In this Issue

- Making the voice of science heard in Brexit
- Genetics Society Centenary preparations
- London Fly Meeting - SIG in the spotlight
- Research and travel grant reports

The Genetics Society News is edited by Lynsey Hall and items for future issues can be sent to the editor by email to HallL10@cardiff.ac.uk.

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Cover image: Chelsea Flower Show as part of 2019 - A Year Of Celebration: The Genetics Society Centenary. See page 22 for details.
A word from the editor

Welcome to Issue 78

Dear Readers,

Welcome to the latest addition of the Genetics Society newsletter. Since the last newsletter, preparations are now well underway for a series of events in 2019 to celebrate The Genetics Society Centenary. In this issue we are pleased to introduce our newly appointed Centenary project manager - Cristina Fonseca, who outlines some of the upcoming Centenary events in the feature article 2019 - A Year Of Celebration: The Genetics Society Centenary. More internationally, Brexit negotiations have moved forward in anticipation of the UK leaving the European Union in March 2019. Due to the collaborative nature of research, how these negotiations progress are of substantial interest to our community. As such, we thought it timely to include a guest feature from Dr Sarah Main, the Executive Director of the Campaign for Science and Engineering (CaSE), on Making the voice of science heard in Brexit. Organizations such as CaSE, whose mission is to ensure the UK has the skills, funding and policies to enable science and engineering to thrive, are integral to representing the interests of research in the UK during this process.

I hope you enjoy this issue, and all of the reports on the various research and meetings which we have been delighted to fund.

Best wishes,
Lynsey Hall

Brexit negotiations have moved forward in anticipation of the UK leaving the European Union in March 2019. Due to the collaborative nature of research, how these negotiations progress are of substantial interest to our community.
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www.genetics.org.uk
A Genetics Society Workshop

Communicating Your Science
A Genetics Society Workshop for PhD students and postdocs

April 23rd – 25th 2018, Chicheley Hall, Chicheley Road, Newport Pagnell, Chicheley

An important part of science is getting your results and ideas across to others, through papers, presentations, theses, grant proposals, conversations and interviews. Your audience may include specialists in the field, those from other disciplines, industry, or the general public.

How can you best communicate your science?
This workshop brings together experts in different fields - writers, broadcasters and presenters - to help you explore and develop your communication skills. Working together with others on the course you will learn how to structure presentations, develop writing skills, bridge disciplines and have hands-on experience of broadcasting.

The Genetics Society will cover costs of travel, accommodation and meals for successful applicants.

Tutors and Speakers include
Armand Leroi (author, broadcaster and professor of Evolutionary and Developmental Biology, Imperial College, London)
Enrico Coen (author and Professor of Genetics at the John Innes Centre, Norwich)
Helen Keen (Award winning comedy writer and performer; author of the Radio 4 series, “It Is Rocket Science!”)
The Naked Scientists (Presenters of the award winning Naked Scientists radio show and podcast)
Alison Woollard (Presenter of the 2013 Royal Institution Christmas Lectures and Lecturer at University of Oxford)

Organisers
Jonathan Pettitt (Reader in Genetics, University of Aberdeen)

For registration, visit www.genetics.org.uk
More detailed information and links to event websites can be found at www.genetics.org.uk/Conferences/Externalmeetings.aspx
We will happily include any announcements for genetics-based meetings in this section. Please send any items to theteam@genetics.org.uk

Connectome to behaviour: modelling C. elegans at cellular resolution
**Date:** 29th - 30th January 2018  
**Location:** The Royal Society, London  
**Contact:** scientific.meetings@royalsociety.org  
**Website:** royalsociety.org/science-events-and-lectures/2018/01/mind-of-a-worm/

Festival of Genomics
**Date:** 30th - 31st January 2018  
**Location:** Excel Exhibition Centre, London  
**Registration deadline:** 8th January 2018 (early bird); 30th January  
**Website:** www.festivalofgenomicslondon.com

The 100,000 genomes project - mainstreaming genomic medicine in the NHS
**Date:** 2nd February 2018  
**Location:** Royal Society of Medicine, London  
**Registration deadline:** 2nd February 2018  
**Website:** www.rsm.ac.uk/events/mgk02

Genomic Medicine 2018 Edinburgh Conference
**Date:** 18th - 19th April 2018  
**Location:** Radisson Blu Hotel, Edinburgh  
**Registration deadline:** 31st January, 10th April, 18th April 2018 (varying rates)  
**Website:** biotexcel.com/event/genomic-medicine-2018edinburgh/

Genomics of Brain Disorders
**Date:** 23rd - 25th April 2018  
**Location:** Wellcome Genome Campus, Hinxton, Cambridge  
**Deadline(s):** 30th January (early bird registration), 13th February (bursary), 27th February (abstract submission), 27th March (registration) 2018  
**Website:** coursesandconferences.wellcomegenomecampus.org/Conferences.wt

Complex Trait Analysis of Next Generation Sequence Data
**Date:** 18th - 22nd June, 2018  
**Location:** Max Delbrück Center for Molecular Medicine Berlin, Germany  
**Registration deadline:** 1st March 2018  
**Website:** statgen.research.bcm.edu/index.php/ComplexNGS2018

Genetic Association
**Date:** 17th - 21st September 2018  
**Location:** Max Delbrück Center for Molecular Medicine Berlin, Germany  
**Registration deadline:** 15th June 2018  
**Website:** statgen.research.bcm.edu/index.php/Genassoc2018

Single Cell Biology
**Date:** 6th - 8th March 2018  
**Location:** Wellcome Genome Campus, Hinxton, Cambridge  
**Registration deadline:** 6th February 2018  
**Website:** coursesandconferences.wellcomegenomecampus.org/Conferences.wt

Genomics of Rare Disease
**Date:** 26th - 28th March 2018  
**Location:** Wellcome Genome Campus, Hinxton, Cambridge  
**Registration deadline:** 27th February 2018  
**Website:** coursesandconferences.wellcomegenomecampus.org/Conferences.wt
The Genetics Society helps support several sectional interest groups by providing meeting sponsorship. We currently have 15 groups who organise sectional interest meetings with the organizers and dates of any forthcoming meetings are listed below. If you are interested in any of these areas, please contact the relevant organiser. Groups who wish to be considered for sectional interest group status should contact the Scientific Meetings Secretary Dominique Kleyn (dominique.kleyn@btinternet.com) in the first instance.

**Arabidopsis**
Organiser: Geraint Parry
(geraint@garnetcommunity.org.uk)
Website: www.garnetcommunity.org.uk

**Archaea Group**
Organiser: Nick Robinson (n.robinson2@lancaster.ac.uk)
Website: www.microbiologysociety.org/events/society-events-and-meetings.html

**British Yeast Group**
Organisers: Daniela Delneri (d.delneri@manchester.ac.uk) and Graham Pavitt (graham.pavitt@manchester.ac.uk)

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

**E-ACTG (Edinburgh Alliance for Complex Trait Genetics)**
Next meeting: Biannually (usually March and October)
Organisers: Chris Haley (chris.haley@roslin.ed.ac.uk) and Josephine Pemberton (j.pemberton@ed.ac.uk)
Website: www.wiki.ed.ac.uk/display/eactg/Edinburgh+Alliance+for+Complex+Trait+Genetics

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

**Evolutionary Genetics and Genomics**
Next meeting: 20th March 2018
Organiser: Frank Jiggins (fm1001@cam.ac.uk)
Website: evolutionarygenetics.heliconius.org/eggs/

**South-West Fly**
Next meeting: 7th March 2018, 13th June 2018
Organiser: James Hodge
(James.Hodge@bristol.ac.uk)
Website: http://www.bristol.ac.uk/phys-pharm-neuro/events/fly-meetings/

**Genetics Society Pombe Club**
Next meeting: 2018 (date to be confirmed)
Organiser: Jacky Hayles (j.hayles@cancer.org.uk)

**London Fly meetings**
Next meeting: 3rd Wednesday of the month
(Francis Crick Institute, Lincoln’s Inn Fields laboratory, London)
Organisers: Nic Tapon (nic.tapon@crick.ac.uk) and Barry Thompson (barry.thompson@crick.ac.uk)
Website: lists.londonflymeeting.org/listinfo/lfm

**Mammalian Genetics and Development**
Organisers: Nick Greene, Andrew Copp, Andrew Ward (ich.mgdwshop@ucl.ac.uk)
Website: www.ucl.ac.uk/ich/research/developmental-biology-cancer/DBCmeetings/MDW/mgw_workshop

**Mammalian Genes, Development and Disease**
Next meeting: 7th July 2017.
Organisers: Rosalind John (johnrm@Cardiff.ac.uk), David Tosh (d.tosh@bath.ac.uk), David Allard (d.allard@exeter.ac.uk)

**Meiosis group**
Organiser: Isabelle Colas (isabelle.colas@hutton.ac.uk) and Alexander Lorenz (a.lorenz@abdn.ac.uk)

**Population Genetics Group**
Organiser: Jon Bridle (jon.bridle@bristol.ac.uk)
Website: populationgeneticsgroup.org.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).
Honorary Secretary’s Notices

Jonathan Petitt. Honorary Secretary, University of Aberdeen

Committee Changes, Elections and Vacancies

The Committee has established a new post of Policy Officer, whose remit will be to build strong networks with policy makers, advisory bodies, and think tanks and thereby identify and support opportunities to strengthen Genetics Society engagement on public policy. Professor Rebecca Oakey (King’s College, London) was nominated to this position at the Committee Meeting held on 22nd November 2017. She will take up her post on the 1st May 2018.

The Committee is currently seeking nominations for an Ordinary Committee Member (Cell and Developmental Genetics) to take up position 1st May 2018. Any member in good standing is eligible to submit nominations (including self-nominations) to Jonathan Pettitt (j.pettitt@abdn.ac.uk).

Life Membership in the Genetics Society

Have you reached the age of retirement (65), but wish to continue with your involvement in the Society? If so, and you are an ordinary member who has discharged any arrears that 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).

2018 Medals and Prize Lectures

The Genetics Society is pleased to announce the recipients of our 2018 Medals and Prize Lectures. Additional information about the recipients and awards can be found on pages 10 - 13 in this newsletter and on the Genetics Society website.

The Mendel Medal is awarded by the President of the Genetics Society to an individual who has made outstanding contributions to research in any field of genetics.

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 Genetics Society Medal is an award that recognizes outstanding contributions to genetics by a currently active researcher.

The JBS Haldane Lecture recognises an individual for their outstanding ability to communicate topical subjects in genetics research to an interested lay audience.

The Mary Lyon Award recognizes an outstanding contribution to genetics research by a scientist in the middle of their research career.

Nominations are open for our 2019 awards. Any member in good standing is eligible to submit nominations to the Honorary Secretary, Jonathan Pettitt (j.pettitt@abdn.ac.uk). More information can be found at www.genetics.org.uk/Prizes/ MedalsandLectures.aspx.

www.genetics.org.uk
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.

As part of our plans for the Society’s Centenary Celebrations in 2019 we would like to increase the involvement of the Local Representatives with the Society’s activities. Further details will be available in the coming months. Currently, we have local representative vacancies in Ascot, Hinxton, Plymouth and Richmond. 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, Jonathan Pettitt, by e-mail at j.pettitt@abdn.ac.uk.
# Genetics Society Local Representatives

