases”. In this session along with various interesting talks, Prof. Anu Suomalainen-Wartiovaara explained the use of whole-exome sequencing which is widely used in mitochondrial research.

The second day of the conference had three sessions on Mitochondria in Neurodegeneration and Neuroinflammatory Disorders, Mitochondria in Oncological Diseases and the Immune system and Mitochondria in Development and Ageing. In the afternoon there was the first poster session where I discussed my work with other people and had very useful feedback. Prof. Nils-Goran Larsson explained about the recent findings and calculations of nuceloid structure and size. Furthermore, Sherine Chan explained the use of the model organism zebrafish for screening bioenergetics. The last talk of the second day was a keynote lecture from Dr. Nick Lane who is a scientist and a writer. Dr. Lane gave a very stimulating talk about mitochondria and evolution of complex life with some very interesting visual and mathematical examples.

Third day of the conference was the most intense. There were three sessions entitled mitochondrial life cycle, mitochondrial DNA metabolism and expression in disease and import, assembly and turnover of mitochondrial proteins. Luca Scorrano’s talk on Opa1, Ian Holt’s talk on nucleoids and Zofia Chrzanowska’s talk on role of poly(A) tail was amongst the other very interesting talks. I had more discussion about my research at the poster session and already started planning the experiments I need to start after the conference.

At the end of the day we were all tired and had a lot of questions on our minds, however having a wonderful gala dinner at night was very useful to socialize with other researchers. Next day which was sadly the last day of the conference, we all had a chance to listen the talk of Prof. Douglas Wallace who has been working in mitochondrial field for a long time. Title of his talk was “A Mitochondrial Etiology of Complex Diseases” and focused on energy levels.

Overall I have enjoyed my time at the conference and found it very useful to attend one of the most important conferences in mitochondrial science. I would like to thank Genetics Society for sponsoring me and helping me to have this great experience.
1st Austria Evolutionary Genetics Workshop 2011

19th – 23rd September 2011, Klosterneuberg, Austria

Anna Muir . University of Glasgow

The IST Austria Evolutionary Genetics Workshop 2011 was held between the 19th and 23rd of September 2011. The Institute of Science and Technology Austria (IST Austria) is a new Institute, opened in 2009, dedicated to research and graduate education in the natural and mathematical sciences. The Institute is situated in the beautiful Vienna woods, in the city of Klosterneuburg, 18 km from the center of Vienna. The aim of this intensive four day course was to give a thorough introduction to evolutionary genetics through techniques used to model evolutionary processes. The course was jointly run by IST Austria and the Vienna Graduate School in Population Genetics.

Arrival at the Institute for the welcome reception was accompanied by torrential rain and the walk from the main building along a forest track to the traditional Austrian Hütte left the participants rather bedraggled. However, the warm wooden clad interior, traditional food and Austrian beer soon lifted our spirits and everyone left looking forward to the start of the workshop. The workshop was attended by students from a diverse array of European countries and Institutions, joining those from IST Austria and the University of Vienna, to make 41 participants.

Lectures began on Tuesday morning with introductory sessions from Nick Barton (IST Austria) discussing the history of evolution and key open questions in the field. Nick was joined throughout the week by Reinhard Burger, Joachim Hermisson and Ines Hellmann (University of Vienna) to make up the instructors on the course. The workshop packed in an array of topics during the week, covering random drift and inbreeding, neutral theory, the coalescent, selection, molecular population genetics, population structure and evolutionary genetics from a modelling viewpoint.

Lectures were accompanied by practical sessions using simulation software, a number of which were developed at IST Austria, allowing students to visualise and play around with parameters that had been described.

Magnus Nordberg (Gregor Mendel Institute) gave a very interesting guest lecture on Thursday afternoon about the difficulties of analysing genetic data from structured populations and discussing some on his own research on genome-wide association mapping.

As the week went on the weather turned sunny and allowed the beautiful surroundings to be explored. Staying and eating on campus allowed students to discuss research interests and current projects, highlighting the diverse background of participants, from molecular biologists to mathematicians studying a wide array of topics and species. A mid-afternoon finish on the final day allowed time for a look around Vienna in the sun and an evening meal in the city before departure. The IST Austria workshop will be run again in 2012 and I would recommend it to anyone interested in a thorough and broad introduction to modelling evolution genetic processes. I would like to thank the Genetics Society for support to attend this interesting workshop.
This was the first time that I had been to an ESEB congress; the scale of which was considerably larger than that of previous scientific meetings I had attended. Over four days there were approximately 1300 attendees, 350 talks and 700 posters. Needless to say, even before I had left Sheffield I was excited to see the most recent projects and developments across the field of evolutionary biology.

Attempting to be eco-friendly with my travel plans, I set off from Sheffield by train with my dismantled bike in a very large bag. I was a little nervous about travelling across Europe with such a large piece of luggage but to my relief encountered no problems, only bemused looks from fellow passengers. Indeed as soon as I boarded the Eurostar and left the UK rail network everything was very easy. After a relaxing but long journey, I arrived at my out of town hotel. I quickly reassembled my bike and headed into Tübingen for the evening registration and welcome session. It was a great evening and a perfect opportunity to catch up with friends from other institutions under one roof.

The next morning the congress formally opened with plenary talks from Mike Siva-Jothy and Duur Aanen. There was quite a subject contrast between Mike’s talk on sexual conflict and traumatic insemination in the bed bug and Duur’s talk on cooperation in mutualistic mushrooms. Soon it was the first coffee break and a chance to locate my poster contribution and rapidly choose the talks from the next session that I wanted to attend. Over the course of the congress there were a staggering 30 symposia of which my highlights were; “Speciation by natural versus sexual selection”, “Mutualism: Causes and consequences” and “Evolutionary ecological genomics”.

The remaining plenary talks were varied and included Michael Ruse, a philosopher and historian from Florida State University who gave an entertaining talk and sparked some debate by calling into question the importance of JBS Haldane in population genetics. In opposition to this, Brian Charlesworth provided some strong defence during his presidential address on the final day. Brian also highlighted other issues in Evolutionary Biology for discussion; notably problems with detecting selection when it acts weakly and is widespread throughout the genome. Another speaker to highlight was the JMS-Prize Laureate Rowan Barrett who gave a very clear and interesting talk on “The Genetics of Adaptation”, combining theory, lab and field studies in the stickleback.

The conference organisers did a great job in promoting student research. There was the chance for poster presenters to invite other conference attendees to meet them at their posters during allocated sessions. Another opportunity for student academic interactions came in the form of the “meet a silverback” program during which small groups of students were able to spend an evening over dinner with an established academic, courtesy of the Volkswagen Foundation. I had the pleasure of dining with Walter Salzburger, whose work predominantly focuses on the diversification of the East African cichlid fishes. There was plenty to discuss, particularly as his research group was probably the best represented at the congress, with a wide range of talks and poster presentations.

Overall, attendance at a large congress provided me with an in depth encounter with a diverse range of projects. There was plenty of scope to meet academics and find out about life at other institutions. I feel that all too often as PhD students we get caught up in our own project and associated problems. ESEB allowed me to take a step back from my research and to look at the wider picture of evolutionary research. This was both refreshing and re-assuring and I would like to thank the Genetic Society for supporting my attendance.
In early September of this year, just as I was entering into my 4th and final year of my PhD and thanks to the award of a Genetics Society junior scientist travel grant, I was lucky enough to be able to attend the conference on Plant Genome Evolution in Amsterdam.

This was the second in a new series of conferences sponsored by Current Opinion journals and was to be the first major international conference I had attended.

The conference focused on bringing together the diverse range of plant genomic and evolutionary research and the many recent, rapid advances in the field. The conference was organised into six sessions over 2 days with a reception, plenary talk and poster session on the preceding evening and second poster session at the end of the first day. Session topics spanned from fundamental research such as the influence of gene and genome duplication and genome structural diversity moving through to more applied research such as plant systems biology, the association of genomics and transcriptomics to phenotype and finally to future directions in plant genomics. The aim of the conference was putting emphasis on the latest and unpublished results and providing extended discussion periods and opportunities to interact with the speakers, so promised to be an exciting few days.

Arriving into Amsterdam quite early on the day the conference was due to start I was able to enjoy a walk round some of the city’s sights and a canal side drink before registration opened. The conference was held in the impressive Grand Hotel Krasnapolsky, right on the city’s main square. Sitting in the expansive lobby reading through my delegate pack with its list of speakers and their pictures it was quite exciting to start to identify people whom until that point I recognised only as names on research papers. Slowly getting over that shock I started to realise the value and potential of such conferences.

The conference opened with an introduction from Yves Van de Peer followed by a great plenary talk from Maarten Koornneef illustrating just how much the Arabidopsis model has contributed to plant genomics and describing identification of genetic variation involved in environmental adaptation. The first of the poster sessions followed and provided an initial opportunity, both daunting and exciting, to start to introduce myself and talk to some of those names I recognised. Poster sessions, lunch and coffee breaks were all held in the hotel’s beautiful glass-roofed courtyard and provided a great setting for some lively discussion of posters and talks.

The next day got off to great start with sessions on gene and genome duplication and genome structural diversity. Susan McCouch gave a particularly interesting talk which documented gene flow, selection and exchange in rice that as ultimately produced modern domesticated rice as did Chris Pires speaking on whole genome duplication and its impact on gene regulatory networks. The function and description of these networks turned out to be a prominent feature of many of the talks throughout the conference. Pat Heslop-Harrison and Chris Pires maintained a twitter commentary throughout the conference that did a great job of condensing even the most difficult parts of some the talks into concise, take-home messages. In one of the later presentations of the day Dr. Bomberly talked about his research on changed gene expression patterns in polyploids which was particularly relevant to my own work and left me reeling with ideas and notes to apply to my own work. Fortunately this talk came just before a coffee break and although I wasn’t able to meet with Dr. Bomberly directly I was able to discuss the talk with other delegates gaining their opinion and perspectives and perhaps tempering my own runaway enthusiasm!

The evening poster session yielded more great conversations and finished off the day nicely leaving me with a little time to spend exploring the city.

The second day yielded more great talks, with the day’s sessions focusing...
more on the applied aspects of research. Amongst the many excellent presentations D. Zamir gave an engaging talk considering future crop yields and highlighted the important issue of a shortage of trained plant breeders and the general failure of high school graduates to take up plant science education.

