GENETICS SOCIETY NEWS

JANUARY 2010  |  ISSUE 62

In this issue
- Darwin and Development Meeting
- Genetics and the Causes of Evolution Meeting
- Obituary for Hugh Rees
- A Taxi Driver Writes
- Student Travel Reports
- Heredity Fieldwork Reports

The Genetics Society News is edited by Steve Russell and items for future issues can be sent to the editor, preferably by email to s.russell@gen.cam.ac.uk, or hard copy to Department of Genetics, University of Cambridge, Downing Street, Cambridge CB2 3EH. The Newsletter is published twice a year, with copy dates of 1st June and 26th November.

Drosophila montana collected in Finland as part of a Heredity fieldwork study by Paris Veltsos of St Andrews University. See the Report on page 35. Image © Paris Veltsos.
Welcome to issue 62.

This issue welcomes in the new decade: if we consider the breathtaking progress biology has made since the turn of the Century, particularly due to advances in genome sequencing, then the next 10 years should be truly remarkable for genetics. The prospect of very cheap genome sequencing promises new insights into all areas of genetics, particularly in the field of population and evolutionary biology and not least in areas of human genetics and disease. There is purportedly an old Chinese curse - “May you live in interesting times” - We certainly do, although I’m not sure scientists would consider this a misfortune.

In this issue we have meeting reports from the organisers of the one-day session, Darwin and Development, included as part of the International Society for Developmental Biology meeting in Edinburgh and from the two-day discussion meeting on Genetics and the Causes of Evolution held in conjunction with the Royal Society. Both meetings highlighted the importance of Darwin’s work in framing a theory underpinning evolution. We also have reports for sponsored events including the John Innes Centre Centenary Symposium, an institute with longstanding connections with the Genetics Society, and a meeting on Epigenetics celebrating 25 years of this thriving field.

As usual we have a collection of meeting reports from students who have received travel grants and in this issue I have also elected to focus on reports from Heredity Fieldwork Grants. These are available to any society member, irrespective of age or qualification, and can facilitate fieldwork or visits to other labs. We also have a number of reports from Genes & Development Summer studentships available from the website since most are generally too long to make it into the print issue.

In the last issue I wrote a Taxi Driver piece on the accessibility of published scientific data and this issue sees a couple of responses to this. The editor of Heredity, Roger Butlin, has written a piece describing the journal’s new Data Policy and highlighting the initiatives it is taking to try and deal with data types where there are no public repositories or standard formats. It seems to me that the journal is moving forward in a sensible and pragmatic way, anyone with any comments to make should contact Roger. My fellow Taxi Driver, and weather beaten Soay sheep expert Josephine Pemberton, highlights the problems of making difficult to collect longitudinal data immediately freely available on first publication. Clearly policies designed to allow free access to data need to be cognisant of the efforts of particular research groups. I also had a few emails from readers supporting the general concept of data availability. Tom Moore from University College Cork raised the issue of the way the commercial suppliers of reagents or resources frequently fail to disclose critical details (antigen epitopes or vector sequences), citing commercial confidentiality, that leave researchers in difficult positions. Clearly the whole area is complex but without open and rational debate we will not arrive at a position where free data availability improves research outputs but protects considerable personal (or commercial) investment.

I am driven by disquiet to get a wee bit political and draw attention to the campaign to keep libel laws out of science. As many readers will be aware, English Libel laws are being increasingly used to stifle critical discussion of some medical practices and scientific evidence. The use of the courts in this way is seen by many to be the thin edge of the wedge in terms of free and open scientific debate. Progress in science has always relied on open discussion in public fora and literature: there is a growing concern that valid scientific criticism will be suppressed by well-funded bullies. I urge readers to visit the website of the Libel Reform Campaign (www.libelfreform.org), a coalition of groups including Sense about Science, Index on Censorship and English PEN, seeking changes to a libel law that is rapidly becoming an international laughing stock.

Cheers

Steve Russell

University of Cambridge
2010 Spring Meeting

**Mouse Genetics** Think Globally, Act Locally


The meeting will highlight complementary approaches at the forefront of mouse genetic research, from work focussed on specific genes or systems to large-scale genomics and mutagenesis programmes. It will include Lectures by Steve Brown (2009 Genetics Society Medal) and Andrew Jackson (2010 Balfour Lecture).

**Scientific Organisers**
- Ian Jackson
  MRC Human Genetics Unit, Edinburgh
- Anne Ferguson-Smith
  University of Cambridge
- Andrew Ward
  University of Bath

**Speakers**
- Dave Adams
  Wellcome Sanger Institute, Cambridge
- Kathryn Cheah
  University of Hong Kong
- Gary Churchill
  The Jackson Laboratory, Bar Harbor, USA
- Elizabeth Fisher
  Institute of Neurology, UCL
- Jane Hurst
  University of Liverpool
- Bill Skarnes
  Wellcome Sanger Institute, Cambridge
- Emma Whitelaw
  Queensland Institute of Medical Research, Australia

**Featuring**
- Steve Brown
  MRC Mammalian Genetics Unit, Harwell
  2009 Genetics Society Medal
- Andrew Jackson
  MRC Human Genetics Unit, Edinburgh
  2010 Balfour Lecture

for registration, visit
www.genetics.org.uk

---

---
2010 Autumn Meeting

Lessons from Cancer for Biology and Genetics

Friday 12th November 2010. The Royal Society, Carlton House Terrace, London.

Genetics has become one of the most widely used tools to study a wide range of biological phenomena. Studies in genetics require the presence of variation to compare and contrast the same system in different states opening the way to deciphering broader biological mechanisms. Cancer studies use the same principle of comparing the functioning of perturbed and “normal” tissues. Over the past three decades since the advent of molecular biology, we have learnt a great deal about developmental control and the functioning of normal cells from the study of aberrant cancers. Our hopes for better cancer treatments are also based on our improved understanding of how malignant transformation and progression might be reverted to normal control.

Speakers
Terry Rabbitts
Leeds Institute of Molecular Medicine, UK

Ken Kinzler
Johns Hopkins University, Baltimore, USA.

Ashok Venkitaraman
Cambridge Cancer Centre, UK

Karen Vousden
Beatson Institute, Glasgow, UK

Andrew Feinberg
Johns Hopkins University, Baltimore, USA

Anne Ridley
King’s College London, UK

Peter Ratcliffe
Oxford, UK

Stuart Orkin
Harvard, USA

Hans Clevers
Hubrecht Laboratory, Utrecht, The Netherlands

Scientific Organisers
Veronica van Heyningen
MRC Human Genetics Unit, Edinburgh

Terry Rabbitts
Leeds Institute of Molecular Medicine

Andrew Ward
University of Bath

The meeting will include the 2010 Mendel Lecture to be delivered by Susan Lindquist, Whitehead Institute, MIT.

Cancer cell chromosomes showing specific translocation

for registration, visit www.genetics.org.uk
The Mammalian Genetics and Development Workshop

An annual meeting of the Genetics Society

Thursday 19th – Friday 20th November 2009
Institute of Child Health, UCL, 30 Guilford Street, London

The Mammalian Genetics and Development Workshop is a small annual meeting that aims to cover any aspects of the genetics and development of mammals. Meetings are based on the submitted abstracts, and usually include diverse topics ranging from early mammalian development (not exclusively human or mouse), imprinting and positional cloning of disease genes to human population genetics and association studies. In recent years, presentations on other model systems (such as chick and zebrafish) have also been included where these relate to general developmental questions or disease models.

The meeting is traditionally a venue for post-docs and PhD students to talk rather than laboratory heads and so is an excellent training ground and friendly, informal forum for discussing new results. In keeping with this objective, we offer up to four prizes to individual post-graduate/post-doctoral presenters who, in the opinion of a panel of judges, have given an outstanding presentation.

Further information will be posted on the Genetics Society website (www.genetics.org.uk) or you can join the MGDW electronic mailing list by sending an email to MGD.Workshop@ich.ucl.ac.uk
We will happily include any announcements for genetics-based meetings in this section. Please send any items to the editor.

**British Meiosis Meeting**  
29th March 2010  
University of Leicester, UK  
[http://tinyurl.com/britishmeiosis](http://tinyurl.com/britishmeiosis)

**54th Ecological Genetics Group Meeting**  
6th – 8th April 2010  
University of Stirling, UK  
[www.sbes.stir.ac.uk/egg/](http://www.sbes.stir.ac.uk/egg/)

**Annual Drosophila Research Conference**  
7th - 11th April 2010  
Washington, D.C.  

**Experimental Biology 2010**  
24th - 28th April 2010  
Anaheim, California  

**3rd Human Variome Project Meeting**  
10th - 14th May 2010  
Paris, France.  
[www.humanvariomeproject.org/meetings/paris/](http://www.humanvariomeproject.org/meetings/paris/)

**The Biology of Genomes**  
11th - 15th May 2010  
Cold Spring Harbor, New York  
[http://meetings.cshl.edu/meetings/genome10.shtml](http://meetings.cshl.edu/meetings/genome10.shtml)

**40th Annual Behaviour Genetic Association**  
2nd - 5th June 2010  
Seoul, Korea  
[www.icts2010.net](http://www.icts2010.net)

**Nuclear Organization & Function**  
2nd - 7th June 2010  
Cold Spring Harbor, New York  
[http://meetings.cshl.edu/meetings/symp10.shtml](http://meetings.cshl.edu/meetings/symp10.shtml)

**Evolutionary Biology of Caenorhabditis and Other Nematodes**  
5th - 8th June 2010  
Wellcome Trust Genome Campus, Cambridge  
[https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=171](https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=171)

**Genomic Epidemiology of Malaria**  
9th - 13th June 2010  
Wellcome Trust Genome Campus, Cambridge  
[https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=172](https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=172)

**European Human Genetics Conference**  
12th - 15th June 2010  
Gothenburg, Sweden  

**WT/P3G Biobank Summer School 2010**  
30th June - 4th July 2010  
Wellcome Trust Genome Campus, Cambridge  
[https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=173](https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=173)

**SEB Annual Meeting**  
30th June - 3rd July 2010  
Prague, Czech Republic  
[www.sebiology.org/meetings/Prague/Prague.html](http://www.sebiology.org/meetings/Prague/Prague.html)