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<thead>
<tr>
<th>Local representative</th>
<th>Location</th>
<th>Institute</th>
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<tbody>
<tr>
<td>Dr Anne Donaldson</td>
<td>Aberdeen</td>
<td>University of Aberdeen</td>
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<td>Dr Dylan Phillips</td>
<td>Aberystwyth</td>
<td>Aberystwyth University</td>
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<td>Vacant</td>
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<td>Dr Alexander Papadopoulos</td>
<td>Ascot</td>
<td>Silwood Park, Imperial College London</td>
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<td>Dr Araxi Urrutia</td>
<td>Bath</td>
<td>University of Bath</td>
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<tr>
<td>Dr Declan McKenna</td>
<td>Belfast</td>
<td>University of Ulster</td>
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<tr>
<td>Dr Lindsey Leach</td>
<td>Birmingham</td>
<td>University of Birmingham</td>
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<tr>
<td>Dr Charlotte Rutledge</td>
<td>Brighton</td>
<td>University of Birmingham</td>
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<tr>
<td>Dr Felicity Z Watts</td>
<td>Bristol</td>
<td>University of Sussex</td>
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<td>Professor Patricia Kuwabara</td>
<td>Cambridge</td>
<td>University of Bristol (SOMs)</td>
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<tr>
<td>Howard Baylis</td>
<td>Cambridge</td>
<td>Zoology Department, University of Cambridge</td>
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<tr>
<td>Philip Weir</td>
<td>Cambridge</td>
<td>Sainsbury Laboratory, Cambridge University</td>
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<tr>
<td>Dr Ben Longdon</td>
<td>Cambridge</td>
<td>Genetics Department, Cambridge University</td>
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<tr>
<td>Dr Bénédicte Sanson</td>
<td>Cambridge</td>
<td>Phys, Dev and Neuro Department, Cambridge University</td>
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<tr>
<td>Ian Henderson</td>
<td>Cambridge</td>
<td>Plant Sci Department, University of Cambridge</td>
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<tr>
<td>Dr Simon C Harvey</td>
<td>Canterbury</td>
<td>Canterbury Christ Church University</td>
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<tr>
<td>Dr Timothy Bowen</td>
<td>Cardiff</td>
<td>University of Wales College of Medicine</td>
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<td>Dr William Davies</td>
<td>Cardiff</td>
<td>Cardiff University</td>
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<td>Oliver Breeze</td>
<td>Dublin</td>
<td>University College Dublin</td>
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<td>Dr Michael JR Stark</td>
<td>Dundee</td>
<td>University of Dundee</td>
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<td>Dr Ian Jackson</td>
<td>Edinburgh</td>
<td>MRC Human Genetics Unit</td>
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<td>Dr Douglas Vernimmen</td>
<td>Edinburgh</td>
<td>The Roslin Institute</td>
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<td>Dr Jarrod Hadfield</td>
<td>Edinburgh</td>
<td>Institute of Evolutionary Biology</td>
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<td>Professor Eileen Wall</td>
<td>Edinburgh</td>
<td>SRUC</td>
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<td>Dr Antonio Marco</td>
<td>Essex</td>
<td>University of Essex</td>
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<td>Dr Sarah Planagan</td>
<td>Glasgow</td>
<td>University of Exeter</td>
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<td>Dr Iain Johnstone</td>
<td>Glasgow</td>
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<td>Dr Kevin O'Dell</td>
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<td>Dr Fiona Green</td>
<td>Guildford</td>
<td>University of Surrey</td>
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<td>Dr Paul Potter</td>
<td>Harwell</td>
<td>MRC Harwell</td>
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<td>Vacant</td>
<td>Hinxton</td>
<td>Wellcome Genome Campus</td>
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<td>Dr Heather M Sealy-Lewis</td>
<td>Hull</td>
<td>University of Hull</td>
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<td>Prof Nick F Tuite</td>
<td>Kent</td>
<td>University of Kent</td>
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<tr>
<td>Dr Paul Ashton</td>
<td>Lancashire</td>
<td>Edge Hill University</td>
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<td>Dr Peter Glen Walley</td>
<td>Liverpool</td>
<td>University of Warwick</td>
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<td>Prof Tony Flagg</td>
<td>Liverpool</td>
<td>University of Liverpool</td>
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<tr>
<td>Dr Craig Wilding</td>
<td>Liverpool</td>
<td>Liverpool John Moores</td>
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<tr>
<td>Dr Andrew Peel</td>
<td>Leeds</td>
<td>University of Leeds, School of Biology</td>
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<tr>
<td>Dr Ed Hollox</td>
<td>Leicester</td>
<td>University of Leicester</td>
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<tr>
<td>Dr Marie Nugent</td>
<td>Leicester</td>
<td>University of Leicester</td>
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<tr>
<td>Dr Claire Russell</td>
<td>London</td>
<td>Royal Veterinary College</td>
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<td>Professor Simon Hughes</td>
<td>London</td>
<td>King's College London</td>
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<tr>
<td>Dr Francesca Mackenzie</td>
<td>London</td>
<td>Kingston University</td>
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<td>Professor Harald Schneider</td>
<td>London</td>
<td>The Natural History Museum</td>
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<td>Professor R M C Fisher</td>
<td>London</td>
<td>UCL Institute of Neurology</td>
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<td>Professor Andrew Pomiankowski</td>
<td>London</td>
<td>UCL Department of Genetics, Evolution and Environment</td>
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<td>Professor Richard A Nichols</td>
<td>London</td>
<td>Queen Mary and Westfield College</td>
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<td>Dr Emanuela Volpi</td>
<td>London</td>
<td>University of Westminster</td>
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<td>Dr Yalda Jamshidi</td>
<td>London</td>
<td>St George's University of London</td>
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<td>Dr Michalis Barkoulas</td>
<td>London</td>
<td>Imperial College (Hammersmith)</td>
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<td>Dr James Turner</td>
<td>London</td>
<td>Francis Crick Institute</td>
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<tr>
<td>Dr Catherine Walton</td>
<td>Manchester</td>
<td>University of Manchester</td>
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<td>Miss Rebecca Collier</td>
<td>Manchester</td>
<td>University of Manchester</td>
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<td>Dr Kirsten Wolff</td>
<td>Newcastle upon Tyne</td>
<td>University of Newcastle (Biol Sci)</td>
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<td>Professor Enrico Coen</td>
<td>Norwich</td>
<td>John Innes Centre</td>
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<td>Dr Tracey Chapman</td>
<td>Norwich</td>
<td>University of East Anglia</td>
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<td>Dr Richard Emes</td>
<td>Nottingham</td>
<td>University of Nottingham (Sutton Bonnington Campus)</td>
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<td>Professor John Brookfield</td>
<td>Nottingham</td>
<td>University of Nottingham (University Park Campus)</td>
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<td>Dr S L M Fischer</td>
<td>Oxford</td>
<td>University of Oxford (Zoology)</td>
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<td>Professor Andrew O M Wilkie</td>
<td>Oxford</td>
<td>University of Oxford (John Radcliffe Hosp)</td>
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<td>Professor Liam Dolan</td>
<td>Oxford</td>
<td>University of Oxford (Plant Sciences)</td>
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<td>Professor Jonathan Hodgkin</td>
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<td>Dr Ravinder Kanda</td>
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<td>Dr Louise Johnson</td>
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<td>Dr Jon Slate</td>
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<td>Dr Mark A Chapman</td>
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<td>Professor Mike Ritchie</td>
<td>Stirling</td>
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<td>Dr Mario Vallego-Marin</td>
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<td>Dr Lewis Eagle</td>
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<td>Dr George Johnson</td>
<td>Warwickshire</td>
<td>University of Warwick</td>
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<td>Dr Jose Gutierrez-Marcos</td>
<td>York</td>
<td>University of York</td>
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Michael Bevan studied biochemistry at Auckland University in New Zealand before moving to Cambridge University to study for a PhD in the Biochemistry Department. He became interested in DNA after a lecture by Fred Sanger in 1976, and studied Agrobacterium tumefaciens T-DNA transfer into plants cells under the guidance of Mary-Dell Chilton at Washington University in St Louis. This work led to methods for transferring and expressing any gene in a plant, laying the foundations for GM agriculture. Since returning to the UK in 1982, he worked at the Plant Breeding Institute in Cambridge, then moved to the John Innes Centre in Norwich in 1989. He initiated and led an international collaboration to sequence the genome of Arabidopsis thaliana, completing the project in 2000. Following this, he has been involved in sequencing several grass genomes, most recently that of bread wheat.

His interests in wheat genomics are now focussed on understanding how pseudogenization, epigenetic modifications and gene expression are influenced by the formation of new wheat hybrids, as such changes generate new traits in hexaploid wheat.

Linked to this work, he is exploring applications of genomics to improve the precision and efficiency of wheat breeding. He has also identified novel molecular mechanisms controlling organ and seed size, phenotypes making important contributions to crop yield.

He was elected to the European Molecular Biology Organisation in 2001, and to the Royal Society in 2013. He was awarded the Rank Prize for Nutrition in 1987 for his work on plant transformation and the Kumho Award in 2001 for sequencing the first plant genome.

His interests in wheat genomics are now focussed on understanding how pseudogenization, epigenetic modifications and gene expression are influenced by the formation of new wheat hybrids, as such changes generate new traits in hexaploid wheat.
Balfour Lecture
Ludmil B. Alexandrov

Ludmil Alexandrov is an Assistant Professor of Cellular and Molecular Medicine and Bioengineering at the University of California, San Diego. He earned his Bachelor of Science degree in Computer Science from Neumont University and received his Master’s of Philosophy in Computational Biology as well as his Ph.D. in Cancer Genetics from the University of Cambridge.

Ludmil’s research has been focused on understanding the mutational processes in cancer. In 2013, he developed the first comprehensive map of the mutational signatures in human cancer. More recently, Ludmil mapped the signatures of clock-like mutational processes operative in normal somatic cells, demonstrated that mutational signatures have the potential to be used for targeted cancer therapy, and identified the mutational signatures associated with tobacco smoking.

Ludmil has 64 publications in peer-reviewed journals from which 15 publications in Nature, Science, or Cell and another 20 publications in Nature Genetics, Cancer Cell, Nature Medicine, or Nature Communications.

In 2014, Ludmil Alexandrov was recognized by Forbes magazine as one of the “30 brightest stars under the age of 30”. In 2015, he was awarded the Prize for Young Scientists in Genomics and Proteomics by Science magazine and SciLifeLab, and he also received a Harold M. Weintraub Award by the Fred Hutchinson Cancer Center.

In 2016, Ludmil was awarded the Carcinogenesis Young Investigator Award by Oxford University Press. Ludmil is currently one of six co-investigators leading the Mutographs of Cancer project, a £20 million initiative to identify the unknown cancer-causing factors.

More recently, Ludmil mapped the signatures of clock-like mutational processes operative in normal somatic cells, demonstrated that mutational signatures have the potential to be used for targeted cancer therapy, and identified the mutational signatures associated with tobacco smoking.
JBS Haldane Lecture
Turi King

Turi King is a Reader in Genetics and Archaeology and Professor of Public Engagement at the University of Leicester. She is perhaps best known for leading the genetics analysis in the King Richard III case leading to the identification of his remains in 2014 which led to his reinterment in Leicester Cathedral in 2015.

Turi has an unusual background in that she started her career in archaeology in her native Canada and then reading for a BA in Archaeology and Anthropology at the University of Cambridge where she specialised in Biological Anthropology.

It was here that she became interested in how genetics could be used to answer questions in history and archaeology and moved to the University of Leicester to study molecular genetics. Her award winning PhD examined the link between British Surnames and the Y chromosome. All of her subsequent work has combined genetics with history, archaeology, geography, forensics and epidemiology.

Alongside this, she began to develop a public engagement strand to her career, becoming the most prodigious member of staff at the University of Leicester for Public Engagement work. Alongside giving talks and workshops at schools she gives numerous lectures ranging from family history groups to a Congressional Breakfast on Capitol Hill.

She has advised on and appeared in numerous television and radio programmes and has recently been made a Professor of Public Engagement at the University in recognition of the contribution she continues to make in making science accessible to the general public.

Turi has an unusual background in that she started her career in archaeology in her native Canada and then reading for a BA in Archaeology and Anthropology at the University of Cambridge where she specialised in Biological Anthropology.
Mary Lyon Medal

Sarah Teichmann

Sarah did her PhD at the MRC Laboratory of Molecular Biology, Cambridge, UK with Dr Cyrus Chothia, FRS and was a Beit Memorial Fellow at University College London with Professor Dame Janet Thornton, FMedSci, FRS. She started her group at the MRC Laboratory of Molecular Biology in 2001.

In 2013, she moved to the Wellcome Trust Genome Campus in Hinxton, Cambridge, jointly with the EMBL-European Bioinformatics Institute and the Sanger Institute. In January 2016 she became Head of the Cellular Genetics Programme at the Sanger Institute. She is also a Director of research in the Cavendish Laboratory, University of Cambridge and Senior Research Fellow at Churchill College.

Sarah is an EMBO member and a Fellow of the Academy of Medical Sciences, and her work has been recognized by a number of UK and international prizes, including the Lister Prize, Biochemical Society Colworth Medal, Royal Society Crick Lecture and EMBO Gold Medal.

Sarah Teichmann is Head of Cellular Genetics at the Wellcome Trust Sanger Institute. Her work focuses on deciphering the immune system with genomics and bioinformatics approaches. She co-chairs the international Human Cell Atlas Consortium together with Aviv Regev (Broad Institute).
The 5th Annual Drosophila Cell & Developmental Biology workshop at the Burn house of the Goodenough College in the Scottish Highlands featured 22 scientists from all over the United Kingdom. This workshop was introduced in 2013 to provide a platform for scientists working on various aspects of Drosophila developmental cell biology to exchange unpublished data, ideas and observations. The workshop also promotes gender balance and the interaction of senior and junior principal investigators in a casual atmosphere. The workshop covered the following topics:

**Early embryos:** Arno Muller (Dundee/Kassel) discussed the labs efforts to investigate zygotic transcriptional requirements for early embryogenesis by extending the use of chromosomal aberrations using transgenic rescue of known zygotic genes. James Wakefield (Exeter) reported on the results of a large proteomic analysis of microtubule-associated proteins, and discussed the role of the replication factor C complex in mitosis in early embryos.

**Cytoskeleton:** A number of presentations were concerned with the role of the actin-myosin cytoskeleton during morphogenesis. Katja Rooper (Cambridge) discussed the role of the actin and myosin filament systems in salivary gland morphogenesis in the embryo and presented a quantitative dynamic analysis of the process in three dimensions. Benedicte Sanson (Cambridge) reported on the role of myosin cables in orienting cell divisions during the gastrulation and germ band elongation process in the early embryo.

Yanlan Mao (London) spoke about her labs efforts into investigating the consequences of how tissues are coping with mechanical stress and presented methods to determine the consequences when external mechanical stress applied to tissues.

