Collecting saltwater samples in the Dead Sea, part of a fieldwork grant. See page 39
A word from the editor

Welcome to issue 67.

Welcome to another issue of the Newsletter. We include the usual interesting range of articles, student reports, meeting reports and so on, but I am also very pleased to include the biographies of our newest Honorary Members, a group of outstanding geneticists who have all made great contributions to the field. I wonder what they would make of an amusing, yet somewhat depressing commentary published in a recent issue of Genome Biology (Goodbye Columbus: Genome Biology 2012 13:155)?

The article places Columbus before the King and Queen of Spain after his funding application to sail west to seek the Indies has been rejected. The reasons for the rejection are explained and Columbus is advised to seek funds for something he has done before, something that will not fail (why not at trip to Lisbon instead?). It includes the amusing dialog;

‘Columbus: “But your guidelines say that a lot of preliminary data are not required for proposals of high impact”.

Ferdinand: “And you believe that? Hahahaha! What an idiot”.

The article makes some excellent points and makes them well. It is a must-read, and reviewers and panels should remember that if it cannot fail and if we know the answers beforehand, it is not really science.

Read on and enjoy, and I can only hope that the summer weather where you are, is a darn sight better than here.

Best wishes

David Hosken

The article places Columbus before the King and Queen of Spain after his funding application to sail west to seek the Indies has been rejected.
2012 Autumn Meeting

At the cutting edge of molecular biology
25 years of Genes & Development

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

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

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

Speakers
Sharon Dent
Steve Smale
Jerry Workman
Ken Zaret
Titia de Lange
Steve Elledge
Steve Jackson
Susan Gottesman
Elisa Izaurralde
Narry Kim
Jim Manley
Joan Steitz
Hans Clevers
Elaine Fuchs
Nick Hastie
Rich Losick
Eileen White

Chairs
Terri Grodzicker
Hans Clevers
Rudi Grosschedl
Winship Herr
Davor Solter

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

Features
Steve West
The 2012 Genetics Society Medal recipient

for registration, visit
www.genetics.org.uk
2013 Spring Meeting

A joint meeting held by the Genetics Society and BSHG

Genomics for Health and Society

19 April. The Royal Society, London

This meeting is jointly organised by the Genetics Society and the British Society of Human Genetics, and brings together excellent speakers with a broad range of perspectives on the medical and societal implications of genomics. Each speaker is an expert in their own domain, from DNA fingerprinting to consumer genomics, from genealogy to genomic medicine, from the legal implications of genomics to the therapeutic opportunities.

Genomics promises to revolutionize medicine and health care, with the potential for highly personalised treatments for the very first time. This meeting will focus on these and related issues, with presentations on clinical and societal issues that arise from these new horizons. Discussion of the legal implications of genomics, neuromuscular diseases and clinical genetics will be included.

Speakers
Kate Bushby University of Newcastle
Sir John Burn University of Newcastle
Jim Lupski Baylor College of Medicine, Houston
Mark Henderson Head of Communications, Wellcome Trust
Jane Kaye University of Oxford
Mark Jobling University of Leicester
Alec Jeffreys University of Leicester

A full list of speakers will be available soon on the Genetics Society web site.

Scientific Organisers
Matt Hurles, Chris Ponting and Bill Newman

for registration, visit
www.genetics.org.uk
2013 Autumn Meeting

From Genes to Shape

Thursday 7 – Friday 8 November. The Royal Society, London

How does digital information in a linear DNA sequence lead to the dynamic shape of individual cells, such as pollen tubes and neurons, and growing multicellular structures such as flowers or wings? Recent advances in genetics, imaging, cell biology, biophysics and computational biology are being used to address this problem at a mechanistic level for the first time.

This two-day meeting brings together scientists working at the interface of these disciplines to unravel the mechanisms underlying shape generation from the subcellular to the tissue scale. Topics include cytoskeleton dynamics, cell polarity, growth and deformation of cell sheets and formation of primordia and appendages. The meeting will highlight unifying principles by ranging over microbial, plant and animal systems.

Speakers include
Anja Geitmann Université de Montréal
Ray Goldstein University of Cambridge
Verônica Grieneisen John Innes Centre, Norwich
Max Heiman Harvard Medical School
Frank Jülicher Max Planck Institut, Dresden
Stan Leibler Princeton and Rockefeller Universities
Sophie Martin University of Lausanne
Benedicte Sanson University of Cambridge
James Sharpe EMBL-CRG, Barcelona
Jan Traas ENS, Lyon

Meeting organisers
Enrico Coen and Buzz Baum

for registration, visit
www.genetics.org.uk
Population Genetics Group

The Population Genetics Group (PGG or PopGroup) is a yearly international meeting held in the UK. It is an informal meeting covering all aspects of Evolutionary Genetics with typically 150-200 participants, and an excellent place for PhD students to present their work.

Popgroup45 (Nottingham) was a smoothly run and highly successful meeting, with a particularly high standard of presentations and cutting edge developments in the use of advancements in sequencing technologies for population genetics applications; we hope to maintain this high standard at the next meeting.

The meeting has so far obtained sponsorship from the Genetics Society, Nature Reviews Genetics, Heredity, Royal Society Publishing, and the Institute of Biodiversity, Animal Health & Comparative Medicine at the University of Glasgow.

In addition, the Glasgow City Marketing Board has provided substantial support both in terms of logistics and financing, including arranging for a Civic Reception prior to the Conference Dinner.

Speakers include
Rod Page (University of Glasgow)
Mike Arnold (University of Georgia)
Charlie Baer (University of Florida).

Opening Reception
Held on December 18th at Jurys Inn, Central Glasgow. The rest of the meeting will be held at the Gilmorehill campus of the University of Glasgow, situated in the west end.

Accommodation
Accommodation for the conference has been bulk booked at the Jurys Inn in central Glasgow (close to Central Station)

For more information
Please contact pgg@populationgeneticsgroup.org if you have any questions. Additional details about the meeting can be found on the website www.populationgeneticsgroup.org, including information on subscribing to the email list.
We will happily include any announcements for genetics-based meetings in this section. Please send any items to the editor.

Drosophila Genetics and Genomics
12-20 August 2012, Downing College, University of Cambridge, UK
https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=293

Rapid evolution during biological invasions
Fribourg, 6-7 September 2012
www.unifr.ch/biol/ecology/CUSO/EEday2012/index.html

British Human Genetics Conference 2012
17-19 September 2012, Warwick, UK
www.bhgc.org.uk

The Genomics of Common Diseases 2012
19-22 September 2012, Bolger Center, MD, USA
www.nature.com/natureconferences/gcd2012/index.html

Infectious Disease Genomics and Global Health
1-3 October 2012 Churchill College, Cambridge
https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=297

Molecular Genetics of Aging
9-13 October 2012, Cold Spring Harbour USA
http://meetings.cshl.edu/meetings/aging12.shtml

Epigenomics of Common Diseases
12-15 October 2012, Johns Hopkins University, Baltimore, USA
https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=298

62nd Annual Meeting of the American Society of Human Genetics (ASHG)
6-10 November 2012, San Francisco, CA, USA
www.ashg.org/2012meeting

RNA: a key to coordination of gene expression
7-11 November 2012, Roscoff France,
www.cnrs.fr/insb/cjm/2012/Prats_e.html

Human Genetic Diversity
www.galtoninstitute.org.uk/conferences.htm

Rat Genomics and Models 2012
3-6 December 2012, Cambridge, UK
https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=286

Population Genetics Group
18-21 December 2012, Glasgow, UK
www.populationgeneticsgroup.org/popgroup46-glasgow/

14th Congress of the European Society for Evolutionary Biology
19-24 August 2013, Lisbon, Portugal
www.eseb2013.com/

8th European Zebrafish Genetics and Development meeting
9-13 July 2013, Barcelona, Spain
http://zebrafish2013.org/
The Genetics Society helps support several sectional interest groups by providing meeting sponsorship. We currently have 11 groups who organise sectional interest meetings with the organizers and dates of any forthcoming meetings are listed below. If you are interested in any of these areas, please contact the relevant organiser. Groups who wish to be considered for sectional interest group status should see the Society website for further details.

**Arabidopsis**  
Organiser: Ruth Bastow  
(ruth@garnetcommunity.org.uk)  
www.garnetcommunity.org.uk

**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)

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

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

**London Fly meetings**  
Organisers: Manolis Fanto and Nic Tapon  
(manolis.fanto@kcl.ac.uk) and  
(nic.tapon@cancer.org.uk)

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

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

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

**The Zebrafish Forum**  
Organiser: Rachel Ashworth (r.ashworth@ucl.ac.uk),  
Caroline Brennan (C.H.Brennan@qmul.ac.uk),  
Corinne Houart (corinne.houart@kcl.ac.uk).

There are meetings at 5.30pm-8.00pm on the first Thursday of every other month. Room G12, New Hunt’s House, King’s College - London SE1 1UL
Committee changes and elections

The Committee has seen a number of new changes this year, and we acknowledge the valuable contributions of all outgoing members. The Society is particularly grateful to the outgoing President, Veronica van Heyningen, for her four years at the helm, which were much appreciated by all.

Veronica retires at the end of this year after a distinguished career in Genetics, and we wish her well, but do not say goodbye: she hopes to attend many future Genetics Society meetings. Our Corporate and External Affairs have been well looked after by Vice Presidents Ian Jackson and John Brookfield, respectively, who have been generous with their time and commitment to Society business.

Patricia Kuwabara has completed her term as Honorary Secretary, and has done an excellent job of ensuring smooth and efficient running of the Society. We are grateful to Adam Eyre-Walker and Tom Weaver for their contributions to the Committee as representatives for Areas ‘E’ (Evolutionary, ecological and population genetics) and ‘F’ (Corporate genetics and biotechnology), respectively. We also thank Lynne Harris as outgoing Postgraduate Representative.

Four new Executive Committee members were elected to office at the Annual General Meeting, held at the Royal Society on Friday 20th April 2012. We welcome Enrico Coen (John Innes Institute) as President. Rico has been shadowing Veronica for the past year; she promises that he will bring a ‘stylish approach’ to the running of the Society. Rebecca Oakey (King’s College London) takes over as Vice President for External Affairs, while Elizabeth Fisher (University College London) takes up post as Vice President for Corporate Affairs. As the new Honorary Secretary, I wish to express my sincere thanks to Patty, who has helped me find my way and been patient with my numerous questions!

Three new Ordinary Members were also elected to the Committee: Colum Walsh (University of Ulster) will complete Rebecca Oakey’s term representing Area ‘A’ (Gene structure, function and regulation); Judith Mank (University College London) will represent Area ‘E’ (Evolutionary, ecological and population genetics), and Dominique Kleyn (Bioindustries Association) will represent Area ‘F’ (Corporate genetics and biotechnology). Adam Hargreaves (Bangor) takes over as Postgraduate Representative. We welcome all new Committee members and hope that they will find their time on the Committee rewarding and enjoyable.

We also welcome the 160 new members that were formally elected by the Society at the AGM; we look forward to seeing them at future meetings and hope that they, in turn, will help to recruit new members.

Minutes of the April 2012 AGM and a list of Committee members can be found on the Society’s website.
Medal and Prize Lecture Announcements

The Genetics Society is pleased to announce the award of the following Medals and Prizes to scientists for their outstanding contributions to the study of Genetics. Additional information about these individuals and their research are posted elsewhere in this Newsletter.

2013 Genetics Society Medal
Robin Allshire,
University of Edinburgh

2013 Balfour Lecture
Simon Myers,
University of Oxford

2013 JBS Haldane Lecture
Mark Henderson,
The Wellcome Trust

Please note that the Society is now seeking nominations for awards to be made in 2014. Details can be found in this edition of the Newsletter. Any member in good standing is eligible to submit nominations.

Honorary Members

Four distinguished and eminent members of the Genetics community were elected by the Committee as Honorary Members of the Society

Professor Dame Kay Davies FRS
Professor William Hill FRS
Professor Sir Alec Jeffreys FRS
Professor Paul Nurse FRS

Life Membership in the Genetics Society

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

Committee vacancies

Six Committee posts will be falling vacant as of 1st May 2013:
1. Postgraduate Representative
2. Newsletter Editor
3. Ordinary Committee Member: Area ‘A’ (Gene structure, function and regulation)
4. Ordinary Committee Member: Area ‘B’ (Genomics)
5. Ordinary Committee Member: Area ‘C’ (Cell and developmental genetics)
6. Ordinary Committee Member: Area ‘D’ (Applied and quantitative genetics)
7. Executive Committee: Honorary Treasurer

Please note that the post of Honorary Treasurer will be falling vacant as of 1st May 2014, but nominees are elected with a shadowing year, and so will be invited to join the Committee from 1st May 2013.

Members of the committee will nominate a ballot of candidates; however, all members in good standing are welcome to nominate individuals for these upcoming vacancies from members of the Society. Nominations should be sent via email to the Honorary Secretary, Tanya Whitfield (t.whitfield@sheffield.ac.uk) in time for a deadline of Friday, November 30th, 2012. Nominations must be made with the nominee’s consent.
2014 The JBS Haldane Lecture

The JBS Haldane Lecture will recognise an individual for outstanding ability to communicate topical subjects in genetics research, widely interpreted, to an interested lay audience. This speaker will have a flair for conveying the relevance and excitement of recent advances in genetics in an informative and engaging way. The annual open lecture will be delivered on a topic, and in a place, agreed with the Genetics Society. In addition to delivering the Lecture, the recipient will receive an honorarium of £1000 and a three-year membership of the Society. The recipient of the JBS Haldane Lecture 2013 is Mark Henderson (Head of Communications, The Wellcome Trust).