**CSHL/Wellcome Trust Systems Biology**  
11th - 15th August 2010  
Wellcome Trust Genome Campus, Cambridge  
[http://meetings.cshl.edu/meetings/netwrkuk10.shtml](http://meetings.cshl.edu/meetings/netwrkuk10.shtml)
<table>
<thead>
<tr>
<th>Event</th>
<th>Dates</th>
<th>Location</th>
<th>Website</th>
</tr>
</thead>
<tbody>
<tr>
<td>Personal Genomes</td>
<td>10th - 12th September</td>
<td>Cold Spring Harbor, New York</td>
<td><a href="http://meetings.cshl.edu/meetings/person10.shtml">http://meetings.cshl.edu/meetings/person10.shtml</a></td>
</tr>
<tr>
<td>Infectious Disease Genomics &amp; Global Health</td>
<td>12th - 15th September</td>
<td>Wellcome Trust Genome Campus, Hinxton, Cambridge</td>
<td><a href="http://meetings.cshl.edu/meetings/pathuk10.shtml">http://meetings.cshl.edu/meetings/pathuk10.shtml</a></td>
</tr>
<tr>
<td>Genome Informatics</td>
<td>15th - 19th September</td>
<td>Wellcome Trust Genome Campus, Hinxton, Cambridge</td>
<td><a href="http://meetings.cshl.edu/meetings/infouk10.shtml">http://meetings.cshl.edu/meetings/infouk10.shtml</a></td>
</tr>
<tr>
<td>Mammalian Genetics &amp; Development Workshop</td>
<td>11th - 12th November</td>
<td>Institute of Child Health, London</td>
<td><a href="mailto:MGD.Workshop@ich.ucl.ac.uk">MGD.Workshop@ich.ucl.ac.uk</a></td>
</tr>
<tr>
<td>American Society of Human Genetics</td>
<td>2nd - 6th November</td>
<td>Washington, DC, United States</td>
<td><a href="http://www.conferencealerts.com/seeconf.mv?q=ca1mishs">www.conferencealerts.com/seeconf.mv?q=ca1mishs</a></td>
</tr>
</tbody>
</table>

If you run an interest group and hold regular meetings, our new web site forum is the perfect place to promote your activities. Simply visit [www.genetics.org.uk](http://www.genetics.org.uk), log in to our forum and tell us all about it.
The Genetics Society helps support several sectional interest groups by providing meeting sponsorship. We currently have 8 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 contact the Treasurer, Josephine Pemberton, in the first instance.

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

**Archaea group**
Organiser: Thorsten Allers
(thorsten.allers@nottingham.ac.uk)

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

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

**Drosophila**
Organiser: David Ish-Horowicz
(david.horowicz@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
Contact: mgd.workshop@ich.ucl.ac.uk

**POP group**
Organiser: Mike Bruford
(BrufordMW@cardiff.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

**54th Ecological Genetics Group Meeting**
6th – 8th April 2010
University of Stirling
http://www.sbes.stir.ac.uk/egg

**Mammalian Genetics & Development Workshop**
11th – 12th November 2010
Institute of Child Health, London
MGD.Workshop@ich.ucl.ac.uk
The Genetics Society
Annual General Meeting

Friday 23rd April 2010. The Wellcome Trust, Sanger Institute, Hinxton.

The 2010 Annual General Meeting of the Genetics Society will take place on Friday 23rd April 2010, in the context of the Society's Spring Meeting on Mouse Genetics held at the Sanger Institute, Hinxton, Cambridge. The business includes the election of new members to the Society, and of new members to the Society's Committee, including the post-graduate representative. In addition, due to early resignations from members of the Committee, individuals will be elected to fill these posts only until the time at which the previous office-holder’s term would have expired (May 2011), in the first instance.

The business will also include the election of an Honorary Treasurer (who will shadow the present Honorary Treasurer for 1-year) and a Newsletter editor; approval will also be sought to extend the present Meetings Secretary’s term of office by 1-year.

A list of new members proposed for election to the Society will be publicised via emails to members, and on the Society’s website http://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.

Important Note

The 2010 AGM will allow advance voting by email 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 email voting. To ensure involvement in the AGM by this mechanism, please check that the Society has your correct email address. As a check, you should have received an email communication from the Society (Christine Fender: christine.fender@genetics.org.uk - on Mon, 16 Nov 2009) inviting nominations for the Balfour and GS Medal competitions; if you did not receive this message, please contact mail@genetics.org.uk with an email address update.

Provisional Agenda

1. Minutes of previous General Meeting (Friday May 8th 2009); matters arising
2. President's Report
3. Honorary Treasurer's Report
4. Honorary Secretary's Report and Business for Transaction
   (a) Balfour Lecturer 2010
   (b) Genetics Society Medal 2010
   (c) Mendel Lecturer 2010
   (c) Applications for new membership
   (d) Election of new Committee members
   (e) Election of Honorary Treasurer to shadow present Honorary Treasurer; election of Newsletter editor; one-year extension to the present Meetings Secretary’s term of office

5. AOB
New Genetics Society Website Launched

After a great deal of effort by our office staff Christine Fender and Hazel Hutchison, working alongside Dave Moxey from Round and Red Creative, the new Genetics Society website is now live. We believe the new site is much cleaner and easier to navigate. As you can see the design incorporates the new branding but, more importantly, it’s the changes under the hood that make it much easier for the office to maintain and update. We hope that online registrations will now be much smoother and we are working to add functionality such as online applications for Society grant schemes. When you register with your membership number you will have free access to Heredity and also be able to view your membership details, change your subscription and more. The new site also features a forum, we hope you will help us make this an exciting discussion board by posting anything of interest, news of forthcoming meetings or if you simply need to get something off your chest that relates to the genetics community. We look forward to reading your posts.

Genetics Society Meetings

As I am sure most are aware, given the excellent attendances we have, the Society organises a regularly series of one-day meeting throughout the year. Generally we hold Spring and Autumn meetings, but we often have three in a year. Meetings are usually held at the Royal Society in London for ease of organisation but other venues across the country can be used. Ideas for one-day meetings come from a broad constituency and the committee always welcome suggestion for meeting topics, which can be focused on any area of genetics. Suggestions, including the names of potential organisers (generally two people) and an indication of the likely range of talks, can be submitted to the Scientific Meetings Secretary, a.ward@bath.ac.uk.
Data archiving progress at *Heredity*

In mid-2009, *Heredity* introduced a new ‘Data Policy’ in its instructions to authors. It says the following:

> Authors are strongly encouraged to follow established minimum guidelines for the reporting of biological data, wherever appropriate. Guidelines for many relevant data types are available from MIBBI: Minimum Information for Biological and Biomedical Investigations (www.mibbi.org).

DNA sequences published in Heredity must be deposited in a publicly available database, usually EMBL / GenBank / DDBJ, and accession numbers must be included in the final version of the manuscript. Where public databases exist for other data types, such as microarray data (see www.ebi.ac.uk/Databases/microarray.html, for example), they must be used and the relevant reference should be included in the manuscript. Where no public database exists, authors are strongly encouraged to provide the data on which their analyses are based as Electronic Supplementary Information. The data should be formatted for use in a relevant, readily available software package, ideally one which allows data export in a variety of formats (such as CREATE for population genetic data: https://bcrc.bio.umass.edu/pedigreesoftware/node/2). Sufficient metadata (such as sample locations, individual identities, etc.) should be provided to allow easy repetition of analyses presented in the manuscript.

Heredity proposes to make public archiving of data a requirement for publication in the near future and welcomes feedback from authors on this proposal (please address comments to heredity@shef.ac.uk).
Readers will immediately notice the difference between ‘must be deposited’ for sequence and microarray data and the rather different ‘strongly encouraged’ for other data types. This reflects the uncertainty discussed by our Newsletter Editor, Steve Russell in his TaxiDriver piece (Issue 61): we have all benefitted enormously from the universal archiving of sequence data in GenBank, and almost all scientists agree that the data on which published papers are based should be available for re-analysis or further study, but we are not sure how far to extend mandatory archiving to other data types.

Heredit introduced this interim policy because there were several concerns about rapidly adopting mandatory archiving. It would be good to take a lead on this issue but might be risky if other journals were not adopting similar policies. It is not clear that Supplementary Information provides a suitable archive where data can be stored in a useable form and easily retrieved. A suitable archive should also allow temporary embargoes on some data types, to allow authors to exploit their data more fully before release or to protect sensitive information.

An ideal archive should allow easy submission of many data types, with metadata, integrated with the manuscript submission process.

The outlook is now changing rapidly. Several major journals in ecology and evolutionary biology (American Naturalist, Evolution, Molecular Ecology, Journal of Evolutionary Biology) have joined together in a joint data archiving initiative. Heredit’s field of interest overlaps substantially with these journals and the policy they propose to adopt fits closely with our planned development. Therefore, we will join the other journals in publishing closely linked statements on data archiving early in 2010. This will make archiving of all data types a requirement for publication. We will be expecting referees and editors to police this requirement: a small extra load, I am afraid, but one that will be well worth the effort.

These journals are also supporting an initiative by NESCENT, the US National Evolutionary Synthesis Center (www.nescent.org) to create a data repository suitable for the very varied forms of data generated in evolutionary biology, including evolutionary genetics. The result is DRYAD (http://datadryad.org). Dryad operates like a data library, allowing it to contain any data type but restricting the types of searches that are possible compared with sequence data, for example. Data submission can be linked to the electronic manuscript submission systems of member journals. Embargoes can be requested. There is basic curation of data and metadata files and the data are given a unique identifier which is linked to the appropriate publication. The joint data archiving initiative will recommend Dryad as a data repository but will not restrict the use of other repositories. The Genetics Society Committee is currently considering whether to join the Dryad Consortium. If you have views on Dryad, or data archiving more generally, please do contact me or any committee member.
During the last International Society for Developmental Biologists (ISDB) congress in Edinburgh, the Genetics Society organised, in conjunction with the British Society for Developmental Biology and the British Society for Cell Biology, social events for younger conference attendees. Between 300 and 400 students and post-docs as well as a few principal investigators joined a pub-crawl running around Edinburgh’s historic Old Town and a Latino-themed evening including Salsa class as well as Capoeira and Salsa performances in El Barrio, one of Edinburgh’s centrally located clubs.

Attendees have agreed that both events were a great icebreaker and helped students get to know each other in a friendly environment outwith the official conference centre. We were pleased to receive very positive feedback and will continue such initiatives in the future. A Facebook group “ISDB 2009 Student Social” was created following the Edinburgh meeting to help students and younger scientists who attended the social events to network, exchange opinions and swap information about meetings or sponsorship opportunities.