**Hemocytes:** Tom Millard (Manchester) presented data on the regulation of the actin dynamics during wound healing and a novel quantitative imaging approach to study the developmental migration of the hemocytes in the embryo. Iwan Evans (Sheffield) presented data of his lab trying to dissect the heterogeneity of hemocytes in the embryo using imaging and molecular techniques.

**Epithelial Biology:** Franck Pichaud (London) demonstrated the interactions of the Par and Crumbs polarity complexes and their regulation using the developing eye as a model. Natalia Bulgakova
The summer UK Circadian Clock Club took place this year at the University of Bristol. The one-day meeting allowed established and young researchers in the fields of circadian rhythms and sleep biology to present their new research, spanning a considerable breadth of experimental systems and questions. The meeting attracted about 140 delegates from both the UK and other European countries.

**Mechanosensation:** Barry Denholm (Edinburgh) presented data on the role of a novel membrane protein in the mechanisms of mechanosensation in the heart. Nick Brown (Cambridge) discussed the role of the integrin complex protein vinculin and its relationship to Talin and the binding of the integrin complex to actin.

**Cell Signaling:** Sarah Bray (Cambridge) spoke about the laboratory's effort in studying the response of the Notch receptor using in vivo single molecule tracking in the nucleus of the responding cells. Yuu Kimata (Cambridge) discussed the role of cell cycle regulation in Wingless signaling and presented their findings on the APC/C-Nek2 module in this pathway.

**Cell polarity:** Jens Januschke (Dundee) presented data on symmetry breaking controlling the direction of cell division in asymmetrically dividing neuroblasts. Rita Sousa-Nunes (London) discussed the mechanisms that govern quiescence in these cells and reported on the unexpected discovery of a role of components of nuclear pore complex in the process. Helen Strutt (Sheffield) presented their data on the role of phosphorylation of Strabismus as a molecular switch regulating feedback in planar polarity in the wing imaginal disc. Tony Southall (London) spoke about progress on the neuroblast differentiation gene lola and the identification of a small peptide as novel polarized protein in neural stem cells. David Strutt (Sheffield) discussed the problem of how the different core components of the planar polarity complex interact with each other to produce an information flow that could explain the generation of planar polarity in the wing imaginal disc.

**Transport:** Helen White-Cooper (Cardiff) presented an unexpected link between the mRNA nuclear export pathway and muscle degeneration. Clive Wilson (Oxford) introduced the male accessory gland cell as a model system to study sub-compartmental and endosomal control of exosome and regulated secretion.

**Centrosomes:** Paul Conduit (Cambridge) presented work on how centrioles duplicate only once per cell cycle discussing the potential involvement of the nuclear envelop in early fly embryos in this process. Finally Jordan Raff (Oxford) showed recent results building on super resolution microscopy shedding light on the mechanism that governs how centrioles grow to particular sizes.

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**Summer Circadian Clock Club 2017**

29th June 2017, Wills Memorial Building, University of Bristol, UK

**Dr James Hodge, University of Bristol**

The summer UK Circadian Clock Club took place this year at the University of Bristol. The one-day meeting allowed established and young researchers in the fields of circadian rhythms and sleep biology to present their new research, spanning a considerable breadth of experimental systems and questions. The meeting attracted about 140 delegates from both the UK and other European countries.

At this Clock Club, Prof. Martha Merrow from the University of Munich delivered the keynote Biochemical Society Lecture, “Circadian rhythms in non-photosynthetic prokaryotes.” Her far-reaching lecture introduced important concepts for new researchers in the field, and addressed important questions such as whether rapidly-dividing microbes might benefit from having a circadian clock.

The other 13 research talks covered topics ranging from the temporal investigation of collective mood through analysis of twitter content to molecular aspects of the functioning of the circadian oscillator in experimental systems such as plants, animals and humans.
The EMBO Conference on Eukaryotic RNA Turnover was the second in an EMBO Conference Series, which grew out of an informal biennial series starting in 2003, and has generated substantial interest among participants in the RNA field.

The conference was mainly supported by the European Molecular Biology Organisation (EMBO) but also received sponsorship from the Genetics Society and the RNA Society as well as industrial sponsors. The Conference was organised by Chris Norbury (University of Oxford) with the Co-Organisers Professor Sarah Newbury (University of Sussex) and Professor Cecilia Arraiano (Universidade Nova de Lisboa, Portugal). The conference was attended by 127 participants from all over the world and comprised 11 sessions with a total of 60 oral presentations. The talks were complemented by five ‘flash’ presentations, where early career scientists had an extra opportunity to present their work, and two poster sessions.

The focus of the Conference was on RNA turnover, with an emphasis on its relevance to human disease. Presentations spanned a wide range of topics from structural biology of RNA-binding proteins to new information on the exoribonuclease Dis3L2 and its role in repressing cell proliferation, RNA binding proteins and their role in inflammation and also trypanosomal RNA degradation systems. Highlights included the presentation of elegant work on specificity of deadenylation complexes by Lori Passmore (LMB, Cambridge), who showed that RNA-binding proteins such as Puf3 provide specificity for targeted deadenylation.

The importance of codon usage as a major determinant of mRNA half-life in trypanosomes and humans was also illustrated by Mark Carrington (University of Cambridge) and Olivia Rissland (Hospital for Sick Children, Toronto). The biological consequences of impeding the progress of the exoribonuclease XRN1 were explained by Jeff Wilusz (Colorado State University) who showed data on the repression of ribonucleases by flaviviruses (including Zika virus), and Carol Wilusz (Colorado State University) on the binding of muscleblind 1 protein to the structures formed by CUG repeats, which impede the progress of the progressive exoribonuclease...
XRN1, resulting in accumulation of toxic RNA fragments.

An interesting talk was also provided by Mike Kiledjian (Rutgers University) on the capping of RNAs by NAD+ and the enzymes that remove this unusual cap. Roberto Gherzi (IRCCS AOU San Martino IST, Genova) also described his recent work on the long non-coding RNA Inc-EPR which binds KHSRP and functions as an RNA but also encodes a functional peptide. Beautiful work was presented by Bob Schneider (NYU School of Medicine) on the role of the mRNA Decay Protein AUF1 in muscle stem cell differentiation and disease. The plant world was well represented by talks on the plant exosome by Dominique Gagliardi (University of Strasbourg), cap quality control by Joanna Kufel (University of Warsaw) and the involvement of the exoribonuclease XRN4 in NMD and environmental responses by Pam Green (University of Delaware).

The Genetics Society provided generous support for the poster sessions and PhD student poster prizes. The lively poster sessions included 51 posters, which included 25 from PhD students. The posters were all of very high quality and the judges had such a difficult time deciding on the prize-winners that they agreed that three PhD students should all win a 1st prize! The students who were awarded the prizes were Oliver Rogoyski (University of Sussex; pictured), Jeremy Scutenaire (University of Perpignan) and Ramona Weber (Max Planck Institute for Developmental Biology, Tübingen; pictured). Oliver Rogoyski had previously been awarded a Genetics Society Summer Studentship and also attended the associated Genetics Society Workshop.

Two further highlights of the meeting included a banquet dinner in the dining hall at Keble College and after dinner entertainment by the IMMposters, a local band of biomedical scientists. The meeting has already been highlighted as a great success, therefore another meeting in the series is planned for July 2019 in Montreal. The organisers would like to thank all the participants for supporting a wonderful meeting.

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**Norwich-Cambridge Student Symposium (NoCaSS)**

17th August 2017, Norwich

**Nicola Capstraff, University of East Anglia**

PhD and undergraduate summer school students from Norwich and Cambridge met for a symposium featuring talks from students, two prominent keynote speakers, poster competitions and networking. Student delegates who attended were from a range of institutes with research predominantly with a plant or microbial theme. Participating institutes included the John Innes Centre, Sainsbury Laboratory in Norwich, Quadram Institute, Earlham Institute, University of East Anglia, University of Cambridge and National Institute of Agricultural Botany.

The day featured 8 varied and insightful talks from students across these institutes, detailing their current PhD work which lead to interesting and sometimes unforeseen questions from the mixed audience. During Ben White’s presentation (EI) discussing ‘Identifying sex determination loci in the highly heterozygous white guinea yam’ one student exclaimed how she had never realised a sweet potato and a yam are different things, which then lead into a stimulating discussion during the next coffee break on the problems of engaging the public into discussing where our food comes from.

Two highly prestigious scientists also came to present on the day. Prof Neil Bruce from the University of York led us through his decade long journey of work on the phytoremediation of explosives, with the advice that one of the advantages of this project is that you visit strange and dangerous places; old TNT manufacturing sites and secret US army military bases! Prof Dame Carol Robinson from University of Oxford ended the day with an inspirational look at her scientific career, with
her talk being open, honest and passionate. She spoke about how you need to find the right balance and that ‘there’s no one path through science, follow what you love’. We are incredibly grateful for each of these scientists joining us for the day.

Poster competitions were also featured at NoCaSS, all of which were sponsored by various organisations. We are grateful to the Genetics Society for the funding of the ‘Epigenetics and transcriptional regulation’ category, which was won by Emily Hawkes (JIC) for her studies on ‘conserved long non-coding RNA in the transition to flowering’.

During the lunchbreak, we were treated to a networking activity by OpenPlant, who also sponsored the lunch, and gave a short presentation about their funding opportunities for collaborations between Norwich and Cambridge students. Their talk and all the others that day were graphically recorded by the talented Rebecca Osborne, giving a creative edge to each session.

We hope NoCaSS will continue next year at Cambridge to provide another platform for PhD students to share their work with one another, as well as socialise in a comfortable atmosphere. For those interested in finding more please visit nocass.org. We are extremely grateful to the Genetics Society for their sponsorship of both the poster competition and the day’s refreshments.

The 16th International Conference on Pseudomonas
5th - 9th September 2017, Liverpool

Robert W. Jackson, University of Reading and Craig Winstanley, University of Liverpool

This biannual meeting on all things Pseudomonas was held for the first time in the UK on September 5-9th 2017. Organised by Craig Winstanley and other Pseudomonas researchers around the UK, the conference attracted over 330 delegates from across the globe. And what a treat they were in for because the meeting was held in the grand old St George’s Hall in Liverpool, a fitting venue for such a distinguished bacterial species.

The Pseudomonads are widespread in the environment, occupying a wide variety of niches, from soil and plant roots to the inside of plants and animals. The genus has a remarkable ability to adapt to a wide range of challenges and consequently the conference had a strong focus on mechanistic processes employed by the different species of Pseudomonas. And of course, genetic analysis was prevalent in almost every talk – thus, the GS sponsorship was much appreciated and was devoted towards supporting attendance of early/mid-career researchers Jens Klockgether, Mark Silby and Ashleigh Griffin.

All three GS-sponsored talks described approaches to understanding how the ecological settings of Pseudomonas bacteria influence their evolution. Klockgether described how in the human lung environment, P. aeruginosa is able to rapidly adapt, though mutation rates can vary. Adaptations can lead to a variety of phenotypes, including antibiotic resistance and changes in the biosynthesis of alginate, though the populations of evolved strains can vary from a dominant single clone to mixtures of genotypes. This can then influence the course of the infection and potentially treatment. Silby described how dual interactions of Pseudomonas and Pedobacter leads to the manifestation of motility on hard agar, whereas each strain alone is normally sessile. Over time, the strains co-evolve via changes in flagellum activity and polysaccharide synthesis. Griffin addressed the theme of behavioural ecology, discussing the social dynamics of P. aeruginosa in the CF lung, and highlighting issues such as adaptive and cooperative evolutionary behaviour in relation to iron acquisition.

There were many other excellent talks describing genetic analysis of Pseudomonas. These included Jake Malone describing the post-transcriptional regulation RimABK system, which appears to control the transition of Pseudomonas between active and sessile lifestyles. Mike Brockhurst provided a fascinating insight to how plasmids introduce regulatory genes, like rsmA, that can interfere with cellular regulation systems, probably to promote plasmid
replication and dispersion. Paul Rainey described the epic work of Honour McCann who has been working in the forests of China, Korea and Japan to carry out an elegant population genetic analysis of the kiwifruit pathogen *Pseudomonas syringae pv. actinidiae* – and to potentially pinpoint the source of the pathogen in Korea and Japan. However, Cynthia Whitchurch delivered perhaps the most “incendiary” talk at the conference, on explosive cell lysis and its role in releasing eDNA to the bacterial community to help with cellular aggregation. She provided a series of stunning images showing the rod cells taking on a spherical shape before exploding – a process mediated by an endolysin and three holins.

Finally, a mention for two young researchers – Maxwell Fishman from Cornell and Vanessa Francis from Exeter. They both described advances in our understanding of *Pseudomonas* signalling systems. Vanessa detailed the relationship between RetS and GacS and how different phosphorylation activities can influence decision making processes in the cell. Max, on the other hand, described the two-component sensor regulator CvsSR, which is activated by *Pseudomonas syringae pv. tomato* inside the plant. It is induced by calcium and activates alginate production, potentially indicating a switching mechanism of the bacterial pathogen, from early infection immune suppression to late infection biofilm colonisation. It will be fascinating to see how these studies develop.

Thanks to the Genetics Society for supporting the *Pseudomonas* meeting and its research community.