Prof. Heslop-Harrison’s talk on genome evolution gave a great deal of insight into the information we may be able to obtain from domesticated crop genomes talk and was again especially relevant to my own work, resulting in more furious note taking. The conference ended on an especially high note for me with Julian Hibberd’s talk in the final session. His brilliant and engrossing talk on the evolution of C₄ photosynthesis that left me with yet more frantic note scribbling with the main problem being trying to scribble not only enough notes on the scientific content but also on the delivery style and presentation so that I might use them to inspire my own future presentations.

Attending this conference has been a great experience for me. It has presented me with great opportunities and given me insight into the higher scientific life and the wider field into which your own work is placed. Conferences provide an intense and absorbing experience where you can become totally immersed in science, to see how your work may relate to others and to formulate new ideas and routes your own research may follow.

I would like to take this opportunity to thank the Genetics Society for awarding me this travel grant which allowed me to attend this conference. It was a fantastic and rewarding experience for which I am enormously grateful.

The Genomics of Common Diseases 2011

30 August – 2 September, Wellcome Trust Conference Centre, Hinxton UK

Fayeza Fatima Khan . University of Nottingham

This year saw the 5th Genomics of Common Diseases meeting, which is jointly organized by Nature Genetics and the Wellcome Trust. The conference program included seven sessions of talks with three keynote lectures and two poster viewing sessions spread over a three-day period. The topics covered in the seven sessions were: exome and whole genome sequencing, functional genomics, clinical translation and pharmacogenetics, infectious diseases, population and statistical genetics, cancer and emerging technologies and their applications.

While the first meeting was held at the time when Genome-wide Association Studies (GWAS) had just taken off, this year’s meeting came at a time when whole-genome/exome sequencing has become cheap and accessible enough to be applied widely across biological research and to allow large-scale studies such as sequencing-based GWAS.

The challenges involved with whole-genome/exome sequencing today are similar to what genome-wide genotyping faced and mostly deal with three general areas as one could gather from the talks: study designs to maximize power of finding association, statistical tools to deal with the resulting data and making biological sense of the results. For example, most studies aimed to choose subjects that are at the tail-end of the phenotypic spectrum of the trait in question and many speakers acknowledged the usefulness of using family members versus unrelated individuals to increase power to detect rare variants associated with disease.

Similarly, the use of model organisms and relevant experimental techniques in elucidating the effects of human genetic variants was highlighted. While speakers mulled over the challenge of converting data from the multitude of whole-genome/exome sequencing projects into meaningful biological answers, they could also show examples of interesting success stories where variants associated with phenotypes were experimentally shown to be involved in relevant biological pathways.

As was shown in one talk, these latest sequencing technologies could be put to use in a different way when it came to infectious diseases: sequencing pathogen genomes to work out the relationship between the strains causing outbreaks in different places. Findings from such an investigation...
help in tracking and controlling the spread of disease.

Overall, learning about new discoveries of disease-causing variants, including cancer-associated ones, and seeing how facts gathered on the functional elements in the human genome shed insight on its complex workings, was very inspiring.

There are projects underway to sequence thousands of individuals that will allow a much more comprehensive map of sequence variation in the human genome. Researchers from the ENCODE project and others showed how they are involved with comprehensively assaying non-coding regions of the genome and assigning functional elements to them. All of the data generated from sequencing and functional element studies is shared with everyone through online databases which is only part of the increasing amount of collaboration between researchers worldwide to unravel complex trait and disease mechanisms in humans. All these interesting talks and research presented in the form of posters gave way to a lot of discussion amongst the 250 or so delegates attending the conference. There was a good amount of time for interaction over tea breaks, drinks receptions or during one of the well-arranged delicious meals.

As a PhD student coming from a ‘locus-specific’ research background whose genome-wide technology know-how had largely come through literature reading, it was a wonderful opportunity to hear first-hand of the recent developments and interact with the researchers, and also to present my own work. I will take this opportunity to thank the organizers of the event and the Genetics Society for the travel grant.

The Snake Genomics and Integrative Biology Meeting

5th-8th October 2011, Vail, Colorado

Adam Hargreaves . Bangor University

The snake genomics and integrative biology meeting was the first of its kind held in the beautiful surroundings of Vail in the Rocky Mountains. The meeting was attended by all major research groups working in the area of snake genomics and transcriptomics and consisted of two days of talks followed by a day of collaborative discussion. The core aims of the meeting were to discuss on-going and planned research projects utilising or producing genomic and transcriptomic data from snakes, to encourage the formation of collaborative relationships, and to ensure all work efforts are of greatest use to the scientific community.

Both days of talks covered a wide variety of topics, from isochore evolution in reptiles to snake venom gene evolution, with a troubleshooting Q&A session conducted by an Illumina representative thrown in for good measure. It was obvious that what had once been a largely neglected area of research is now rapidly attracting attention, which is understandable considering the many unique features of snakes involving Hox genes, eye evolution, aerobic metabolism and transposable element activity. The two main hot topics were the recently completed genomes for the Burmese python (Python molurus bivittatus) and the King Cobra (Ophiophagus hannah), one of which (Burmese python) is currently freely available on GenBank and one (King Cobra) which is soon to be released. These sequenced De Novo genomes present an invaluable resource which will aid in research involving snakes, as well as broader-ranging studies in comparative genomics and vertebrate evolution.

Several talks at the meeting revealed upcoming snake genome sequencing projects including the corn snake, the saw-scaled viper, the garter snake, the western diamondback rattlesnake and the blind snake, all being undertaken by research groups with very different research interests. Numerous transcriptomes from a number of species are also planned to be released in the near future. It is evident that a large body of fascinating work and useful information will be released in the next year or two which promises to be an exciting time for snake genomics.

Overall the meeting was a great success with all talks being extremely interesting and many collaborations being formed and discussed. From a personal point of view it gave me an opportunity to discuss my work with researchers working in a similar field and also to find out what work is being done in this exciting and rapidly expanding research area.

A review paper of the meeting is currently being written should anyone want further information. Alternatively, you can visit the website www.snakegenomics.org.

Finally, I would like to thank the Genetics Society for awarding me a Junior Scientist Travel Grant which allowed me to attend this meeting.
Bioinformatics of Human and Animal Genomics

14th – 18th November 2011, Suzhou, China

Claudia P Cabrera . University of Edinburgh

Next-generation sequencing technologies are dominating the genomics research environment, nevertheless the lack of consensus and standardized methodologies for analysis of the data generated was reflected in the program of this conference.

“In bioinformatics, we are all chasers of technology...” (Prof. Rebecca Doerge). This phrase could not explain better the current situation; technology develops at a greater speed than researchers, developers and analysts can cope with. Now, the real challenge is not assembling the puzzle but understanding it, and bioinformatics has become the bottleneck.

Therefore, networking and meetings, where collaborations and research groups can exchange and present new developments and tools, are an essential part of research.

Next-generation sequencing technologies are dominating the genomics research environment, nevertheless the lack of consensus and standardized methodologies for analysis of the data generated was reflected in the program of this conference. Cutting-edge research was presented on how the availability of these technologies is changing the future of cancer treatments into personalized medicine.

Professor Lincoln Stein’s group is performing clinical trials on cancer patients who did not respond effectively to chemotherapy. They are studying the feasibility of routine genomic analysis of cancer patients’ biopsies in order to aid genetic diagnosis and treatment.

Time is a crucial aspect on these studies. Their goal is to obtain the genotype results within three weeks from the time of the patients consent, and inform them of possible treatments they would respond better to, according to their mutations and affected pathways. In addition, they developed a Cytoscape plug-in (Reactome Functional Interaction (FI) Network) and applied it to breast cancer, identifying prognostic signatures. This program aims to find network patterns related to cancer and other diseases, and it covers almost 50% of the human proteins.

The ENCODE group presented an interesting example of how the RNA expression levels can be predicted from the chromatin modification patterns. The Beijing Genomics Institute (BGI) is coming through with amazingly sized projects as well. The BGI is now famous for sequencing the panda and releasing the sequence of the German E.coli (the strain responsible for many fatalities in 2011) just after three days of the outbreak. Their mission is to sequence any organism, important for various reasons (i.e. economically, food supplies, industry/textile applications, endangered, or even just because they appear “cute” to humans).

I also had the opportunity to discuss very interesting developments being implemented in the software Galaxy (galaxy.psu.edu). Galaxy is a freely available web-based software, that allows the centralization and easy reproducibility of ‘data-intensive’ analyses. Because of its flexibility,
user friendliness and wide range of integrated tools (i.e. from sequence analysis, EMBOSS tools, UCSC integration and GWAS analyses, including LD and QC), it is being widely accepted within the research community.

In this conference, young, senior and experienced scientists were given the opportunity to present their work.

Dr. Yinyin Yuan, presented a very interesting methodology of the use of imaging technologies and their integration with DNA copy number and gene expression profiles for tumour classification and refinement of molecular signatures.

I was also given the opportunity to present my work about the use of circular genomic permutation as means to assess the significance of pathway-trait associations; this talk was in the same session as Prof. Anders Krogh’s. He is very well known for introducing Hidden Markov Models in bioinformatics and co-developing SAM (Sequence Alignment and Modeling). His talk was on improvements to the mapping performance for short reads, using quality scores in a probabilistic framework, which would be very useful for ancient DNA and small RNAs.

CSHA provided an excellent atmosphere to talk, exchange and discuss ideas, also great hospitality.

I want to express my deep gratitude to the Genetics Society for awarding me with the travel grant, allowing me this great experience.

International Federation of Placenta Associations

14th European Placenta Group Meeting 2011

14th – 17th Sept, Geilo, Norway

Norah Fogarty . University of Cambridge

The International Federation of Placenta Associations meeting was held in the small mountain resort of Geilo, located 4 hours west of Oslo. This meeting brings together Placenta research organisations from Australia and New Zealand, Europe, Japan and the Americas. The town is a national park, famed for its ski slopes and nature. The conference centre was situated beside a huge lake which provided us with lovely walks and fresh air to clear our head after intense sessions.

The theme of the meeting was "Placenta: Predicting Future Health" and had a special focus on the epidemiology of placenta pathologies and the effects on maternal and offspring health. The meeting opened with a plenary session on Evolution, development and lifelong health with presentations from Prof. Mark Hanson and Prof. Graham Burton.