The Genetics Society will continue its strong involvement in student activities via this type of social event sponsorship. In addition, applications for funding, including meetings sponsorship, heredity fieldwork, training or junior scientist grants are always welcome. Please refer to the recently refurbished Genetics Society website for more information about application procedures for our recently expanded grants portfolio available for young scientists. Additional information can be found on the newly created Facebook group “The Genetics Society”, moderated by the postgraduate representative of the Society, where students can post their questions, views and opinions as well as share valuable information about meetings and other topics.

Salsa lessons and demonstrations proved popular at the social event. Senzala Group UK performed a Capoeira show and a Salsa performance was thanks to the Edinburgh University Salsa Society.
Heredity

Published on behalf of The Genetics Society

The essential resource for geneticists, keeping readers informed about the latest genetics research with an evolutionary perspective

Visit www.nature.com/hdy and discover more:

- sign up for your FREE Table of Contents e-alerts
- FREE access to Heredity podcast
- weekly Advance Online Publication of papers
- submit your research paper

www.nature.com/hdy
As we have previously reported, the Biosciences Federation and Institute of Biology have now officially merged to create the Society of Biology and those interested can find out more at the new website www.societyofbiology.org/. As with the Biosciences Federation, the Society is active in responding to matters relating to science policy and education. In addition, the Society has a network of regional branches that act as a focus for local activities and is also interested in promoting professional development for biologists; see the website for details of these activities. The Society of Biology will be officially launched at an invitation only event in London in March this year with guest speakers Sir Paul Nurse and Sir David Attenborough.

The Society has recently responded to a number of consultations including the Science and Technology Committee policy on the treatment of scientific advice provided to the Government, the HEFCE consultation on the Research Excellence Framework, the House of Lords Science and Technology Committee report on funding priorities for research and The Science and Learning Expert Group report on science education. Details of the Societies response to these and other consultations are all available from the website. The Society website also holds details of local and national events of interest to biologists. In contrast to the Biosciences Federation, and more like the Institute of Biology, the Society also allows individual membership for those interested in obtaining professional accreditation or personally contributing to aspects of the Societies business, again details are available from the website.

The Society of Biology will be officially launched at an invitation only event in London in March this year with guest speakers Sir Paul Nurse and Sir David Attenborough.
The International Congress of Developmental Biology takes place every four years and is the largest conference worldwide in the field of developmental biology. The previous three Congresses, in Utah, Kyoto and Sydney, each attracted over a thousand delegates, putting considerable pressure on the UK to host a similarly attractive meeting in 2009. In the end, expectations were surpassed and a record attendance of 1500 delegates attended the 16th Congress held at the impressive Edinburgh International Conference Centre. The Genetics Society generously sponsored a full-day ‘double session’ at the Congress, plus an associated Plenary Lecture, and was rewarded by an exceptional turn-out of delegates, a series of cutting-edge talks, and wide exposure for the Society. For topical reasons, the subject chosen for the Genetics Society symposium was ‘Darwin and Development’. The reason, of course, was to commemorate the 200th anniversary of Darwin’s birth and the 150th anniversary of the publication of ‘The Origin of Species’.

Despite the historical significance of the year 2009, the aim of the symposium was not to look back at Darwin’s work. From the outset, the intention was to hold a symposium that discussed the latest research on topics that would have interested Darwin were he alive today, particularly within the subject of evolutionary developmental biology and genetics. The structure of the symposium roughly followed the order of topics in the Origin of Species, or at least those topics relevant to genetics and development. Chapter 1 of the ‘Origin’ was entitled ‘Variation under Domestication’, and accordingly this topic was addressed by two speakers in the morning session. John Doebley (University of Wisconsin-Madison, USA) discussed his research on the domestication of maize, focussing on genetic differences underlying morphological differences between maize and its wild relative Teosinte. Enthusiasm for domestication as a model for natural selection has waned somewhat since Darwin, but through comparative analysis with other systems John was able to show that the artificial and natural selection targeted the same sorts of loci underpinning trait variation.

Continuing the theme, Elaine Ostrander (National Institutes of Health, USA) was invited to speak on the genetic basis of differences between breeds of domestic dog. Although Elaine was unable to attend the meeting, she did not let this small complication stop her from presenting an excellent talk, live by telephone from Washington DC. The audience was given a remarkable demonstration of how high-resolution genetic mapping in multiple pedigree lines, together with a reference dog genome sequence, enabled specific traits such as long hair or curly hair, or the presence of facial ‘furnishings’ (a sort of canine moustache), to be traced to variants in single, identified genes. There were even implications for Barack Obama; his chosen household pet (a Portuguese Water Dog) has all three characters.

Darwin followed his discussions of domestication with a survey of ‘Variation under Nature’, and accordingly three talks in the morning session addressed this topic.
Flowers, finches and fish were the principle focus. Cris Kuhlemeier (University of Bern, Switzerland) used QTL mapping and behavioural experiments to dissect the genetic differences and selection pressures underpinning the divergent morphologies, and distinct ecologies, of three closely related Petunia species pollinated by different agents: bees, hawkmoths and hummingbirds. Arkhat Abzhanov (Harvard University, USA) described the search for the developmental basis of differences in cranial morphology between divergent species of Darwin’s finches and also between their relatives on Caribbean islands. Yingguang Frank Chan (formerly at Stanford University, USA; now at MPI, Plön, Germany) brought the audience up-to-date concerning the intriguing story of Pitx1 mutations and spine reduction in stickleback evolution, showing exciting new data on the actual mutations present in natural populations.

The afternoon session focussed on other areas that were of interest to Darwin, including phylogeny, homology, the fossil record and the dawn of animal life. In 1857, Darwin wrote to T.H. Huxley “the time will come, I believe, though I shall not live to see it, when we shall have very fairly true genealogical trees of each great kingdom of nature”. He would have enjoyed the talk by Michael Akam (University of Cambridge) who gave an overview of the ‘new animal phylogeny’ assembled from molecular data by many groups over the past two decades. Further research is still needed to resolve problematic components of the phylogeny, for example among the spiralian and the ecdysozoan phyla. Michael also emphasized the importance of genome projects for animals such as centipedes to facilitate research into some difficult topics in evolutionary biology such as the origin and evolution of segmentation.

Michael also emphasized the importance of genome projects for animals such as centipedes to facilitate research into some difficult topics in evolutionary biology such as the origin and evolution of segmentation.

Serial homology and the variation of characters were topics discussed by Jukka Jernvall (University of Helsinki, Finland, and Stony Brook University, USA) and Nicola Illing (University of Cape Town, South Africa), using examples from their research on dentition in mammals, and limb development in bats, respectively. Jukka showed that underlying developmental rules have constrained evolutionary variation of dentition patterns, while Nicola showed differences in gene expression profiles that underpinned differential growth of digits in bat wings. Darwin was particularly concerned with ‘the imperfection of the geological record’, but the discovery of fossilised embryos speaks both to his concerns on the absence of Precambrian fossils and to the paucity of soft tissues in the fossil record. Philip Donoghue (University of Bristol) used synchrotron X-ray tomography on Ediacaran fossil embryos to reveal their precise cell number and organisation. The fossils show no embryological characteristics of bilaterians but it is remains unclear whether this is an artefact of post mortem decay or reflects their biology.

Michael Ruse once wrote “Of all the scientists in the world today, there is no one with whom Charles Darwin would rather spend an evening than Sean Carroll.” It was fitting, therefore, that Sean Carroll (University of Wisconsin-Madison, USA) should end the day on ‘Darwin and Development’ by presenting the Genetics Society Plenary Lecture. A few words are insufficient to sum up his whirlwind tour of ‘Endless Flies most Beautiful’, except to say that it swept effortlessly from natural variation to ecology, from experimental genetics and development to evolutionary biology, and kept a packed auditorium riveted.
As part of the Darwin 200 celebrations, the Royal Society and the Genetics Society held a joint meeting at the Royal Society’s headquarters in London, on November 12-13th. Organised by Mike Bonsall and Brian Charlesworth, the aim of the meeting was to show how advances in the field of genetics have been essential in aiding our understanding of the mechanisms of evolutionary change that operate across all biological systems.

As may be expected from the remit of this meeting, diversity was high, with both the audience and the speakers coming from a wide range of disciplines. The format of the meeting was such that ample time was left for discussion between sessions. This allowed a detailed examination of presenters’ findings and also an opportunity for more general questions to be raised by audience members. The main topics of this meeting were similar to those that Darwin himself had studied in-depth: variation under domestication, adaptation by natural selection, cross and self-fertilisation, the descent of man and, of course, the origin of species.

One of the unifying themes of the meeting was how the rapid advancement of genotyping and sequencing technologies, and a corresponding reduction in their price, has led to an explosion of work tracking adaptation in non-model organisms. Indeed, the first talk by Josephine Pemberton, about quantitative traits in wild populations of Soay sheep, set the standard and tone for much of the rest of the meeting. Hopi Hoekstra presented elegant work identifying specific genetic changes that have led to lighter coat colour in the beach mice, a subspecies of the deer mouse *Peromyscus polionotus*. Different mutations in geographically isolated populations of beach mice have led to similar phenotypic outcomes, illustrating the convergence at the phenotypic level need not occur at the genetic level. In contrast Holly Wichman, illustrated the abundance of convergent evolution at the genetic level in lines of φ174 phage that were evolving independently in the laboratory. Both Dolf Schluter and John Willis showed further examples of how adaptive phenotypes in local populations could be
mapped and subsequently tracked genes differing in the wild.

In a short section of the meeting, one that Darwin himself was extremely interested in, Spencer Barrett spoke about sexual systems in plants and the transition between different sexual systems. Leading on from this was a fascinatingly graphic talk by Tracey Chapman on sexual conflict in *Drosophila*. The topic that stimulated the greatest public interest was that of speciation. Jerry Coyne laid out the arguments for a stricter definition of sympatric speciation (one that includes a requirement for a genetic basis for reproductive isolation) and provided evidence that few good examples of sympatric speciation have really been seen in nature.

In one-way or another, much of the rest of the conference related to humans and the impact of humans on other organisms or *vice versa*. Talks on tracking domestication events in cattle and cataloguing biodiversity in plants from Dan Bradley and Anthony Brown respectively, illustrated how humans, throughout their history, have had a profound impact on patterns of diversity observed in domesticated species today. Naoyuki Takahata presented estimates of ancestral effective population sizes in human-chimp ancestors while Anna DiRienzo presented work, carried out in collaboration with Graham Coop and Jonathan Pritchard, that aims to detect genetic adaptations due to novel environmental challenges during recent human colonisation events. Paul Sharp presented an illuminating overview of the evolution of the chimpanzee and human immunodeficiency viruses (SIV and HIV respectively) and provided evidence that SIV increases mortality in chimpanzee, by CD4+ T cell depletion, albeit by a different mechanism from HIV. Following on from this Ben Kerr and Steven Frank presented very different studies on how pathogen virulence evolves and is, or can be tailored, to evade host defences and the potential consequences of adopting different lifestyles.