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11th Mammalian Genes, Development and Disease Meeting
7th July 2017, Cardiff

**Professor Rosalind John, Cardiff University**

The 11th MGDD meeting has been funded by the Genetics Society for 11 years and rotates through the GW4 Universities: Cardiff, Bath, Bristol and Exeter. The purpose of the meeting is three-fold: to showcase research in mammalian system in SW England/Wales region; to develop a community of collaborating researchers; and to aid the career progression of early career researchers with the opportunity to give short talks at a small but friendly meeting.

This year we had the great pleasure of hosting Professor Yves Barde, the Welsh government’s first Ser Cymru (Stars of Wales) appointment, as our keynote speaker. Yves, recently elected to the Royal Society, is most renowned for his discovery of brain derived neurotrophic factor (BDNF), a protein important in the development and maintenance of a healthy nervous system.

His work led to the identification of the related proteins - the neurotrophins. The keynote lecture was a masterclass for the neurotrophin field, providing an overview of the discovery of four processed secretory proteins: BDNF, NGF, NT3 and NT4. He presented details of the mechanistic studies that formally demonstrated the importance of BDNF in neuronal survival, synaptic plasticity and memory. He went on to discuss more recent work exploring the potential for using BDNF to rescue the neurodevelopmental disorder, Rett Syndrome, and the development of bespoke drugs and biological approaches with the potential for therapeutic application.

Our invited speaker was Dr Adele Murrell (Bath University), a leading expert in the study of long range
epigenetic regulation of 3D nuclear architecture with a particular focus on cancer. The talk discussed examining epigenetic regulation over megabases of the genome, with a mechanistic focus on the DIRAS3 locus. DIRAS3 encodes a vas homologue which functions to suppress proliferation and which is downregulated in some cancers. Adele presented her data demonstrating that expression of DIRAS3 is regulated by this non-coding RNA providing an example of the phenomenon of transcriptional interference.

We also had talks from a number of early career researchers, predominantly from across GW4, who were chosen from submitted abstracts. Selected talks were from cancer, neuroscience and developmental disciplines.

Within the cancer field, we had our first talks from Dr Karen Reed (Wales Gene Park) who presented her work on the function of Apc2 in cancer. We also had a presentation from Dr Alex Greenhough (Bristol University) on his work exploring hypoxia in colorectal cancer. Our third cancer-focused talk was from Dr Marianna Szemes (Bristol) presenting her work which used RNAseq analysis of neuroblastoma exposed to R-spondin to identify Wnt targets with potential prognostic value.

Within the Neuroscience discipline, Jasmine Donaldson (Cardiff University) presented work which examined the relationship between CAG repeat length in Huntington’s Disease and time of onset. Dr Isabel Martinez Garay (Cardiff University) presented her work on the function of PCDH19 gene in cortical development, using in vivo electroporation with siRNAs at key developmental timepoints to determine the effect of loss of function on neuronal migration. Dr Asami Oguru-Ando (Exeter University), spoke on her work on CNTN4, and reported on consequences for behaviour, such as social discrimination and fear conditioning, using ex-vivo techniques to examine spine density and electrophysiology.

The final neuroscience talk was from Dr Lucia Cardo (Cardiff University) describing her work on SETBP1 in neural stem cell regulation, Lucia’s novel approach is to engineer mutations in human ES cells to examine the phenotypic response focusing on neuronal differentiation in culture, and gene expression analysis.

We had two further talks within the Developmental Biology theme, both with a placental focus. Isabel Garcia-Martin (Cardiff), a second year PhD student, presented her work measuring placental telomere length using the highly sensitive technique called Single Telomere Length Analysis (STELA). This technique amplifies from single telomeric molecules to reveal the full detail of telomere-length distributions. Her work revealed a striking heterogeneity within samples not previously been reported for the placenta. Dr Thomas Breke (Bangor) spoke about his beautiful work on hybridisation between closely related species and he definitely had the best images to show of tigrons and ligers. He work focused on Dwarf hamsters (P. sungorus and P. campbelli) only one of which displays paternal care. Depending on the parent-of-origin, the resulting fetus and placenta can either be hugely over grown or growth restricted, highlighting the existence of differential genomic imprinting regulation between the two. He was able to show a disrupted imprinting network in the hybrid placenta using RNAseq and SNP calling with evidence for genes on the X chromosome in the placental phenotype.

Prizes were awarded to Jasmine Donaldson (PhD best talk) and Alex Greenhough (Postdoc best talk).

The next meeting will be held in July 2018 in Bristol.
More information and details on registration can be found on The Genetics Society website at: genetics.org.uk/Conferences.aspx and selecting “Genetics Society Sponsored” from the drop down menu.

UK Clock Club
12th January 2018, University of Leicester

On January 12th 2018, the UK Clock Club will meet for its biannual one-day conference in Leicester, hosted by the Genetics and Genome Biology department and organised by Prof Bambos Kyriacou. The meeting allows PhD and postdoctoral students to present their work in an informal and supportive atmosphere and most of the UK’s clock researchers and PIs attend, with the majority using genetic and molecular techniques to dissect various biological rhythms. This meeting is “timely” (excuse the pun) given the recent award of the 2017 Nobel Prize for Physiology or Medicine to three American clock researchers, Jeffrey Hall and Michael Rosbash from Brandeis University and Michael Young from Rockefeller University, who won it for their genetic and molecular dissection of the fruitfly’s circadian oscillator. Bambos Kyriacou worked with Hall and Rosbash for 20 years has been invited to attend the Nobel ceremony in Stockholm on December 10th. He will report back to the Clock Club with films and interviews of the laureates during this memorable weekend. Anyone interested in attending, please register at the website below. There is no cost for the meeting which is supported by the Genetics Society.

Oxford Brookes BMS Seminar Series: “From genes to brains; how can we make sense of genes related to reading abilities and handedness”
7th February 2018, Oxford Brookes University

This talk will be given by Dr Silvia Paracchini from the University of St Andrews. Silvia’s group is studying the genetic basis of complex cognitive and behavioural phenotypes. Their focus is on the biology of dyslexia. More recently Silvia has become interested in handedness and the complex link between dyslexia and laterality.

The BMS seminar series offer students and academics the opportunity to meet scientists from their research field for scientific exchange. By providing time for 1:1 meetings before the talk, students and researchers can meet Silvia and discuss her work, future collaborations and career opportunities. The talk will be followed by an informal wine reception for networking and additional questions.

Enquiries to: brookesseminarsbms@gmail.com
For full programme and updates, follow us on Twitter @OBU_BMSSeries

10th Annual British Meiosis Meeting (2018)
24th – 25th May 2018, Brighton

The 10th annual British Meiosis Meeting (#BMM2018) will gather together UK researchers with interests in meiosis, with an emphasis on presentations by postdocs and students and informal discussions between the talks.

The meeting will cover all aspects of meiosis, ranging from research into the molecular mechanisms that promote pairing, recombination and chromosome segregation in model organisms to how these events impact on human fertility and crop breeding.

This two-day event will provide an excellent forum for PhD students and Postdocs to present their research as an oral and/or poster presentation. During the two-day meeting there will be time for 15 oral presentations that will be selected from submitted abstracts. Students and Postdocs are encouraged to apply!

Researchers whose abstract is not selected for an oral presentation will have the opportunity to present a poster. Posters will be on display during the entirety of the meeting and attendants will be able to view them during coffee breaks and lunches, and following the evening meal.

In addition, this year, the plenary speakers are world-class scientists Prof Eva Hoffman (Novo Nordisk Foundation Young Investigator, Centre for Chromosome Biology, University of Copenhagen) and Prof Scott Keeney (Memorial Sloan Kettering Cancer Center, New York, USA). Both are successful leaders in meiosis research with an excellent reputation of engaging with and supporting early-career researchers within the meiosis community.

All enquiries should be sent to bmm2018@sussex.ac.uk

Fisher 1918 Celebratory Event
9 October 2018, The Royal College of Surgeons, Edinburgh

Further details to follow on The Genetics Society website.
In this edition of the Newsletter, we have three feature pieces. The first feature introduces our centenary project manager Cristina Fonseca and some of the events that are part of the centenary programme spanning 2018 and 2019. The second feature is part of an extended series designed to promote each of our Sectional Interest Groups in turn, to provide our membership with more insight into what these meetings are like and encourage attendance. The last feature is a guest piece by Dr Sarah Main which gives an overview of the role of the Campaign for Science and Engineering in making the voice of science heard amidst Brexit negotiations. We hope you enjoy these features. If you have an idea for future features or would like to contribute a feature, please contact the newsletter editor (HallL10@cardiff.ac.uk).

The aim is to encompass a diverse range of activities; from live events to digital content with something for adult and family audiences alike.

**Centenary project manager, Cristina Fonseca**

Cristina is from Portugal and is a Biomedical Engineer by background. After an ERASMUS at the University of Cambridge she moved to Edinburgh to pursue a PhD in Clinical Neuroscience. During her PhD she was involved in outreach and public engagement activities and decided to follow a career in this area. Cristina is based at the Royal Institution in London, with whom the Genetics Society has established a collaboration and will be a partner during the centenary celebrations. Various events during 2019 will be delivered at the Royal Institution, a place with great history in science communication. As the Genetics Society Centenary Project Manager, Cristina’s role is to plan, execute and evaluate an exciting programme of activities celebrating genetics throughout 2019, which seek to entertain, inform and engage a broad section of the public across the UK with all aspects of genetics. The programme of events has been guided by a working group, comprising members of the Genetics Society. The aim is to encompass a diverse range of activities; from live events to digital content with something for adult and family audiences alike.

**Chelsea Flower Show**

The Genetics Society was founded by William Bateson in 1919 and is one of the oldest “learned societies” devoted to Genetics in the world. The Society acts to support and promote research and teaching of Genetics in the UK. As part of its centenary celebrations in 2019, the Genetics Society aims to develop an exhibition at the Chelsea Flower Show (CFS) Discovery Zone to not only commemorate 100 years of the Society but also its link with the Royal Horticultural Society (RHS). RHS was the first to publish Mendel’s work in English, which was translated by William Bateson. Mendel’s Glasshouse will be featured at the Discovery Zone, an area showcasing scientific and educational exhibitions.

Following the Chelsea Flower Show an adapted garden based on this exhibition will tour some of the UK science and musical festivals. As part of the collaboration between the Genetics Society and the Royal Botanic Garden, a permanent genetics themed garden will be in residence in Edinburgh.

**2019 - A Year Of Celebration: The Genetics Society Centenary**
Public engagement grants

We want all our member to help us celebrate our centenary and to support them in their public engagement activities. We have launched the Public Engagements Grants (members can apply for grants up to £500). Applications are currently accepted on a rolling basis and will be sent to reviewers at the start of each month for assessment. If you have never done public engagement and/or need some new ideas, we have a public engagement booklet available on our website comprising a “How to guide” and outreach resources/instructions.

History of Genetics in 100 objects (members to submit objects)

As part of our centenary we are also celebrating the fantastic advances achieved in the field of genetics in 100 objects. This project will be hosted in our new website, and we will use different media such as animations, podcasts, infographics and interviews to detail their importance in the history of genetics. We would love for our members to be involved and to submit their ideas for objects we should cover. Please email Cristina or use twitter #GenSoc100 for your submissions.

In the Issue 79 of the Genetics Society newsletter (July 2018) there will be another feature dedicated to events taking place as part of the Centenary programme.

Sectional Interest Group in the spotlight: The London Fly Meetings

The London Fly Meetings (LFMs) are monthly gatherings of Drosophila groups in the London area held at the Francis Crick Institute on the third Wednesday of each month. These meetings are supported by the Genetics Society and organised by the London Fly Group to bring together fly researchers from all the major London universities, as well as Bristol and Sussex. The meetings start with an informal mixer, during which reagents and ideas are freely exchanged. This is followed by one or two speakers. Usually, the speakers are from participating labs, but we also occasionally host external speakers. It is a great forum for students and postdocs to present and discuss their latest data in a relaxed atmosphere.

The past year has been particularly exciting for the LFM community! Following the opening of the Francis Crick Institute in August 2016, the meetings relocated from the Crick auditorium with talks by Yutaka Matsubayashi (Stramer lab, KCL) on extracellular matrix remodelling in the embryo and Clara Fons (Gould lab, Francis Crick Institute) on brain sparing during CNS development. In February 2017, the LFM was introduced by special guest and former London fly community member Phil Ingham. In the past year, LFM speakers covered a broad range of topics from immunity and metabolism (Jess Sharrock, Dionne lab, ICL) to sleep (Utham Valekunja, Reddy lab, Francis Crick Institute). The LFM also welcomed several external speakers such as Ken Irvine (Waksman Institute, USA), who presented his lab’s work on biomechanical regulation of organ growth and Hippo signalling.

In September 2017, members of the LFM community hosted the 25th
European Drosophila Research Conference at Imperial College's South Kensington campus.