There was a wide range of topics covered in 12 workshop sessions, including placenta immunology, stem cells, comparative placentology, placental and fetal circulation and biomarker identification. It was difficult to choose which to attend! The workshop on epigenetic and microRNA regulation of gene expression was particularly interesting.

Presentations dealt with DNA methylation, imprinting, X-chromosome inactivation and microRNA-dependent gene regulation in the placenta, and their impacts on placental development and fetal growth. Dr. J. Richard Chaillet from University of Pittsburgh gave an interesting round-up of the molecular mechanism of genomic imprinting and the role of imprinting in placental development and function. He discussed his work on Dnmt 1o knock-out mice in which embryos from homozygous Dnmt1 o/o female mice fail to maintain imprints during preimplantation development, and develop abnormalities in placental structure and gene expression during the second half of gestation.

I presented a poster on my investigative work into the functional and morphological differences between nuclei in syncytial knots and sprouts in the syncytiotrophoblast of the human placenta. A lot of people showed interest in my work and offered some useful insights for me to consider in my future

The theme of the meeting was “Placenta: Predicting Future Health” and had a special focus on the epidemiology of placenta pathologies and the effects on maternal and offspring health.
work. I also presented a workshop oral presentation in the session on Trophoblast Differentiation. This session generated stimulating discussion and again, I got some good advice from other people in this specialised field.

The most important feature of IFPA meetings is the great attention and support that is afforded to New Investigators. We are encouraged to get involved at all opportunities; to give oral presentations, to participate actively in discussions and not to be shy about offering up our opinions. Two special sessions were organised for us to help us with career development. These focused on building research groups and the skills behind writing successful grants. Everyone who attended the grant session found the advice to be invaluable and were greatly appreciative to the organisers for arranging such a worthwhile session.

The meeting was concluded with a gala dinner featuring such local treats as Juniper berry smoked trout and reindeer.

I really enjoyed IFPA 2011 and have returned to my bench full of enthusiasm and motivation for placenta research. I would like to extend my gratitude to the Genetic Society for enabling me to travel to this meeting which will certainly be of benefit to me as I begin the final year of my PhD.

Gordon Research Conference on Epigenetics
7th – 12th August 2011 Stonehill College, Easton, Massachusetts.

Elizabeth Radford . University of Cambridge

The Gordon Research Conference on Epigenetics takes place every two years, and is eagerly anticipated by the epigenetics community. The scope of the meeting is broad, ranging from research focussed on understanding epigenetic mechanisms, epigenetic reprogramming and inheritance to the interface between epigenetics and the environment, ageing, behaviour and disease in a wide range of model organisms. Speakers are encouraged to discuss unpublished data. This fosters an open, collaborative atmosphere with stimulating discussion during the talks, poster presentations and after dinner. The overall quality of the poster presentations was extremely high, making this conference particularly rewarding to be a part of.

My work has focussed on the role of imprinted genes and epigenetics in a transgenerational model of developmental programming, and so I was particularly interested in the sessions examining the mechanisms of epigenetic reprogramming and inheritance in different model organisms.

Anne Brunet presented intriguing data demonstrating that an H3K4 histone methyltransferases regulates longevity in C. elegans, with intergenerational effects; while Ryszard Maleszka made a compelling argument that the honey bee has much to teach us regarding developmental programming and the role for epigenetics in this process. Diet during early development in the bee determines whether an individual develops into a worker or a queen. This involves changes in DNA methylation which alter the developmental programme of gene expression. Petra Hajkova sounded a cautionary note regarding the role for the TET enzymes in the methylation reprogramming of the mouse zygote, while Bernardo Lemos stressed the importance of genetic background with an elegant series of experiments demonstrating trans-effects of Y-linked polymorphisms in Drosophila. Kazufumi Mochizuki and Mariusz Nowacki’s work on Tetrahymena and Oxytricha respectively, demonstrated the role of RNA-directed epigenetic regulation of DNA rearrangement in these organisms, and argued persuasively for the value of studying more unusual model organisms. Finally, Rob Martienssen gave a thought-provoking talk on the role of small RNAs in sexual reproduction in Arabidopsis, which raised some fascinating questions regarding the co-evolution of transposition and meiosis.

I am very grateful to the Genetics Society for the opportunity to attend this meeting. It was a hugely stimulating week, and a privilege to discuss exciting science in such a congenial atmosphere.
Invasive populations are thought to be under strong selection for evolution of specific life-history traits. Theoretical simulation work, supported by empirical studies, suggests that individuals at the wave-front of an expanding range should allocate more resources to reproduction and dispersal, leading to accelerating rates of range expansion. For example, in Australia, cane toads (Rhinella marinus) at the front of the expanding invasive population show evidence of increased reproductive effort and increased dispersal compared to individuals in previously colonized areas. Species may also lose parasites as they expand their ranges, so increased investment in reproduction and dispersal may be traded-off against reduced investment in immunity.

The bank vole (Myodes glareolus, formerly Clethrionomys glareolus) was first recorded on Ireland in 1964, in County Limerick in the south-west of the country. Although there had been plenty of field-based studies on Irish small mammals prior to this time, voles had not previously been detected.

The first systematic survey to establish the distribution of the bank vole in Ireland was carried out in 1969/70. This survey found that the bank vole was restricted...
to an area of about 6,000 sq. km in the vicinity of Limerick. Another complete resurvey was carried out in 1982, showing that the bank vole had approximately doubled its area, had now colonized much of the south-west of Ireland and was expanding in all directions at rates of 1 to 4.5 km per year. From the observed distribution and extrapolation of these rates of spread, it was estimated that the bank vole first began expanding its range in Ireland in the 1940s or 1950s. In continental Eurasia, the bank vole is found from northern Scandinavia to the Mediterranean and from Siberia to Spain and must have been inadvertently introduced to Ireland by people from somewhere within that natural range.

Previous parasite analysis of vole populations revealed a very restricted distribution of the vole-specific flea *Malaraeus penicilliger* along the southern estuary of the River Shannon, suggesting that this might have been the site of introduction, with fleas being lost from the bank vole population as it invaded new habitat. Mitochondrial DNA studies found only two distinct haplotypes, consistent with a single introduction event with few founders. The bank vole is continuing to expand its range in Ireland, and the process of invasion is not being modified by an eradication program. The bank vole in Ireland can therefore be considered an excellent model system for the study of evolution during range expansions.

I have an interest in understanding how populations are able to survive and adapt to new environments despite being small or having passed through severe bottlenecks, and obviously the Irish bank vole is an intriguing example of this. In 2010, I began an EU Marie Curie Fellowship to investigate the population genomics of the bank vole expansion in Ireland. Fieldwork for this project was supported by the Heredity Fieldwork Grant. The aim of this project is to reconstruct the invasion history of the bank vole, and to determine whether there is any genetic evidence of adaptation to invasion. In October 2010, I went to Ireland to sample voles. As genetic effects may be restricted to the wavefront of the population expansion, I first tried to find the current limits of the bank vole range. Having found the limits, I then sampled along transects, running from the supposed core of the invasion in County Limerick in three directions: one north to Galway, one north-east to Lough Ree, and one heading east to Waterford. The use of replicate transects is important, as genes identified as being under selection may be false-positives. If they are identified in all three transects, this gives us greater confidence in the result.

Now back in Cornell, I am using novel next-generation sequencing techniques to genotype many thousands of loci located randomly throughout the bank vole genome. With these data, I will use an approximate Bayesian computing (ABC) approach to reconstruct the demographic history of the invasion. In particular, I am interested in the number of founding individuals, rates of invasion and local effective population sizes. I should also be able to determine the influence of landscape features on the invasion process, and whether or not the invasion has been slowed by barriers to dispersal, such as rivers and motorways.

I will also use various techniques to detect genes under selection. Range expansions have been shown to cause a genetic phenomenon called ‘allele surfing’. Basically, alleles present in the small populations at the wavefront of an expansion will tend to drift to fixation and spread over large geographic areas. This phenomenon can generate similar genetic signals to those expected under natural selection. Therefore, I will explore various ideas of how these two processes might be distinguished. Any loci identified as being under selection will be followed up in future research projects. I am particularly interested in any loci relating to dispersal, reproduction, growth and functioning of the immune system.

Trapping in Ireland was very successful; I sampled 140 voles from 7 sites for genetic analysis. Further fieldwork later this year should provide me with enough samples to complete my project. I would like to thank Dr Sarah Perkins at Cardiff University for assistance in the field, and Dr Colin Lawton at NUI Galway and Prof. Jeremy Searle at Cornell University for providing me with traps and other equipment.

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Evolutionary responses to climate change: shifts in host plant preference during species range expansion

James Buckley, previously University of Bristol and currently University of Glasgow

Recent climate change has been associated with poleward range expansions in a wide range of taxa, but has been particularly well documented for butterflies whose geographical distributions, particularly in the UK, are well known. British butterflies show substantial variation in the rate of range expansion, with some undergoing significant northward range shifts and others either showing no distributional change or even declines in distribution. These differences can partly be explained by the ecological requirements of different species, with a greater proportion of habitat generalist species expanding northwards relative to habitat specialist species.

Understanding these contrasting effects of habitat fragmentation and climate change is therefore important for predicting the likelihood of species range expansions across taxa. There is also increasing evidence that evolutionary change in key ecological traits (particularly dispersal ability) is necessary for the successful movement across a fragmented landscape to colonise newly suitable sites. Given the importance of habitat preference in the ability to undergo northward range expansions, there is limited evidence for evolutionary change in traits associated with habitat preference during species’ range expansions.

The Brown Argus butterfly, Aricia agestis, has almost doubled its range in the UK over the past 30 years and is continuing to expand northwards with ongoing climate change. The Brown Argus uses host plants in two distinct families for larval growth: the Geraniaceae (e.g. Geranium molle) and the Cistaceae (solely Helianthemum nummularium). These host plants dominate different habitat types and are distinct in their geographic distribution across the UK. G. molle, for example, occupies a diverse range of disturbed grassland habitats and is widespread across the UK, whereas H. nummularium is restricted to chalk grassland habitats. Variation in the population-level host preference among four sites across the range of the Brown Argus provided evidence for adaptation to the different habitat types, as well as a potential shift to preferring G. molle.
in recently-colonised parts of the range. However, these population-level host preference estimates were based on the average number of eggs laid by free-flying females on potted host plants placed randomly around a site and do not identify individual variation in host preference within a site. In addition, a population genetic analysis using AFLP molecular markers, identified selection on loci associated with populations occupying the different habitat types, as well as during the colonisation of new sites. These data suggest that there is evolutionary divergence in host plant preference (and associated habitat use) across the expanding range of the Brown Argus. To confirm whether evolutionary change in host preference has been associated with the ability to colonise new sites it is important to identify differences among individuals in host preference and then explore the genetic basis of this important ecological trait using genomic sequence data from individuals assayed for differences in their host plant preference.