Rounding off this successful meeting was a more theoretical session, with the first talk from Laurent Duret dealing with the contentious issue of biased gene conversion and its effects upon genome scans for positive selection. As a fitting end to the meeting, Nick Barton gave a stimulating talk on the problem of the maintenance of recombination. As neither the removal of deleterious mutations, nor the rate of advantageous mutations appear to be high enough to satisfy theoretical requirements for the maintenance of sex and recombination, a more complicated scenario of local adaptations in structured populations needs to be given consideration; a process that was empirically illustrated by many of other speakers.

This year's Genetics Society Mendel lecture was given by Wen-Hsiung Li, after which he was awarded the Mendel medal by the former president Brian Charlesworth. The Mendel medal and lecture invitation are the highest honour the Genetics society bestows. In recent years, Professor Li has made the remarkable transition from theoretical and molecular population genetics to functional and evolutionary genomics, embracing yeast as a model organism and using next generation sequencing to study the evolution of gene expression regulation in this and other systems. In his lecture, Professor Li touched on many aspects of his more recent work, including the finding that more gene expression variation within species is due to trans acting factors than between species, where most observed changes in gene regulation occur in *cis*. In the last part of his talk, Professor Li charted the evolutionary history of a microRNA and the stepwise expansion of the surrounding regulatory network in more recently evolved orders of life. Professor Li's lecture was the conclusion of this highly stimulating and enjoyable meeting and was itself a demonstration of how much progress in the field of genetics has led to a deeper understanding of the processes of evolution.
The history of John Innes and the Genetics Society is as closely entwined as the two strands of the DNA helix. So it was an honour that we were able to sponsor The Bateson Lecture given by Professor Sir Paul Nurse, at the John Innes Centenary Symposium to celebrate Genetics 100 Years On in September.

William Bateson, the first Director of John Innes co-founded the Genetics Society in 1919 and in the early years John Innes staff formed a high proportion of the membership. Six past Presidents of the Society were from JI (Haldane, Darlington, Mather, Lewis, Riley and Hopwood) and numerous JI staff have also served as Secretaries, Senior Secretaries and Vice Presidents over the years. Bateson founded the Journal of Genetics in 1920, and in 1947 Darlington and Fisher founded the journal Heredity. In the mid 1980s David Hopwood, then President, and Dick Flavell, Senior Secretary, both of John Innes, spearheaded the Genetics Society discussions and negotiations that led to the founding of the journal Genes and Development. The John Innes visitors’ books record individual visitors to the Institution and shows that the Society met there often in the early years. The John Innes Centre also looks after the archives of the Genetics Society beginning from their first meeting in 1919.

The Centenary Symposium attracted a distinguished list of speakers including Nobel prize winners Sydney Brenner, Paul Nurse and Eric Wieschaus and provided an in depth examination of genetics in historical terms, as well as raising contemporary and future issues from personalised medicine, stem cells and biometrics to ethics, identity and GM. Genetics Society support of the Bateson Lecture enabled the Organising Committee to fully fund attendance by over 20 young researchers and students. The complete video recorded presentations are freely available on demand via the Centenary website http://www.jic.ac.uk/centenary/index.htm
2009 marked the 25th anniversary of the publication of two seminal papers in the journals Nature and Cell in the field of genomic imprinting. Studies, led by Davor Solter (Institute of Medical Biology, Singapore) and Azim Surani (University of Cambridge) reported the failure of androgenetic (two paternally inherited genomes) and parthenogenetic (two maternally inherited genomes) mouse embryos to develop to term. These findings proved the functional non-equivalence of maternal and paternally inherited genomes in the development of the mammalian conceptus. Subsequent work identified genomic regions that were subject to parental origin effects, work predominantly piloted by Bruce Cattanach (MRC Mammalian Genetics Unit, Harwell) and his colleagues. In 1991 the first imprinted genes were identified; genes expressed according to their parental origin whose dosage was perturbed in the bi-parental conceptuses made by Solter and Surani.

The past 15 years has seen further analysis identify the mechanisms by which the transcriptional machinery of the cell can tell the difference between the two parental chromosomes. This has elucidated epigenetic modifications such as DNA methylation, post-translational modifications of core histones, and the involvement of non-coding RNA transcripts as key players in the epigenetic control of gene activity and repression at imprinted loci. However, not only is genomic imprinting a fascinating research area in its own right touching areas of evolutionary biology, normal and abnormal mammalian development and physiology and functional genomics, but it also has become a very good experimental paradigm for investigating the epigenetic control of genome function and the role of non-coding RNA transcripts in the process. The field of epigenetics is now recognized as an important one influencing most areas of contemporary genetics.

Today, the advent of new technologies for exploring genomes and epigenomes has resulted in the integration of these earlier findings into a wider genomic context that has changed the face of chromosome biology. This progress has not been possible without genetic and epigenetic studies in model systems and model organisms notably in plants (which also undergo genomic imprinting) and Drosophila where the epigenetic influence of repressive chromatin on adjacent sequences has long been recognized and provided the some of the earliest genetic tools to identify many of the key players regulating epigenetic processes.

From 4-6th September 2009, approximately 200 international participants working in epigenetics came to the University of Cambridge to celebrate the remarkable progress that has been made since the elucidation of genomic imprinting in mouse in 1984. The meeting took place at Peterhouse and King’s College and was organised by CellCentric with additional sponsorship from The Genetics Society and The Company of Biologists. Sessions focused on Epigenetic Control of Developmental Processes, Interactions between the Genome and Epigenome, the Epigenome in Health and Disease, Parental Origin Specific Epigenetic Control and covered areas ranging from the roles of macro and small non-coding RNA in epigenetic regulation to the influence of histone modifications on genome architecture.
and function. Germ line epigenetics and stem cell programming featured prominently in several presentations, as did topics around DNA methylation in a range of normal and disease processes. Whole genome analysis of epigenetic states in a range of model systems and model organisms is providing useful reference epigenomes and novel mechanisms of epigenetic control. Highlights of the meeting included the Genetics Society Speaker, Steve Henikoff (Fred Hutchinson Cancer Research Center, Seattle), presenting work entitled ‘Chromatin dynamics and imprinting in Arabidopsis’. Azim Surani and Davor Solter’s talks on ‘Resetting the epigenetic state in the mouse germline’ and ‘Epigenetic control of oocyte to embryo transition in mammals’ addressed fundamental developmental epigenetic questions which new advances have now rendered tractable. In a year in which Cambridge University achieved its 800th anniversary and amidst the local excitement and events surrounding Darwin’s bicentenary, the Genetics Society contributed to a successful and stimulating meeting in which a part of epigenetic history was honoured and the future of epigenetics was celebrated.

Human genomics, the study of genetics and the human genome, is poised to become part of UK science lessons thanks to a new programme launched by Nowgen, the Manchester-based centre for genetics in healthcare. The ‘Nowgen Schools Genomics Programme’ will bring cutting-edge scientific research into schools, exciting pupils about the pace of discovery and engaging them in thinking about how advances in genetics will affect their future lives.

Traditionally, it can take 10 years or more for new scientific discoveries to become integrated into science teaching. Nowgen’s Schools Genomics Programme aims to address this - narrowing the gap between genomics research and classroom genetics. The project, funded by The Wellcome Trust, will include seminars for examiners on the latest developments in genomics and healthcare, offer students opportunities to visit research establishments and result in the production of three new Teachers TV programmes for students and teachers. The innovative three-year programme will be run by a team of Nowgen clinicians, scientists and educationalists. As well as influencing how genetics is taught in schools, the project will look at new ways of integrating contemporary content into traditional science and within science related courses such as A-level Science in Society and The History and Philosophy of Science. Peter Finegold, leader of the Schools Genomics Programme said: “Every day we read stories in the newspapers about how scientists have found genetic predictors for common diseases, such as cancer, diabetes and rheumatoid arthritis. Nowgen’s Schools Genomics Programme will help young people to interpret what these news stories are saying, by providing greater insight into the complexity of the science, and into the implications on our society of applying this knowledge in a healthcare context.”

The project team expects to see some of the outcomes of its work included into GCE A-level specifications in England within the next five years and hopes it will be included in the major review of the GCSE science curriculum, due to be carried out in 2011. Early discussions are also underway with key curriculum developers in Scotland.
Obituary

Professor Hubert (Hugh) Rees DFC, FRS
1923 – 2009

Professor Neil Jones. Aberystwyth University

Professor Hubert Rees DFC, FRS, a leading British scientist and decorated wartime pilot, died on Sunday 13 September 2009 at Aberystwyth.

Hubert Rees, always known to his friends and associates as Hugh, was born on October 2, 1923, the son of Owen and Tugela Rees, and was educated at Llandovery and Llanelli Grammar Schools. He left school to volunteer for the RAF, and after training in UK and Canada he joined 75 Squadron (RNZAF) in 1944 to pilot Lancaster bombers. At the end of his first tour of 30 operations he was awarded the DFC and then volunteered for a second tour but, soon after commencing, his aircraft was critically damaged over Homberg, Germany. He was able to retain sufficient control to allow the crew to bail out and, unusually, all survived. Following capture, Hugh and fellow officers were sent to Stalag Luft 1 on the Baltic coast, where they remained until liberated by the Russian advance in May 1945. Posted as missing in November 1944, it was not until 2 months later that his family received notification of his survival and internment, together with a laconic personal message from Hugh that he was “playing quite a lot of bridge”, a pastime shared with his wife Mavis that continued until late in life. In transit to his POW camp Hugh was caught in a night time RAF raid which he was again lucky to survive. In notes made at the time he described the experience as “unpleasant,” a clear understatement judging from the rare occasions when he later spoke of these events.