The European Drosophila Research Conference (EDRC) has been the main scientific meeting for the European fruit fly research community for 50 years and is held every two years in a European city. EDRC 2017 was the largest yet, with 800 delegates from all over the world. With a stellar cast of plenary speakers and outstanding workshops, platform and poster sessions, the conference brought together the cream of Drosophila research from Europe and beyond. Among the many highlights were spectacular opening plenaries in which Ruth Lehmann (NYU, USA) presented her lab’s latest work on the diversity of mechanisms through which germ line cells escape somatic differentiation and preserve totipotency, and Marc Freeman (Vollum Institute, USA) demonstrated that glial cell function extends far beyond their known role in supporting neuronal homeostasis, to being active participants in neurotransmission. A busy four days of fly research was concluded by the announcement that EDRC 2019 will move to Lausanne!

Most recently, the LFM went on the road for the first time, with the October 2017 meeting hosted by Rita Sousa-Nunes at King’s College London’s Guy’s Hospital Campus. As well as enjoying a trip south of the Thames, attendees heard great talks from Andrea Chai (Sousa-Nunes lab, KCL) presenting a new tool for spatiotemporal genetic manipulations to study non-autonomous effects and David Mazaud (Fanto lab, KCL) on the role of glial cells in adult brain homeostasis. This year, we look forward to the LFM Xmas special lecture, which will be given on December 13th by Isabel Palacios (QMUL), the newest member of the London fly community.

For details about the monthly meetings, please contact Barry Thompson (barry.thompson@crick.ac.uk), Nic Tapon (nic.tapon@crick.ac.uk) or Georgina Fletcher (georgina.fletcher@crick.ac.uk).

Making the voice of science heard in Brexit
A guest feature by Dr. Sarah Main

Sarah is the Executive Director of the Campaign for Science and Engineering and oversees all aspects of CaSE’s work. She started out as a molecular biologist researching mechanisms of cancer, DNA replication and virology for Cancer Research UK and the Medical Research Council in London and Cambridge.

She moved in to science policy at the Medical Research Council working on research funding boards, overarching investment strategy and research careers. She gained first-hand experience of spending review preparations whilst on secondment to the Department for Business, Innovation and Skills (BIS), where she wrote a report on the leveraging power of public investment in science and research for the UK economy.

The Genetics Society supports travel and discovery by geneticists through grants but also, through its membership of the Campaign for Science and Engineering (CaSE), supports engagement with Government and politicians to ensure that the UK has an environment in which genetics and all other forms of science and engineering can thrive.

The membership of CaSE numbers over one hundred organisations and many hundreds of individuals, spanning academia, industry and research charities.

We work with the Genetics Society and our other members to address the issues that determine how easy or difficult it is to get great research done. We provide a voice for science in Parliament, engaging with Government ministers, departmental officials and MPs from all political parties to raise the issues under Government control that impact on science. So you won’t be surprised that Brexit features high on our agenda.

Through our work building relationships with Government and Parliament, and the strength of our voice from our broad membership, CaSE has earned a place at the table in a number of key Brexit fora. CaSE is a member of the Science Minister’s high-level stakeholder group on
science and Brexit, is a contributor to discussions of the Shadow Brexit team, has appeared as a witness to the Brexit inquiry by the Commons Science and Technology committee, and holds regular dialogue on Brexit with Government officials.

The picture I can paint for you is a tumultuous one. You might have heard of the swan that glides serenely on the water whilst paddling hard underneath? Well, my impression is of the swan trying to glide purposefully and serenely while the legs underneath paddle furiously, but in contrary motion.

Civil servants are heavily burdened and politicians within and between parties are pushing in very different directions. Alliances are being drawn up across party lines along different Brexit positions: to exit at all costs, to exit and ‘make the best of it’, or to stop Brexit altogether. On one day, I held meetings with three different MPs from the same party, who each held a different Brexit position. And each of them was working extremely hard to make their position a reality. So, you can see, a great deal of paddling is going on beneath the surface but in very different directions.

Into this tumult, CaSE must deliver clear, well-evidenced messages in a non-partisan way, that make clear what the needs of the science community are to ensure that genetics, and the other sciences, cannot just survive, but flourish.

CaSE has worked hard with its members to understand these needs and formulate policy positions to convey to Government. In our document, ‘Vision and priorities for the new Government’ we characterise the features of an environment in which science and engineering can thrive in the UK, and set out goals in six areas to achieve: education, immigration, collaboration, investment, regulation and evidence.

Each has a goal along with specific policy recommendations. In recent months, we have been focussing on three of these areas: immigration, investment and regulation.

On immigration, we have built up relationships of trust in key areas of government and have been able to create a ‘safe environment’ for officials to test their thinking against the concerns and expectations of our members, thus enabling us to get messages across effectively while policy is being formed. One of the key messages from my political conversations is that there is every expectation that the rights of EEA nationals in the UK will be secured. Negotiations on this appear to be at quite a technical level now, which implies to me that they are quite advanced.

On investment, CaSE took a leading position in the campaign to make a step change in science funding, resulting in the additional £4.7bn announced at the last Autumn Statement. We are now pressing Government on how to achieve its target of 2.4% of GDP to be spent on R&D by 2027, double the current spend, and are pushing for transparent and trusted processes to set research priorities and inform funding decisions.

At the Science Minister’s forum, CaSE is involved in discussions about priorities for future participation in European research programmes. It is clear that there is ambition on both sides for the UK to remain a participant and, whilst the bigger politics will have enormous sway on the outcome, I am hopeful that the UK will continue to participate in EU programmes in a substantive way.

On regulation, CaSE is raising with Government the potential of Brexit to impact on the regulatory framework for scientific activity and illustrating this with examples from our members. We will also be putting forward how the scientific community can help support the technical aspects of trade negotiations with the Department for International Trade and its new Chief Scientific Adviser.

CaSE will be marking the first anniversary of the triggering of Article 50 with a body of work to reflect the views of our members and the scientific community a year into the negotiations. Look out for a survey from us soon!

1 Equip providers to deliver high-quality STEM education and training that is open to all
2 Create a migration system that supports mobility for excellence, skills, education and collaboration
3 Grow the UK’s leadership and collaboration in research & innovation internationally
4 Invest at a level and in such a way as to enhance the UK’s research & innovation environment
5 Deliver a stable regulatory environment that facilitates trade, access to markets and innovation
6 Champion the use of evidence and science advice in all government decisions, documents and messaging
The Mobile Genome: Genetic and Physiological Impacts of Transposable Elements

Christopher Todd

The “Mobile Genome: Genetic and Physiological Impacts of Transposable Elements” at the picturesque EMBL Advanced Training Center in Heidelberg is one of the most comprehensive conferences on the topics of the role transposable elements in evolution and development. With 54 talks and almost 100 posters this 4 day conference provided an intense experience but extensive insight into this rapidly expanding field.

As a PhD student in my final year of study I was excited to attend and present a poster entitled “Lineage specification of early development through epigenetic control of transposable elements”, which aimed to investigate the role specific transposable elements have in regulating the genome in early development. I will soon be preparing a manuscript detailing the findings of this functional assessment, and therefore insights provided by members of the conference were invaluable in addition to potential collaborations that were discussed.

Among the many fascinating talks were several findings and theories which resonated with my own research and interests.

Of particular note were: the role the host vs transposon arms race can play in speciation (William Theurkauf), the co-option of transposable elements in Drosophila to facilitate stress responses (Josefa González), a group of new regulatory proteins resulting from KRAB-transposase fusions (Cedric Feschotte), and the ability for transposons to effect chromatin organisation in early embryonic development (Juanma Vaquerizas). The poster sessions also provided a diverse selection of research for members to digest with one particular poster that stood out to me detailing a novel barcode-ChIP-Seq technology for unbiased detection of protein binding to transposons in yeast (Ila van Kruijsbergen).

Overall the impressively broad range of the research discussed at the meeting highlighted why researchers, including myself, should be interested in mobile genomic elements with various topics arising within the field including: the role of transposons in the evolution of genomes, the interplay between host defence mechanisms and transposons, the mechanisms by which transposable elements achieve their mobility, and the co-option of transposable elements to serve host functions.

The poster sessions also provided a diverse selection of research for members to digest with one particular poster that stood out to me detailing a novel barcode-ChIP-Seq technology for unbiased detection of protein binding to transposons in yeast (Ila van Kruijsbergen).
The 2017 Congress of the European Society for Evolutionary Biology (ESEB)

Patricia Landaverde-González

The congress of the European Society for Evolutionary Biology (ESEB) is a biannual meeting and considered one of the largest scientific meetings in Europe. This meeting is also a very exciting and enriching experience on the current knowledge of evolutionary biology in the world. This year consisted of eight parallel sessions that covered subjects of evolutionary biology ranging from evolution of communication signs, fitness landscape, evolution of immune diversity, phylogenomics, evolution of infection diseases to urban evolution distributed within 35 symposia. During the congress there were around 300 oral presentations and around 1000 posters from different investigators and PhD students working in the research field of evolution.

The 2017 ESEB congress was held in August 20-25th 2017 in Groningen (Netherlands), a small university city that was the perfect scenario for this amazing congress. The highlights included some keynote lectures from expert in different areas of evolutionary biology such as Svante Pääbo, who has been working since 30 years on the development of methods to study DNA of ancient humans and the evolution of our own species. His team was the first to generate and analyse the genome of Neanderthals and of a new undescribed hominin species Denisova and thereby identified novel genomic features unique to modern humans.

In the second keynote lecture Nicole Dubilier described how symbionts from the deep-sea acquired multiple evolutive benefits due to horizontal gene transfer and symbiont diversity. Andreas Wagner held the third keynote lecture, in which he discussed the power of recombination to create new evolutionary adaptations and innovations. In the fourth keynote lecture Renée Duckworth showed on the example of two passerine birds how important is an understanding and integration of concepts such as community formation, evolution of the ranges of species and the dynamics of hybridization for understand the mechanism underlying evolutionary processes of species. Finally in the last keynote lecture Chris Jiggins showed how polygenic selection maintains differences in Heliconius butterflies species even when gene flow exists.

The rest of the meeting was just as amazing and interesting as the keynote lectures. I had the opportunity to learn about other spatial evolutionary studies and about studies on eco-evolutionary dynamics and the new research area of urban evolution that tries to understand how organisms adapt to the growing urban areas, which I find particularly interesting and promising.

Overall, the quality of the talks was excellent and the congress provided a fantastic overview of the current state of the art research in all the different areas of evolutionary biology. The conference provoked scientific debate, provided me with information about new technology and new analysis methods and stimulated new collaborations. I got positive feedback for my research and learned about new analysis approaches applicable to my own data. The meeting ended with two very interesting lectures of the winners of the John Maynard Smith Prize (MS) prize that is given each year in order to distinguish an outstanding young evolutionary biologist. The MS prize winner 2016 was E. Keith Bowers, who presented the consequences of maternal stress and the maternal immune system on offspring development. The MS prize winner 2017 Amanda Kyle Gibson discussed how the cost of sexual reproduction could be maintained during host-parasite coevolution. I want to thank the Genetics Society that gave me the great opportunity to attend this great conference.
The 10th European Zebrafish Meeting 2017 (EZM2017)

Vanessa Chong-Morrison

The 10th European Zebrafish Meeting 2017 (EZM2017) was held in Budapest to commemorate the birthplace of George Streisinger, leading pioneer of zebrafish research. With approximately 700 researchers from 39 countries in attendance, EZM2017 is the largest conference on this year’s calendar for the global zebrafish community. Covering a diverse range of topics, EZM2017 provided an unrivalled learning as well as networking opportunity for those interested in the use of zebrafish for scientific research.

Thanks to the generosity of the Genetics Society, I was fortunate enough to receive a Junior Scientist Travel Grant to attend this meeting. I presented a short talk in the Emerging Technologies I session, describing our recently published biotagging technology - a binary in vivo biotinylation genetic toolkit for analysis of small cell populations in zebrafish.

Parallel sessions were held to accommodate all the talks available, which meant having to pick between sessions based on different research themes. Fortunately, regular coffee breaks provided opportunities to chat and discuss science with fellow attendees in between every session, as well as to visit the exhibition booths of companies and organisations providing services and tools for zebrafish research. There was also an impressive array of posters on display from every field one can think of. I personally find posters intriguing and interesting as they often include unpublished data. Unsurprisingly, going around and speaking to a number of the presenters proved to be very fruitful - I certainly picked up a thing or two that I had not expected to learn about! Two award talks were also presented during this meeting; the Chi-Bin Chien Award to Marc Wolman and the Christiane Nüsslein-Volhard Award to Didier Stainier.

The Keynote Speakers line-up did not disappoint either. Monte Westerfield (University of Oregon), who is no stranger to the zebrafish community, gave the opening address which is more than apt as Monte personally worked with George Streisinger early in his career. It was insightful to hear a first-hand account on the beginnings of zebrafish research, with a story that developed through the years towards Monte’s current research work tackling the molecular genetics of human diseases. Elly Tanaka (IMP Vienna) followed with a beautiful story of scientific discovery and unexpected results during the course of her research elucidating regenerative mechanisms of the axolotl. Last but not least, Jean-Paul Vincent (Francis Crick Institute, London) wrapped up the conference in style with a good dose of elegant Drosophila genetics, describing the role of Wnt signalling in maintaining growth and patterning of imaginal discs.