Nominations are now being invited for the 2014 JBS Haldane Lecture. The recipient will be selected by a committee chaired by the Genetics Society’s Vice President for the Public Understanding of Genetics (Chris Smith) from nominations made by Society members. Nominees need not be members of the Society, but should be active researchers working in the UK.

To make a nomination, please confirm that your candidate is willing to be nominated, and then submit both a two-page CV and a short explanation of how the candidate meets the criteria above. These documents must be submitted electronically to the Honorary Secretary of the Society, Tanya Whitfield, by Friday, November 30, 2012, at t.whitfield@sheffield.ac.uk.

2014 Balfour Lecture

The Balfour Lecture, named after the Genetics Society’s first President, is an award to mark the contributions to genetics of an outstanding young investigator. The Balfour Lecturer is elected by the Society’s Committee on the basis of nominations made by any individual member of the Society. The only conditions are that the recipient of the award must normally have less than 10 years’ postdoctoral research experience at the time of nomination. Any nomination must be made with the consent of the nominee. Those making nominations must be members of the Genetics Society, but there is no requirement for the nominee to be a member, nor is there any restriction on nationality or residence. Simon Myers will present the 2013 Balfour Lecture at the Genetics Society Spring meeting, 2013, at The Royal Society.

Nominations are now being invited for the 2014 Balfour Lecture. Note that there is no restriction on the subject matter of the Balfour Lecture. To make a nomination, please confirm that your candidate is willing to be nominated, and then forward a two-page CV of the candidate, together with a list of his or her ten most important publications, plus a one-page letter of recommendation outlining why you feel their contributions to the field have been outstanding. These documents must be submitted electronically to the Honorary Secretary of the Society, Tanya Whitfield, by Friday, November 30, 2012, at t.whitfield@sheffield.ac.uk.

The Sir Kenneth Mather Prize

We are seeking nominations for this annual prize, of £150, to reward a BSc, MSc or PhD student of any UK University or Research Institution who has shown outstanding performance in the area of quantitative or population genetics. Nominations should be made between July 1st and November 1st 2012 through the local Head of Department or School of the nominee. Nominations should consist of no more than one page of A4, setting out the case for the nomination, including relevant comparison with other students where possible. Nominations should be sent to the Head of School, School of Biosciences, The University of Birmingham, Birmingham, B15 2TT, clearly labelled as a nomination for “The Sir Kenneth Mather Memorial Prize”.

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 Genetics Society. Decisions will be announced in December 2012.
Genetics Society Medal 2014

The Genetics Society Medal is an award that recognises outstanding research contributions to genetics. The Medal recipient, who should still be active in research at the time the Medal is awarded, will be elected annually by the Committee on the basis of nominations made by any individual member of the Society. Those making nominations must be members of the Genetics Society, but there is no requirement for the nominee to be a member, nor any restriction on nationality or residence. Neither current members of the Committee nor those who have retired from office in the past four years may be nominated for the award. The recipient will be invited to deliver a lecture at a Genetics Society meeting, where the medal will be awarded, in the year following his/her election. Robin Allshire will present the Genetics Society Medal lecture for 2013 at the Genetics Society Autumn meeting, 2013, at The Royal Society.

Nominations are now being invited for the 2014 Genetics Society Medal. To make a nomination, please confirm that your candidate is willing to be nominated, and then forward a two-page CV of the candidate, together with a list of his or her ten most important publications, plus a one-page letter of recommendation outlining why you feel their contributions to the field have been outstanding. These documents must be submitted electronically to the Honorary Secretary of the Genetics Society, Tanya Whitfield, by Friday, November 30th, 2012.

JBS Haldane Lecture 2013

Mark Henderson

After studying Modern History at Oxford as an undergraduate, Mark joined the Times as Science Correspondent 2000, becoming Science Editor in 2006. He was instrumental in founding Eureka, the newspaper’s monthly science magazine, and has won several awards for his journalism.

The Genetics Society is pleased to announce that the 2013 JBS Haldane Lecture will be awarded to Mark Henderson (The Wellcome Trust). The JBS Haldane Lecture recognises an individual for outstanding ability to communicate topical subjects in genetics research, widely interpreted, to an interested lay audience.

After studying Modern History at Oxford as an undergraduate, Mark joined the Times as Science Correspondent 2000, becoming Science Editor in 2006. He was instrumental in founding Eureka, the newspaper’s monthly science magazine, and has won several awards for his journalism: three prizes from the Medical Journalists’ Association (all for genetics stories: cancer treatments, genetic diagnosis of MODY diabetes and the first pre-implantation genetic diagnosis for BRCA genes), the Royal Statistical Society’s prize for statistical excellence in journalism (investigation into risks revealed by over-the-counter genetic testing), and the European Best Cancer Reporter prize from the European School of Oncology.

His first book, 50 Genetics Ideas You Really Need to Know, was published in 2009. His second book, The Geek Manifesto, which explores the relationship between science and politics, was published in May 2012. Mark Henderson joined the Wellcome Trust as Head of Communications in January 2012.
Balfour Lecture 2013
Simon Myers

The Genetics Society is pleased to announce that the 2013 Balfour Lecture will be awarded to Dr Simon Myers (University of Oxford).

The Balfour Lecture, named after the Genetics Society’s first President, is an award to mark the contributions to genetics of an outstanding young investigator.

Following his undergraduate training in mathematics at the University of Oxford, Simon Myers became interested in the application of probabilistic models to studying patterns of genetic variation in natural populations. He gained a PhD in mathematical genetics in 2002 with Professor Bob Griffiths FRS at the Department of Statistics in Oxford, working on complex graph structures that arise in coalescent models that include recombination. His work, initially on theoretical properties of these graphs, turned towards trying to make sense out of empirical data; in particular, to how it is possible to ‘count’ the number of historical recombination events that must have occurred in the history of a sample of DNA sequences. This naturally led to a deeper interest in the problem of learning about recombination from patterns of genetic variation and, through a postdoc with Professor Peter Donnelly FRS and collaboration with Gil McVean also at the Department of Statistics in Oxford, he became involved in the International HapMap Project and the development of statistical methods to identify recombination hotspots from the wealth of genome-wide SNP data arising from the project. By application of these methods he identified large numbers of hotspots across the human genome, discovered that a DNA sequence ‘motif’ marks the positions of these hotspots and, in 2010, identified that the PRDM9 protein binds to the motif, and thus specifies the positions of tens of thousands of hotspots throughout the human genome.

During this period he spent two years at Harvard and MIT, working with David Reich and colleagues on methods for analysing genetic variation in admixed populations.

In 2007 Simon became a Lecturer in Bioinformatics in Oxford, where he has continued to work to understanding recombination and patterns of genetic variation in natural populations. In a landmark paper, published in 2011, Simon showed how patterns of admixture provide rich information about the location of hotspots and identified an African-specific motif, bound by a distinct variant of PRDM9. He has also developed methods for learning about population history from genetic variation, which have provided new and detailed insights into diverse populations, from the UK to the plains of Central Asia.

Simon spent two years at Harvard and MIT, working with David Reich and colleagues on methods for analysing genetic variation in admixed populations.
Genetics Society Medal 2013
Robin C. Allshire

The Genetics Society is pleased to announce that Professor Robin Allshire (University of Edinburgh) will be awarded the 2013 Genetics Society Medal for his outstanding research contributions to the fields of epigenetics and chromosome biology. Robin Allshire studied genetics as an undergraduate in Trinity College Dublin before moving to Edinburgh to study for a PhD in the MRC Mammalian Genetics Unit under the guidance of Chris Bostock and Ed Southern. During this time he investigated factors affecting the behaviour of vectors for propagating DNA in mammalian cells, an interest that naturally led to studies of telomere and centromere structure that have occupied him since.

Robin spent four years as a postdoc with Nick Hastie in what is now the MRC Human Genetics Unit, where he cloned human telomeres and studied their behaviour in cancers. He showed that telomere length decreases with age and proposed that telomerase is inactive in somatic tissues. Robin then spent a year as a visiting scientist in the Cold Spring Harbor Laboratory where he started to work with *Schizosaccharomyces pombe* before returned to Edinburgh to establish his own research group, again at the MRC Human Genetics Unit. In 2002 he became a Principal Fellow of the Wellcome Trust within the Wellcome Trust Centre for Cell Biology at the University of Edinburgh.

Robin's attention has turned from telomeres to centromeres and he and his colleagues have demonstrated that normal centromere activity requires that centromeric DNA is in heterochromatin and is dependent on histone modifications, particularly those on Histone H3 and the related protein CENPA. More recently they have shown that these modifications are added in response to components of the RNAi pathway linking transcription of centromeric sequences to histone modification and centromere integrity.

Robin is recognised internationally as a world leader in the field of epigenetics and chromosome biology. He was elected a member of the European Molecular Biology Organisation in 1988, a Fellow of the Royal Society of Edinburgh in 2002, and of the Royal Society, London, in 2011.

Robin spent four years as a postdoc with Nick Hastie in what is now the MRC Human Genetics Unit, where he cloned human telomeres and studied their behaviour in cancers.
New Honorary Members

The Genetics Society is delighted to announce the following have been elected to an Honorary Membership, in recognition of their outstanding contributions to the study of genetics.

Professor William G. Hill, FRS, OBE

Bill Hill is one of the world’s leading quantitative geneticists, with a distinguished research career spanning 40 years, focussed on the variability in complex traits arising from the joint effects of genetic and environmental factors. Raised on a Hertfordshire farm (which the family still owns), Bill came into genetics via an interest in livestock improvement. After studying Agriculture at Wye College London and Genetics at UC Davis, Bill moved to Edinburgh to undertake a PhD in quantitative and population genetics with Alan Robertson. Apart from occasional periods abroad to work with his many collaborators, he has stayed in Edinburgh since, building on the historical strength in quantitative genetics developed by Douglas Falconer, Alan Robertson and others.

Bill’s research is primarily theoretical, using mathematical and computer models of the behaviour of genes in populations to understand the genetic basis of quantitatively varying traits. His contributions have included studies of how genetic variation is maintained in natural populations, and how selection (both natural and artificial) changes the structure of genetic variation. He has made numerous very influential advances in our understanding of the effects of finite population size and mutation on variability and selection responses, notably the role of mutation in maintaining continued responses to selection. In addition to his purely scientific work, he has made many important contributions to the application of genetics to animal improvement, which have had a major impact on the livestock breeding industry. He is a sought-after consultant by both public agencies and private businesses in this area.

Of especial importance has been his work on linkage disequilibrium, the non-random associations between genetic variants at different sites in the genome. Such associations now provide an immensely important tool for geneticists seeking to map and identify genes involved in disease and other complex traits, and Bill’s work provided a basic framework for modelling and analysing linkage disequilibrium, which he went on to apply to genetic mapping. As a PhD student with Alan Robertson, Bill demonstrated how selection acting at a locus interferes with that happening simultaneously at linked loci. The Hill-Robertson effect has become one of the most influential ideas in population genetics, finding a new lease of life in its ability to explain patterns of molecular evolution and diversity revealed by the genomic revolution. Within recent years, his work has helped to shape our understanding of what genome-scale data sets can tell us about complex traits and relatedness within populations.

Bill has served with distinction in several important academic administrative posts, culminating in the position of Dean of the Faculty of Science and Engineering at the University of Edinburgh until his official retirement in 2002. He continues to be highly active in the fields of quantitative genetics and animal breeding and has inspired many generations of scientists through his teaching and supervision. He was elected to the Royal Society of Edinburgh in 1979, the Royal Society of London in 1985 and appointed OBE in 2004, in part for his contribution to the UK animal breeding industry.
Kay Davies is the Dr Lee’s Professor of Anatomy in the Department of Physiology, Anatomy and Genetics, Honorary Director of the MRC Functional Genomics Unit and Associate Head of Division (Development, Impact and Equality) at the University of Oxford. Her research interests lie in the molecular analysis of human genetic disease, particularly the genetic basis of neuromuscular and neurological disorders. She began her career in Oxford as a chemistry undergraduate, followed by a DPhil in Biochemistry. After a short postdoc in France she joined Bob Williamson’s department in St Mary’s Hospital in London where she began work on Duchenne Muscular Dystrophy (DMD) which is caused by the absence of dystrophin. She has been working on the molecular analysis of this devastating progressive muscle wasting disease for more than 30 years. She initially developed the first DNA probes for prenatal diagnosis and carrier detection and currently focuses on the development of effective treatments for DMD. She identified the dystrophin-related protein utrophin and demonstrated that increasing levels of this protein could prevent the pathology in a mouse model of the disease. She co-founded Vastox plc (now Summit plc) in order to take drugs that increase levels of utrophin to the clinic for DMD. In 1999, she set up the MRC Functional Genetics (now Genomics) Unit which aims to use genome information for the analysis of the function of genes to aid the development of new treatments for neurological disorders. Over the last ten years, she has been using ENU mouse mutants to model movement and behavioural disorders. One of these mutants links synaptic dysfunction for the first time to abnormal circadian rhythms and schizophrenia endophenotypes. Professor Davies has won numerous prizes for her research and published more than 350 peer reviewed papers. She has an active interest in the ethical implications of genomics research and in promoting public understanding of science, appearing at Science Festivals, in newspaper reports on television and on radio (including Desert Island Discs). She has served on many Committees for charities and government organisations and has been a Governor of the Wellcome Trust since 2003. She is founding editor of the journal Human Molecular Genetics. She is currently a Director of the American Society of Human Genetics, the first year Europeans have been elected to this role. Professor Davies is a founding fellow of the Academy of Medical Sciences and was elected a Fellow of the Royal Society in 2003. She was awarded a CBE in 1995 and a DBE in 2008 in recognition of her many contributions to medical research.
**Professor Sir Alec Jeffreys FRS**

Prof. Sir Alec Jeffreys studied biochemistry and genetics at Merton College, Oxford. Following an EMBO Postdoctoral Fellowship at the University of Amsterdam where, with Dr Richard Flavell, he was one of the first to discover split genes, he moved in 1977 to the Department of Genetics at the University of Leicester where he currently holds the positions of Professor of Genetics and Royal Society Wolfson Research Professor.