Some of these wartime experiences undoubtedly had a lasting influence on his outlook, but it was in character that after return to the UK at the age of 22 he pursued his peacetime ambitions with drive and energy. On demobilisation in 1946 he married his childhood friend, Mavis Hill, and enrolled as a student at Aberystwyth University, graduating with a First in Agricultural Botany in 1950. He was encouraged by his tutor Professor P T Thomas to specialise in plant cytogenetics, and spent a few months at the John Innes Horticultural Institute under the tutelage of C D Darlington before taking up an appointment as Lecturer in Cytology at the newly-formed Department of Genetics at Birmingham University under Professor Kenneth Mather. Here he successfully applied the techniques of quantitative genetic analysis to the genetic control of chromosome behaviour in plants, from which he later built his scientific reputation.

In 1958 he returned to Aberystwyth as Senior Lecturer in Agricultural Botany, being promoted Reader in 1966 and ultimately Professor and Head of Department. He rapidly built up an internationally acclaimed school of study on chromosome genetics, and on evolutionary changes in chromosome organisation with
particular reference to plant-breeding. He was elected a Fellow of the Royal Society in 1976. An excellent teacher with a powerful intellect, he also had the talent to inspire his students and to evoke in students and staff a lasting feeling of respect, regard and loyalty. Many would go on to high achievement in research and university teaching, and all would remain his friends.

Hugh was also a well known figure in the UK Genetical Society (as it was known at the time), when genetics was still a unified science. He would regularly present his latest ideas and findings, and could be relied upon to ask the critical questions of others and to spark lively debate.

An illustration of his involvement in Departmental activities, and of his singular leadership style, was the initiation of each new intake of his students to the joys of the countryside especially through the climbing of Cader Idris. He used to tell them that if they remembered only one thing from their time at Aberystwyth, this should be it. He continued the activity even when, as he joked, the effort of reaching the summit left him too breathless to address his new charges. The Departmental Christmas parties were famously festive occasions; Hugh’s customary and colourful rendering of Lewis Carroll’s “Jabberwocky” will long be remembered by successive classes of students. Such activities also reflected his eclectic interests and voracious reading habit, extending beyond scientific matters in a wide range of English and Welsh literature.

Throughout his career Hugh was intent to focus on the way that the results of his research could be brought to bear on improving the consistent yield of food crops from diminishing resources to feed an ever expanding world population. During his tenure at Aberystwyth he was at pains to strengthen the traditional links in research between the Department of Agricultural Botany and the Welsh Plant Breeding Station and to foster collaborative research between them and the Department of Genetics at Birmingham University under Professor John Jinks; an arrangement that enhanced the international reputation of all three centres.

Hugh had a rare capacity for quickly perceiving the crux of a problem in his own or related fields of research or, indeed, generally. He was a forceful presence in scientific meetings or committee and could be relied upon to ask a critical question on the crucial issue early in the proceedings, initiating strong debate. Consequently, in parallel with his scientific research he was much in demand for advisory or administrative duties. In the College he served on several committees and on various administrative posts including that of Vice Principal. Further afield he served on a number of advisory groups and governing bodies, including those of the Welsh Plant Breeding Station (subsequently The Institute of Grassland and Environmental Research and now part of the Institute of Biological, Environmental and Rural Sciences) and the Plant Breeding Institute, Cambridge (subsequently part of the John Innes Centre). Through the British Council and the University of Malawi he was also active in promoting academic and technical interactions with the Bundu College of Agriculture with lasting mutual benefits. Throughout his career he spent several study tours abroad in a number of different countries either as a Research Fellow or as Visiting Professor; most notably in 1977 when he taught at the Australian National University at Canberra.

Hugh combined his heavy work load with a rich and varied social life. He liked nothing more than to entertain friends, associates and visitors to the Department from the UK and abroad, to evenings at his home with the unstinting support of his wife Mavis, and their family. Generous hosts, their parties rarely ended before the early hours. Hugh was an excellent raconteur, with an enviable eye for detail, and a talent for spotting the bizarre and quirky in any situation. Many of his memorable and humorous tales recalled pre-and post-war life in the villages of South Wales, student life in the overcrowded “digs” of post-war Aberystwyth, and incidents on river-banks and lakes of mid-Wales where he avidly pursued his hobby of fly fishing.

In retirement, Hugh also remained a keen painter, bridge player and gardener. Later he took to gentle cycling with a small group of friends through various regions of France as a means of exploring the different wines and cuisine. Inevitably, since cycling in France is a cult, his distinctive patriarchal appearance and his decidedly unconventional garb often attracted the attention of photographers from the local press; while his charismatic presence at the lively evening festivities would lead to a gradually expanding entourage of other cyclists who would adapt their itineraries so as to join in.

Hugh is survived by his wife, a son and two daughters. Another son predeceased him.
The SET awards are provided by the Parliamentary and Scientific Committee and aim to encourage, support and promote Britain’s early-stage and early-career research scientists, engineers and technologists who are the “engine-room” of continued progress in and development of UK research and R&D. Many will be Britain’s future scientific and technological leaders and are a vital asset and investment for the UK.

This year’s winner in the Biological and Biomedical Sciences category was Xiaoqi Feng, in the third year of a DPhil in Plant Sciences at Magdalen College, Oxford. Her winning poster presentation, ‘Male meiotic cells and their tapetal nurse calls are derived from distinct cell lineages in higher plants’, looked at a discovery about plant reproduction which could help with developing new strategies for seed production. Xiaoqi Feng found the event useful. ‘I am very happy I won – it came as a real surprise, especially considering the high standard of the other entries I saw! But what was even more rewarding was getting the opportunity to meet young researchers in different fields from all over the UK and to find out about their cutting-edge research.’ She notes that her work would not have been possible without the support she has received from colleagues and friends. ‘I am also very grateful for the funding for my study and research provided by the Clarendon Scholarship and the ORS Award – without it, none of this would have been possible.’ She added: ‘It is essential that young scientists are able and willing to communicate with the general public and politicians, to make sure that science stays in touch with real life and to promote science-friendly policy that can benefit society.’

It has been a busy 12 months for Xiaoqi Feng since she also won the Society for Experimental Biology Young Scientist Award 2009 and was part of the University of Oxford team that won the UK Environment Young Entrepreneurs Scheme.
A Taxi Driver Writes...

**Josephine Pemberton**. Institute of Evolutionary Biology, University of Edinburgh

**Dear Steve-the-taxi-driver,**

Thank you for your article in the last GS news about the need to make the data behind published papers accessible to other workers, and especially for highlighting the potential issues surrounding long term projects, such as my study of Soay sheep in the pouring rain and howling gales of St Kilda.

I should like to enlarge on the potential problems of long term data sets by reference to a specific evolutionary genetics article published by the Soay sheep project in the last few years. I believe it illustrates two kinds of difficulties: the need to clarify the exact data authors are to upload and the need to safeguard the interests of those who conduct long term projects where data accrual leads to the potential for ever more sophisticated analyses. I am not against the overall mission here, but I am seeking some deeper thinking.

Overall *et al* (2004)\(^1\) investigated heterozygosity-fitness correlations in neonatal traits in Soay sheep lambs, finding none: I am always proud to publish a null result!

The data underlying the paper consisted of, for each lamb and its mother, a range of measures of heterozygosity plus inbreeding coefficients, birth date, birth weight, twin status and whether or not the lamb survived the neonatal period. The various heterozygosity estimators were calculated from genotype data across up to 24 microsatellite

---

*Spot the sheep – A typical balmy day on St Kilda!*
loci in such a way that the entire data set of genotypes (for all animals ever genotyped, not just the focal lambs and their mothers) was required. Estimating the inbreeding coefficients required a pedigree which required paternity analysis which also required the entire back-catalogue of genotypes as well as information on which individually-identified males were known to be alive in the relevant mating season. The final statistical analysis required data on population density and the winter North Atlantic Oscillation (a measure summarising the severity of winter weather) for each year in which the focal lambs were born.

Which level of data would we be required to upload with respect to a future article of the same kind? Would it just be the final data set on which we did the stats, consisting of the derived measures of heterozygosity and inbreeding coefficient for each focal individual, or would it be the entire underlying relational database which would allow other researchers to use their own methods to reconstruct the pedigree and derive alternative estimators of heterozygosity (a new one of these, ‘heterozygosity by loci’[2] has been suggested in the interim, so this might be useful)?

If large, multidisciplinary data sets such as the Soay sheep data set are made publicly available as a result of publishing journal articles, how will research groups like the Soay sheep researchers be protected from competitors immediately conducting analyses that the original authors themselves plan to do? I am currently involved in a manuscript which uses almost precisely the same dataset as was used for Overall et al (2004), albeit updated, to ask a different question. If others had thought of this newer analysis five years ago, would they have been within their rights to carry it out and publish it? I know that current plans would allow authors to place a time lag on the accessibility of their data, but I am not sure this is sufficient protection from my perspective.

I suggest that we are conflating two issues here: (1) the conservation of data in a way that keeps it for posterity. The funding agencies that I deal with have been remarkably lax at requiring response mode grant-holders to do this and I applaud any action, including by journals, which makes this a requirement. (2) The availability of data for re-analysis. I believe data should generally be available for re-analysis, but I also think the authors who obtained the data have a right to say whether they accept data release for re-analysis, on a case-by-case basis.

I am not saying this is the best model, but what we actually do with the Soay sheep data at present is as follows: current information on all 7,404 individuals, plus associated population, vegetation and weather data is held in a relational database on a server. If anyone wants to analyse the data in pursuit of a specific question, they are asked to email in a synopsis of their plans. This is sent round the current project group to identify comments or conflicts in plans. If there are none, the applicant gets the data, often by getting a login to the server so they can download successive data updates; effectively they become part of the current project group. Over the last few years, I can’t actually remember a case where a non-clashing reasonable request was turned down. In a similar manner, I would like to see whatever the journals invent allowing researchers to hide their data, but reveal it to what seem like bona fide requests.

References

TRAVEL GRANTS FOR JUNIOR SCIENTISTS

The 17th International *C. elegans* Meeting

June 24th-28th 2009. University of California, Los Angeles

Elizabeth Marsh, University of Birmingham

Arriving hot, bothered and severely jet-lagged, we collected our textbook-sized abstract book from the registration desk; a quick flick-through demonstrated that it was to be a superb conference with some high profile speakers. Beside them was my name, as I was to be giving my first presentation at a meeting three days later. Fortunately, jumping straight into the first of five plenary sessions helped dispel the nerves that were beginning to take hold and the meeting was kicked off with a lecture from the keynote speaker, Barbara Meyer.