A big well done to the organisers for putting together such a fantastic meeting, I am certain to be one of many looking forward to EZM2020 in Prague!
The meeting started with a welcome reception on the moonlit waterfront of the conference centre, before we began the exciting series of talks, poster presentations and networking events prepared by the organizing committee. In total there were 3 keynote address talks, 6 symposiums and over 100 posters to see – including mine! I was presenting my research on the importance of the environment during early life. What a bird experiences while it is in the egg and just after it hatches has consequences, for example a stressful environment can increase dominance and gregariousness. I’m interested in whether the mechanisms behind these social behaviours are also affected throughout development.

The talks spanned the many different approaches to studying the links between the neuroendocrine system and behaviour. The researchers at SBN studied rats, mice, prairie voles, poison frogs, cichlid fish, poultry, songbirds and humans, and it was great to hear that they chose the species they work with because it was best suited to the question they were asking.

I found one symposium particularly useful, as it focused on the new techniques used in our field. I learnt about the use of calcium imaging to study the links between brain and behaviour (Zoe Donaldson, University of Colorado), and CRISPR gene editing to understand which genes are crucial for the control of reproductive behaviour (Scott Juntti, University of Maryland).

One training workshop was held by Nancy Wayne, an advocate for women in science. In small groups we discussed the barriers we have faced as scientists and why we might feel like don’t deserve to be in the position we’re in (sometimes called ‘imposter syndrome’). Nancy explained that these feelings are almost always completely false – most people who progress to PhD level and above are more than qualified for their positions, but their lack of confidence leads to feelings of inadequacy and causes many young scientists, especially women, to abandon their careers in academia.

Nancy’s goal is to support women in this position, and as a woman aspiring for a career in academia who sometimes has doubts about not being good enough, I found her workshop really useful and inspiring!

I want to thank the Genetics Society and the Physiological Society for the travel grants which enabled me to attend this meeting, my supervisors Simone Meddle and Karen Spencer for their support and advice about my presentation, and my funding body BBSRC EASTBIO for my PhD scholarship.
Every two years the top researchers in vision science from around the world come together to discuss their most recent data at the FASEB Biology and Chemistry of Vision Conference. This year the event, organised by Marie Burns and David Williams, took place in Steamboat Springs, Colorado, USA – a quaint city best known for its Ski Resorts. In June however, there was little snow to be seen and the city was instead surrounded by lush green mountains, providing a beautiful backdrop for an exciting few days. The conference was held in the Steamboat Grand Hotel where the majority of attendees also stayed, providing a welcoming and inclusive atmosphere.

Sessions ranged from the basic science of phototransduction to the latest advances in the treatment of patients with blinding diseases. The conference consisted of eight chaired sessions and two poster sessions, each supplemented with DataBlitz presentations. These fast-paced DataBlitz sessions allowed each participant a maximum of two slides and three minutes to describe their most exciting findings, giving trainee scientists an opportunity to sell their poster and encourage other attendees to stop by.

The conference began with a keynote address from Samuel Jacobson, detailing his seminal work which led to the first human clinical trial of a gene therapy for inherited retinal degenerations, and introduced the translational theme that ran throughout the meeting. The first session covered the latest research into how the photoreceptor cell functions.

A particularly striking talk was delivered by Yoshikazu Imanishi, who detailed the use of Dendra 2 photoconversion to distinguish between old and newly synthesised rhodopsin molecules in Xenopus Rod cells and stunned the audience with beautiful images obtained by this technique. Dendra 2 photoconversion will no doubt prove useful for many of the researchers present, seeking to locate their protein of interest in the photoreceptor outer segment.

The remaining sessions covered a vast number of topics, from new developments in understanding phototransduction to mouse models of human retinal disease. Roxana Radu presented her recent work using ABCA4 knockout mouse as a model of Stargardt’s disease. She observed partial rescue of the retinal degeneration phenotype by re-introducing the ABCA4 gene exclusively to the RPE cells. This work highlighted the complex relationships between cell types within the retina and the importance of considering this when designing new therapeutic strategies.

The focus on treatment strategies continued, with talks examining the application of CRISPR and stem cell therapies to treat human retinopathies and, in the final keynote address, Paul Sieving’s work with the audacious goals initiative from the National Eye Institute, which seeks to restore vision by regenerating the human retina.

This meeting excellently highlighted the substantial progress that has been made in our understanding of the science of vision and how these findings may lead to new treatments for patients suffering from devastating blinding diseases. The strong collaborative atmosphere of this meeting will no doubt encourage new collaborations between researchers and aid progress in the field. The next FASEB Biology and Chemistry meeting is scheduled for 2019 and is set to be another exceptional meeting. I for one am excited to see the developments in the field over the next two years!
In the interests of space, only five reports have been selected for inclusion in the newsletter, however contributions were also received from:

Isobel MacGregor – EMBO conference on meiosis.
Zane Duxbury – 2017 International Conference for Arabidopsis Research
Yiru Wang – The 21st International C. elegans meeting
Toni Beltran – International Worm Meeting 2017
Thomas Nicol – Mitochondria, metabolism and heart failure
Thomas Laver – Precision medicine in diabetes: EASD-SGGD conference
Sarah-Jayne Mackin – 50th Anniversary Meeting of the European Society of Human Genetics
Patrick Martin – Nuclear Structure and Dynamics: EMBO
Olga Sedelnikova – XIX International Botanical Congress
Ngang Heok Tang – The 21st International C. elegans meeting
Michaela Holzem – Gordon research conference: Wnt signaling
Michaela Agapiou – 25th European Drosophila Research Conference
Lorenz Fuchs – 2017 European Molecular Biology Organization Meiosis Conference
Leong Yeh Chwan – ISSCR annual meeting 2017
Laurence Newman – The 21st International C. elegans meeting
Joshua Roworth – The 20th International Congress of Nitrogen Fixation
James Burgon – Evolution Conference 2017
Ian Wilson – The Genome 10K and Genome Science Conference 2017
Harsh Sheth – 50th European Society of Human Genetics annual conference
Hannah Wilson – International Botanical Congress 2017
Goncalo Faria – European Society for Evolutionary Biology 2017 meeting
Ghislain Gillard – 25th European Drosophila Research Conference
Georgina Donati – Behavioural Genetics Association Meeting 2017
Emeline Favreau – 2017 Congress of European Society for Evolutionary Biology
Elspeth Ransom – SEB Annual Meeting and New Breeding Technologies in the Plant Sciences
Elizabeth Mittell – Evolution 2017
Elena Meusa – International Society for Gastrointestinal Hereditary Tumours
Eleanor Raymond – EMBO Conference on Meiosis
Dominic Pearce – 3rd EACR Conference on Cancer Genomics
Daniel Sachs – 28th International Conference on Yeast Genetics and Molecular Biology
Daniel Dodd – Cold Spring Harbour Asia: Cilia and Centrosomes 2017
Colette Baxter – The G4thering: The 6th International meeting on Quadruplex Nucleic Acids
Bharat Pokhrel – The 21st International C. elegans meeting
Arunkumar Ramesh – ISEMPH and ESEB joint meeting
Ariadna Navarro Aragall – Vascular Biology 2017
Anna Schönauer – 2nd Biennial Meeting – Pan-American Society for Evolutionary Developmental Biology
Anastasia Kishkevic – Gordon Research Seminar and Conference on Cell Growth and Proliferation 2017
Amey Redkar – the 5th International Conference on Biotic –Plant Interactions (ICBPI)
Alexander Hull – Cold Spring Harbour Laboratory – Neurobiology of Drosophila
Aleix Arnau Soler – XXVth World Congress of Psychiatric Genetics
Alberto Micheletti – 16th Congress of the European Society for Evolutionary Biology
A Stormy Affair: The Role of the Major Histocompatibility Complex in Seabird Mate Choice

Alexandra McCubbin

Mate choice in animal systems is a complex matter. Choosing a mate that is behaviourally and genetically compatible can be a critical decision, especially where individuals mate for life and parental investment is high. Genetic theory of mate choice suggests that, to maximise offspring fitness, individuals should choose mates that are not closely related. This outbreeding can target the whole-genome level, or be restricted to Major Histocompatibility Complex (MHC) loci, which are involved in immune defence. Supported by a Heredity Fieldwork Grant, we are investigating mate choice targets in two recently diverged species of Atlantic seabird, Monteiro’s storm petrel (Hydrobates monteiri; Vulnerable) and band-rumped storm petrel (Hydrobates castro; Least Concern).

The MHC is comprised of highly specific cell-surface proteins which facilitate antigen destruction by immune cells, such as T-lymphocytes. MHC loci are highly polymorphic, enabling organisms to respond to a wider range of pathogens. It is thought that choosing mates with dissimilar MHC results in offspring with more diverse MHC alleles, translating into potentially higher fitness.

Already demonstrated in some taxa, this MHC dissimilarity may be detectable by scent. As ‘tube-nosed’ seabirds (Order: Procellariiformes), storm petrels presumably benefit from well-developed olfactory capability, making them model organisms for MHC-related studies.

Originally considered a single species, our study species were recently recognised as two separate, partly sympatric species that have seasonally distinct breeding populations. The band-rumped storm petrel is found across the Atlantic and Pacific, breeds on the Azores in winter and has an estimated
Using an opening in the top of the chambers, we could efficiently collect blood samples and record morphometrics from breeding birds with minimal disturbance, following precautions to maintain animal welfare standards.

breeding population of ca. 13,000-13,700 individuals globally. In contrast, Monteiro’s storm petrel is endemic to the Azores and breeds during the summer, with an estimated population of just 328-378 breeding pairs. Our study requires DNA obtained from blood samples of mated pairs, and The Heredity Fieldwork Grant funded a valuable trip to Praia Islet, Azores, to sample Monteiro’s storm petrels during their breeding season.

Praia islet is a Special Protected Area (SPA), with visitors prohibited unless authorised by The Nature Park of Graciosa, and one of two proven breeding grounds for Monteiro’s storm petrel. A seabird haven, it supports a rich and diverse assortment of breeding species, and is classed as an Important Bird and Biodiversity Area (IBA) by Sociedade Portuguesa para o Estudo das Aves (SPEA). This biodiversity is especially evident through the night, when a chorus of shearwaters, terns and storm petrels picks up. To encourage and facilitate breeding of storm petrels, ca. 150 artificial nesting chambers have been installed since March 2000. Both study species have now utilised these for over a decade, providing exciting opportunities to study these elusive, nocturnal birds that spend most of their lives out at sea.

Using an opening in the top of the chambers, we could efficiently collect blood samples and record morphometrics from breeding birds with minimal disturbance, following precautions to maintain animal welfare standards. If produced, faecal samples were also collected for use in separate dietary analysis. During the winter season, our collaborators will repeat this sampling for us, to provide data on the band-rumped storm petrel pairs. Back in Cardiff, we will sequence MHC loci using Illumina MiSeq technology, which will be compared to genotyping data from loci across the genome. This comparison will allow us to investigate how relatedness influences mate choice, and if so, whether this relatedness is a genome-wide feature or restricted to the MHC. By comparing the two species, we will investigate how mate choice may affect speciation and evolve in small populations with low genetic variability. Ultimately, we hope this knowledge will contribute to protecting the vulnerable Monteiro’s storm petrel.

I want to thank the Genetics Society making this field work possible, and my supervisors Dr Frank Hailer, Dr Renata Medeiros-Mirra, Dr Carsten Muller and Dr Rob Thomas for their support. I also want to thank The Nature Park of Graciosa and SPEA for permitting access to the islet and getting us safely there and back, especially in uncertain weather conditions. I also want to thank Verónica Neves from the University of the Azores, for assistance in sampling blood. Finally, I also express gratitude to Dr Joel Briëd, who has generously supplied blood samples taken from mated storm petrel pairs from previous years, enabling us to determine long-term patterns of mate choice and expanding our dataset considerably.

This work was carried out with the permission of The Nature Park of Graciosa. Permits were acquired from Secretaria Regional da Energia, Ambiente e Turismo, Direcção Regional do Ambiente da Região Autónoma dos Açores, under licence numbers 33/2017/DRCT and N060/2017/DRA.

An adult Monteiro’s storm petrel and chick from Praia Islet.
Invasion-related traits in a successful invader – a comparative study of the Common Myna (Acridotheres tristis)

Tali Magory

The Common Myna (Acridotheres tristis) is a notorious starling native to south-east Asia and the Indian subcontinent, which has invaded parts of every continent but Antarctica. As such successful invaders, mynas raise interesting questions regarding the role that ecology, behavior, genetics and morphology play in biological invasions.

Common mynas were able to successfully invade nearly every place they have been introduced to, even in areas where other species of similar size, diet or breeding strategy were not, making them an ideal model species for the study of avian invasions. Therefore, as part of my Ph.D. research supervised by Dr. Roi Dor (Tel Aviv University), we set out to compare invasion-related traits between common mynas in different invasive stages. In order to study these questions in an extensive spatial and temporal framework, we took part in a collaborative effort that involved researchers from several institutes across the globe, which included a recent invasion (Israel), an old invasion (Australia) and the native range (India).