Sir Alec’s research at Leicester has focussed on exploring human DNA variation and the mutation processes that create this diversity. He was one of the first to discover inherited variation in human DNA, then went on to invent DNA fingerprinting, showing how it could be used to resolve issues of identity and kinship. His current work concentrates on developing new approaches to analysing variation and mutation in human chromosomes.

Sir Alec’s work has received widespread recognition, including his election to the Royal Society in 1986 and a Knighthood for services to genetics in 1994. Other awards include the Louis-Jeantet Prize for Medicine (2004), the Lasker Award (2005) and the Heineken Prize (2006). He was also one of the four finalists for the Millennium Prize in 2008.

**Paul Nurse FRS**

Paul Nurse is a geneticist and cell biologist who has worked on how the eukaryotic cell cycle is controlled and how cell shape and cell dimensions are determined. His major work has been on the cyclin dependent protein kinases and how they regulate cell reproduction.

He is President of the Royal Society and Director of the Francis Crick Institute in London and has served as Chief Executive of Cancer Research UK and President of Rockefeller University. He shared the 2001 Nobel Prize in Physiology or Medicine and has received the Albert Lasker Award and the Royal Society’s Royal and Copley Medals. He was knighted in 1999 and received the Legion d’honneur in 2003.
Heredity is an official journal of the Genetics Society, and publishes original research in all areas of genetics, with a particular focus on population, evolutionary and quantitative aspects, animal and plant breeding and cytogenetics. Primary research papers are complemented by Reviews covering currently developing areas and News and Commentary articles keeping researchers and students abreast of hot topics. Here is just a selection of some of our hottest content.

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M J Sillanpää

Genetic basis of sexual dimorphism in the threespine stickleback Gasterosteus aculeatus
T Leinonen, J M Cano & J Merilä

Evolution of sex-specific wing shape at the widerwing locus in four species of Nasonia
D W Loehlin, L S Enders & J H Werren

Genetic variation of copia suppression in Drosophila melanogaster
W Vu & S Nuzhdin

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Local Representatives

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

We seek to fill vacancies and to update our database of Local Representatives on a yearly basis. Should you wish to volunteer as a local representative or if existing representatives wish to update their contact details, please contact the Honorary Secretary, Tanya Whitfield by e-mail at t.whitfield@sheffield.ac.uk.

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The Inaugural Scottish Drosophila Conference took place in Edinburgh in 2009 and was a great success. The 2nd Drosophila meeting was now held in Dundee on 9 December 2011 with the generous support of the Genetics Society. The theme of the second conference was ‘Cell Differentiation in Development and Disease’ and attracted 77 delegates from all over Scotland. The conference was held in the University of Dundee’s Dalhousie Building, which provided a stimulating atmosphere for discussions and networking. The main programme of the conference featured 7 main speakers and 6 short talks selected from the abstracts. One of the highlights of the meeting was the poster session with 26 posters by PhD students and postdoctoral researchers covering a large range of original research that stimulated intense discussions. A jury selected three posters to be equally outstanding and the posters of Dr. Manuel Breuer (Edinburgh) on karyosome formation, Mr. Michal Janiszewski (Edinburgh) on the role of Invadolysin in regulating chromosome structure and Dr. Daniel Mariyappa (Dundee) on the role of O-GlcNAcylatation in Fibroblast Growth Factor signalling were each recognized by an award. Following the ‘tradition’ of the first meeting the presentations were arranged in four sessions and commenced with a keynote lecture by a non-fly scientist, who made major contributions in the field. Professor Kate Storey (Dundee) gave an overview on early neural development in vertebrates using the chick embryo as a model. Her talk provided an excellent introduction into the field of cell differentiation and highlighted the importance of the spatio-temporal control of cell signalling and gene expression during neural development and differentiation. In her fascinating presentation, Professor Storey also described novel results demonstrating the importance of epigenetic changes underlying the onset of neural differentiation. The next speaker, Professor Andrew Jarman (Edinburgh), introduced the transcriptional control of cilia cell differentiation. Professor Jarman demonstrated a mechanism of how the transcriptional regulator Atonal controls gene expression and morphogenesis in mechano-sensory cilium formation in Drosophila. In the final talk of the session, Dr. Douglas Armstrong (Edinburgh), introduced the transcriptional control of cilia cell differentiation. Professor Jarman demonstrated a mechanism of how the transcriptional regulator Atonal controls gene expression and morphogenesis in mechano-sensory cilium formation in Drosophila. In the next session Dr. Douglas Armstrong (Edinburgh) impressively showed how the Virtual Fly Brain online resource integrates 3D image data with annotated brain regions and neuronal identities allowing complex searches using a large range of characteristics. In the second session Dr. Mikael Bjorklund (Dundee) talked about his systems-oriented approaches to understand the genetic control of cell growth. Using Drosophila cell based screens, Dr. Bjorklund identified many genes that are involved in cell growth and proliferation and presented approaches to validate these hits in cell and whole organism models. Professor Julian Dow (Glasgow) then introduced how to use adult flies to model renal function in health and disease. Professor Dow gave a brilliant presentation on the use of genetics to model kidney disease such as nephrolithiasis highlighting the extensive functional similarities of the renal systems in Drosophila and humans. The use of Drosophila as a model for human disease was further expanded upon by a very interesting short presentation by Mr. Stuart Forrest (Edinburgh) on a fly model for Amyotrophic Lateral Sclerosis (ALS).

The third and fourth sessions focussed on cell biological principles important in differentiation and cancer. Professor Hiro Ohkura (Edinburgh) described the function and genetic control of the formation of the karyosome a characteristic chromosome configuration that occurs during meiosis in human and Drosophila oocytes. Professor Ohkura presented his exciting work on the function of the NHK-1 kinase in this process. In the following presentation, Professor Margarete Heck (Edinburgh) reported on her elegant work on Invadolysin, a very interesting metalloprotease, which is involved in cell division and cell migration and exhibits an unexpected subcellular distribution to lipid droplets. Mr. James Catterson (Edinburgh) presented in his short talk an approach using the Fly Atlas gene expression database and sequence comparison in order to study genes required for adult
fly heart biology and relate these to human heart function. This was followed by a short presentation of Dr. Selim Terhazaz’s (Glasgow) work about the capa peptide receptor, capa GPCR, and its role in regulating desiccation stress-response. His work suggested a close functional relation of capa GPCR and human NeuromedinU receptor.

The final session was dedicated to fly models of cancer biology. Dr. Mark Ditzel (Edinburgh) described his interesting findings on the tumour-suppressor Hyperplastic discs (Hyd) and how his group is trying to understand the mechanisms of Hyd function in growth control. The meeting was rounded up by two short presentations. Dr. Juan Macagno (Glasgow) communicated his exciting data on a link between oncogenic stress, cell differentiation and cell survival. Dr. Villo Muha (Dundee) described the role of growth factor signalling and small GTPases in a Drosophila model for epithelial mesenchymal transition.

The Drosophila community in Scotland is very grateful for the support given by the Genetics Society for their Research Conference 2011.

The Conference was a great success and helped to further connect researchers using fly genetics to resolve important questions in biology and biomedical sciences. Given the consistently excellent scientific interactions and responses, the meeting series will be continued to take place in Glasgow in the summer 2013 organised by Professor Julian Dow (University of Glasgow) and Dr. Marcos Vidal (The Beatson Institute).

22nd Mammalian Genetics and Development Workshop

A meeting of The Genetics Society. 17th November 2011.

Kin Pong U & Nick Greene. UCL Institute of Child Health, London

The annual Mammalian Genetics and Development Workshop was held, as in recent years, at the Institute of Child Health in London. Labs from across the UK were represented with all the talks by Post-docs and PhD students, in keeping with the tradition of this meeting of providing an opportunity for platform presentations by less established researchers.

A range of topics relating to genetics and developmental biology were covered and it was good to hear directly from the people who are hands on in the lab.

The meeting started with talks on the theme of stem cells and developmental biology. Jorn Lakowski (UCL) presented findings on use of cell surface markers for isolation of photoreceptor precursors for stem cell therapy in retinal degenerative disease. Ana Rolo (UCL) gave the first of several talks related to studies of neural tube development, highlighting the functional importance of Rho-family GTPases, in this process. Next, we heard about ear development from Hannah Thompson (King’s College London), whose studies investigated cavitation in the middle ear, abnormalities of which are a possible cause of conductive hearing loss. To end the session, Sophie Pryor (UCL) discussed the role of non-canonical Wnt/PCP signalling in convergent extension movements that appear to play an important contribution in development of the spinal neural tube.

The next session focussed on epigenetics and imprinting. Heba Saadeh (King’s College London) presented findings of bioinformatics-based studies to identify consensus sequences that might serve as targets for DNA methyltransferases at imprinting control regions (ICR). Nozomi Takahashi (Tokyo University of Agriculture) highlighted the role of imprinting in regulation of non-coding RNAs (ncRNAs), illustrating this with findings in a mouse teratoma model. Stuti Mehta (University of Oxford) showed how genomic imprinting can be mediated between paternal and maternal gene cluster. Using the GNAS Imprinting Control Element (ICE) as a model, she proposed a possible mechanism by which the non-coding RNA is able to silence Nesp on the paternal allele. Also studying the function of the GNAS cluster, Nicolas Nunn (University of Liverpool) presented work on XLas, a signalling protein transcribed from the paternal allele of the imprinted Gnas locus. These studies focussed on the effect of altered XLas expression on metabolism, via deregulation of the sympathetic nervous system.

To begin the next session Gemma Swiers (University of Oxford) gave a beautifully illustrated talk on tracking of endothelial cells during development and their commitment to the haematopoietic lineage. Dragos Leordean (MRC Harwell), presented bioinformatics-based
analysis suggesting a mechanism of FoxA2 regulation of Pkd1l1, that is conserved between species and may play a role in left-right asymmetry. Leena Joshi (King’s College London) described identification of Eya1 gene mutation in branchio-oto renal syndrome (BOR) and proposed using Eya1 mice as models for understanding conductive deafness as they exhibit several phenotypes found in BOR.

The next two talks also focussed on birth defects, specifically neural tube defects. Sarah Escuin (UCL) spoke about the RhoA signalling pathway in regulation of the actomyosin cytoskeleton and apical junction complex and described experiments to test the function of these in spinal neurulations. Caroline Hirst (UCL) ended the session with a talk describing investigation of the mechanisms by which either loss or gain-of-function of the Grainyhead-like 2 transcription factor cause neural tube defects.

The final session was kicked off by Iain Dykes (UCL) with a talk on Hic2, a gene associated with a DiGeorge syndrome-like phenotype in mice. He presented data to show a role of Hic2 in post-transcriptional regulation, through binding of mRNA, with a focus on Wnt pathway genes. Gordana Palovska (University of Bath) showed some of her findings using a combination of in situ hybridization method, Optical Projection Tomography (OPT) and image processing to allow visualisation of spatio-temporal expression patterns of multiple regulators of the cell cycle. The final two talks of the meeting focussed on the molecular basis of the cilia disorder, primary ciliary dyskinesia (PCD). Miriam Schmidts (UCL) showed that mutation or loss of PF22 gene, encoding the dynein axonemal assembly factor 3, resulted in the reduction of dynein stability in the cytoplasm and abolishes ciliary movement, thereby giving rise to PCD. Saloni Patel (MRC Harwell) described analysis of a mouse model, inversus vicerum (iv), which may be useful for long term study of PCD, providing a model for study of the equivalent human condition.

In summary, the Mammalian Genetics and Development Workshop showcased a range of high quality talks covering developmental biology, genetics and models of human disease. The competition for best presentations was very close, and the judges awarded prizes to Stuti Mehta (MRC Harwell), Jorn Lakowski (UCL Institute of Child Health), Gemma Swiers (Oxford University) and Leena Joshi (Kings College London). The meeting organisers are grateful to the Genetic’s Society and Mammalian Genome for their sponsorship of the meeting. Meeting abstracts will be published in Genetics Research. The 2012 meeting will be held on 22-23rd November, please look out for the meeting email in the summer. If any colleagues would like adding to the mailing list please send an email to Nick Greene (n.greene@ucl.ac.uk).