To collect these data I visited field sites across the UK range of the Brown Argus in the Summer of 2011 to conduct assays of individual female egg laying preference for either G. molle or H. nummularium. Females were placed in small cages with both host plants and a temperature datalogger and left to lay eggs for a short period. The aim was to assay individual variation at up to ten sites across the UK covering both habitat types in both long-established (butterfly present since before 1970-82) and recently-colonised (butterfly present since 1995-99) parts of the range and collect samples for subsequent RNA extraction. However, a cool, wet and windy August across the UK resulted in low butterfly population sizes and my attempts to find two consecutive days when it did not rain proved more challenging than expected… Sample sizes were lower than predicted, but despite these difficulties, I did manage to assay individual host preference for 50 females from five different sites (30 of which laid eggs). This was combined with another dataset from a previous year’s fieldwork resulting in a dataset of 77 females with individual host preference data from 9 sites across the range of this species. Variation in host preference among individuals within sites was high, but there were also consistent differences among those sites differing in habitat type. Specifically, a greater frequency of individuals laid eggs on H. nummularium at those sites where H. nummularium was the dominant host plant. This pattern was seen in both long-established and recently-colonised H. nummularium-dominated sites, although only one recently-colonised, H. nummularium-dominated site could be assayed.

Of particular interest for future work are the 24 females (5-7 individuals from each of 4 sites, 2 long-established and 2 recently-colonised) I collected and stored for subsequent RNA extraction. The extracted RNA from each individual will be pooled by population and then enriched for mRNA (reducing the number of rRNA transcripts). The pooled RNA for each population will then be sequenced with one lane of a Roche 454 sequencer (using funding obtained through a NERC Biomolecular Analysis Facility small projects grant) to enable the development of a preliminary transcriptome database for developing SNPs and characterising genes expressed in individuals from populations varying in host preference. This preliminary project should hopefully identify candidate SNPs, which could then be genotyped in a greater number of individuals from a wider range of sites across the long-established and recently-expanded distribution of this species. A larger-scale genotyping strategy would also allow us expand on recent results by identifying signatures of selection on potential candidate genes. This approach would allow us to more directly test for evolutionary change in important ecological traits during climate-driven range expansion.

I would like to thank the Genetics Society for providing the field grant to fund the collection of host preference data and samples for RNA extraction. I am also extremely grateful to Dr Jon Bridle (University of Bristol) for his advice and supervision during my PhD, as well as the numerous field assistants for their help and support in the field. I must also thank the various landowners (the Kent, Lincolnshire and Norfolk Wildlife Trusts, Natural England and the National Trust) who gave me permission to conduct this work.
The United Nations declared 2011 as the Year of Forests to highlight the importance of woodlands all over the earth. To mention just a few statistics: 31% of land is covered by woods, they are crucial for the livelihoods of more than 1.6 billion people and are the home of 80% of our terrestrial biodiversity. Therefore, it is recognised that awareness must be raised to maximise the conservation and sustainable management of all types of forests for the future. The Heredity field grant allowed us to visit and sample lime woods across Europe. Although lime (Tilia) species are an important component of many European woods, our knowledge of its genetics lags far behind that of many other well studied European woodland species, such as, oak, pine and beech.

Lime (both small-leaved lime, *T. cordata* and large-leaved lime, *T. platyphyllos*) was one of the dominant woodland trees across much of lowland Britain and northwest Europe by 6000 yr BP but is now one of Britain’s rarest native tree species. Where lime is present today, it often occurs as very old coppice stools, and it may have a link with prehistoric ‘wildwood’. Lime trees provide the key habitat for many rare species of plants, fungi and animals, forming unique communities reliant on lime woods for long-term survival. In the face of future climate change it is vitally important that the current status of lime woodland is understood to enable informed decision-making about how best to preserve this unique and ecologically important part of the landscape.

Lime woods in Britain are also important because of the roles they have played in human history. In ancient times lime was used for fodder, rope, hedging, honey and wax. Lime trees are planted central in many European towns and villages as a meeting point or for commemorative reasons. Its ecosystem services as food source for bees are important; a flowering lime tree is noted by its strong smell and the noise of the busy bees. From interactions with woodland managers and specialist interest groups it is clear there is an enormous interest in lime trees and woodlands.

We started to investigate the evolutionary genetics using the existing extensive body of excellent ecological research in lime. The population genetics of lime has been influenced by several processes. Firstly, after the ice age lime must have spread from its ice age refugia into regions where it is currently found. According to pollen records this was largely from southern and south-eastern European regions. *T. cordata* has reached a wider and more northerly distribution than *T. platyphyllos*. Secondly, the cooling climate from approximately 5000 BP has meant that sexual reproduction diminished at the northerly edges of its distribution. There the species have persisted through asexual reproduction and are potentially thousands of years old. Thirdly, humans have managed the trees to maximise fodder production through pollarding and coppicing (two types
of pruning). The effect of this is a lack of flowering, preventing sexual reproduction. Fourthly, the species can hybridise and form *T. x europea*, which seems to have regularly occurred in England.

There should still be a genetic signature of these processes in wild populations because lime has not been planted to any extent in woods (except in parks and along avenues). We have already received many samples from several researchers and interest groups from the UK and from many countries all over Europe. However, it was important to fill some gaps and visit some locations to meet local researchers and see the trees ‘in the flesh’. The Heredity Field grant helped us, myself and field assistant Arthur Leewis, achieve that. Our first location was in Colbitz (Germany), where the sign declared the wood the largest ‘Lindenwald’ in Europe. The wood consisted of about 60% lime trees, often what seemed to be huge clones of a single original tree that could well be a thousand or more years old.

We also stopped at three ancient lime trees in villages along the way; a book of 400 impressive lime trees in Germany was the source for these. We then drove through the Czech Republic and sampled a wood that seemed much younger with a few seedlings in a sunny moist spot. The next, again contrasting, wood was along the river Thaya, the border of Austria and the Czech Republic. Here, the trees were on a very rocky slope to the river, with huge self-coppiced trees that appear to be of extremely high age.

The national park headquarters in Hardegg had an interesting exhibition on the wildcat, including two live animals cared for by the head forester Wolfgang Riener. That day it was 38 degrees C: the next day we visited a site near Innsbruck with 7 degree C. This site (Stams) had a rare remnant of oak-lime wood in the Inn valley, surrounded by 2000m high Alps.

Our collection in Switzerland was made easy because live samples of both species from about 30 different locations in northwest Switzerland had been collected and grafted on stems in an orchard, to conserve genetic variation of the two species for the region. As more than one sample was grafted on the same stem Urs Rohner and Peter Rotach kindly helped us collect.

After that we visited several woods in France that happened to be in otherwise also interesting regions, namely the Burgundy and Champagne regions. Both Donald Piggott and Bruno Chopard had given us directions, which were easy to follow. We met Bruno in one of the locations where he told us that it is likely that woods that have a large amount of lime trees are likely to have been protected over the centuries by nearby abbeys.

All in all we collected some 333 samples, which we dried and sent to Newcastle. Here, they were safely put in a freezer, for DNA analyses. My PhD student, Prattana Phuekvilai, will undoubtedly make good use of them for her phylogeographic analyses. Further, they are crucial for finding species specific markers, and studying hybridisation and introgression. We will also be able to place the UK samples in the Europe wide spectrum. The samples form a solid basis for our research. Having seen the actual locations and growth forms of the trees has given a good insight and highlighted a few specific research questions. In addition, meeting local researchers will enable further collaboration.

I am grateful for the Genetic Society to have given me this opportunity.
Evolution of the Retinoic Acid Signalling Pathway

**Student** Samuel Downes  . **Supervisor** Tetsuhiro Kudoh, University of Exeter

Retinoic acid (RA) is a potent morphogen in vertebrates, regulating the development of many embryonic tissues, including the patterning of the head to tail axis by controlling hox gene expression. While hundreds of genes have clearly been shown to be affected by RA, only around twenty reveal functional Retinoic Acid Response Elements (RAREs). RAREs, constructed principally from heterodimers of Retinoic Acid Receptors (RARs) and Retinoid X Receptors (RXRs), undergo a conformational change when bound to all-trans RA, thus allowing the binding of transcriptional coactivators which either stimulate or inhibit the transcription of nearby genes.

The RXR has been found to be widely distributed in the animal kingdom, suggesting that retinoid signalling systems evolved before the development of invertebrates, and not, as previously believed, during the evolution of chordates. However, RXRs bind only to 9-cis RA, a derivative of RA which has not been detected endogenously within the vertebrates and thus appear to function only as a binding partner for the RAR in vertebrates. RA metabolism in vertebrates begins with the importation of retinol. However, only a single alcohol dehydrogenase gene, which is crucial in RA metabolism, resides in the genomes of invertebrates. Therefore, the oxidative metabolism of β-carotene has been characterised as the ancestral route of RA production. Recently, a RAR has been discovered within mollusces, suggesting that mollusc species may have been some of the earliest metazoans to have acquired a RA signalling pathway based upon all-trans RA. One study has shown that most organisms ranging from bacteria to vertebrates have a complement of enzymes that can be used in the RA signalling pathway, or at least some of which could be useful in the evolution of variants of such pathways. The aim of this project was to elucidate the role of the RA signalling pathway within mollusc embryonic development with the use of pond snails (*Lymnaea stagnalis*) as a model animal.

One group has also suggested that the hox1 gene is specifically expressed within the shell gland, an embryonic structure which leads to the formation of the shell, in different gastropod embryos. We have also obtained preliminary data showing that RA treated Japanese purple mussel, pond snail and limpet embryos failed to form shell structures. This investigation involves both RA and DEAB treatments, the latter of which inhibits retinaldehyde dehydrogenase function in the formation of RA. The majority of the embryos treated with RA before the ten hours post fertilisation (hpf) stage and exposed to concentrations of 10⁻⁶ M suffered mortality. In certain respects this highlights the significance of controlled RA signalling within invertebrates, although it may also represent the potential toxicity of the chemical. Embryos treated beyond 10hpf have undergone a significant period of unrestricted development; thus many of the embryos analysed for morphology at 24h intervals showed few or no differences when compared to control snails. However, treated snails suffered a visible reduction in size, which possibly reflects differences in hox gene expression.