One of my favourite talks of the conference was the next morning; “Life is not fair: larger chromosomes are transmitted to males in *C. elegans*” from John Wang at the University of Lausanne, Switzerland. Their finding that allele transmission can be biased, even with differences of only a few kb (just single gene deletions), has begun to upset the dogma that genetic information is segregated equally during reproduction; I believe this is why I found it so interesting. Sperm, but not oocytes, were found to display the transmission skew suggesting that this transmission bias may happen during spermatogenesis. From an evolutionary perspective, the transmission of smaller chromosomes to hermaphrodite progeny may henceforth mean that deletions are likely to propagate in *C. elegans*.

Another talk from Emily Troemel, newly independent at the University of California San Diego, described the parasite Microsporidia (*Nematocida parisii*) as a natural pathogen of *C. elegans*. These microbes were found to cause an intracellular infection of the intestinal epithelium and were capable of being transferred from worm to worm. A series of EM pictures showed ‘grooves’ in the intestine caused by the displacement of gut cells, which was thought to be the Meront stage, followed by the appearance of rod-shaped microbes; the spore stage. The innate immune response of *C. elegans* to *N. parisii* does not require the p38 MAPK or Insulin-like signalling pathways typical of the response raised by the animal to infection with other pathogens, indicating that there is a specific interaction between the host and this natural parasite.

The climax of the meeting was a superb lecture from Nobel Laureate Marty Chalfie, who gave fascinating insights into his lab as he detailed the history of his 1994 *Science* paper on GFP. It was truly inspirational to see the scraps of paper Marty had used to jot down his original ideas for GFP and *C. elegans* after hearing a seminar on bioluminescent proteins in 1988, as well as extracts from the lab books of his team as they conducted the first experiments. Other highlights were the Worm Art Show: there were some incredible entries (I wish I was creative!), and, of course, the Worm Comedy Show by P.I.s Morris Maduro and Curtis Loer...yes, it’s all geeky in-jokes, but they were hilarious all the same! The show included renditions of *Baby got back* (*Wormy got back*) and *Nessun Dorma* (*Nessun Worma*), I guess you had to be there...

As I have alluded to by my description of the abstract book, there were around 250 talks, just under 1,000 posters and about 1,600 delegates at the meeting! As a result the meeting was remarkably intense but, conversely, the opportunity to attend an international conference and hear talks from renowned *C. elegans* scientists about the rigorous nature of research at this level was one that has enthused and inspired me and my work. My own talk went well, somehow my nerves disappeared when I was speaking and I actually enjoyed it! It has been good to receive feedback on my own work directly and the discussions we had have opened many doors for collaborations. I would like to take this opportunity to thank the Genetics Society for helping fund my attendance at this conference.
The European Society for Evolutionary Biology (ESEB) Congress

24th -30th August 2009. Turin, Italy.

Rebecca Ross . University of Oxford

As a plant evolutionary ecologist, I can only give you a limited idea of what was going on for the rest of the sessions, which spanned parasites to humans, genomics to ecosystems, and everything in between.

The tone of the Congress was set by the opening reception held in the magnificent 18th century Rectorate Palace. Champagne flowed, beef was carved and networking proceeded apace. Keen to see what the programme would be for the next five days, we started looking through the tome of abstracts. With five parallel symposia on each day, just working out what to see required military precision and there was a fair amount of friendly competition between the ‘flitters’ and the ‘stickers’.

Each day began with a plenary talk from a leader in their field. We started with Hanna Kokko and the strange tale of the Amazonian fish that reproduce asexually; yet rely on sperm from another species of fish to trigger embryogenesis. Men: can’t live with ‘em, can’t live without ‘em. Massimo Pigliucci gave us some food for thought in the form of future trends in thinking about evolution. Further plenary talks ranged from genome evolution to human evolution, and finally planet scale co-evolution from John Thomson. The talks were streamed from the main theatre to several smaller ones to enable everyone to listen in.

As a plant evolutionary ecologist, I can only give you a limited idea of what was going on for the rest of the sessions, which spanned parasites to humans, genomics to ecosystems, and everything in between. So, a few highlights from my perspective to follow….Andreas Wagner on the links between evolutionary innovation and robustness: how the number of neighbours a sequence has which produce
the same overall phenotype could determine its evolutionary dynamics. Carol Lee (Wisconsin) gave us a whistle-stop tour of her great body of work on parallel evolution in copepods invading freshwater lakes. Mohammed Noor (Duke) addressed a packed lecture theatre about insights into hybridisation through fine-scale genome comparison in Drosophila. Francisco Ubeda (Tennessee) presented a new explanation for the role of genomic imprinting in Prader-Willis and Angelman syndromes, which was enough to make everyone angry with their fathers! Kevin Foster (Harvard) on social behaviour in biofilm-forming bacteria, with some really cool models. Matt Robinson (Sheffield) using a long-term data set in Finns to investigate environmental effects on birth intervals. Matthias Stoeck (Berkeley) on the weird and wonderful mating patterns and ploidy in the green frog hybrid zone in Kyrgyzstan. My hero, Loren Rieseberg (UBC) talked about some new work on the importance of hybridisation in historical speciation events, and particularly the role for polyploidy... and many many others!

Amidst the packed programme of seminars, there was a little time for R and R. The organisers put on a range of events one afternoon, from visits to the cinema museum and the Egyptian collection for the culture-vultures, to trips up Mont Blanc for the more adventurous.

There were also two poster sessions, with over 200 posters in each one, which made it a fairly epic journey to get round them all. The whole experience was somewhat reminiscent of the assembly rooms in Jane Austen’s Bath – the company circled, the rooms got hotter, and sadly there was no Willoughby to rescue me. However, it was a great chance to get some new ideas for my analysis and pick some tips from other people’s posters.

So, heads reeling with Science, keen to put some new ideas into practice, and even keener to have a cold beer first, it came to Saturday afternoon and the end of the conference. The organisers put on a splendid conference banquet in the Turin Armoury, a magnificent brick building in downtown Turin. The conference dinner showcased the best of Piedmontese cuisine, starting somewhat surprisingly with a cheese course. We continued to a more traditional steak, and an array of delicious dolce. The evening was rounded off with music, and lounging on the grass under a starry Italian sky. Writing this in rainy London in October, wish I were there!

18th Association for the Advancement of Animal Breeding and Genetics Conference

24th September-6th October 2009. Barossa Valley, Australia

Jennifer Gill. The Roslin Institute, Edinburgh

The 30th anniversary conference of the Association for the Advancement of Animal Breeding and Genetics (AAABG) was held in the famous Barossa Valley, 60 km Northeast of Adelaide. The conference, which is held every two years at locations throughout Australia and New Zealand, was located at the Novotel resort, directly behind Jacob’s Creek, which lends its name to the famous brand of wine based in the region.

The conference kicked off with
a comparative genomics workshop, attended by more than 200 delegates. The workshop included interesting sessions on, among other things, regulation of gene expression, genome evolution and genome structure as well as an impressive tribute dinner to Frank Nicholas, Emeritus Professor at the University of Sydney, which was the first of many social activities arranged throughout the week. One of the most fascinating talks of the workshop came from Jennifer Marshall Graves who amused everyone in the audience by stating that she believes mice are an alien life form sent from space to confuse us! She concluded her talk by stating that the Y chromosome could disappear within 5.8 million years - which amused only half of the audience.

After a day and a half of the genomic workshop it was time for the 18th conference to begin. The conference was opened by famed Australian cook and TV presenter Maggie Beer who urged us all to explore as much of the Barossa valley as possible. However, the packed conference timetable, which consisted of 3 plenary, 18 concurrent and 2 poster sessions over 4 days, left limited time for exploration. One of the first talks of the conference came from Frank Nicholas, author of “Charles Darwin in Australia”, who gave a fascinating insight into Darwin’s visit to Australia in 1836. The concurrent sessions of the conference included talks on the delivery of genomics to industry, genomic selection, beef cattle genetics, disease resistance and statistical methods. This latter session consisted of two very well attended talks on the mixed models used in animal breeding by Arthur Gilmour and Robin Thompson who developed ASReml, a computer program used routinely in animal genetics research. The most interesting sessions as far as I was concerned were the two on Beef Cattle genetics, the subject of my PhD thesis. Alison Van Eenennaam (University of California) gave a thought-provoking talk on the necessity for validation of DNA tests for quantitative beef cattle traits whilst Matt Walcott (AGBU), who discussed the use of genetic tests for meat tenderness in Brahman cattle, gave an interesting insight into the incorporation of genetic marker test results into BREEDPLAN, the Australian genetic evaluation system for beef cattle.

There was a packed and varied social programme consisting of both informal buffet dinners and a Bavarian barbeque and a more formal conference dinner at the Roseworthy campus of the University of Adelaide. Along with the poster sessions, where 51 posters were perused over wine and cheese, these social events were an ideal opportunity to mix with some of the key players in the field of animal genetics. Furthermore, Wednesday afternoon was set aside for conference tours to enable us to explore some of the Barossa. Tour options included golf, pig breeder tours, a visit to a sheep farm and a wine tasting trip. Needless to say, the majority of people picked the wine tour resulting in five busloads of people transported around various wineries.

I was also lucky enough to be able to attend the Australasian Conference on Statistical Methods for Genomic Data Analysis which was held in the beautiful botanic gardens of Brisbane. This two-day conference included interesting talks by Peter Visscher, Mike Goddard and Bill Hill and was an excellent opportunity to catch up with the new contacts made the week before at the AAABG conference. In conclusion, the AAABG conference was a fantastic experience and I was thrilled to be able to present my work to a group of highly respected scientists. I would like to take this opportunity to thank the Genetics Society for awarding me a Junior Scientist Travel Grant which enabled me to travel to Australia for the conference.
I have always wished to attend the annual American Society of Human Genetics meeting, and 2009 was no different as it was held on the Hawaiian island of O‘ahu. This tropical setting was the perfect place to meet many internationally world-renowned researchers, at a rather large gathering of nearly 5,000 scientists. The meeting was an opportunity to engage with researchers in similar research fields, develop collaborations and instigate new projects. As the meeting was large, the range of topics was varied so I learnt about new aspects of human genetics, cutting edge technologies and novel analytical techniques that I hope to apply to our research at the Centre for Cognitive Ageing and Cognitive Epidemiology, University of Edinburgh. From discussions at the conference, it is clear that the field is moving beyond genome-wide association studies to genome-wide sequencing such as the 1000 genomes project and incorporating techniques such as Microfluidic protein chip and single cell analysis. Furthermore, there are more sophisticated methods to investigating genome-wide association data to perform pathway analysis and test for genetic interactions. I presented my work as a poster on “Variation in the uric acid transporter gene (SLC2A9) is associated with memory performance” where I was asked many questions which lead to some interesting discussion and correspondence beyond the meeting itself.