**11th UK Archaeal Conference, Newcastle University**

5 – 6th January 2012. **Bernard Connolly**. University of Newcastle

The meeting was attended by 59 delegates, 43 from the UK, 15 from Europe and 1 (the plenary speaker, John Reeve) from the USA. There were 17 oral presentations, 15 of which, in keeping with the spirit of the meeting, were given by early stage researchers (PhD students, postdoctoral research associates and newly appointed tenured staff). There were 14 poster presentations. In an excellent plenary lecture John Reeve outlined the historical development of methods to genetically manipulate the archaea and the emergence of *Thermococcus kodakarensis* as an organism amenable to genetic transformation. The usefulness of genetic methodologies in the archaea was illustrated by examples taken from John’s work on hydrogen production and DNA replication. The talks and posters covered a wide area of archaeal species with the topics spanning genetics, cell biology, biochemistry and biophysics. Subjects presented included DNA replication, repair and recombination, transcription, translation, protein folding, cell motility and metabolism. An impressive variety of techniques were discussed which ranged from novel genetic manipulation methods through to biophysical approaches such as single molecule studies.

The best oral presentation prize was awarded to Rosalie Driessen (Leiden University) for a biophysical investigation, using force-microscopy methods, into archaeal chromatin protein. Best poster prize was given to Tamzin Gristwood (University of Oxford) for an elucidation of the sub-cellular location of the replication machinery in *Sulfolobus*.
British Yeast Group Meeting
Adele Marston and Robin Allshire. University of Edinburgh

The 2012 Genetics Society sponsored meeting of the British Yeast Group took place on 21st-23rd March in Edinburgh. The meeting was blessed with an exceptional three days of glorious spring sunshine in the University’s South Hall complex with the spectacular Arthur’s Seat as backdrop. Many aspects of yeast biology were presented and discussed by over 140 delegates from both the UK and further afield.

The opening session focused on chromosome replication and repair. Tony Carr (University of Sussex) discussed the problems caused by inverted repeats at replication forks and Luis Aragon (Imperial College) described mechanisms that regulate cohesin’s role in DNA damage. Carolin Muller (University of Nottingham) told us about her work comparing replication dynamics in several yeast species and Anne Donaldson (University of Aberdeen) presented a proteomic analysis of replication factor C-like complexes.

RNA and chromatin formed the theme of the second session. Jon Houseley (Babraham Research Campus, Cambridge) demonstrated the importance of non-coding RNA degradation in meiosis and Keerthi Chathoth (University of Edinburgh) described a checkpoint monitoring splicing.

A link between nuclear pores and gene expression was the focus of Kristine Willis’s (Georgetown University, USA) presentation. The session concluded with an impressive quantitative analysis of the fission yeast transcriptome and proteome in cycling and stationary cells by Jürg Bähler (University College London).

Wednesday evening concluded with a lively poster session followed by dinner and ample informal networking and discussion in the bar.

Thursday kicked off with a metabolism theme. Several talks focused on oxidative stress. Campbell Gourlay (University of Kent) discussed a new RAS-dependent signaling pathway that is activated by damaged mitochondria and Jonathon Brown (University of Newcastle) presented his work on the role of the Pnp1 transcription factor in oxidative stress. Markus Ralser (University of Cambridge) told us about the role of feedback loops in preventing oxidative stress upon shifts between fermentation and respiration.

The plenary speaker was John Kilmartin (MRC laboratory of Molecular Biology) who presented a fascinating description of the yeast spindle pole body with his beautiful EM images and new insights into the duplication process. Aply, this was followed by several talks on microtubule organizing centres. Kayoko Tanaka (University of Leicester) told us about a novel structure associating with the spindle pole body in meiosis and Ken Sawin (University of Edinburgh) presented his work on activation of the fission yeast gamma-tubulin complex.

In the next session, Ed Louis (University of Nottingham) discussed the role of chromatin regulators in silencing at telomeres, Marion Dubarry (University of Newcastle) presented her work on heterochromatin formation and Rita Cha (National Institute for Medical Research, London), discussed how double strand break formation is regulated in meiosis. Carol Munro (University of Aberdeen) reminded us of the importance of yeast as pathogens with a talk on cell wall remodeling in Candida albicans and its role in antifungal drug resistance.

With the science leaving no questions as to the wide value of yeast as a model organism, we turned our attention to another important use for yeast when we tasted the wares of a local microbrewery (Stewart Brewing, Edinburgh). Following a buffet dinner featuring Scottish dishes such as haggis and cranachan, the evening concluded with traditional Scottish entertainment provided by the excellent Lomond Ceilidh Band along with comprehensive tuition for novices.

Despite a full dance floor into the wee hours, the final session on Friday morning was well attended and featured talks on the cell cycle and chromosome segregation. Iain Hagan (CRUK Paterson Institute for Cancer Research, Manchester) described events on the SPB that affect mitotic commitment and Jane Atkin discussed the role of Tor in mitosis. Kok-Lung Chan (University of Oxford) presented recent findings on the mechanism of cohesion establishment and Martin Singleton (London Research Institute, CRUK, London) told us about his structural analysis of cohesion establishment proteins. Three talks on the spindle assembly checkpoint followed. Jonathan Millar (University of Warwick) described a motif in the Spc7/Spc105/KNL1 protein that recruits the checkpoint kinase Bub1 to kinetochores; Kevin Hardwick (University of Edinburgh) presented work on functions of...
The Population Genetics Group

4th – 7th January 2012. University of Nottingham

John Brookfield

The 45th Population Genetics Group meeting took place at the University of Nottingham. This successful series of specialist meetings has been granted sponsorship by the Genetics Society for a number of years, and, as organisers, we were very grateful that the Society was again able to offer funds to the meeting. Organisation was by Angus Davison, Tamsin Majerus, Sara Goodacre and myself.

Population genetics has changed greatly since the first of these forty-five meetings. The early years were dominated by the study of visible polymorphisms and the genetic variation in enzyme charge detected by gel electrophoresis. The latter was the focus of the heated debate between selectionists, who regarded enzymic variation as being acted on by natural selection, and the neutralists, who thought it more likely that almost all this variation is neutral in its effect on fitness. Now, with the age of next generation sequencing and genomics, the need for population genetic insight into the interpretation of intraspecific DNA sequence variation has never been greater, and some of the iconic polymorphisms from population genetics history are starting to yield their secrets at the molecular level.

The delegates assembled on Wednesday, the 4th January, staying at the Hugh Stewart Hall on the main University of Nottingham campus, and we had presentations throughout the Thursday and Friday, and until midday on Saturday, the 7th January 2012. The 225 delegates included 160 from the UK, but a further 17 nations were represented. Of those from outside the UK, the countries featuring most strongly were Austria, France, Sweden, Germany and the USA.

Following the tradition of the population genetics group, almost all of the one hundred and twelve talks were contributed presentations. But each of the three days started with a plenary talk, from Michael Lynch from Indiana University on the Thursday, Hopi Hoekstra from Harvard University on Friday and Steve Jones from University College, London, on Saturday morning. The talks included forty-six from graduate students, providing the next generation of population geneticists with an opportunity to present their work. Many population geneticists, including the author, have, down the years, made their first conference presentation to the population genetics group.
With so many talks, parallel sessions were inevitable, and there were four on Thursday, and three throughout Friday and Saturday morning. As always, the task of organising parallel sessions in a way that leaves everyone happy was difficult. The diversity of population genetics creates the particular problem of whether talks should grouped by organisms or by questions or by methodology. In addition, all student talks had to be on the Thursday and Friday, so that they could be eligible for the student talk prize to be awarded at the conference dinner on the Friday night.

All delegates were invited to judge the posters, and all non-students judged the student talks that they had seen, and, for symmetry, students were asked to judge the non-student talks. Posters and talks were graded on a four-point scale. There was some discussion beforehand about the best way to collate the marks, given that there was enormous variation between talks in the numbers of sets of judges’ marks and comments that they received. In the end, prior to looking at the votes, a complex scoring system was created which rewarded a contribution receiving a high average score from a large number of voters.

The winner of the student talk prize was Paul Richards of the University of Nottingham, with his description of using the RAD technique to map the *Cepaea nemoralis* colour and banding loci. Second was Toni Gossman, from Sussex, for a simulation study of the use of the McDonald-Kreitman test under conditions of fluctuating selection, and third was Katie Charneski from the University of Bath with her study of the A-T skew (unequal usage of the two bases on the lagging and leading strands) in Fermicute bacteria. In the posters, the joint winners were Dalia Abu Awad from the University of Lille with a study of the effect of deleterious mutations on extinction rates in selfing and outcrossing species, and Alyia El Nagar from Nottingham with a study of the heritability of parasite resistance in the stickleback. Third was Robert Verity, from Queen Mary, University of London, for his work on new approaches to isolation by distance.

There was also a non-graduate student talk prize, for which speakers on the last morning were unfortunately but inevitably ineligible. Here, the Prize was won by Ceridwen Fraser from the Free University of Brussels with her talk about sub-Antarctic kelp and Belgian bark beetles. Steve Jones’ talk on snails was second, with Clare Marsden, from the University of California at Davis, who described her work on introgression between the incipient species of *Anopheles gambiae*, being placed third.

The Prizes were awarded at the conference dinner, in the East Midlands conference Centre. Afterwards delegates were entertained by the legendary Funtime Frankies. One strength of these conferences is their relaxed and informal atmosphere. No only do students get to present their first
talk, but also the have a chance to see their supervisors in a very different light, and even on the dance floor in some cases.

The plenary speakers collectively illustrated the range of questions that population genetics encompasses. Michael Lynch discussed the determination of mutation rates, and the ways in which mutation, in conjunction with differences in typical effective population sizes between the domains of life, determines differences in genome structure. Hopi Hoekstra focussed on one species, *Peromyscus maniculatus*, and the selection acting on its polymorphic and quantitative variation, and its relationship with environmental variation, thereby allowing the process of adaptive evolution on a local scale to be investigated from the selective cause right through to the response in allele frequency change measured at the molecular genetic level.

Steve Jones’ plenary talk, on the final morning, gave an opportunity to reflect on the history of the population genetics group itself. Steve was Bryan Clarke’s first graduate student when they started the Population Genetics group.

Steve’s presentation was introduced by Bryan Clarke and chaired by Sara Goodacre, who was Bryan’s last graduate student. Steve was the only person to give two talks to the meeting, describing his latest snail data on the Friday in what was the best attended of all the contributed talks. Steve’s plenary talk, “Scientists find a gene for…”, was concerned with science in the media, and, in particular, the BBC Trust’s Review of Impartiality and Accuracy in the BBC’s Coverage of Science, which Steve was responsible for in 2011. The strongest point is that there is a paradox inherent in trying to deal with scientific controversies in the balanced and impartial way that is the BBC’s goal. Public understanding of science would not be served by giving equal time and weight to, on then one hand, a broadly-held scientific consensus and, on the other, a minority and discredited opposing view.

The Genetics Society’s journal *Heredity* was strongly represented at the meeting. The Editorial Board meeting took place on the Wednesday, the 4th January, and a “Meet the Editors” session on the Thursday, chaired by the Editor Roger Butlin, with support from Rebecca Vickerstaff from Nature Publishing Group, was well-attended.

The next meeting will be at the University of Glasgow, organised by Barbara Mable and her team. We would like to thank our other sponsors, Royal Society Publishing, Roberts and Company Publishers, Nature Publishing Group, Cambridge University Press and Oxford University Press. We would also like to thank the Nottingham team, which included Faisal Almathen, Féaron Cassidy, Harry Clifford, Emily Clingain, Takele Desta, Aliya El Nagar, Lisa French, Jie Han, Olivier Hanotte, Beth Hellen, Moses Ilori, Harriet Johnson, Emily Kostas, Joram Mwacharo, Eric Politt, Paul Richards, Salha Saad, and David Wragg.

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**Genetics Society Sponsored Events**

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

Sian Davies . School of Life Sciences, University of Warwick, UK

R.C. Punnett was appointed Arthur Balfour Professor of Genetics in the University of Cambridge in 1912, the first professorship of genetics anywhere. Remembered for his discovery of linkage with William Bateson and Edith R. Saunders in 1905, his name lives on in ‘Punnett’s Square’. To celebrate the centenary of the Professorship and Punnett’s appointment to it, here A.W.F. Edwards, himself a Fellow of Gonville and Caius College, records an imaginary conversation at its High Table in April 1906 between Punnett (elected Fellow 1901), R.H. Lock (elected Fellow 1902) and the President, John Venn (elected Fellow 1857). Lock was another of those associated with Bateson in the heady days in Cambridge following the rediscovery of Mendel’s paper in 1900. Punnett was in due course to be succeeded in the Professorship by another Caiian, R.A. Fisher (Fellow 1920-26, 1943-62).

LOCK
[Coming into the Senior Combination Room before dinner]
Good evening Punnett – do you know who is presiding tonight?

PUNNETT
I think it’s the President himself.

LOCK
I hope he doesn’t mind if I ask you something about your work with the sweet-peas, but perhaps you can answer my question before dinner is called.

PUNNETT
If it is not too difficult.

LOCK
Bateson tells me that he has included the useful square diagram you invented to map the sixteen genotypes from an F1 cross with two factors [Figure 1] in the third Report of the Evolution Committee to the Royal Society now in press, and I wondered whether I might include it in the book I’m writing.

PUNNETT
Have you asked Bateson?