Future studies may well need to assess the critical timing of treatment and/or modify the concentration of RA to which the embryos are exposed. Zygotic mRNA production begins approximately 3hpf, replacing the effects of maternal mRNA, and would seem an ideal checkpoint. Immunostained embryos, with the use of ACE anti-acetylated tubulin, which visualises cilia, were analysed in particular for the absence or reduced presence of structures as a result of RA or DEAB treatment. A reduction in mantle cilia was consistent in DEAB treated embryos; structures which perhaps have a role in shell formation. A clearer result was apparent from in-situ analysis. Control embryos showed a band of strong engrailed
expression in the region of the shell gland, but this band was absent in treated embryos. Due to the limited availability of *L. stagnalis* probes at the time of writing, due to incomplete sequencing of the species' genome (this will assessed in the future with the collection and sequencing of inbred specimens), the expression of engrailed, rather than hox, was determined. Engrailed has a significant role in protoconch (embryonic shell) formation, as described in gastropods, and it is plausible that engrailed, hox and RAREs coevolved as genetic precursors for shell construction; the results of which are possibly related to the sudden appearance of shelly fossils during the Cambrian era. If true, and RA affects only Hox gene transcription and not that of Engrailed, then perhaps transcription of only the latter is enough to cause the formation of a shell, but one which is prone to damage due to the insufficient production of shell proteins or hormones.

The fluorescent dye Bodipy C5-ceramide clarifies cell outlines of live embryos, making it easier to judge the roles of different cells in embryonic development. Live embryos were also treated with the fluorescent dye FM-143 in order to further investigate neuronal development, a key indicator of embryonic advancement. Both revealed the development of organs and specialised tissues sometime earlier than the 24hpf stage, although there was not sufficient time for RA or DEAB treated embryos to be analysed. In using RA and DEAB treatments, we have to consider the possible effects of the chemical upon other molecules within an organism. Does Aldh2, inhibited by DEAB, oxidise or reduce other molecules? Thus, the possible effects apparent in *L. stagnalis* could result from reactions not considered here. Does RA have other unconsidered effects? If the RA signalling pathway is present in invertebrates, then does it play a role in the development of tissues besides the shell, areas which should receive closer attention?

Changes in foot morphology and eye development seem to have been caused by RA and DEAB treatment (and may well be caused by changes in hox transcription, due to the pluripotent nature of the genes involved).

This study has highlighted the significance of retinoic acid within invertebrates, and provides further evidence that the RA signalling pathway evolved long before the evolution of chordates. However, the role and nature of this pathway needs to be elucidated, in particular its links to hox expression and the head to tail axis, itself inextricably linked to the evolution of a phenomenal diversity of organisms. I am grateful to the Genetics Society for giving me my first research opportunity and to Tetsuhiro Kudoh, Sulayman Mourabit and Sarah Derry for all their help and advice.

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**Detailed Expression Analysis of Notch Pathway Components in Axial Tissues of Developing Chick and Mouse Embryos**

*Student* Hannah Cook  . *Supervisor* Dr Shona Gray and Dr Kim Dale, University of Dundee

During my summer studentship I assisted on a project aiming to observe and document the mRNA expression of notch signalling components during early embryonic development. Expression of the selected signalling components was observed at three stages of chick development and at one stage of mouse development.

In the chick the selected signalling components were the receptors *cNotch1* and *cNotch2*; ligands *cDelta1*, *cSerrate1* and *cSerrate2*; and targets *cHairy1*, *cHairy2* and *cLfng*. Each was observed at chick stages HH4, HH5/6 and HH7/8 (HH – Hamburger Hamilton). In the mouse the selected signalling components were receptors *mNotch1*, *mNotch2*, *mNotch3* and *mNotch4*; ligands *mDelta1*, *mDelta3*, *mDelta4* and *mJagged1*; and targets *mHes1*, *rHes5*, *mRfng* and *mLfng*. All notch components in the mouse
The staining patterns created by the probes were observed and recorded by photography in both the whole embryo and in transverse embryonic sections along the entire body axis.

were observed at embryonic day (e)8.5. The location of each mRNA was identified through the use of a specific labelled antisense probe. To ensure experimental accuracy, each probe was observed in five different embryos at each selected developmental stage. The staining patterns created by the probes were observed and recorded by photography in both the whole embryo and in transverse embryonic sections along the entire body axis. These photographs were recorded and data from them extracted and entered manually into an Excel expression analysis table.

Preparation of Embryos for Analysis

The first stage of the process involved the harvest of embryonic mice and chicks. Additional to dissection of the required stages, I also gained experience of dissecting older embryos – chick stages HH11, HH22, HH24 and mouse stage e10.5. Following harvest the embryos were placed into a 4% Fix/2mM EGTA/PBS solution, before dehydration using increasing concentrations of EtOH in PBST (PBS; 0.1% Tween 20) solution (up to 100% EtOH).

Labelled probe preparation involved use of a restriction digest protocol to isolate the required DNA fragments, with purification using a Qiaquick PCR purification kit (Qiagen), before implementing in-vitro transcription to transcribe them into their RNA counterparts with purification using an RNeasy Mini-kit (Qiagen).

The probe was then applied to the embryos making use of a well-established in situ hybridisation protocol that allows the labelled probe to bind to the target RNA and the signal to be amplified and then detected under a dissection scope. In the interest of time many of the in situ hybridisations were performed using an automated robot over an approximate two day period.

After the in situ hybridisation protocol was completed, whole mount photographs of the embryos were collected. The prepared embryos were mounted in agar and frozen, before being sectioned in 25µ divisions along the transverse plane using a cryostat. The sections were mounted onto slides, allowing the specific areas of interest to be identified and photographed using a Leica DM500 microscope and associated camera.

Analysis of Notch Component Expression

Expression of the selected notch components was analysed in selected regions along the cranio-caudal axis. All embryos were analysed in the region of the progenitor cells, primitive streak and prenode/prechordal area – with additional analysis in the region of the notochord, emerging somites and presomatic mesoderm in the later chick and mouse stages. Expression was analysed according to location within each of these regions, and strength of the colour reaction. These findings were recorded in the Excel expression analysis table for publication in conjunction with the embryonic images. For each notch signalling component at a specific stage, the embryo in the best condition and displaying the most accurate representation of the mRNA distribution was selected to have its associated images assembled into panel form for publication.

Summary

During the project, I completed analysis of over 190 embryos and participated fully in every stage of preparation and analysis. I was also able to begin mid-sagittal sectioning of mouse embryos for each notch signalling component, however due to time restrictions and developing methods, I was unable to complete this area of the study. The data I have amassed will constitute part of a manuscript that we hope to submit for publication towards the end of the year.

I would like to thank the Genetics Society for their financial support – without which I would have been unable to take advantage of this wonderful opportunity and develop my skills and interest in the field of developmental biology. I would like to thank Shona and Kim, whose support and expertise was unfaltering and invaluable, and all of the JKD lab, who made my summer go very very quickly indeed.
Comparative study of rate of DSB repair in *Saccharomyces cerevisiae*

*Student* Constantinos Drousiotis . *Supervisor* Dr.Alistair Goldman, The University of Sheffield

**Background Information**

DNA double-strand breaks (DSBs) are a major source of genome damage, and their accurate repair is essential to maintain genome integrity and stability. DSBs can be caused by: hydroxyl radicals, ionizing radiation, UV light by increasing ROS (reacting oxygen species) and nuclear enzymes such as Topoisomerase II, which releases supercoiling during DNA replication. This study concentrated on repair of a DSB caused by HO-endonuclease at the MAT locus, which is required for mating type switching in *Saccharomyces cerevisiae*. The DSB is repaired by homologous recombination (gene conversion) between MATa and HML (hidden MAT left) or MAT and HMR (hidden MAT right). HO cuts within MAT and various proteins including MRX complex along with Sae2 and Exo1 are recruited to allow competent resection of the single strand ending 5´ at the DSB site. They trim DNA in a 5´->3´ direction leaving single-stranded 3´ overhangs. The MRX complex includes Mre11, Rad50 and Xrs2 proteins is thought to be involved more in the damage signaling pathway and recruitment of e.g. Exo1m rather than in directly catalysing DNA removal. The single-stranded DNA attracts Rad51 that binds single-stranded DNA and catalyses invasion of the donor cassette, HML or HMR. Mre11 does have nuclease activities that are required for resecting modified DNA ends, such as DSBs stimulated during meiosis and covalently bound to Spo11. Recent published work in this laboratory has led to the conclusion that contrary to the work of other groups, Mre11 nuclease activity is active during processive resection in meiosis (Hodgson et al 2011 DNA repair 10:138). My project was designed to retest Mre11 nuclease dead alleles for their influence on HO-DSB repair in mitotic cells. We used diploids which expressed different alleles of MRE11 i.e. mre11A/MRE11, mre11A/mre11-58S, mre11A/mre11-H125N and compared the abilities to repair the HO-endonuclease induced DSB.

**Methods**

We undertook our experiments using diploid yeast, *Saccharomyces cerevisiae*. One parent haploid strain contained a galactose inducible HO-endonuclease gene, and was deleted for MRE11. This was mated with strains deleted for HO-endonuclease and expressing one of MRE11, mre11-H125N or mre11-58S. HO-endonuclease gene was induced in galactose medium in each of the diploids expressing different MRE11 alleles. Expression of HO was allowed to continue for 1.45h and stopped by returning cells to glucose medium. Cells were sampled for DNA extraction before, during and after HO expression. The DNA was restriction endonuclease digested and displayed by native agarose gel electrophoresis and Southern Blotting, using a probe adjacent to the MAT locus.

The Southern analysis detected two bands, a parental MAT locus and a fastest moving band representing the MAT locus with an HO-induced DSB. By measuring the relative intensities of these bands, we set out to compare the rates of repair in cells expressing each of the MRE11 alleles.
DSB. By measuring the relative intensities of these bands, we set out to compare the rates of repair in cells expressing each of the MRE11 alleles.

**Results**

In the short time available, the system was tested and we determined the time needed for good induction of the HO-endonuclease and repair after washing out the galactose. Two strains were analysed in some detail, one expressing MRE11, and one expressing mre11-58S.