One highlight was a Trainee-mentor lunch with Professor Robert Elston of linkage analysis fame, whose algorithms I used frequently in my PhD studies. Prof. Elston was very encouraging to all the budding scientists at his table, telling us to do what we want! He also discussed the importance of choosing journals for publishing papers, obtaining tenure track positions in the US and the difficulties of working mothers. Furthermore, he told us that understanding the genetics of human traits and disease is beyond biallelic SNPs and we should look towards developing analysis methods to investigate other types of genetic variation, and we should look towards functional work such as proteomics. Finally he warned us to use computational resources and programmes with caution. This was echoed by Professor Edward R. B. McCabe during the Presidential address “Beyond Darwin? Evolution, Coevolution and The American Society of Human Genetics”, who advised caution when using genetic analysis software as we must try to understand and be careful about how we feed experimental data into a black box, how the software authors, commercial or otherwise, deal with the data and then how we interpret the results.

From this meeting, I have reported back to our group on current work in our field, exciting developments and new analytical methods, from which we have developed future research strategies. Indeed, collaboration with a group in Australia has arisen from the meeting. Finally, I am very grateful for the Genetics Society Travel Award and the opportunity to attend my first American Society of Human Genetics meeting.
How many genes need to change in a fly before it becomes a new species? The quest for discovering such 'speciation genes' has been based on either top-down (start with lab mutants in candidate genes) or bottom-up (start with population analyses leading to genomic regions) approaches. We aim to combine the two by conducting a QTL (quantitative trait locus) study based on a pedigree of wild-caught flies. QTL studies are, at a basic level, correlations between phenotypes and genotypes. Advances in sequencing technology allow for the genotypes to include both candidate genes and neutral markers, hence the marriage of the bottom-up and top-down approaches. When asking evolutionarily relevant questions, it is very important for the genotypes studied to represent natural genetic variation. For example, while mutants in candidate genes display relevant phenotypes, they are usually identified in the lab and might never have survived in the wild. Collection of flies from the wild is therefore an essential part of the project.

Our phenotypes of choice are potentially essential for mating: they characterise the systems of courtship song and cuticular hydrocarbons - fly pheromones. The male-female interactions during courtship can be thought of as sender-receiver systems, albeit in a language we are not used to: song, smell and taste. Compatibility between the actual and expected message, determines the chances of mating. Given enough time, the courtship systems can evolve to different directions in different populations. Populations evolving independently can end up 'tuned out' of each other so that, if they were to meet, the individuals from one would avoid mating individuals from the other. This seems to be the case for courtship song frequency in the fly *Drosophila montana*, where the female preference has evolved to

http://biology.st-andrews.ac.uk/parisveltsoslab/
different directions in US and Finish populations.

The study will increase our understanding of the genetic basis of variation in important traits to reproductive isolation, and hence, potentially, the first steps in speciation. The availability of multiple pedigrees will allow to scratch the surface on tantalising questions. For example is the same genetic architecture responsible for trait variation in different populations? Is evolution predictable i.e. is the same result reached independently in different populations through the same genetic pathways? We hope to successfully establish pedigrees from Colorado and Kuusamo, and compare them to the one established from Vancouver last year. The field grant provided by The Genetics Society, has funded a collection at a field station near Kuusamo, Finland. This is a location from which the group of Prof Anneli Hoikkala, with which we collaborate, have been consistently sampling with success in the past. (This year they collected from Colorado, see http://mountainflyers.wordpress.com/).

The trip from Edinburgh was quite adventurous, requiring a 5 hour drive preceded by 3 flights, before reaching the field station. But it was definitely worth it, as the remoteness of the location contributes to its beauty and calmness. The first 3 days were very disappointing, as the temperature was below 5oC and there were brief instances of snowing - conditions far from ideal for fly collection. We took the opportunity to visit the Kiutakongas rapids, the most impressive in the country, at least according to the local national park sign. Eventually the weather did improve and by the end of the 10 day trip we had about 300 flies, which should be sufficient for obtaining the offspring of 40 D. montana females - our aim for the founders of the pedigree. We will only know how many D. montana were caught after they are interviewed: 3 species coexist and they are indistinguishable except for when they are allowed to sing. I would like to thank The Genetics Society for making the trip possible.


Fly traps in the beautiful Finnish countryside. © Paris Veltsos
Coping with climate change: patterns of genetic variation, phenotypic variation and dispersal in six species of dragonfly

Helena Johansson. Institutionen för Ekologi, Miljö och Geovetenskap, Umeå University, Sweden.

Global climate change is expected to profoundly alter conditions for existence for numerous species. In order to cope with increasing temperatures species will have to genetically adapt to new conditions, migrate to areas with suitable conditions or their reaction norm in critical traits must allow for adaptation without genetic changes (Gienapp et al 2008). In addition, there is some debate over the function and fate of populations at range margins; are these populations more vulnerable to climate change because they tend to be smaller, fragmented and may harbour less genetic variation than central populations, or do they represent potential source populations of locally adapted individuals with high potential for further adaptive change (Bridle and Vines 2006)? Studying central and peripheral populations of congeneric species that differ in their geographic distribution and other life history characters may give insight into which factors (or combinations of factors) facilitates survival in a changing global climate, and also into the relative role of peripheral populations.

We are studying six species from the Coenagrion family of damselflies: two species, *C. johanssoni* and *C. armatum*, are found in the north of Europe, *C. puella* and *C. pulchellum* have wide ranging central European distributions, and *C. scitulum* and *C. mercuriale* are found in southern Europe. They are all small, bright blue damselflies with black markings, and can be seen flying and mating by various water bodies across Europe on summer days when the sun is shining and the wind is still. In 2008 and 2009 sampling of the northern species was carried out by researchers based at Umeå Universitet (Frank Johansson, Viktor Nilsson), and in central Europe by a researcher based at K.U. Leuven (Robby Stoks). The aim is to sample nine localities for each species: three from...
centre of the species range, and three localities in their northern and southern range margins.

Sampling for the southernmost localities for *C. scitulum* and *C. mercuriale* was carried out in Spain in June with the aid of a Genetic Society travel grant. With only scant information available for potential sampling sites, and with some collaborators tied up with sampling elsewhere, we allocated two weeks in this region to locate and collect samples from both species.

After a wet and cold start in northern Andalusia, when these damselflies do not fly, three localities were successfully sampled (in beaming hot sunshine) for *C. mercuriale*. We found this species at two previously unknown localities and at one locality that had been sampled as part of a biodiversity inventory by Junta de Andalusia. Between nine and 16 females were caught when mating, and their eggs retained for hatching and subsequent growth experiments. Damselflies lay their eggs in water, where the larvae also develop. Growth rate in eggs and larvae is dependent on water temperature, making this a potentially important functional trait for coping with climate change (Van Doorslaer and Stoks 2005). There is a plastic component to damselfly growth rate (Van Doorslaer and Stoks 2005), and spatial variation in the reaction norm (mean trait value) is being investigated in these six species using common garden experiments (at three different temperatures) in a laboratory setting.

In addition, damselfly legs were collected at each locality to make up a total sample number of 30 (including the egglaying females). Taking a leg does not affect mortality or mating success in damselflies, and is acceptable when collecting rare or protected species such as *C. scitulum* and *C. mercuriale*. From these 30 samples genetic variation (allelic richness, expected heterozygosity) will be assessed using microsatellite markers and other population parameters, such as effective population size and dispersal, can be estimated from these data.

After the successful collection of *C. mercuriale*, the journey went to the Spanish south coast to sample *C. scitulum*. A promising locality near Huelva (recorded in 1995) was found covered in concrete, so it was promptly decided to travel further east towards the (less concreted) Jerez de la Frontera region where one sampling record from 2003 existed. Here, two ponds were found in which *C. scitulum* resided; one previously recorded and the second one a new locality. Rain did not stop the sampling here, however wind in the afternoon promptly ended sampling activity at 2pm (compared to 6pm for *C. mercuriale*). After a weeks work, three females from each pond were caught and had laid eggs, and a further 10-15 *scitulum* were found at each site for DNA sampling.

Later in June, sampling continued by V. Nilsson in northern Spain and southern France (with the aid of local entomologists) where the remaining localities for the two species were added to the collection. *Coenagrion scitulum* was found to exist in more profuse numbers further north, indicating that we indeed did find populations at the very southern limit for this species.

The larvae that hatched from the eggs are now growing in the laboratories, and the legs are awaiting DNA extraction and genotyping in the near future. I would like to thank the Genetic Society for the award of this Heredity Fieldwork grant.

References


High-throughput yeast phenomics

Francois Cubillos, University of Nottingham

D
ifferent strains of *Saccharomyces cerevisiae* exhibit a wide genetic and phenotypic diversity, which makes this organism an attractive model for mapping quantitative trait loci (QTLs). Haploid strains of opposite mating types can be easily crossed to obtain a large number of segregants that can be quickly genotyped across the small genome. The identification of individual functional polymorphisms allows the dissection of complex phenotypes and advances our understanding of the molecular basis of natural variation.

The *Saccharomyces* Genome Resequencing Project (SGRP) released genome sequence of 72 *S. cerevisiae* and *S. paradoxus* strains. A neighbour joining phylogenetic tree based on pairwise SNP differences shows the presence of five well-defined *S. cerevisiae* lineages (Liti, et al., 2009). The same set of strains was also exposed to a vast array of 67 conditions to obtain a global phenotypic picture. Several strains showed extreme phenotypic variation like resistance to metal ion stress or environment sensitivity.

Currently in my PhD project with Prof. EJ Louis and Dr. G Liti, I have selected one strain from different geographic origins (Asian, European, American and African) and generated a grid of six crosses between the strains in order to map loci responsible for phenotypic variations. I generated 576 segregants (96 per F1 hybrid) and genotyped them using 170 markers evenly spaced along the genome (1 marker every ~70 kb). This set of segregants represents a valuable tool for the yeast genetic community for studying the genetic basis underlying natural variation. In this project, we collaborate with Prof. A Blomberg and Dr. J Warringer at Gothenburg University, who have established a high-throughput methodology for generating precise phenotypic profiles of yeast strains under multiple conditions (Warringer & Blomberg, 2003). We started to phenotype the 576 F1 segregants under several conditions in order to perform linkage analysis. Preliminary results indicate continuous distribution of the phenotypic profiles typical of complex traits, where several genes are involved and regulated by complex interactions. QTL mapping is currently underway for several of these conditions (e.g. Paraquat and Copper resistance).