LOCK
Not directly, but anyway he says it was your idea. To be frank, I’m quite keen to maintain my distance, and although in the preface of my book I shall thank him warmly for introducing me to genetics and for his continual encouragement, I will also say that I have deliberately refrained from consulting him during the writing so that the book might retain some traces of individuality.

PUNNETT
Quite right – he is inclined to dominate any discussion and one needs to cherish one’s own independent thoughts. Yes, of course you can use my diagram, though as a matter of fact I use a slightly different version in the second edition of my Mendelism which I am in the middle of preparing.

THE FELLOW’S BUTLER [Addressing Dr Venn]
President, dinner is served.

Fig. 1. Punnett’s square showing the 9:7 ratio.
PUNNETT
We’ll have to go up to Hall now and continue this later.

The Fellows proceed to Hall, Grace is said, and dinner begins. After some general conversation with other Fellows, Lock and Punnett renew their discussion.

LOCK
You said you are going to use a different diagram in your second edition. In what way is it different?

PUNNETT
It’s difficult to describe without a figure, but if the President isn’t looking I’ll draw one on the back of the menu [Sketches the figure - Figure 2].

LOCK
That looks just the same as the one Bateson showed me except for the lettering.

PUNNETT
Well, of course it is really, though it is shaded for the 9:3:1 segregation and not just 9:7. The only difference is the way I put it together. Just think of the four-square diagram for the ‘A’ factor alone, and the similar one for the ‘B’ factor. Now drop this ‘B’ diagram into each of the four squares of the ‘A’ diagram and the result shows all sixteen genotypes. Mind you, some genotypes are repeated in all such diagrams of course because each heterozygote appears twice.

LOCK
I see. And in the other format you simply head the four columns with the male gametes and the four rows with the female gametes, and obtain the sixteen genotypes by addition, as it were. [He puts the menu in his pocket]

PUNNETT
Yes, it’s only a matter of taste.

After dinner is over, Venn, Punnett and Lock are the only Fellows who continue to the Combination Room for dessert.

VENN
What were you drawing on the back of the menu at dinner, Punnett? I’m inclined to think that’s a finable offence.

PUNNETT
Surely, President, a necessary adjunct to an intellectual conversation has protected status?

LOCK
I plead guilty too, as an accomplice, and enter the same defence.

VENN
Let the evidence speak for itself. Lock produces Punnett’s drawing and hands it to Venn, who examines it carefully.

PUNNETT and LOCK
What’s that?

VENN
It’s a logic diagram very similar to the one I have here in front of me. It was invented by Alexander Marquand the year after I published my own logic diagram as an alternative to it. I published my three-circle diagram in 1880 – perhaps you are not familiar with it – but it is difficult to generalise to more than three classes, so Marquand invented his square alternative which can be multiplied up, as it were, indefinitely. I recently put an example of it in the second edition of my Symbolic Logic.

PUNNETT
Are we exonerated?

VENN
Only so that I may myself draw Marquand’s diagram on the menu. [He does so - Figure 3]

Fig. 2. Punnett’s square showing the 9:3:3:1 genotypic ratio.

Fig. 3. The Marquand diagram.
PUNNETT  
Shall we despatch the Junior Fellow to the Library to get a copy?

Lock leaves the table and returns a short time later with a copy of Venn’s second edition. Venn examines it

VENN  
Here it is, on page 140 [Figure 4]. [He passes it to Punnett]

PUNNETT  
I don’t believe it! I think that is the same as the three-factor square we have put in the third Report! Well, at least it looks very much like it, and the principle is the same. As a matter of fact it was Francis Galton who suggested the arrangement we used, in a letter to Bateson in October 1905. I can get them from Bateson and show them to you tomorrow if you like [Figure 5].

VENN  
Yes, please do. But in the meantime let’s be satisfied with four sets and look up my form of logic diagram to match your 4x4 square. You can’t do four sets with circles like you can three sets, but I was pleased to discover that four ellipses will do. Here it is, on page 127. It’s in the first edition too. You could use it for the two-factor case (if I understand the genetics correctly) and colour it up to represent the 9:3:3:1 ratio. I expect it would be quite pretty.

But just then the Fellows’ Butler came in to clear away the silver and the spell was broken. It was to take 105 years before another Fellow of Caius married up Venn’s Four-set Diagram and Punnett’s Square for two diallelic factors [Edwards, 2012 - Figure 7]. A version of it appeared on the cover of Nature Genetics for September 2011 (Volume 43 Number 9).

Bibliography
- Venn, J. (1894) Symbolic Logic. London: Macmillan (2nd ed.).

Acknowledgment
- This fantasy draws on the following account with the kind permission of the editors of the journal Edwards, A.W.F. (2012) Punnett’s Square. Studies in History and Philosophy of Biological and Biomedical Science 43, 219–224.
Go in search of bighorn sheep’s ‘horny’ genes; cross paths with a hybrid Oxford Ragwort, and catch up with Heredity’s Editor Richard Nichols who is reporting from a meeting of the ‘ConGRESS’ Network.

Corresponding papers from the Heredity:

QTL mapping for sexually dimorphic fitness-related traits in wild bighorn sheep
J Poissant, C S Davis, R M Malenfant, J T Hogg and D W Coltman
Heredity (17 August 2011) | doi:10.1038/hdy.2011.69

Genetic and phenotypic divergence of homoploid hybrid species from parental species
B L Gross
Heredity advance online publication 14 September 2011 | doi: 10.1038/hdy.2011.80

Molecular genetic and quantitative trait divergence associated with recent homoploid hybrid speciation: a study of Senecio squalidus (Asteraceae)
A C Brennan, D Barker, S J Hiscock and R J Abbott
Heredity (10 August 2011) | doi:10.1038/hdy.2011.46
ResearchGate was founded by the virologist Ijad Madisch, who wanted to create an online platform to facilitate research and collaboration. Since its beginning in 2008, ResearchGate is now the largest professional network for scientists and researchers with over 1.2 million members. You can ask questions and get answers from over 6000 geneticists by joining the genetics topic discussions.

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Sign up to ResearchGate at www.researchgate.net and start networking with other geneticist.
At the Tübingen Congress in August 2011, the ESEB Council decided to institute a new award, to be presented for the first time at the joint meeting in Ottawa this July. This new award is intended to recognise outstanding contributions to evolutionary biology by a mid-career scientist. The award is to be in the gift of the three Presidents in post at the time (Past-President, President and President-Elect) and so will be known as the Presidents’ Award. The recipient will give an address at the joint meeting and therefore we expect this award to be made once every six years.

The current Presidents, Siv Andersson, Brian Charlesworth and Roger Butlin, considered a shortlist of 10 truly outstanding evolutionary biologists for the first Presidents’ Award and the recipient was Professor Adam Eyre-Walker of the University of Sussex.

Adam Eyre-Walker is one of the world’s leading researchers in the field of molecular and genome evolution. Adam was one of the pioneers of the use of DNA sequence databases to extract useful information about the patterns and processes involved in the evolution of genomes. He has consistently been an innovator in making creative use of the information extracted in this way, combining bioinformatic methods with evolutionary models based on population genetics theory. He established his reputation by his work on the evolutionary forces affecting DNA base composition and codon usage, and the use of species comparison of gene sequences to infer the rate of occurrence of deleterious mutations.

He has subsequently developed new methods for estimating the frequency of adaptive changes to protein sequences, and for estimating the fitness effects of nonsynonymous mutations, by combining information on within-species polymorphism and between-species sequence divergence. He has an impressive record of publications, mostly in leading journals, and has trained many excellent postgraduate students and post-doctoral fellows.

Siv, Brian and Roger

The free Heredity podcasts provide the latest research news from Heredity, in the words of the researchers themselves. Informal interviews are used to make the science in Heredity more accessible. The authors explain the basic foundations of their topic, and draw out the key findings of their paper.

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International Congress on Transposable Elements
21st – 24th April 2012, St. Malo, France

Michael Cowley . King’s College London

Geneticists from across Europe and the Americas gathered in the historic walled city of St. Malo, France, to explore recent developments in our understanding of transposable elements (TEs).

Recent elegant studies have demonstrated that some TEs, in particular a subset of LINE1 (L1) elements, are still active in the human genome, contributing to phenotypic as well as genetic diversity. This congress aimed to distil, discuss and debate several aspects of TE biology. What is the impact of retrotransposition on the genome? How is transposition controlled? What are the mechanisms of transposition? How have TEs evolved?

On Saturday evening, Jef Boeke (Johns Hopkins) delivered a stimulating keynote lecture, illustrating the potential for new technologies in addressing fundamental questions about TE behaviour. For example, Jef and his team have utilised deep sequencing of Ty1-flanking sequence amplicons to understand more about the sites of integration of these elements in the yeast genome. These studies have revealed a preference for integration at RNA pol III-dependent genes, including tRNA genes. Jef has used similar technology to catalogue retrotransposon insertion polymorphisms in human populations, and has discovered huge variability in polymorphism frequencies, underscoring the active nature of transposition in the modern human genome.

Sunday morning began with an exploration of the impact of TEs on the genome. Mark Batzer (Louisiana State) picked up on the theme of active transposition in primate genomes, coined the ‘primate mobilome’, demonstrating that many mobile element insertions that are fixed in humans are nonetheless human-specific. Mark utilised the distribution of Alu, L1 and SVA elements to resolve discrepancies in the phylogenetic relationships of gibbons, with a view to aiding conservation and captive breeding programmes that currently suffer from a lack of understanding about the genetic variation of distinct gibbon populations.

Rita Rebollo (Vancouver) is interested in addressing how TE insertion can affect local chromatin structure. She showed how intracisternal A particles (IAPs) can induce heterochromatin spreading over distances of up to 5 kb, but that such changes are not usually permitted by the genome if heterochromatinisation might impact on host gene expression. Indeed, Rita showed an antagonism between TEs and host genes, such that TEs near to transcription start sites (TSSs) are most heavily methylated at the end furthest from the TSS, and are relatively hypomethylated close to the TSS, presumably to prevent interference with host gene activity.

After suffering an intense downpour of rain during the two-minute run from the hotel to the conference venue on Monday...
morning, our wet feet were warmed and dried by the under-seat heaters in the seminar room as we explored how transposition is controlled. Pascale Lesage (Paris) demonstrated how yeast activate Ty1 element transposition in response to stress, including in a model of severe adenine starvation. This may induce mutations that could confer selective advantages in the host. During this session, I was also able to present my work on imprinted retrogenes that have arisen through L1-mediated retrotransposition.

We reconvened after a terrific three-course lunch to explore the evolution of TEs. Mojca Tajnik (Ljubljana and Cambridge) described how Alu elements situated within gene introns can be incorporated into processed transcripts, a system coined 'exonisation'. This is an important tool for genome and transcriptome evolution, but must be suppressed for the majority of the time. Mojca identified the factor hnRNP C as a suppressor of this process, by competing with the splicing factor U2AF65 for binding at the intronic Alu.

The mechanisms of transposition were the focus of the final session. Alan Schulman (Helsinki) discussed how TEs face a conflict between the two opposing roles of their transcripts: translation and reverse transcription. Using the BARE retrotransposon of barley as a model, which is relatively simple with a single open reading frame, Alan identified distinct pools of RNA that arise from its transcription. Some transcripts are fully processed, including capping, splicing and polyadenylation, and exported to the cytoplasm for translation. Molecules in this RNA pool cannot be reverse transcribed. A distinct pool of RNA molecules are not processed, but destined instead for packaging into virus-like particles, and ultimately reverse transcription. This system is the first demonstration of how the conflict between translation and reverse transcription can be balanced.

The congress closed with an extravagant banquet in a room with panoramic views across the beach to the National Fort. The feast provided the last opportunity to forge collaborations and discuss future directions, aided of course by the flow of fine French wine.

Microtubules: Structure, Regulation and Functions

23rd – 26th May, EMBL Advanced Training Center, Heidelberg, Germany.


This was the second conference of the series, aimed to gather researchers from all over the world who study microtubules using different scientific approaches. This conference covered a wide range of microtubule research, including complex microtubule assemblies, microtubule-based transport, microtubule dynamics and regulation, microtubules in cell division, microtubule interactors, microtubules in differentiated cells, microtubules in disease mechanisms and microtubule organization in mitotic spindle. The conference lasted for 4 days, with 47 talks and 253 posters in total.

The first day of the conference started with registration and lunch in the foyer, giving chance for the attendees to interact with each other. The first scientific session started with a few talks focusing on microtubule assemblies. I especially enjoyed Daniela Nicastro’s (Brandeis University, USA) talk on microtubule inner proteins (MIPs) in Chlamydomonas. By using cryo-electron tomography (cryo-ET), which provides excellent structure preservation and high resolution of sample imaging, her works showed that B-tubule of doublet microtubules contain 10 protofilaments (PFs). This resolves
the long-standing question on total number of PFs present in B-tubule. Besides, microtubule inner proteins (MIPs) were observed in the lumen of microtubule. It was fascinating to realise for the first time that microtubule is not a “hollow” structure.

The first evening was scheduled for a lecture from the keynote speaker, Eva Nogales (HHMI/University of California at Berkeley, USA). Unfortunately, she was unable to attend the meeting due to problems with her flight. This is a big loss to me since I am very keen to hear about her work on interaction of microtubule and kinetochore complexes. However, I did enjoy the evening with a longer dinner with some German beers and another good opportunity to interact with other participants.