The HO-DSB was made efficiently in both strains, reaching 100% of MAT DNA after 1.45h. After washing out the galactose and providing glucose medium the DSB-band diminished and the parental band reappeared representing repair. By 0.5h after reintroduction into glucose rich medium all DSBs detectable were repaired. We could not distinguish between the two strains for timing of repair. However, the pattern of gel bands is similar and this suggests that the mutant strain (ie.mre11-58S) may employ other exonucleases with redundant action to carry out MRE11 activity.

Further experiments are required with more frequent sample to confirm this result and test the mre11-H125N strain. These experiments will be undertaken by current undergraduate project students.

I would like to thank Genetics Society for funding my project which gave me the opportunity to gain valuable lab experience and transferrable skills. I really appreciated the help I received from my supervisor Dr.Goldman Alistair, his master’s student Miss L Mawlong and PhD students in the laboratory.

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**Sexual Selection and Wolbachia**

*Student* Daniel Soanes-Brown  
*Supervisor* Dr Damien Smith, University of Exeter

Wolbachia (Wol) is an endosymbiont that infects *Drosophila* species and many other arthropods found throughout the world. Some Wol live as parasites within their hosts, whilst others maintain a more mutualistic relationship. The detrimental strains of Wol are known to decrease host fitness by reducing population productivity (number of offspring per generation), reducing sperm competitive ability and increasing the risk of extinction by decreasing the genetic diversity of a diminishing population size. In contrast, Wol has also been implicated in increased host fitness, for example by improving resistance of *Drosophila melanogaster* to RNA viruses including the Nora Virus and West Nile Virus. Wol occupies cells throughout the host’s body, but most notably the cells of the testes and ovaries, so their interactions with host reproduction are of particular interest. Male killing, feminization and cytoplasmic incompatibility (CI – a paternally transmitted form of embryonic lethality) have been attributed to the presence of Wol and related to their drive within host populations.

Our interest in the bacterium stems from a previous 30 generation experimental evolution study on Australian *Drosophila simulans* that displayed anomalous fitness trends across treatment groups. After exhausting other possible explanations for these results, and given the potentially profound effect of Wol on host reproduction and fitness, we decided to determine the infection status of our experimental evolution lines by PCR diagnostic. Wol frequencies were found to be high at generation 1 across all the lines. Intriguingly, while we found that Wol frequency in populations which were undergoing sexual selection had decreased over time, those without sexual selection had maintained higher infection frequencies. To determine why sexual selection influences the frequency of Wol we needed to first determine the exact nature of the Wol phenotype. We hope that this can then inform further investigation of the subsequent population dynamic feedback between Wol and its host.

Preliminary multi locus sequence typing (MLST) concluded that the specific Wol genotype infecting our *D. simulans* populations was 100% matched to a previously identified genotype responsible for CI. We produced Wol-infected isolines from one of the experimental evolution lines and, through subsequent tetracycline curing, parallel Wol-cured flies so that for each isoline we had Wol-infected and Wol-cured populations. A pilot study of these
flies did not reveal CI, but did expose a possible male fertility effect in Wol-infected males.

Further experiments were conducted to determine the effects of male and female infection status on mating behaviour and fitness components, including fecundity and egg viability, as well as total adult offspring production. These consisted of full factorial (for male and female infection status) mating assays followed by female egg laying over consecutive days, and either assessment of fecundity and egg hatching or of total offspring eclosed from each day’s laying.

Preliminary results suggest that, in our *D. simulans* populations, Wol does affect non-competitive mating behaviour and also has significant fitness effects. Future studies will be directed at determining competitive mating effects including both pre- and post-copulatory measures of male mating success.

I would like to thank the Genetics Society for funding my studentship, and everyone in the biosciences department at Exeter University for their help and guidance during the project.

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**Development of bioinformatic methods for the analysis of human DNA methylation**

**Student** Harry Clifford  
**Supervisor** Dr Richard D. Emes, University of Nottingham

The term epigenetics refers to heritable changes in gene function which are not related to changes of the underlying genomic material. One such epigenetic control mechanism is DNA methylation. Methylation of DNA is a major component regulating gene expression, and plays a central role in both deciding cellular identity and differentiation, and in directing cellular development. Generally, methylation of the cytosine residues in a CpG dinucleotide within CpG islands is associated with reduced gene expression. However, inappropriate methylation can cause genome-wide effects. For example genome-wide hypomethylation can lead to chromosomal instability and potentially an increase in the frequency of DNA breaks. Determining differential methylation of human samples is becoming a more common approach in basic and clinical studies. A recently developed method to determine DNA methylation across the human genome is Illumina’s Infinium methylation beadchip. The 27k array simultaneously measures the relative methylation level of 27,578 individual CpG sites across 14,495 genes resulting in an intuitively interpretable beta-value. Beta-values vary between zero and one corresponding to a completely unmethylated or completely methylated CpG respectively. Recently this platform has been extended to measure approximately 450,000 CpGs. Methods to identify differentially methylated sites are often based on comparisons of samples to identify those sites which are statistically different between *a priori* defined groups. However, methods to determine these groups and visualise membership within them have proved hugely valuable in either confirming expectations or identifying novel avenues of research. Cluster analysis is one such approach to provide this information. Cluster analysis is an approach to separate data into groups or clusters based on similarities. Hierarchical clustering can proceed using various linkage and distance methods. The distance method determines how the distance between two observations is calculated, for example, the shortest distance between two points, is
The linkage method is used to decide the position in a cluster from which measure the distance to merge two clusters. For example the distance of the furthest points may be used, known as Complete Linkage. We applied these methods to compare the methylation profiles of fetal DNA samples born to mothers on Anti-epileptic drugs to those not. All samples were collected as part of a World Cancer Research Funded, UK Clinical research network portfolio study with full local NHS ethical approval (EFFECT-M, UKCRN study ID 6864).

Methods
The software environment and programming language R was used for development of a script to carry out hierarchical clustering using a combination of algorithms. Twenty-eight different hierarchical cluster analyses were conducted combining seven linkage methods, with four distance methods. The seven linkage methods used were Average/UPGMA, Centroid, Complete, Mcquitty/WPGMA, Median, Single, and Ward’s. The four distance methods used were Canberra, Euclidean, Manhattan, and Maximum. The silhouette width was used to determine the relatedness of samples in a cluster and the separation of different clusters. The maximum mean silhouette width was used to rank and determine the most appropriate combination of linkage and distance measures.

The output of this software is a collection of dendrograms showing the clustering of the samples. Optionally, the pvclust package which quantifies the uncertainty of each node in a hierarchical cluster can be implemented from within the developed software. In this way the internal resolution of the clusters can also be determined. This approach therefore provides a robust framework for the investigation of data. The script is freely available at http://www.nottingham.ac.uk/~svzrde/software.htm

Results and Discussion
For the 18 patients, the clustering with the highest silhouette width was obtained using the Canberra distance method with Ward’s linkage. Two clusters were identified with very good bootstrap support. Although little change is seen between the individual anti-epileptic drug patients, there is a clear reproducible difference in global methylation between the cord blood DNA of babies born to mothers on anti-epileptic drug treatment and the control group. Few consistent changes were identified using NIMBL. A single gene SMYD4, a potential tumour suppressor gene was identified as having an average difference of ≥ 20% methylation between groups. This suggests that the differences seen in the dendrogram are due to a large number of small differences which possibly have an accumulative effect.

The general applicability of the clustering approach for investigating methylation data was tested by simulation of 1000 datasets of 18 patients. The ability of the various method combinations to accurately cluster the simulated data was determined using the Rand method. The approach developed to rank distance and linkage combinations was shown to be an accurate method to determine the most robust clustering for a given set of data.

I would like to thank The Genetics Society for funding this studentship project. I would also like to thank my supervisor Dr. Richard Emes for supervision, and PhD student Frank Wessely for advice. The data was produced in collaboration with the Fetal Epigenomics group, Professors Bill Farrell (Keele University), Khaled Ismail and Tony Fryer (UHNS NHS Trust) and Will Carroll (Derby Childrens Hospital).
Developing cytogenetic tools to analyse tropical Begonias

Alex Twyford. University of Edinburgh and Royal Botanic Garden Edinburgh

Begonias are one of the most familiar herbaceous plants to tropical botanists, with more than 1500 species found throughout the tropics. I returned from a productive collection trip to Mexico in the Spring 2010 (see Genetics Society News issue 64) with lots of material ready for genetic analysis. I was particularly keen to characterise potential hybrid plants I had collected which were intermediate in morphology between two weedy Begonia species. My plan was to assess how much gene flow occurs between two species that have distinct habitat preferences. Before the collection trip I had developed nuclear microsatellites, which could give a preliminary insight into the degree of gene flow at a handful of loci. However, getting a genome-wide snapshot requires a different set of genetic tools.

Cytogenetic analyses, such as genomic in situ hybridisation (GISH), is one such technique that can do this. In this method, fluorescent probes are made that are complementary to total genomic DNA of the putative parent plants. Different coloured probes, corresponding to different parents, are then annealed to chromosome preparations of the hybrid plants. After a series of washes to remove background signal, the chromosome preparations are examined under a fluorescent microscope, and, in theory, chromosome segments where the probes anneal fluoresce in the colour corresponding to the parent that contributed them. Therefore a typical F1 hybrid may have one set of homologous chromosomes with the colour to match parent A, and the second set of chromosome matching the colour of parent B. Over successive generations of backcrossing this clear pattern of fluorescence will break down as recombination occurs. So, GISH gives a valuable insight into the chromosome number and the relative contribution of genetic material from each parent in early generation hybrid plants.

The genetics society co-sponsored a training visit for me to learn this technique in the lab of Prof. Andrew Leitch, at Queen Mary University London. My aim was to pick up the technique using tobacco plants (genus Nicotiana), which they routinely study, and attempt this technique on my Mexican Begonia plants. My time in London was limited to just 5 weeks, so this would be quite a challenge. Overall I had some success during my short training visit. Begonias have very small chromosomes, about a tenth of the size of tobacco plants. It took a couple of weeks to perfect my squash technique, to get an even spread of these tiny chromosomes on the slide. I also succeeded in getting the positive control to work. For this, we used a probe for ribosomal DNA (rDNA), which is ubiquitous in all plants. We saw a faint signal corresponding to a few hundred rDNA repeat units – roughly an order of magnitude less than what you can see in tobacco. However, the genomic probes I designed didn’t work well and this may be due to a number of reasons, such as the quality of the original DNA that I extracted.