The richness of the Indian colors, culture, language, food and music can only be matched by its diversity of Wildlife. In August of 2017, through the generous Heredity Fieldwork Grant by the Genetics Society, I set out on a trip to Dehradun, a vibrant city in the state of Uttarakhand, North India, where I was to begin joint fieldwork with two of our collaborators, Dr. Suresh Kumar of the Wildlife Institute of India and Dr. Manoj Nair of the India Forest Service. We planned to capture Common Mynas in order to test traits that are traditionally correlated with invasion success and were hoping that these birds will give us an insight into the natural, basic state of this species in its original environment. Once caught, the birds were meant to be measured, sampled for genetic purposes and given behavioral tasks. However, the mynas had other plans.

Dr. Manju Siliwal, a renowned arachnologist and Dr. Kumar’s wife, has coined what will later be remembered as the birds’ nickname – ’Cheeky birds’ – following yet another early morning trapping expedition during which the birds taunted us by dodging our traps despite our best efforts. At first, they seemed to comply with our capturing attempts and we managed to catch the first batch of birds. This lot did well in the behavioral tasks and taught us some very important lessons on myna behavior. However, as the weeks went by, these early mornings were often discouraging, having caught not a single bird despite targeting the better part of the Dehradun cowsheds (they would often frequent cowshed digging up insects in cow dung). At one time, I had sunk so deep in cow dung while trying to retrieve a Magpie Robin from one of the mist nets that I had to be pulled out by two men. At other times, I was battling Rhesus macaques to stop eating the food we had baited the traps with.

Exploring the Indian landscape also allowed me to meet local Dehradun Valley people and get a glimpse into their daily lives. In order to trap
this elusive bird, cooperation of the resident community was essential. We roamed around mostly on an old but trustworthy scooter and experienced early morning light with cowshed farmers and curious neighbors. Often we were offered fresh milk tea (Indian Chai), and conversations – though not always completely verbal – were fascinating. Once the tests were over, the mynas were released back into the wild in the exact location where they were caught, as the house owners take active part in their release. This created a sense of personal investment and pride within the community, which often resulted in people relishing at the sight of the ringed birds in the following weeks. Despite trapping fewer mynas than expected, we succeeded in establishing a database for the native population, retrieving behavioral, morphological and genetic data. We proceeded to conduct successful DNA extractions and preliminary PCR work at the Wildlife Institute Conservation Genetics lab which will subsequently be analyzed at the genome level to determine the levels of genetic diversity, differentiation and population structure. While still preliminary, the behavioral tests analysis showed a significant difference in some of the traits between Israeli (introduced) and Indian (native) populations. These exciting results open a gateway for a better understanding of invasion mechanisms. While I eventually went back to Israel, India stayed with me. This project would not have been possible without the generous funding from the Genetics Society. It was an honor for me to be a recipient of this grant and to get a glimpse of the Indian Wildlife. We continue our collaboration, eagerly anticipating answers to our questions as new questions arise. We have already witnessed exciting findings in the beginning of our work, and we hope that the future brings more life-changing adventures like this one.

**The effectiveness of environmental DNA metabarcoding for surveying Lake Tanganyika’s diverse littoral fish communities**

**Chris Doble**

**M**easures of species diversity are central to both our understanding of ecological communities and our ability to monitor their responses to anthropogenic and natural stressors. Despite this, gaining accurate diversity measures for freshwater fish communities remains a significant challenge, with traditional survey methods often having associated biases as well as being costly and destructive.

Like all higher organisms, fish species continually emit DNA into their environment through excreta, shed cells, gametes and decaying material. In recent years researchers have increasingly looked towards this environmental DNA (eDNA) as a source of diversity information. eDNA metabarcoding enables the identification of multiple species through combining broad range primers with high throughput sequencing. Applications of this approach within aquatic habitats have highlighted its sensitivity for surveying fish communities, often outperforming traditional techniques in detecting the presence or absence of species, particularly those that are rare or elusive. As a result, eDNA metabarcoding holds the potential to improve our ability to both monitor and investigate the ecology of aquatic ecosystems. Despite this, applications of eDNA metabarcoding within natural systems remain in their infancy, limiting our ability to evaluate its effectiveness at surveying fish communities across different habitats and scales. Notably, there have been few applications within highly diverse freshwater ecosystems particularly within the tropics. Compared to their temperate counterparts these systems have different fish community structures, often contain more closely related
species within radiations and are likely to have different eDNA degradation rates. Therefore, the ability of eDNA metabarcoding to detect and distinguish between species is likely to differ. As much of the world’s freshwater fish diversity exists within tropical ecosystems, it is important to understand the extent to which eDNA metabarcoding can accurately detect species within diverse assemblages.

Our work aims to help address this issue, through applying eDNA metabarcoding methods to Lake Tanganyika’s littoral fish communities, dominated by the cichlid fishes. This represents a highly diverse habitat for which there is a rich availability of sequence data thanks to the lake’s fishes being popular models in evolutionary biology research.

This habitat provides two unique challenges to metabarcoding methods. Firstly, very high local diversities are commonly found, particularly across stretches of rocky habitat. Secondly many of these species exist within adaptive radiations, often resulting from rapid speciation events. Our research will therefore provide information on the effectiveness of eDNA metabarcoding for detecting species within highly diverse ecosystems, as well as distinguishing between species within adaptive radiations.

Thanks to the Heredity Fieldwork Grant, I was able to undertake a field season to Lake Tanganyika in May and June 2017 to collect eDNA samples and fish community data across a number of sites within Lake Tanganyika. These sites were located along the lake’s Kigoma region coastline in Tanzania.

At each site a water sample was collected, stored on ice and later filtered to concentrate and capture the eDNA. Following this a series of SCUBA visual surveys of the littoral fish communities were undertaken with local field researcher George Kazumbe, following a method we have established during previous field seasons to the lake. I was also able to undertake experiments investigating the degradation rates and DNA size structure within the water column that will enable us to better understand the sources of eDNA within our samples. As a result, this fieldwork has enabled the collection of multiple unique eDNA samples, as well as a valuable visual dataset against which our metabarcoding data can be compared. We are currently undertaking the molecular and analysis work associated with this project and look forward to presenting the results in the future.

I would like to thank the Genetics Society for providing the Heredity Fieldwork Grant, enabling me to undertake this fieldwork.

I am also very grateful to Dr Julia Day and Dr David Murrell (both UCL) as well as our collaborator Dr Chacha Mwita (University of Dar es Salaam) for all their support and assistance with this research. Finally thank you to George Kazumbe for his help throughout this year’s field season.

In the interests of space, only three reports have been selected for inclusion in the newsletter, however contributions were also received from:

Sandar Moreno-Medina – Phenotypic plasticity and behavioural reprogramming in solitary insects.
Further to the website and newsletter, the Genetics Society has been engaging with its membership via the social media platforms LinkedIn, Twitter and Facebook. In order to ensure that all content on the groups are meaningful to you, both LinkedIn and Facebook groups are moderated. This means that when you join the group this needs to be formally approved, but as long as we can see you are active in a genetics related area this is not a problem. This prevents a lot of indiscriminate postings from online recruiters that have affected some of the Genetics related groups. As a member of the LinkedIn and Facebook groups you will be updated on our activities but you can also comment and add your own events.

linkedin.com/groups/Genetics-Society-UK-4574262

facebook.com/groups/207531925428/

twitter.com/GenSocUK
CRISPR/Cas9 is taking the genetic community by storm, and this is perhaps especially the case within the world of insect genetics. Genetic engineering has varied applications, from uncovering developmental-genetic pathways in flies to creating mosquitoes capable of crashing entire populations. Whilst previous gene editing technologies were limited to particular model species, CRISPR is applicable to any insect and requires minimal prior sequencing information. With no holds barred, the next generation of non-model transgenic insects are ready to revolutionise genetics.

In the quiet town of Rockville, away from the bustle of the main University of Maryland campus, a team of microinjection specialists spend every day injecting insect eggs, ranging from beetles to bugs and moths to mosquitoes. This is the IBBR Insect Transformation Facility and, for one week each year, they put their microinjection service on hold in order to teach the tools of their trade to the next generation. In July, 2017, I was lucky enough to be one of twenty-four students on this course. In just six days, I learnt more about insect transgenesis than I have in a year of my PhD.

Insect Transgenesis with CRISPR/Cas9 can be considered a four-part process. First, the insects must be reared, and their eggs collected fresh after laying. Second, collected eggs are cleaned and their chorion removed, ready for injection, before being aligned on glass. Finally, the aligned eggs are injected, using a finely pulled glass needle, with a combination of Cas9 exonuclease, RNA guides, and the DNA of interest. When developing the use of a novel insect model, each of these aspects carries unique challenges, to be dealt with in turn. For want of time, the ITGRCN injection course focussed upon the final stage – that of physically implanting insect embryos with foreign genetic material. Easily written, but there is a nebula of complexity behind this apparently straightforward step. ‘The key to transgenesis is a very sharp needle.’ A phrase stressed time and again by Robert Harrell, an injection expert on the course. Inducing genetic material to reach nuclei within the early insect embryo, without rendering the embryo completely inviable, requires skill, preparation and perfect conditions. The egg must be in an exact period of development such that genetic material, injected in picogram quantities, can contact free floating nuclei, before they are enveloped by the blastoderm. Fused-quartz needles are custom-pulled so long and thin that they are capable of entering and exiting a cellular membrane without allowing cellular material to escape.

Once genetic material reaches the nucleus, successful transgenesis becomes a molecular problem. Short RNA sequences guide the Cas9 enzyme to its desired cut site in the genome, but their effectiveness and specificity depends entirely on a high level of theoretical and in-vitro testing. Bill Reid, an expert in CRISPR experimental design, explained various cutting edge strategies for increasing the probability of a transgenic event occurring within the nucleus. For example, pre-forming complexes between the guide and the enzyme
sprouted new ideas for transgenic insect applications. Alterations of honey bee communication genes to study evolution; development of transgenic moths capable of crashing wild populations; suppression of developmental genes to investigate insect body plan formation – the list of possibilities goes on and on.

A whole week of CRISPR mentoring with the masters, and what is the message? Insect transgenesis requires a sharp needle, but an even sharper imagination.

When developing the use of a novel insect model, each of these aspects carries unique challenges, to be dealt with in turn. For want of time, the ITGRCN injection course focussed upon the final stage – that of physically implanting insect embryos with foreign genetic material.
Planning, generating and analysing a RADseq dataset on a non-model organism using STACKs software

Dr Kirsten Thompson . University of Exeter

My PhD research focused on using a number of genetic approaches to study beaked whales in the Southern Hemisphere. Investigating the biology of these whales is particularly challenging as they are very rarely seen alive and most of what we know is derived from stranded specimens. Beaked whales are extremely deep divers, foraging to up to 3000m depths, with offshore distributions and elusive surface behaviour. In my PhD, the central focus of my research was to use mitochondrial and species-specific microsatellite markers to investigate genetic population structure, demographic change and kinship within stranded groups of Gray’s beaked whale (Mesoplodon grayi). This work has provided some interesting insights into the biology of this species and sheds light on how beaked whales live in such an extreme environment.

The Genetic Society Training Grant funded my attendance at a week-long intensive RADseq Workshop run by Dr Julian Catchen, author of the STACKS software (University of Illinois) and facilitated by Dr Konrad Paszkiewicz, Director of the Wellcome Trust Biomedical Informatics Hub (University of Exeter) and Dr Josie Paris (University of Exeter). The workshop was hosted at the Earlham Institute in Norwich and was attended by researchers from all over the world – Africa, Europe, Canada and the United States. Aimed at researchers with all levels of experience, it provides an opportunity to meet people working in research from early stage PhD students to professors. As researchers working on wild non-model organisms, full genome characterisation is often not feasible due to restricted funding. RADseq can provide a powerful alternative to full genome sequencing for understanding population variation and selection – it is cost-effective if the study is designed and analysed well to fit the research question.

The initial sessions of the workshop focussed on essential UNIX coding commands that every researcher working in the field of genomics will need. I have some experience in coding and was encouraged to see that even those who had not used UNIX, or genetic analyses, were well supported through the workshop. We were given detailed lectures on how to plan a study using RADseq data, with details of how to choose your restriction enzyme for a specific species, sequencing platforms, data characteristics and filtering for quality control. Further lectures were delivered on how to analyse RADseq data for population genomic, genome-wide association studies and phylogenomics, in combination with examples of how these data have been applied in current studies. For three days, using test datasets for a number of species, we trial the STACKs software to answer different research questions. At the end of the week, I was proficient in UNIX and now have extensive notes to enable me to carry out future genomic analyses.

Dr Julian Catchen is both a computer scientist and biologist and his lectures provided a unique insight into modern computing and how this relates to evolution and bioinformatics. The workshop was a rare opportunity to learn and apply skills in bioinformatics alongside other researchers working in a similar field, with support from the software developer. In the evenings, after lectures and work ended, there were plenty of opportunities to network with the trainers and other participants.

The workshop has not only given me a firm grounding on how to plan my next study, but I also feel confident that I have the necessary skills to analyse a large RADseq dataset. I am currently applying for both postdoctoral positions and Fellowship funding and these skills are invaluable. I am very grateful to the Genetic Society for providing the timely support that will help me launch into the next stage of my career. I am already in the process of planning further genomics work on beaked whales using RADseq data with the help of a small grant awarded through the American Natural History Museum. This work will further develop links to other institutions and lead to a publication that will investigate gene flow in beaked whales of the Southern Hemisphere.
The Genetics Society Summer Studentships, sponsored by Genes and Development, are grants provided to support vacation research by undergraduate geneticists (usually in their penultimate year). In this issue, we have reports from Harvinder Pawar and Srinand Sundaram.