In the second day, a series of talks on ‘microtubule dynamics and regulation’ were given. Maxence Nachury (Stanford University SoM, USA) presented his work on using permeabilised cells system to study transport into primary cilia. He presented a series of beautiful experiments showing that transport into primary cilia is size-dependent. David Sharp (Albert Einstein College of Medicine, USA) discussed roles of Fidgetin, Fidgetin-like 2 and Kif19 in controlling human cell migration rates. By using total internal reflection fluorescence (TIRF) assay, Melissa Gardner (University of Minnesota, USA) showed that microtubule catastrophe is a multi-step process that requires accumulation of a few defects. The catastrophe frequency is dependent on microtubule age, regardless of tubulin concentration used.

After a short coffee break, we received a special ’Landmarks in microtubule research’ lecture from Susan Horwitz (Albert Einstein College of Medicine, USA). She discussed how Taxol was discovered and isolated from the bark of Taxus tree by Monroe Wall and Mansukh Wani and how she started to study the potential therapeutic effects of Taxol. Today, Taxol is well known as a microtubule stabiliser and is widely used as a drug for ovarian, breast and lung cancer patients. Her lab is now focusing on evaluating new drug combinations with Taxol, aiming to deliver an improved efficacy to treat cancer.

In the third day, Anthony Hyman (Max Planck Institute of Molecular Cell Biology and Genetics, Germany) gave a very interesting talk on importance of XMAP215 and its homologues to bind tubulin dimers. *Xenopus’s* XMAP215 protein contains 5 TOG domains. By mutating two residues in each TOG domain to alanine, he showed that the XMAP215-TOG(AA) mutant does not bind tubulin nor promote microtubule growth. Besides, he demonstrated that an engineered “bonsai” TOG proteins, which contain only two TOG domains with a basic region, has almost full polymerase activity.

My favourite oral presentation was from Richard McIntosh (University of Colorado, USA), who gave a lecture in the second ‘Landmarks in microtubule research’ on the last day. He summarised recent findings from different groups that provide a better understanding on how microtubule dynamics generate force to move cargo. Also, he mentioned some works in his lab showing that during microtubule depolymerisation, microtubule shortens and flares outward. This provides the force to move cargo towards the spindle poles during anaphase.

Something not to be missed out is the ‘Hot topic session’ on the last day. This started with a talk on microtubule studies in bacteria by Martin Pilhofer (Caltech and HHMI, USA). Then, Aditi Maheshwari (ETH Zurich, Switzerland) gave a talk on 3D structure of axonemal microtubule doublet. This is followed by Sabine Petry (UCSF/HHMI, USA), who talked about roles of augmin in microtubule-dependent microtubule polymerisation. The last talk in this session was given by Luke Rice (UT Southwestern Medical Centre, USA) on structural studies of TOG:tubulin complex.

We had two poster sessions in the conference, one in the second afternoon and another in the third afternoon. I presented a poster describing my work on how interaction between the Ndc80 and microtubule associated proteins is critical for stable kinetochore-microtubule attachment. During the poster session, I identified some of the works presented that are closely related to my project. The poster sessions were very useful as I had the opportunity to discuss my project with many scientists who study microtubules in different ways. Overall, I received valuable feedback on my project by presenting my work in this conference.

The conference was a big success and I would like to congratulate the organisers for a fantastic conference. Definitely, I would recommend this meeting to scientists working on microtubule, for the unique experience and discussions. Also, I would like to thank the Genetics Society for the funding to allow me to attend the very first international scientific conference in my life.
RNA Binding Proteins in Neurological Disease and Society for Neuroscience 2011

10th – 16th November, Washington DC, USA

Thomas Ricketts . University College London and Medical Research Council Harwell

A head of the Society for Neuroscience (SfN) meeting in Washington DC, I attended a satellite meeting on RNA Binding Proteins in Neurological Disease. My current research is focused on TDP-43 proteinopathies, including Amyotrophic Lateral Sclerosis (ALS), and understanding the role and function of TDP-43. This meeting was an exciting and intensive two day gathering with leaders in the field studying the involvement of genes involved in neurological diseases, including TDP-43. TDP-43 was identified in 2006 to be causative of ALS. It is also at the centre of a variety of other neurodegenerative diseases, with emerging roles in RNA metabolism thought to be critical in the disease process. The meeting also focused on other causative ALS RNA processing genes such as FUS, and other diseases where RNA metabolism is affected. Advances in the field, and unpublished data were presented and discussed, allowing for investigators to develop and progress the future of their research.

With regards to TDP-43, data from around the world supported both loss and gain of function being important in ALS pathology, as well as further characterising the mechanisms of auto-regulation which may be important in disease. New models were also presented, as well as novel protein biological aspects and global RNA changes/targets, expanding the field’s understanding of TDP-43’s basic biology and roles in pathology. A particular highlight was data presented by Professor Zuoshang Xu, who made a loss of function TDP-43 mouse model using a transgenic RNAi approach, providing a novel and powerful loss of function TDP-43 mouse model. It was also exciting to hear about other diseases where RNA metabolism is altered and the genes and mechanisms associated with these varied neurological diseases. This provided an opportunity to compare similarities and differences with TDP-43, one RNA binding protein of many which cause or are associated with neurological disease.

Following the satellite meeting, SfN was incredibly diverse with around 16,000 posters presented. A huge range of areas in neuroscience were accessible as posters and talks to gain insights into the diversity of science that occurs. There were also a number of special and featured lectures ranging through multiple topics from development to cognition. From the special lectures, Dr Erin M Schuman presented a fantastic review of protein synthesis and degradation at synapses as well as focusing on current developments in technology and directions. Furthermore, within ALS, data was presented for multiple genes known to be causative or associated with ALS, that are not necessarily associated with RNA metabolism alterations, such as SOD1. SfN was also attended by many post docs and students who were at the satellite meeting, providing opportunities to further assess and reflect on the data presented at the satellite meeting. It was refreshing learn about other areas of neuroscience and to gain perspective on the bigger picture rather than focusing on a single gene or disease.

I am grateful for the support of the Genetics Society which allowed me to attend the RNA Binding Proteins satellite meeting and SfN 2011. The satellite meeting provided a focused environment assessing the biology of TDP-43 and SfN provided access to the diversity of neuroscience. I presented posters at both meetings and was able to interact with a wide audience and receive invaluable feedback about the ENU mouse models I am currently working on. Alongside this interaction, I gained invaluable information on the progress and directions of the field studying the biology of TDP-43 and this will be central to future planned experiments.
Every scientific field has its favourite quotation. For evolutionary geneticists it is J.B.S. Haldane’s pronouncement that the Creator has “an inordinate fondness for beetles”. Microbiologists on the other hand have an inordinate fondness for citing Baas Becking: “Everything is everywhere, but the environment selects”. This axiom pithily summarises the observation that all microorganisms appear to be ubiquitous, since almost any prokaryotic species can be isolated from any environment, given the right selection criteria in the laboratory.

If microbes are indeed ubiquitous, then geographic isolation cannot be a significant force in prokaryotic speciation. Indeed, bacteria impose barriers to gene flow at both a physical level (via incompatibility during conjugation) and a genetic level (via mismatch surveillance systems that restrict the recombination of divergent sequences). However, this does not appear to be the case for halophilic archaea, which exchange genetic information promiscuously. In fact, a growing body of research has shown that microbial communities are not ubiquitous but instead exhibit restricted

Evidence is emerging that viruses can also exhibit distinct biogeographical patterns, but this assertion remains contentious. Because viruses drive the adaptation and diversification of their hosts through predation and horizontal gene transfer, viral biogeography is relevant to evolution.
biogeography. This suggests that ecological isolation may be a major determinant of prokaryotic speciation after all.

Evidence is emerging that viruses can also exhibit distinct biogeographical patterns, but this assertion remains contentious. Because viruses drive the adaptation and diversification of their hosts through predation and horizontal gene transfer, viral biogeography is relevant to evolution. The question remains – are viruses endemic to a particular environment or do they transcend biogeographical boundaries?

To tackle this question, we wanted to study the diversity and biogeography of viruses found in hypersaline environments. Natural hypersaline waters maintain dense microbial populations (mainly halophilic archaea) and high concentrations of virus-like particles ($\geq 10^8$/ml). Haloarchaea and their viruses are an ideal system to study biogeography – they are easy to isolate and culture, and the natural salt lakes they inhabit are geographically distinct.

With the kind help of our collaborators at Tel Aviv University, we sampled for viruses at several locations in Israel. Unlike the UK, Israel is home to many permanent and seasonal hypersaline lakes. Our first sampling site was in Eilat, which is located at the southern tip of Israel, on the shores of the Red Sea. We collected five-litre samples from three different evaporation pools, which are part of a sea salt crystallisation plant owned by Israel Salt Industries Ltd. The samples were hypersaline (their salinities ranged from 23 – 29% NaCl) and deep red in colour due to halophilic archaea, bacteria and *Dunaliella salina*).

We then collected saltwater samples from three different locations on the western shore of the Dead Sea, their salinities were all extremely high (around 32% NaCl). Over the past century the waters of the Dead Sea have been steadily increasing in salinity, due to diversion of the Jordan River for agriculture. Consequently, haloarchaeal species that were isolated some time ago (such as *Haloferax volcanii* in 1977) are now extinct in their natural habitat. Indeed, the waters of the Dead Sea are now crystal clear and devoid of most life, apart from a few itinerant humans.

Once back in Tel Aviv, our precious saltwater samples (50 litres in all) were decanted into jerry cans and shipped back to Nottingham. They have now arrived safe and sound, and we will soon be processing them to isolate the viruses. The samples will be pre-centrifuged to remove debris and eukaryotic cells, and then sequentially filtered through 1 $\mu$M glass fiber and 0.2 $\mu$m filters to remove prokaryotic cells. Following this they will be subjected to tangential flow filtration, which will concentrate and purify the viruses further. Finally the viruses will be isolated by precipitation with PEG8000. Once DNA has been extracted, it will be sequenced in our DeepSeq facility at the University of Nottingham using Roche454 technology. The sequence data will be used to construct a viral metagenome, in which we will identify DNA polymerase and helicase genes that will serve as phylogenetic markers. These will hopefully enable us to draw robust conclusions about viral diversity and biogeography.

We would like to thank the Genetics Society for their generous support through a Heredity Fieldwork Grant, and Adit Naor, Uri Gophna and Moshe Mevarech of Tel Aviv University for their invaluable help during our travels in Israel.

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What happens to DNA methylation marks donated to the gametes?

Student Arielle Bennett. Supervisor Gavin Kelsey, Babraham Institute Cambridge

Epigenetics is a fast growing field investigating how modifications to DNA and chromatin that do not alter the underlying base sequence can have an impact on gene expression throughout the life of an organism.

Epigenetic markings include post-transcriptional modifications of histone tails and the chemical modification of DNA by methylation, the area investigated in this project. Correctly setting epigenetic modifications during development is crucial to the normal differentiation of cells and incorrect methylation can affect the expression of genes and has been shown to cause developmental disorders such as the Prader-Willi and Angelman imprinted gene syndromes.

DNA methylation in mammals occurs mostly as methylation of cytosine residues within CpG dinucleotides. Areas rich in CpG nucleotides are known as CpG islands (CGIs), which coincide with many gene promoters and are generally unmethylated. A small subset of CGIs is known to be highly methylated but, intriguingly, only on one of the two parental alleles. Such CGIs are referred to differentially methylated regions (DMRs) and these are often the control regions for imprinted genes, genes which are active on only one parental allele. Relatively few imprinted genes have been discovered; how many exist is still a matter of considerable interest and controversy.

One way to obtain a complete picture of the imprinted genes in the genome would be to perform whole-genome analysis of CGI methylation in the gametes (the egg and sperm), and to follow the fate of these gamete-determined methylation marks into the zygote and developing embryo: imprinted CGIs would be distinguished by their faithful maintenance of the methylation patterns from the gametes. In the summer project I undertook in Gavin Kelsey’s laboratory in the Epigenetics Programme of The Babraham Institute, near Cambridge, I set out to test whether a number of candidate sequences, identified in genome-wide analysis as being highly methylated in the egg but not in sperm, and retaining an intermediate level of methylation in blastocysts, were indeed previously undiscovered imprinted genes.

Since DNA methylation is a chemical modification of cytosines – the addition of a methyl group to the 5-position of the purine ring of cytosines – it can be revealed by a chemical trick. Treatment of DNA with sodium bisulphite converts cytosine to uracil, but methylated cytosine is resistant to conversion. This difference can then be revealed after amplification of DNA and sequencing, or by restriction enzyme analysis (a method known by the acronym COBRA). I selected a number of candidate imprinted CGIs to analyse and designed amplification assays (designing primers for the polymerase chain reaction that match sequences converted by bisulphite is tricky, but fortunately there are programmes available that can do this). I then set about using bisulphite sequencing and COBRA to investigate the methylation of the candidate sequences in a variety of tissues from
mouse embryos. A final refinement of my experimental design was to use hybrid mice obtained by crossing a standard lab mouse strain (C57BL/6J) with a wild-derived strain (Cast/Ei). The abundance of sequence polymorphisms between these two strains would allow me, in cases where I had detected CGI methylation, to infer whether methylation was present on the maternal or paternal allele, or both. As with any method one encounters for the first time (so I’m told), I experienced some technical problems with this project. Bisulphite converted DNA is fragile and primers can have difficulty annealing if the conversion is not complete, resulting in poor amplification. Touchdown PCR, where the annealing temperature is reduced in a stepwise fashion can help to increase the specificity and improve the amplification. Primers can also join together, forming primer dimers. When analysing small DNA fragments such as those produced by COBRA, primer dimers can confound results and make accurate interpretation difficult. Reagents may also degrade and require diagnostic assays to detect the problem. Whilst these problems slowed down the progress of the project, they also allowed me to develop problem solving strategies and gave me the valuable lesson that one should not expect everything to work first time round.