During my stay, I learnt a lot about the ways in which you can study plant genomes from a cytological perspective, which has lost favour in recent years as many researchers have concentrated on using high throughput sequencing to analyse genomes. Seeing the way researchers were using next generation DNA sequencing to generate genomic resources from which cytogenetic probes could be designed illustrated the continued value of using these approaches. Moreover, making cytological observations on the wide range of species that people work on in the lab was an excellent reminder of the dynamic structural differences of plant chromosomes.

We hope to continue this collaborative project to get some good cytogenetic results for future publications on chromosome numbers and genome organization in Begonia. I would like to thank Andrew Leitch, Simon Renny-Byfield, Heike Brinkman, Richard Buggs and Andrew Matthews for their hospitality during my stay and the help they gave me in the lab, as well as the Genetic Society for contributing toward the costs of my visit.
See the relevant web pages and downloadable Funding Application Forms at www.genetics.org.uk

One-off Meeting Sponsorship

Purpose
Sponsorship of genetic research meetings not organised by the Genetics Society.

The Genetics Society receives several requests from members each year to sponsor meetings in the field of genetics. These meetings are usually one-off meetings with an ad hoc organising committee and may be partly sponsored by another Society. The guidelines below indicate a review process for applications and the conditions that must be met for the award of Genetics Society sponsorship.

Review of applications
1) Members may make applications at any time. They should be submitted on the GS Funding Application Form and emailed to Linda Allardyce <Linda.Allardyce@portlandpress.com> using message subject ‘Meeting Sponsorship’ and your surname.
2) The application will be circulated to the full committee for review. The review will cover suitability of the meeting for Genetics Society sponsorship and level of support requested.
3) The committee will be asked to respond within two weeks and the Society aims to respond to requests within four weeks.

Conditions of sponsorship
4) Several levels of sponsorship are possible: (a) single lecture: £200 (b) session: £500-1000 (c) major sponsor: £1500-2000.
5) Genetics Society sponsorship must be mentioned in all pre-meeting publicity (e.g. posters, flyers, website) and in the meeting programme. If the Genetics Society is the major sponsor the meeting should be advertised as a “Genetics Society-sponsored meeting”.
6) Details of the programme of the meeting and registration forms should be sent as far in advance as possible to Linda Allardyce <Linda.Allardyce@portlandpress.com>, for inclusion in the Society’s newsletter and on the website.
7) A short report on a meeting that receives sponsorship of £1000 or more, for possible publication in the newsletter and on the website, should be sent to Linda Allardyce <Linda.Allardyce@portlandpress.com> within one month of the conference taking place.
8) Genetics Society sponsorship may be used at the organiser’s discretion, but budget travel and accommodation options should normally be insisted upon. Any unused grant should be returned to the Genetics Society. The Society will not be responsible for any losses incurred by the meeting organisers.
9) An invoice for the grant awarded should be submitted to Linda Allardyce <Linda.Allardyce@portlandpress.com>. The grant may be claimed in advance of the meeting and no longer than one month after the meeting.
10) The meeting organisers agree to make details of how to apply for Genetics Society membership available to non-members attending the sponsored meeting. Meetings that receive maximum sponsorship will be expected to offer a discounted registration fee to Genetics Society members to encourage non-members to join the Society at the same time. New members may then attend at the discounted rate, once confirmation of their application for membership of the Genetics Society has been received from the Society’s Office.
New Sectional Interest Groups

Purpose

Regular (e.g. annual) funding is available for genetics research communities who wish to run regular series of meetings. Current examples include Arabidopsis, the Population Genetics Group and the Zebrafish Forum.

Members may make applications for new Sectional Interest Groups at any time. Applications should be submitted on the GS Funding Application Form and emailed to Linda Allardyce <Linda.Allardyce@portlandpress.com> using message subject ‘New Sectional Interest Group’ and your surname. The award of Genetics Society support will be subject to review of applications by the committee and subject to the following conditions.

1) The sponsorship of the Genetics Society must be mentioned in all pre-meeting publicity (e.g. posters, flyers, website). It should also be acknowledged in the meeting programme booklet. It is understood that wherever possible, the meeting should be advertised as ‘A Genetics Society Meeting’, however, where the Society’s financial contribution support is only partial, and where this formula of words would conflict with the interests of other sponsors, it is acceptable for the meeting to be advertised as a ‘Genetics Society-Sponsored Meeting’.

2) Details of the programme of the meeting should be made available to all Genetics Society members via the Society’s newsletter, and electronic copy should be sent as far in advance as possible to the newsletter editor, at the latest by the advertised copy date for the newsletter preceding the close of registrations for the meeting. The same details will appear on the Genetics Society website. This information should include the programme of speakers, the topics to be covered, plus details of how to register for the meeting.

3) A report on the meeting, once it has taken place, should be submitted for publication in the newsletter, which is the official record of the Society’s activities. This should be sent as soon as possible after the meeting to Linda Allardyce <Linda.Allardyce@portlandpress.com>, and should include brief factual information about it (where and when it took place, how many people attended and so on), together with a summary of the main scientific issues covered.

4) Genetics Society funds may be used to support speaker travel, accommodation, publicity or any other direct meeting costs, at the organizers’ discretion. It is understood that budget travel and accommodation options will normally be insisted upon. Any unused funds should be returned to the Society. The Society will not be liable for any financial losses incurred by the meeting organizers. Any profits should be retained solely for the support of similar, future meetings, as approved by the Society.

5) A written invoice for the agreed amount of Genetics Society sponsorship should be forwarded to Linda Allardyce <Linda.Allardyce@portlandpress.com>, no later than one month after the meeting date. Funds may be claimed in advance of the meeting, as soon as the amount of support has been notified in writing.

6) Meeting organizers may levy a registration charge for attendance at the meeting as they see fit. However, it is understood that Genetics Society members will be offered a substantial discount, so as to encourage non-members wishing to attend to join the Society at the same time. The meeting organizers agree to make available to non-member registrants full details of how to apply for Genetics Society membership, such as appear on the website and in the newsletter, and may charge such persons the same registration fee as charged to members, upon confirmation from the Society’s Office that their application and remittance or direct debit mandate for membership fees has been received.

7) The meeting organizers are free to apply to other organizations for sponsorship of the meeting, as they see fit. However, organizations whose policies or practices conflict with those of the Genetics Society should not be approached. In cases of doubt, the officers of the Genetics Society should be consulted for advice.
New Sectional Interest Groups (continued)

8) If the meeting is advertised on the Internet a link to the Genetics Society website (www.genetics.org.uk) should be included.

9) For those groupings holding their first such meeting with Genetics Society support, it is understood that the Society’s support for future meetings of the series will be decided on the basis of the success of the first meeting, including adherence to all of the conditions listed above. The first meeting is hence supported on a pilot basis only.

10) The meeting organizers will nominate a responsible person who will liaise with the Genetics Society on all matters relating to the meeting, and whose contact details will be supplied to the Society’s Office. This person will inform the Society if he/she resigns or passes on his/her responsibility for the meeting or series to another person, whose contact details shall also be supplied.

Junior Scientist Grants

Purpose
To support attendance at genetics research meetings by junior scientists. In this section, junior scientists are defined as graduate students and postdoctoral scientists within two years of their PhD viva.

Travel and accommodation to the Genetics Society meetings
Grants up to £150 are available for travel and essential overnight accommodation costs to attend all Genetics Society meetings, including the Genetics Society’s own bi-annual meetings and meetings of our Sectional Interest Groups. The cheapest form of travel should be used if possible and student railcards used if travel is by train. Airfares will only be funded under exceptional circumstances.

How to apply: for the Genetics Society’s own Spring and Autumn meetings, applications should be submitted using the meeting registration form, before the final deadline of the meeting.

For meetings of our Sectional Interest Groups (eg, Arabidopsis, Population Genetics Group, Zebrafish Forum), junior scientist travel claims should be submitted on the GS Funding Application Form at any time and emailed to theteam@genetics.org.uk using message subject “Travel to GS meeting” and your surname.

Other conditions: applicants must have been members of the Genetics Society for at least one year. There is no limit to the maximum frequency at which the grants can be awarded for attending the Genetics Society meetings.

Travel, accommodation and registration cost at other meetings
Grants of up to £750 to attend conferences in the area of Genetics that are not Genetics Society meetings (including sectional meetings) are available to junior scientists.

How to apply: applications should be submitted on the GS Funding Application Form by email in time for one of the quarterly deadlines (1st day of February, May, August and November), to theteam@genetics.org.uk using message subject “JSTG” and your surname. Please ask your supervisor to send a very brief email in support.

Other conditions: applicants must have been members of the Genetics Society for at least one year. Recipients of these grants will be asked to write a short report that may be included in the newsletter. A maximum of one grant per individual per two years will be awarded.
Training Grants

Purpose
To support attendance at short training courses.

Grants of up to £1,000 are available to enable members to go on short training courses in the area of Genetics research. Eligible expenses include travel, accommodation, subsistence and tuition fees.

How to apply: there are two closing dates of 1st March and 1st September each year. Applications should be made on the GS Funding Application Form and should be emailed to Linda Allardyce <Linda.Allardyce@portlandpress.com> using message subject ‘Training Grant’ and the applicant’s surname. Applications from PhD students should be accompanied by a very short supporting e-mail from the supervisor.

Closing date: awards will be announced within two months of the closing date. A maximum of one Training Grant per individual per three years will be awarded.

Heredity Fieldwork Grants

Purpose
Grants of up to £1,500 are available to cover the travel and accommodation costs associated with pursuing a field-based genetic research project or to visit another laboratory for training. The research field should be one from which results would typically be suitable for publication in the Society’s journal Heredity. The scheme is not intended to cover the costs of salaries for those engaged in fieldwork or training, or to fund attendance at conferences.

How to apply: there are two closing dates of 1st March and 1st September each year. Applications should be made on the GS Funding Application Form and should be emailed to Linda Allardyce <Linda.Allardyce@portlandpress.com> using message subject ‘Heredity FW grant’ and the applicant’s surname. Applications from PhD students should be accompanied by a very short supporting e-mail from the supervisor.