In order to strengthen this collaboration, in August 2009 I visited Prof. Bloomberg’s lab to learn the high-throughput phenomics technique; from the experimental design stage through to the data analysis.

Initially, we performed experiments with segregants derived from the American (A) x African (WA) cross. The experiment starts with a pre-cultivation step and then aliquots from this culture are transferred into a plate containing the specific media to be tested. We performed this procedure for several stress conditions: including nutritional stress (media depleted of Biotin), metal ion stress (NaAsO2 5mM), drug sensitivity (Selenomethionine 100 mM) and environmental stress (growth at 40°C). Cell growth was continuously measured during a 72 hour time period, which gave us enough time to share lab experiences, have fascinating science discussions and learn more about the Swedish culture. In this context, I was involved in one of the most exciting traditions in Sweden, the “crayfish party” that gave me a good taste of the Swedish life. Later, back in the laboratory, I was introduced to the data analysis methods, primarily using the Prophecy software (Fernandez-Ricaud, et al., 2005), which allowed me to have a better understanding of the variables affecting traits and the normalization procedures necessary to avoid experimental variations. In this way, during 3 weeks, I was able to collect data from different crosses grown in more than 5 conditions and also get a better point of view of the physiological variables affecting yeast growth. From the growth curve obtained, three traits were extracted: adaptation, rate and efficiency. This dissection allows comparing strain growth at precise stages and determines key points where isolates show strength or deficiencies responsible for growth variation. I will use this data to map genes responsible for the great phenotypic variation detected among natural isolates of *S. cerevisiae*. We are currently working on a manuscript that describes these genotypes and phenotype resource and all the strains will be made publically available.

I would like to thank the Genetic Society for their funding on this fieldtrip, Jonas Warringer, Enikő Zörgő and Anders Blomberg for their incredible help with the lab work and their friendship.

www.genetics.org.uk

Check out the new Genetics Society web site, visit our forum and let us know what you think.
GRANTS

Genetics Society

one-day meetings

Graduate students may apply for travel costs to attend these meetings. The cheapest form of travel should be used if possible and student railcards used if travel is by train. Airfares will only be refunded in exceptional circumstances. Grants for overnight accommodation are not available. Applications for travel grants should be made using the registration form, before the final deadline for the meeting.

Meetings with Genetics Society Sponsorship

These include the annual Arabidopsis, C. elegans, S. pombe and Pop Group meetings. Graduate Students may apply for travel grants to attend these meetings. Applications should be sent to the Genetics Society, at least one month before the meeting. The cheapest form of travel should be used if possible and student railcards used if travel is by train. Airfares will only be refunded in exceptional circumstances.

Genetics Society

Travel Grants for Junior Scientists

PhD students and postdocs (within two years of viva) who have been members of the Genetics Society for at least one year may apply for grants of up to £500 to attend conferences in the area of Genetics that are not sponsored by the Genetics Society. Please note a maximum of one grant every three years will be awarded to any junior scientist. Applications should be submitted by email in time for one of the quarterly deadlines (1st day of February, May, August and November), to the Society Office (mail@genetics.org.uk) using message subject “TGJS application” and your surname. Applications should include a brief outline of the value of the meeting to the applicant, an outline of any presentation to be made at the meeting and estimated costs. Please ask your supervisor to send a very brief email in support. Recipients of travel grants will be asked to write a short report that may be included in the newsletter.

Heredity Fieldwork Grants

Supporting field-based genetic research and training

Purpose: To provide grants of up to £1,500 to cover the travel and accommodation costs associated with pursuing a field-based genetic research project. The scheme is not intended to cover the costs of salaries for those engaged in fieldwork or training, or to fund attendance at conferences. The work should include a strong genetical component.

Eligibility: The scheme is open to any member of the Genetics Society who has been a member for at least one year. The research field should be one from which results would typically be suitable for publication in the Society's journal Heredity. Only one application from any research group will be admissible in any one year. Applications should be made using the form available on the Genetics Society's web page. The application form requests a short summary of the research project for which funds are sought. This should explain the role of the proposed field research in the overall project, and indicate how the grant will be used to facilitate the field research. A detailed budget for the fieldwork will be required, as well as an outline of other possible sources of funding. Applications from PhD students or post-docs should be accompanied by a letter (or e-mail) of support from your supervisor or lab head.

Closing date: There are two closing dates of 1st March and 1st September each year. Awards will be announced within two months of the closing date to allow time for fieldwork preparation. At the end of the grant a short report will be requested from the grant holder. This should be in a format that is suitable for publication in the Genetics Society newsletter. A maximum of one grant per individual every three years will be awarded.
Genes and Development summer studentships
supporting field-based genetic research and training

Purpose: 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.

Eligibility: 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. A maximum of 40 studentships will be awarded. 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.

Applications are invited from members of the Genetics Society who have been members on or before the deadline of March 31st, and who run a research group within a University or Research Institute or a commercial research facility. Applications must be for a named student and must include the student's CV together with a reference from their tutor (or equivalent). Undergraduate students are encouraged to seek a sponsor and to develop a project application with the sponsor.

A panel of members of the Genetics Society committee will review applications. Feedback on unsuccessful applications will not be provided. The successful applicants will be required to submit a short report from the students within two months of completion of the project.

Full details and on-line application form are available at the Genetics Society website

Sir Kenneth Mather Memorial Prize

This is an annual prize of £150 to reward a BSc, MSc or PhD student of any UK University or Research Institute who has shown outstanding performance in the areas of quantitative or population genetics.

Nominations should be made between July 1st and November 1st inclusive of each year 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”.

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 each year.
Personal Subscription
Order Form 2010

Please return this from to: The Genetics Society, Wallace Building, Roslin BioCentre, Roslin, Midlothian, EH25 9PP

The new personal subscription rate for Genes and Development for 2010 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.

Name (BLOCK CAPITALS): ........................................................................................................................................................

Address: ..........................................................................................................................................................................................
..........................................................................................................................................................................................................

Tel: ...........................................................................   Fax: ..........................................................................................................

Email: ............................................................................................................................................................................................

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

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

4. Please debit my Visa/Mastercard

   Credit Card Number .......................................................................................................................................................... Expiry ............. / .............

   Address where bill sent ..................................................................................................................................................
..........................................................................................................................................................................................

   Signed ..............................................................................................................................................................................
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 International 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.
Membership includes free online subscription to Heredity

Please complete this form and return it, along with your payment to, The Genetics Society, Wallace Building, Roslin BioCentre, Roslin, Midlothian, EH25 9PP. 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. 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 registration. In addition, after one year full membership you can apply for a grant of up to £300 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: __________________________

Signature of Head of Department/Supervisor __________________________

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

mail@genetics.org.uk
4. 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 subscription 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 for full and postgraduate members paying by Direct Debit

5. PAYMENT

Option 1: **Direct Debit (UK Bank Accounts only)**

Complete this membership form and send it to the address below. On receipt you will be sent a DIRECT DEBIT MANDATE to complete and return with instructions enclosed.

I wish to pay by direct debit (tick box if applicable) **Paying by Direct Debit saves Full members and Postgraduates £5**

Direct Debit Membership subscriptions are renewed on an annual basis running from 01 June – 31 May or 01 December - 30 November depending on date of application

Option 2: **Cheque**

I enclose a cheque for the sum of £ payable to ‘The Genetics Society’

Option 3: **Card Transaction**

Please note that

- **Visa**
- **MasterCard**

- **Solo**
- **Switch**

* (handling charges apply raising membership fees by 3.6%)

<table>
<thead>
<tr>
<th>Category</th>
<th>Amount</th>
<th>Amount</th>
<th>Amount</th>
</tr>
</thead>
<tbody>
<tr>
<td>Full Member</td>
<td>£25.90</td>
<td>£15.54</td>
<td>£5.18</td>
</tr>
<tr>
<td>Postgraduate</td>
<td><strong>£15.43</strong></td>
<td><strong>£15.43</strong></td>
<td><strong>£5.43</strong></td>
</tr>
<tr>
<td>Undergraduate</td>
<td><strong>£25.43</strong></td>
<td><strong>£25.43</strong></td>
<td><strong>£25.43</strong></td>
</tr>
</tbody>
</table>

Card No: Start Date: Expiry Date: Issue No. (if applicable)

Cardholder Name: Signature of Cardholder:

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 were 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.

Signature of nominating FULL MEMBER (please print name in block capitals after signature)

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, Wallace Building, Roslin BioCentre, Roslin, Midlothian, EH25 9PP marking your envelope MEMBERSHIP APPLICATION.

Please note that the approval of new members is ratified at the Spring Meeting as part of our AGM

OFFICE USE ONLY

<table>
<thead>
<tr>
<th>Date Received</th>
<th>Date Processed</th>
<th>Membership No.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>DD No.</th>
<th>Nominal Code</th>
<th>Membership Pack Sent</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Notification of change of address form

Note that from [ ] my NEW ADDRESS will be:

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

(Print or Type)

Last Name: [ ] First Name: [ ]

Institution: [ ]

Address: [ ]

Postcode: [ ] Country: [ ]

Telephone: [ ] Fax: [ ]

Email: [ ]

Previous address: [ ]

Please return this form to: The Genetics Society, Wallace Building, Roslin BioCentre, Roslin, Midlothian, EH25 9PP marking your envelope CHANGE OF ADDRESS NOTIFICATION.

OFFICE USE ONLY

Date Received [ ] Date Processed [ ]
Heredity

www.nature.com/hdy

Published on behalf of The Genetics Society

What does Heredity publish?
Heredity publishes original research articles, reviews, and news and commentaries in ecological, population and evolutionary genetics, including:

- human population genetics
- genomics and post-genomics as applied to evolutionary questions
- biometrical and statistical genetics
- animal and plant breeding
- cytogenetics

Who reads Heredity?
Researchers with an interest in population genetics, ecological genetics, evolutionary genetics, genomics, cytogenetics, applied genetics, quantitative genetics, plant and animal genetics.

Where can I get more information?
Visit the journal online at www.nature.com/hdy.

Why submit your paper to Heredity?
- Online submission allows you to submit your paper online quickly and easily, and speeds up the acceptance and review process
- Advance Online Publication – articles published online weekly in advance of print
- NPG enhanced Search Tool allows your paper to be identified with all other relevant Nature Publishing Group journals in all keyword searches, meaning your paper can be found on any online search across the NPG journal websites