In the end, I was able to obtain results on the methylation state of CGIs from five genes in a range of tissues. The results indicated a surprising heterogeneity of methylation patterns amongst these loci.

**CGI-1, chr 8**  
Preferential maternal allele methylation confirmed

**CGI-2, chr 10**  
Partially methylated, maternal allele

**CGI-3, chr 17**  
Partially methylated

**CGI-4, chr 5**  
Fully methylated

**CGI-5, chr 8**  
Tissue-specific, partial methylation

Of the loci tested, CGI-1, within a gene that encodes a member of the cadherin family of cell adhesion molecules, showed the best evidence for a new imprinted CGI. COBRA analysis of multiple tissues revealed a consistent pattern of partial methylation. When amplicons obtained from bisulphite treated DNA were cloned and individual clones sequenced, and the sequence profiles assigned parental origin on the basis of the sequence polymorphisms between the C57BL/6J and Cast/Ei parental strains, it could be confirmed that the maternal allele was predominantly the methylated one.

In parallel, work by a student in the lab found evidence for imprinted monoallelic expression of the associated gene specifically in brain mRNA from C57BL/6J x Cast/Ei mouse hybrids. The identification of a CGI within this locus with maternal allele-specific DNA methylation provides important supporting evidence for the imprinting of this gene and identifies the element likely to control its imprinted expression. This is a very promising start, but at the moment it is a mystery why imprinted expression appears to be tissue-specific despite the CGI being partially methylated in other tissues. The significance of imprinting for this gene in brain development is not known and will require detailed investigation in the future; however, in humans, this gene has been linked to intellectual disability.

This summer was a wonderful chance to experience life in a lab and the trials and tribulations of research. The skills I learnt at The Babraham Institute have already proved invaluable with my final year undergraduate project and I am hoping to continue with research once I graduate. I would also like to say a massive thank you to everyone in Dr Kelsey’s lab, in particular Shin-ichi Tomizawa and Natasha Carli whose guidance and advice were invaluable.

The significance of imprinting for this gene in brain development is not known and will require detailed investigation in the future; however, in humans, this gene has been linked to intellectual disability.
CPR5 transmembrane protein involved in a non-transcriptionally based regulation of the circadian clock

**Student** Karche-Guillaume Clémence **Supervisor** Dr Isabelle Carré, University of Warwick

Until recently, the circadian clock was thought to be composed of a set of transcriptional feedback loops. However, it was shown recently in the microalga *Ostreococcus tauri* that the circadian clock could also be regulated by a mechanism that does not depend on transcriptional feedback. Work in Dr Carre’s lab has identified a predicted membrane protein that may play a role in this newly discovered mechanism. Mutations in the *Arabidopsis* CPR5 gene caused abnormal function of the circadian clock. An orthologue was identified in *Ostreococcus tauri* (designated OtCPR5).

The primary aim of my project was to disrupt the function of this gene in *Ostreococcus* and test the effects on circadian rhythms. We designed a disruption cassette containing the antibiotic resistance gene G418 flanked by two regions homologous to the gene OtCPR5. Transformation of wild-type cells with this construct should result in homologous recombination between the upstream and downstream regions of the resistance gene and the genomic CPR5 region of *O.tauri*. Transformed cells would be identified by selection on a medium containing antibiotics. Then homologous recombination events would be identified by PCR screening of individual colonies. All of the steps of the process were optimised, including the concentration of antibiotics to be used for the selection of transgenics. Unfortunately I struggled with the last step of the fusion PCR strategy used to generate the fusion cassette, so we were not able to generate the knock-out mutant within the time frame of the project. This will now be taken over by other members of the group.

While working on this main project I was involved on a number of other projects alongside different members of the laboratory. This included the construction of an antibiotic selection cassette as Gateway entry clone. This will eventually be recombined with three additional fragments to create the final construct, using the Multisite Gateway Technology. I carried out site-directed mutagenesis in order to alter the promoter sequence of the Arabidopsis gene TOC1. I also carried out in vivo imaging experiments to test whether it was possible to measure rhythmic changes in delayed chlorophyll fluorescence in *Ostreococcus*, using a photon-counting camera.

This summer project has been a very important experience for me. It convinced me that I want to go on to a career in research. But it also gave me a lot more. The people that supported me pushed me to think independently. As a result I feel more confident in my way of thinking about biology, and this will be a great help now that I am about to start the first year of a Masters degree.

I thank everyone who has played a role in this project: those that allowed me to do this and those that helped me to do it. I thank you for every thing.
The Effect of Topoisomerase II Inhibitors on Chromatin Organisation and Genome Instability

**Student** Chenchen Song  
**Supervisor** Dr Eugenio Sanchez-Moran, University of Birmingham

During DNA replication and cell division, the double helix DNA structure overwinds in parts to compensate for the relaxation that is required in the replication site to allow the assembly of the proteins involved for this particular cellular process. The double helix overwinding could have detrimental effects if unregulated, potentially causing replication to cease. Topoisomerase II (TopoII) is a chromosome axis protein that is vital to cell survival and correct cellular function, as this essential DNA topology enzyme is recruited by the cell to achieve regulation and to alleviate this problem with overwinding.

TopoII functions via an ATP-dependent two-gate mechanism. It binds to two DNA strands, and a transient double strand break (DSB) is generated in one of the strands - G segment. The second DNA strand, T segment, is passed through the DSB, and TopoII subsequently ligates the DSB to complete the mechanism. Due to the nature of the TopoII mechanism, a range of inhibitors are available that acts on different stages, which results in different phenotypes exhibited by the affected cells. This is employed in this project where we could deduce the action imposed by the inhibitors from the phenotypes that are observed, which would provide a better understanding of the nature of the TopoII enzyme.

In this project, we use *Arabidopsis thaliana* as the model plant for its property of bypassing the apoptosis pathway, which would give an insight into the cytotoxic effects of the TopoII inhibitors. Four known TopoII inhibitors are employed that act on different stages of the TopoII mechanism: netropsin, etoposide, merbarone and ICRF-187. Netropsin binds to the minor groove of AT-rich regions of the double-stranded DNA, and would prevent the TopoII action by competitive inhibition. Merbarone would inhibit the cleavage that is mediated by TopoII. Etoposide prohibits TopoII catalysis between DNA cleavage and ligation of the G-segment. ICRF-187 inhibits the ATP hydrolysis aspect of the TopoII mechanism and significantly affects the enzyme’s turnover rate.

TopoII has already been established as an important target for anti-cancer agents. Therefore the investigation into the mechanism of different TopoII inhibitors would also be highly significant clinically. It is a chromosome axial protein, and its localisation in the area has suggested its vital role in chromosome condensation. We will use the flower buds of *Arabidopsis thaliana* in this project to investigate into this, as they will provide an insight not only into the mitotic stages of the somatic cells, but also into the meiotic stages of the cells that will produce the male gametes (pollen grains). Hence we would be able to gain an integrated understanding of the effects of TopoII and its inhibition in cell cycle.

Wild-type Columbia ecotype Arabidopsis plants were grown and we treated them with the four inhibitors (at different concentrations) at the controlled time lengths of 12 hours, 28 hours and 38 hours. We treated the plants with continuous TopoII inhibition or pulsed inhibition of two hours to observe if there were any differences in the meiotic cells. From observing the different phenotypes resulting from inhibition with these controlled time points, and with respect to the length of meiosis of the plant, we would be able to deduce the specific stage of meiosis these inhibitors act on. Experimental controls were generated where the wild type plants were passed to water containing no TopoII inhibitors, and were fixed and examined in the same way as the plants with TopoII inhibition.

At the specific time points we fixed the flower buds of the plants (where meiosis occurs), which were
Generally, with all four inhibitors, the phenotypes produced demonstrated detrimental damages and abnormalities in meiotic cells. Chromosomal condensation was majorly problematic, and anaphase I bridges were frequently observed that could be causal for the mis-segregation in later stages of meiosis, which are often seen with TopoII inhibition. The great phenotypic similarities observed from plants with continuous TopoII inhibition and those with pulsed TopoII inhibition suggested that the enzyme has a very narrow active time span. With the different time lengths of exposition to TopoII inhibitors, we were able to acquire more information about properties of TopoII. For example, with the inhibition time of 12 hours, although the chromosomes were observed to have abnormalities in the first division of meiosis and in mitosis, second division in meiosis was completely normal, suggesting that TopoII is functional during the pachytene/diplotene stage of meiosis and has no effects in second division.

Thank you to the Genetics Society’s Genes and Development Summer Studentship for funding this project, which has also provided this great opportunity for me to gain research experience and a consolidated insight into research life. I am also extremely grateful to Dr Eugenio Sanchez-Moran for his inspiring supervision, guidance and advice. Thanks must also go to Ms Claire Bauckham for her help and support.
Specificity and memory in the *Drosophila melanogaster* cellular immune response

**Student** Niki McAllister . **Supervisor** Dr Matthew Tinsley, University of Stirling

The invertebrate immune system has traditionally been viewed as non-specific. It has been considered to respond in a relatively uniform way to broad classes of pathogen and, unlike the vertebrate immune response, to lack memory of previous infections. However, this paradigm has been overturned by research showing that following parasite exposure some invertebrates have improved ability to defend against infection. In some studies, these invertebrate immunological memories have been highly specific to the parasite initially encountered.

This project was a preliminary investigation into specificity and memory in the cellular immune response of *Drosophila melanogaster*. I studied the haemocytes of adult flies: these cells phagocyte microbial pathogens and patrol the haemocoel to defend against infection. I began by comparing phagocytosis in different wild-type fly genotypes to determine whether there was general variation between them in their ability to phagocyte, or if variation in the efficiency of phagocytosis was specific to particular microbes. I then investigated the phenomenon of immune memory, determining how phagocytosis by haemocytes was influenced by prior microbial exposure.

*Escherichia coli* bacteria and *Beauveria bassiana* fungal spores were labelled with fluorescein or rhodamine fluorophores so that they could be identified within haemocytes after phagocytosis.

### Part 1

Three wild-type genotypes of *D. melanogaster* (Samarkand, Amherst 3 and Swedish-C) were injected with a suspension of equal concentrations of the two microbes, then bled two hours later to extract haemolymph. Haemocytes were later observed using a fluorescence microscope and phagocytic inclusions counted.

### Part 2

Flies were initially injected with a priming dose of heat-killed *E. coli* or *B. bassiana*, or a control injection of PBS. Three days later flies received a challenge injection containing a mixed suspension of the two microbes, before the flies were bled to assess phagocytosis.

**Part 1: Genetic variation for microbe phagocytosis**

Across all three genotypes, haemocytes more readily phagocytosed *E. coli* than they did *B. bassiana*. However, the relative abilities of the three genotypes to phagocytose *E. coli* and *B. bassiana* differed. In Samarkand and Swedish-C, cells carried ~33% more *E. coli* inclusions than *B. bassiana* inclusions, whereas, in Amherst 3 there was no difference between the microbes. This suggests that the phagocytic response differs in a specific manner between genotypes and that variation in phagocytic efficiency could underlie genotypic differences in the ability of flies to defend against particular infections.

**Part 2: Priming of the cellular immune response:**

I investigated whether the phagocytic response of haemocytes could be primed following microbial challenge. I tested if phagocytosis was more efficient during a secondary microbial encounter, and if this response was specific to the microbe previously experienced. I found exactly this effect: the rate of *E. coli* phagocytosis by haemocytes was 23% greater in *E. coli* primed flies than in controls. This response was specific to *E. coli*, as *E. coli* priming had no impact on the phagocytosis of *B. bassiana* spores.

When primed with *B. bassiana* there was a 42% increase in phagocytosis of *B. bassiana* spores, compared to
flies receiving an initial PBS control injection. Interestingly *B. bassiana* priming actually caused a decline in the ability of haemocytes to phagocytose *E. coli*. Phagocytosis was 35% lower in flies receiving a *B. bassiana* prime injection than in controls. This work demonstrated that the ability of the *D. melanogaster* cellular immune system to phagocytose different microbes varies in a specific manner between genotypes. I also showed that haemocytes display specific immunological memory and have an enhanced phagocytic response when encountering a particular microbe for the second time. It seems possible that this phenomenon may help explain other studies, showing that some invertebrates are more likely to survive pathogen infection when they have previously encountered the microbe.

I would like to thank the Genetics Society for funding this project, I have thoroughly enjoyed the time spent in the laboratory and researching this topic which has enabled me not only to broaden my knowledge in this vast field, but also to learn vital new skills.