A panel of members of the Genetics Society committee will review applications including both information on the student and the proposed project. Feedback on unsuccessful applications will not be provided. Awards will be announced within two months of the closing date.

Other conditions: Applicants must have been members of the Genetics Society for at least one year. Only one application from any research group will be admissible in any one year. Recipients of these grants will be asked to write a short report within two months of completion of the project that may be included in the newsletter. A maximum of one grant per individual per three years will be awarded.
Genes and Development Summer Studentships

Purpose
To support vacation research by undergraduate geneticists.

Grants of up to £3,000 are available to provide financial support for undergraduate students interested in gaining research experience in any area of genetics by carrying out a research project over the long vacation, usually prior to their final year.

Applications must be made by Principal Investigators at Universities or Research Institutes. The application must be for a named student. Studentships will only be awarded to students who have yet to complete their first degree i.e. those who will still be undergraduates during the long vacation when the studentship is undertaken. There are no restrictions concerning the nationality or membership status of the student, and the student does not have to attend a UK university.

How to apply: there is one closing date of 31st March each year. Applications should be made on the GS Funding Application Form which, along with the student’s CV, should be emailed to Linda Allardyce <Linda.Allardyce@portlandpress.com> using message subject ‘G & D studentship’ and the PI’s surname. The student’s tutor or equivalent must also send a reference. Undergraduate students who wish to do vacation research projects are encouraged to seek a PI to sponsor them and to develop a project application with the sponsor.

The studentship will consist of an award of £225 per week for up to 10 weeks to the student plus a grant of up to £750 to cover expenses incurred by the host laboratory. Both elements of cost must be justified. The award will be made to the host institution. The student will receive free membership of the Genetics Society for one year.

A panel of members of the Genetics Society committee will review applications including both information on the student and the proposed project. Feedback on unsuccessful applications will not be provided.

Other conditions: applicants must have been a member of the Genetics Society for at least one year. Recipients of these grants will be asked to write a short report within two months of completion of the project that may be included in the newsletter. A maximum of one grant per individual per three years will be awarded.
Personal Subscription
Order Form

Please return this form to The Genetics Society, c/o Portland Customer Services, Commerce Way, Colchester CO2 8HP

The new personal subscription rate for Genes and Development for 2012 is £128, inclusive of airmail delivery. The subscription runs on a yearly basis from January 1st. The full subscription will be charged and back issues supplied when applications are made after January of each year.

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Payment

Payment can be made by cheque (payable to “Genetics Society”), credit card (add 3.6%) or direct debit. If you already pay by direct debit you do not need to complete a new mandate. If you wish to set up a direct debit for your Genes and Development subscription, a mandate will be sent to you on receipt of this form.

1. I enclose a cheque or Sterling Eurocheque for £128.

2. I instruct you to use my existing direct debit agreement to debit my account in January each year for my subscription to Genes and Development.

Signed ............................................................................................................................................................................................

3. I instruct you to set up a new direct debit agreement to debit my account in January each year for my subscription to Genes and Development and enclose the completed mandate

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4. Please debit my Visa/Mastercard

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The Genetics Society was founded in 1919 and is one of the world’s first societies devoted to the study of the mechanisms of inheritance.

Aims
The Genetics Society was founded in 1919 and is one of the world’s first societies devoted to the study of the mechanisms of inheritance. Famous founder members included William Bateson, JBS Haldane and AW Sutton. Membership is open to anyone with an interest in genetical research or teaching, or in the practical breeding of plants and animals.

Meetings
The main annual event of the Society is the Spring Meeting. This has at least one major symposium theme with invited speakers, and a number of contributed papers and/or poster sessions.

One day mini-symposia are held during the year in different regions so that members from different catchment areas and specialist groups within the society can be informed about subjects of topical, local and specialist interest. Like the spring symposia these include papers both from local members and from invited speakers. One of these meetings always takes place in London in November.

Young geneticists’ meetings
Currently there are three meetings devoted to talks and posters by students and junior postdocs. Promega UK is sponsoring travel to these meetings and prizes for the best contributions, plus costs for the three winners to attend the following Spring Meeting and national finals.

Invited lectures
The Mendel Lecture, in honour of the founder of modern genetics, is given usually on alternate years at a London Meeting by an internationally distinguished geneticist.

To encourage younger geneticists, the Balfour Lectureship (Named after our Founder President) recognises the contribution to genetics of an outstanding young investigator, who must normally have less than ten years postdoctoral research experience at the time of the lecture. The winner gives the lecture at the Spring Meeting.

International links
The Society has many overseas members and maintains links with genetics societies in other countries through the Inter-national Genetics Federation, the Federation of European Genetics Societies and through the International Union of Microbiological Societies.

Publications
The Society publishes two major international scientific journals: Heredity, concerned with cytogenetics, with ecological, evolutionary and bio-metrical genetics and also with plant and animal breeding; and Genes and Development, which is jointly owned with Cold Spring Harbor Laboratories and which is concerned with molecular and developmental aspects of genetics.

Full and student members are entitled to reduced subscriptions both to these journals and also to Genetics Research, published by Cambridge University Press, to Trends in Genetics, a monthly journal published by Elsevier with review articles of topical interest aimed at the general reader, Nature Genetics, published by Nature Publishing company (MacMillan Magazines Limited), Current Biology journals, BioEssays and Chromosome Research.

A newsletter is sent out twice a year to inform members about meetings, symposia and other items of interest.

Specialist interests
Six specialist interest areas are covered by elected Committee Members: Gene Structure, Function and Regulation; Genomics; Cell & Developmental Genetics; Applied and Quantitative Genetics; Evolutionary, Ecological and Population Genetics; Corporate Genetics and Biotechnology. The Committee Members are responsible for ensuring that the various local and national meetings cover all organisms within the broad spectrum of our members’ interests.
Please complete this form and return it, along with your cheque, Direct Debit instructions or credit card to The Genetics Society, Portland Customer Services, Commerce Way, Colchester CO2 8HP, UK. Complete this section carefully. The information you provide will help us to correspond with you efficiently and ensure that your details are accurately held on our membership database.

1. IDENTIFICATION (as data controllers we adhere to the Data Protection Act 1998)

Title: Prof. [ ] Dr. [ ] Mr. [ ] Miss. [ ] Mrs. [ ] Ms. [ ]

Last Name: ____________________________ First Name: ____________________________

Institution: ____________________________

Institution Address: ____________________________

Postcode: ____________________________ Country: ____________________________

Telephone: ____________________________ Fax: ____________________________

Email: ____________________________

Your home address should only be given when there is no alternative. Please ensure that you have included your email address.

2. AREAS OF INTERESTS (tick as appropriate)

Gene Structure, Function and Regulation [ ] Genomics [ ]

Cell and Developmental Genetics [ ] Applied and Quantitative Genetics [ ]

Evolutionary, Ecological & Population Genetics [ ] Corporate Genetics and Biotechnology [ ]

3. MEMBERSHIP FEES

Membership entitles you to reduced rate entry to meetings, discounts on journals, free Society newsletters plus free online access to Heredity. The annual membership charges are as follows (please tick applicable box):

[ ] Full Member: *£25.00 [ ] Postgraduate Member: *£15.00 [ ] Undergraduate Member: £5.00

* there is a reduction of £5.00 from the membership charge for full and postgraduate members paying by Direct Debit

4. STUDENT MEMBERSHIP (if this section is not applicable please go to section 5)

As a student member of the Society you are eligible to apply for a grant to defray the cost of attendance at meetings organised by the Society. Full details regarding grants is available on the web site. In addition, after one year full membership you can apply for a grant for overseas travel to international meetings held outwith the Society.

If you are applying for an undergraduate membership please state year of graduation: ____________________________

If you are applying for a postgraduate membership please state year of starting research degree: ____________________________

Signature of Head of Department/Supervisor ____________________________

Please note: After four years’ postgraduate membership you will be required to pay the full subscription fee.
5. PAYMENT

Option 1: Direct Debit (UK Bank Accounts only)
Complete this membership form and a Direct Debit mandate form, which can be downloaded from our website and send them to the address below.

☐ I wish to pay by Direct Debit (tick box if applicable). Paying by Direct Debit entitles Full members and Postgraduates to a saving of £5.00 from the price of their membership. Direct Debit Membership Subscriptions are renewed on an annual basis.

Option 2: Cheque/Bank transfer

☐ I enclose a cheque for the sum of £____________ made payable to Portland Customer Services

To facilitate identification please confirm:

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Option 3: Credit/Debit Card

I wish to pay by Credit Card.
Credit Card Type: Visa ☐ Mastercard ☐ Switch ☐
I authorise Portland Customer Services to use the credit card details below to pay my membership fees.

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6. MEMBERSHIP NOMINATION

Your application for membership of the Genetics Society will not be accepted without the signature of a FULL MEMBER nominating you for membership. In instances where no full member is available you must submit a copy of your CV along with a short Academic Reference. Your application will then be considered by the Committee. Alternatively, you may contact the Society by email for a list of Society Reps in your area: theteam@genetics.org.uk.

Signature of nominating FULL MEMBER Print name in block capitals Membership No.

☐ I do not have a signature of a nominating member. I enclose a copy of my CV along with an Academic Reference for consideration by the Committee (tick box if applicable)

Please return your membership application form along with any attachments to: The Genetics Society, Portland Customer Services, Commerce Way, Colchester CO2 8HP, UK marking your envelope MEMBERSHIP APPLICATION.

Please note that the approval of new members is ratified at the Spring Meeting as part of our AGM. However, your membership will begin as soon as your application is processed.
# Notification of change of address form

If you wish to notify us of a change of address, you can use our online facility by visiting www.genetics.org.uk or by emailing us at theteam@genetics.org.uk. Alternatively you can complete the form below and return it to:

The Genetics Society, Portland Customer Services, Commerce Way, Colchester CO2 8HP, UK marking your envelope CHANGE OF ADDRESS NOTIFICATION.

Note that from [_________] my new address will be:

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**OFFICE USE ONLY**

Date Received

Date Processed
The latest genetic research from Heredity

Heredity is an official journal of the Genetics Society, and publishes original research in all areas of genetics, with a particular focus on population, evolutionary and quantitative aspects, animal and plant breeding and cytogenetics.

Primary research papers are complemented by Reviews covering currently developing areas and News and Commentary articles keeping researchers and students abreast of hot topics.

Discover Heredity today at www.nature.com/hdy