Investigating candidate loci for sexual antagonism in fruit flies

Harvinder Pawar

**Introduction**
Selective pressures often differ between males and females as a result of anisogamy (Pennell et al. 2013; Innocenti et al. 2010). However the shared genome restricts independent evolution of each sex towards their phenotypic, sex-specific optima (Olito 2016; Pennell et al. 2013). This results in sexual antagonism which is predicted to maintain polymorphism, where each allele is respectively male-beneficial (MB) or female-beneficial (FB).

Sexually antagonistic fitness effects have been documented in both wild and laboratory populations of the model organism *Drosophila melanogaster* (Innocenti et al. 2010; Chippindale et al. 2001). At the level of individual genes, Hill et al. (2017) recently identified numerous genome-wide clustered candidate SNPs associated with sexual antagonism, a subset of which are within the fruitless gene situated on 3R chromosome of *D. melanogaster*. *Fruitless* is promising to study for two reasons. First it is an important regulatory determinant of neurone sexual dimorphism. Second, Hill et al. (2017) found that sexually antagonistic SNPs situated within *fruitless* gene persist over evolutionary time, suggesting that balancing selection is maintaining the polymorphism (Hill et al. 2017). The current study empirically tests whether *fruitless* male and female-beneficial SNPs respectively exhibit fitness effects predicted by Hill et al. (2017).

**Methods**
In order to measure fitness effects of *fruitless* male- or female-beneficial alleles in a homozygous state, we generated two sets of recombinant inbred *D. melanogaster* lines. The inbred lines were initially derived from isogenic North American flies that had undergone full-sibling inbreeding for 20 generations, before having their genomes sequenced (Mackay et al. 2012). The inbred lines were therefore known to carry either the MB or FB allele. To create each set of recombinant inbred lines, we crossed 14 inbred lines carrying one or the other allele respectively in a round-robin design (i.e. lines 1 x 2, 2 x 3, 3 x 4, etc.) using 46 initial flies from each cross (23 virgin males, 23 virgin females). This procedure homogenizes genetic background between sets, while keeping each set fixed for the allele of interest. The round-robin design was also chosen to avoid significant biases of certain initial lines, as each line is heterozygous before mixing (Hawkes et al. 2016; Treusch et al. 2015). Each set was then placed in a cage to generate experimental (‘focal’) flies. As MB/FB cages were set up, we also set up a third cage of ‘competitor’ flies, which are homozygous recessive for the brown-eyed allele (BW, as opposed to the red-eye, dominant, wild-type). See Figure 1 for clarity.

We measured mating success of adult focal MB and FB males by competing them against BW males, over two blocks. In this assay, 8 focal males (MB/FB) competed with 8 competitor males (BW) for access to 16 BW females per vial for 48 hours. After this period, half of the BW females were allowed to oviposit alone for 24 hours (short-term fitness), while the other half were kept with 4 focal and 4 BW males for 120 hours (long-term fitness). Male fitness was measured by counting the ratio of focal (MB/FB) to competitor (BW) offspring produced.
per fitness assay vial 14 days after removal of females.

Mirroring the male fitness assay design, we measured female fitness by placing 8 focal females (MB/FB) and competing them with 8 BW females for fertilisation by 16 BW males per vial. After competing for 48 hours, focal females were allowed to oviposit for 24 hours (short-term fecundity), and transferred to a new vial for an additional 96 hours (long-term fecundity). After 14 days, adult male and female offspring produced by focal (MB/FB) females were counted.

Throughout both assays and for both blocks, environmental variation was minimised by use of standard agar-molasses recipe for food, use of constant temperature rooms (25 degrees Celsius), use of a 12:12 light: dark cycle and use of density control by standardised collection of 250 eggs per cage. Finally, as female fecundity is highly correlated with quantity of yeast provided, we controlled for this by pipetting 15 μL of yeast dilution, concentrated at 0.33g/mL, in each fitness assay vial for both male and female assays.

Results
The short term fitness assays for blocks 1 and 2 produced no significant difference between the MB/FB genotypes, in either male or female flies (see Figure 2).

However, for long-term male fitness assay, MB males had significantly higher fitness than FB males, siring a greater proportion of offspring after 120 hour mating period, after fitting a quasibinomial general linear model (p=0.03, Figure 3a). Female long-term fitness was highly variable between the two experimental blocks (block p<0.001), whereas genotype was not (p=0.33, see Figure 3b) after fitting a quasipoisson general linear model.

Discussion
The short-term fitness assays returned no significant fitness differences between the MB/FB genotypes, suggesting that longer time periods for mating and for oviposition are required to detect genotype-associated fitness effects. This could be expected, as focal flies are derived from wild flies which have been inbred, and thus are not laboratory adapted.

For long-term fitness, MB males had a significant fitness advantage over FB males (p=0.03). Likewise, for female long-term fitness, the effect size was in favour of FB females; however the effect size was small and non-significant (p>0.05).

The lack of a significant effect of genotype in the female fitness was unexpected for a sexually antagonistic locus, but may be due to environmental variance. For example, our results show there was a significant block effect in the female assay, suggesting that additional environmental controls are warranted. Additionally the fitness effect size conferred by FB allele in the female assay may have been too small to detect. Furthermore, given that the focal flies differ at genes other than fruitless, background genetic effects may need to be controlled further to observe genotype-associated female fitness differences.

Finally the experimental design of our assay may not have captured the FB effects of the FB genotype sufficiently, due to fitness differences between the wild and laboratory settings. In light of this fact, experimental evolution may be required, aiming to observe any short-term evolutionary response to selection acting on the sexually antagonistic alleles of interest (Pardo-Diaz et al. 2015). A population cage experiment using skewed initial ratios of the genotypes has been established in the Reuter laboratory and is ongoing beyond the current study’s duration.

Conclusion
Overall we found an effect of genotype (MB/FB) at the fruitless locus on male long term fitness, but female fitness results were inconclusive in D. melanogaster.
Probing the role of ATF4 in modulating DNA replication during morphogenesis in Drosophila melanogaster

Srinand Sundaram

Continuing to synthesise proteins during stress can be dangerous. In Drosophila melanogaster, two stress-sensing kinases trigger an integrated stress response (ISR) that reduces translation following stress while inducing protective genes. GCN2 responds to amino acid starvation, while PERK is activated by endoplasmic reticulum stress (Figure 1). Both kinases phosphorylate the α subunit of eukaryotic initiation factor 2 (eIF2α). Normally, eIF2α helps to initiate translation, but when it is phosphorylated translation of most mRNAs is blocked, although the mRNA encoding a transcription factor called crc (ATF4 in mammals) is translated more efficiently. Targets of crc then help to combat the stress.

Our group has previously studied the role of the ISR in tissue development (Malzer et al. 2013). Over-expression of PERK in the eye impaired eye development, but it remained unclear if this effect reflected reduced translation or if it was mediated by the induction of crc target genes (Malzer et al. 2010). Depletion of crc by RNA interference rescues some eye growth, suggesting that crc can inhibit eye development (unpublished data). When over-expressed in cultured cells, crc down-regulates genes involved in DNA replication leading us to hypothesise that crc might inhibit eye growth by reducing DNA replication (unpublished data). I set out to test this hypothesis in two aims:

1. To determine whether crc expression is sufficient to impair eye development.

2. To determine whether crc expression inhibits DNA replication

**Aim 1:** Crc was expressed in the eyes of flies by using the gmr-GAL4::UAS system, and then comparison was made with animals expressing GAL4 alone (gmr-GAL4 driver control) or GAL4 and an irrelevant protein, eGFP (gmr-GAL4::UAS-eGFP). To examine a range of expression levels, I took advantage of the temperature dependence of the GAL4::UAS system by raising flies at 18°C, 25°C and 29°C. At 18°C and 25°C, expression of GAL4 with or without eGFP had no effect on eye development, while crc caused an obvious rough eye phenotype (Figure 2).

At 29°C the controls also caused roughness and so this condition was excluded from my analysis.

It is worth noting that the darker eye colour of gmr-GAL4::UAS-eGFP animals relates to them having two copies of the mini-wt gene, in contrast to the one in each of the controls. The increase in colour seen from 18°C and 25°C in the controls demonstrates the temperature-dependence of this system.

**Aim 2:** The Drosophila eye develops from a larval tissue called the eye imaginal disc. During development, a wave of differentiation proceeds anteriorly from the posterior end of this structure. As it does so, cells at the ‘wave front’ pass synchronously through S phase, then G2 and eventually mitosis. After I dissected eye imaginal discs from third instar larvae, I marked cells in S phase by incorporating the nucleoside analogue...
In the interests of space, only two reports have been selected for inclusion in the newsletter, however contributions were also received from:

Güniz Göze Eren - Genetic Basis of Cerebellar Expansion in Loxodonta Africana
Hope Haim – Effects of Dis3L2 over-expression on cell proliferation using Drosophila melanogaster
Jon Harper – Remodelling chromatin for DNA repair – SMARCAD1 and TopBP1 interact?
Kieron Killington – Regulation of HIV-1 Gag expression by ACIN1 and SAM68
Kiran Lee – Sexual selection as a defence against sex ratio distorters in the wild in the stalk-eyed fly, Teleopsis dalmanni
Shiyun Liu – Polyploidy of endosymbiont in Dinotoms
Camila Mirow - Ependymin Genes in Branchiostoma lanceolatum
Dennis Walzl – Electrical synapse plasticity in C. elegans oxygen-response behavior

BrdU. I could then visualise this by immunofluorescence microscopy. Staining for phosphorylated histone H3 identified the progression into M phase. Although still preliminary, my experiments suggest that the expression of crc did not impair cell cycle progress and so the synthesis of DNA was not greatly impacted.

Conclusions
Drosophila provides a powerful model system with which to dissect developmental signalling. My findings suggest that part of the inhibitory effect of the ISR on eye growth is mediated by the expression of crc. Since expression of crc did not reproduce the dramatic inhibition of eye development seen previously with the expression of PERK (Malzer et al. 2010), it seems likely that translational attenuation is the major factor mediating the effects of PERK on tissue growth.

Nevertheless, the induction of a rough eye phenotype by expression of crc suggests that transcriptional regulation is also involved in the ISR’s effect on tissue development. My preliminary data do not support a role for reduced DNA synthesis in mediating this effect and so future studies will focus on other targets of crc. Previous work from our group suggested that expression of crc can trigger cell death, although the mechanism remains mysterious. Since activation of apoptosis can manifest as a rough eye phenotype, this is an exciting line of enquiry we intend to pursue.

References
To apply for any of our grant schemes, instructions and downloadable funding application forms are available from the drop down Funding tab on the Genetics Society website - 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 visiting the following website: http://gensoc.fluidreview.com/
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 theteam@genetics.org.uk, 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 theteam@genetics.org.uk 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 theteam@genetics.org.uk. 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 theteam@genetics.org.uk 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 theteam@genetics.org.uk, 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 theteam@genetics.org.uk, 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 three 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 online (https://gensoc.myreviewroom.com) before the registration deadline of the meeting.

For meetings of our Sectional Interest Groups (e.g. 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.

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: Please visit the website https://gensoc.myreviewroom.com in time for one of the quarterly deadlines (1st day of February, May, August and November). The application must be accompanied by a supporting statement from the applicant’s supervisor or head of department, which must be uploaded via the online application form before the deadline.

Other conditions: 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: Applications should be made online via the Genetics Society Grants application site. Deadlines are bi-monthly (1 February, 1 April, 1 June, 1 August, 1 October and 1 December). To apply please visit the website https://gensoc.myreviewroom.com.

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
To support field-based genetic research and training.

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: Applications should be made online via the Genetics Society Grants application site. Deadlines are bi-monthly (1 February, 1 April, 1 June, 1 August, 1 October and 1 December). To apply please visit the website https://gensoc.myreviewroom.com.

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: 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 £2,350 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, and the student does not have to attend a UK university.

**How to apply:** there is one closing date of 31st March each year. 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. Both the PI and the student involved must be members of the Genetics Society.

The studentship will consist of an award of £200 per week for up to 8 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.

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:** 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.
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.

**Medals and Lectures**
The Mendel Medal, named in honour of the founder of modern genetics, is usually given on alternative years at a Genetics Society Meeting by an internationally distinguished geneticist.

The Society also awards the Genetics Society Medal, the Mary Lyon Medal, Balfour Lecture and JBS Haldane lecture on an annual basis. Winners of the Genetics Society Medal and Balfour lectures present their lecture at a Genetics Society 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.

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.
Contacting the Genetics Society

Members and potential members can contact the Genetics Society membership team in the following ways:

By phone:
0203 793 7850

By email:
TheTeam@genetics.org.uk

By post:
The Genetics Society, c/o The Royal Society of Biology, Charles Darwin House, 12 Roger Street, London, WC1N 2JU

The Genetics Society offers a wide range of benefits to its members including:

• Access to generous grants
• Discounted rates for attendance at prestigious Genetics Society meetings
• A biannual newsletter via post
• Free online access to the Society’s journal Heredity

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