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**Genetic studies in *Quercus robur* and *Quercus petraea***

**Student** Charlie Ducker  
**Supervisor** Dr Thorunn Helgason, York University

A recent PhD project showed evidence of a relationship between the timing of budburst within provenances of *Quercus robur* and *Q. petraea* from across Europe and the prevalence of insect herbivores. Early budburst resulted in fewer galls (from herbivorous Oak gall wasps) than later budburst; a result which occurred 2 years in succession within 16 provenances (11 *Q. petraea* and 5 *Q. robur*) at a plot of land in Wykeham, near Scarborough. Insects are thought to choose leaves of the highest quality with which to feed on, suggesting later budburst allowed for higher quality leaf tissue available when the wasps emerge to lay their eggs.

The aim of this project was to determine the genetic variability within and among the provenances. This was done so that the relationship between genetic distance, leaf tissue quality and budburst time can be analysed. In order to achieve this, DNA was extracted from leaf tissue and analysed using previously developed oak genetic markers, including universal chloroplast haplotype and nuclear microsatellite markers, and genetic distance calculated.

Oak trees of both species were sampled on 28/7/11 from all three plots at the site. When leaf tissue was not available from the selected trees, samples were instead taken from the next tree along, or as close as possible. This allowed experience of ecological fieldwork and a view of the wasp gall prevalence in the context of its ecosystem.

In order to elucidate whether leaf or bud tissue was most suitable for harvesting DNA, some samples from each tissue sample were extracted using Quiagen mini kits, initially grinded through the use of Retsch shakers and carbide beads. These were then firstly evaluated via measuring DNA concentration and purity via Nanodrop, with leaf tissue extracts possessing higher concentrations of genetic material. This was followed by running PCR with universal primers ITS1-F and ITS4, with the leaf samples amplifying much more successfully. This was to be expected as there was a small amount of bud tissue available, so leaf tissue was chosen for genetic analysis and all of the plot 3 samples were extracted (64 samples: 44 *Q. petraea* and 20 *Q. robur*), as well as 10 samples from plot 1, and assessed via Nanodrop measurements.

Chloroplast haplotypes were identified via the use of the primer pair trnD [tRNA-Asp (GUC)] and trnT [tRNA-Thr (GGU)]. Chloroplast rather than mitochondrial loci were chosen due to the higher rate of mutation and hence genetic evolution within chloroplasts. These...
were run on PCR thermal cyclers with 1/10 diluted DNA extracts (all extractions), followed by digestion with Taq-1 enzyme, in order to identify different haplotypes. Nuclear microsatellite short tandem repeats were identified with the application of 4 primer pairs spanning 4 separate loci, namely ssrQpZAG1/5 (with repeat unit (GT)6(GA)9), ssrQpZAG9 ((AG)12), ssrQpZAG36 ((AG)19) and ssrQpZAG104 ((AG)9(AT(GA)) from Steinkellner et al.3). ZAG1/5, 9 and 104 loci have been shown to adhere to Mendelian inheritance. Each forward primer was fluorescently labelled, with NED (yellow), VIC (green), 6-FAM (blue) and TET (green) respectively. PCR was carried out on 1/10 dilutions of extracted DNA from all plot 3 extractions, with each primer pair separately. Upon visualisation, PCR product bands were in general, fainter for ZAG104. For analysis on the ABI 3130; ZAG1/5, ZAG9 and ZAG36 PCR products were combined in equal quantities and digested displayed this haplotype. Upon visualisation on agarose gels, products present were of approximate size 200 base pairs. These products were run on the ABI 3130, and resulting fluorescence data was imported into GeneMapper.

Initial analysis suggests there is a wide range of allele lengths. Further analysis of the genetic data is underway. Most notable deviations from expected sizes were in four heterozygous ZAG1/5 isolates, that all showed one allele size of ~128 bp, well below the next smallest allele identified (155 bp). All four were sessile (Q. petraea), with three from the same provenance. Additionally, regarding sessile ZAG9 microsatellite data, an allele at around 181-182 bp was very conserved, occurring in 48% of samples. The genetic analyses carried out collectively suggested substantial genetic diversity within oak provenances at Wykeham, rather than just between species. Chloroplast haplotype digestions suggested some diversity within Q. petraea, which two clearly distinct variants identified. Moreover, ZAG1/5, 9 and 36 alleles were all highly heterozygous within both species, suggesting much allelic diversity, and the size ranges were generally larger than expected, especially within the ZAG1/5 locus. The unusually low allele sizes in four Q. petraea specimens is a potentially interesting discovery, if confirmed, as this was an unambiguous allele and 3 of the 4 occurred in a single provenance. This could possibly be explained by a deletion of a segment of the STR, although this is only speculation.

However, all work carried out in this studentship requires much further analysis, especially of ZAG104, for which results were more difficult to interpret. More scrutiny regarding the microsatellite data is required to deduce the extent of variation, with more stringent data interpretation, such as application of analysis of genetic distance. This will allow quantification of intra and inter species diversity within and between Q. robur and Q. petraea. This is ongoing, and may be included in a publication at a later date.

Whether there is any link between genetic variation, budburst and leaf quality will require further work. Measurement of Nitrogen to Carbon ratios of leaf tissue obtained from the multiple field samplings from Wykeham will be carried out as part of a further project, a task which was initially intended to be carried out in this project, but for time and budget constraints.

Thanks to Jane Hill regarding ecological fieldwork, and Thorunn Helgason for support throughout.
Harmless to Ozone Layer

**Student** Alice Baillie . **Supervisor** Lars Østergaard & Evelyn Körner, John Innes Centre, Norwich

Methyl halide gases cause ozone depletion. While the 1987 Montreal Protocol ended the anthropogenic production of most ozone depleting substances (ODSs), methyl halides arise largely from natural sources. Present models of ozone recovery assume that output from natural ODS sources will remain constant. However, methyl halide emissions from plants are predicted to rise as we increase agricultural output to feed the world’s increasing population. Methyl halide emissions are also expected to increase with rising global temperature – models predict a 10% rise in CH\textsubscript{3}Br and CH\textsubscript{3}Cl emissions from rice for every 1°C rise in ambient temperature.

The biological function of methyl halide production by plants is unclear. Evelyn Körner of the Østergaard group at the John Innes Centre, Norwich, is investigating the function of the *Arabidopsis thaliana* HARMLESS TO OZONE LAYER (HOL) gene (Rhew et al., 2003), which encodes a methyl transferase enzyme that catalyses methyl halide production. This enzyme also catalyses detoxification of thiocyanate ions, which are produced as a by-product of glucosinolate metabolism. As the glucosinolate pathway is specific to the Brassicales order, we might expect HOL homologues from other families not to confer thiocyanate resistance. The primary aim of my studentship was to produce plant lines that will be used to test this hypothesis, by transforming putative HOL homologues from plants from differing evolutionary distances, into *A. thaliana*.

Putative HOL homologues have been identified by sequence similarity in all embryophyte families, as well as in the diatom *Phaeodactylum tricornutum*. Many of these species are known to produce methyl halides. I began by cloning a putative HOL gene from the moss *Physcomitrella patens*, a bryophyte, and two from *Oryza sativa*, a monocot. The genes were inserted into a binary vector for cloning, and transformed into *A. thaliana* (both wild-type and hol-knockout backgrounds) using the floral dip method. Later in my project I also began to prepare constructs containing the putative HOL gene from the diatom, *P. tricornutum*. Methyl halide emissions will be measured from these transformed plants, and compared to emissions from wild-type *A. thaliana* containing its native HOL gene. They will also be plated on medium containing thiocyanate to examine the conservation of detoxification activity in HOL homologues.

A complementary approach to these transformations in investigating the evolution of the HOL gene is knocking out putative HOL homologues in other species. A *Brassica rapa hol* knockout has already been produced, and during my studentship I began making constructs that will be used to knock out the *P. patens hol* gene by homologous recombination in this moss. If, as predicted, these mutants do not emit methyl halides, we can confirm that the putative HOL homologues are responsible for the observed emissions in these species.

In addition to these transformations, I conducted a series of experiments into the effects of various hormones on wild type, hol mutant and 35S::HOL over-expresser lines of *A. thaliana*. One hypothesis for the function of HOL is that it has a role in plant stress responses. I investigated the effects of abscisic acid (ABA), because it is implicated in stress responses. There were no significant differences between the *A. thaliana* lines in the reduction in root length in plants grown on 10µM ABA relative to the control. However, we also grew a HOL::GUS reporter line under each of these conditions. GUS staining appeared to be stronger in the control than in the ABA-treated seedlings.

Treatment of *A. thaliana* with salts such as NaCl and KCl also reduces HOL expression. These paired observations may provide some support for the stress tolerance hypothesis of HOL function.

I look forward to seeing the results of the experiments that are to be conducted using the transgenic plant lines that I have helped to produce. Examination of the relative evolutionary conservation of methyl halide production and thiocyanate detoxification may offer an insight into the contemporary function of the HOL gene.
See the relevant web pages and downloadable Funding Application Forms at www.genetics.org.uk

One-off Meeting Sponsorship

Purpose

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

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

Review of applications

1) Members may make applications at any time. They should be submitted on the GS Funding Application Form and emailed to Linda Allardyce, Linda.Allardyce@portlandpress.com using message subject ‘Meeting Sponsorship’ and your surname.

2) The application will be circulated to the full committee for review. The review will cover suitability of the meeting for Genetics Society sponsorship and level of support requested.

3) The committee will be asked to respond within two weeks and the Society aims to respond to requests within four weeks.

Conditions of sponsorship

4) Several levels of sponsorship are possible: (a) single lecture: £200 (b) session: £500-1000 (c) major sponsor: £1500-2000.

5) Genetics Society sponsorship must be mentioned in all pre-meeting publicity (e.g. posters, flyers, website) and in the meeting programme. If the Genetics Society is the major sponsor the meeting should be advertised as a “Genetics Society-sponsored meeting”.

6) Details of the programme of the meeting and registration forms should be sent as far in advance as possible to Linda Allardyce, Linda.Allardyce@portlandpress.com, for inclusion in the Society’s newsletter and on the website.

7) A short report on a meeting that receives sponsorship of £1000 or more, for possible publication in the newsletter and on the website, should be sent to Linda Allardyce, Linda.Allardyce@portlandpress.com within one month of the conference taking place.

8) Genetics Society sponsorship may be used at the organiser’s discretion, but budget travel and accommodation options should normally be insisted upon. Any unused grant should be returned to the Genetics Society. The Society will not be responsible for any losses incurred by the meeting organisers.

9) An invoice for the grant awarded should be submitted to Linda Allardyce, Linda.Allardyce@portlandpress.com. The grant may be claimed in advance of the meeting and no longer than one month after the meeting.

10) The meeting organisers agree to make details of how to apply for Genetics Society membership available to non-members attending the sponsored meeting. Meetings that receive maximum sponsorship will be expected to offer a discounted registration fee to Genetics Society members to encourage non-members to join the Society at the same time. New members may then attend at the discounted rate, once confirmation of their application for membership of the Genetics Society has been received from the Society’s Office.
New Sectional Interest Groups

Purpose

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

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

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

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

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

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

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

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

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

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

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

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

Junior Scientist Grants

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

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

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

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

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

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

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

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

Purpose
To support attendance at short training courses.

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

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

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

Heredity Fieldwork Grants

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

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

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

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

Purpose
To support vacation research by undergraduate geneticists.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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4. Please debit my Visa/Mastercard

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The Genetics Society

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

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

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

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

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

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

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

International links
The Society has many overseas members and maintains links with genetics societies in other countries through the 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.
Please complete this form and return it, along with your cheque, Direct Debit instructions or credit card to The Genetics Society, Portland Customer Services, Commerce Way, Colchester CO2 8HP, UK. Complete this section carefully. The information you provide will help us to correspond with you efficiently and ensure that your details are accurately held on our membership database.

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

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

Last Name:  
First Name:  

Institution:  

Institution Address:  

Postcode:  
Country:  

Telephone:  
Fax:  

Email:  

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

2. AREAS OF INTERESTS (tick as appropriate)

Gene Structure, Function and Regulation  
Genomics  

Cell and Developmental Genetics  
Applied and Quantitative Genetics  

Evolutionary, Ecological & Population Genetics  
Corporate Genetics and Biotechnology  

3. MEMBERSHIP FEES

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

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

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

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

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

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

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

Signature of Head of Department/Supervisor

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

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

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

Option 2: Cheque/Bank transfer

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

To facilitate identification please confirm:

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Option 3: Credit/Debit Card

I wish to pay by Credit Card.
Credit Card Type: Visa ☐ Mastercard ☐ Switch ☐

I authorise Portland Customer Services to use the credit card details below to pay my membership fees.

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6. MEMBERSHIP NOMINATION

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

Signature of nominating FULL MEMBER

Print name in block capitals

Membership No.

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

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

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

If you wish to notify us of a change of address, you can use our online facility by visiting www.genetics.org.uk or by emailing us at theteam@genetics.org.uk. Alternatively you can complete the form below and return it to:
The Genetics Society, Portland Customer Services, Commerce Way, Colchester CO2 8HP, UK marking your envelope CHANGE OF ADDRESS NOTIFICATION.

Note that from _______________________________ my new address will be:

Title: Prof. □ Dr. □ Mr. □ Miss. □ Mrs. □ Ms. □

(Print or Type)

Last Name: _______________________________ First Name:

Institution:

Address:

Postcode: _______________________________ Country:

Telephone: _______________________________ Fax:

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The latest genetic research from *Heredity*

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

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

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