

Welcome to PopGroup⁵¹ in Bristol!

Dear Friends and Colleagues,

We are very pleased to welcome you to this year's PopGroup in Bristol!

This the 51st meeting in the distinguished history of the Population Genetics Group, which has been assembling almost annually since the late 1960s. We hope that you all have a stimulating and enjoyable time here. We particularly welcome visitors to Bristol from other EU countries, as well as from outside the EU.

Bristol is an exciting, creative city, world-renowned for its contribution to environmental and factual broadcasting. It is home to the BBC Natural History unit, much of BBC Factual Radio, Arkive, Wildscreen, the Soil Association and Bristol Zoo. Bristol was a proud host of the European Green Capital Award in 2015, and is celebrated for its music, artistic and food culture. The latter has a particular focus on locally sourced, seasonal and environmentally sustainable food, something we have tried to reflect in our catering.

If you have some more time to spend in our city, suggestions for places to visit and weblinks are on the PopGroup⁵¹ website. We have also included a short list of our favourite places to eat and drink in Bristol for when you are able to forage for yourselves, but the best advice is to follow your instincts (and/or your favourite eating and drinking app)

We hope you have an enjoyable conference and a Happy New Year!

Jon Bridle (on behalf of the organising committee)

Facebook: Popgroup (@populationgeneticsgroup)

Twitter: any conference-related tweets on talks/posters can use the hashtag #PGG51 and handle @popgroup

Website: populationgeneticsgroup.org.uk

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Key information

Registration

Registration opens at 6 pm on **Wednesday 3rd** January in the Hawthorns on Woodland Road (see *venue locations*). Some nibbles and drinks will be available; there will also be a paying bar until 11 pm. Later arrivals can also register in the School of Chemistry from 8.30 am on **Thursday 4th** January.

Meals & refreshments

Lunch, dinner and coffee breaks are detailed in the programme schedule. Lunch will be served in the Life Sciences Building (LSB) on Tyndall Avenue, break refreshments will be served outside the lecture theatres in the School of Chemistry. The two venues are a 5 min walk apart, up/down Cantock Steps (look for the monkey at their head), and through Royal Fort Gardens (past the Hollow installation).

Conference dinner

This year's conference dinner will take place on **Friday 5th** at the award-winning M-Shed museum located overlooking Bristol's historic harbourside (see *venue locations*; Wapping Road BS1 4RN). Please enter by the main entrance of the M-Shed (next to our historic cranes, and the waterfront). The Museum is c. 25-minute walk/10-minute taxi journey from the Life Sciences Building. A drinks reception will begin at 7 pm with private access to this year's Wildlife Photographer of the Year exhibition. The dinner will commence at 8 pm followed by a Ceilidh at 10.30 pm. There will be a paying bar until 12.30, with proceedings ending at 1 am.

Talks

All talk sessions will take place in the School of Chemistry (see *venue locations*). Plenary talks will take place in Room LT1 and will be 50 minutes, including Q&A. Contributed talk slots are 20 minutes in length, with 15 minutes allotted for the

speaker, 4 minutes of questions and 1 minute for room changes. We ask that the final speaker in each session chairs the talks before them and keeps strictly to schedule.

PopGroup volunteers and AV technicians will be on hand to assist and we ask that all Powerpoint/PDF presentations are uploaded to the session computers by the break before the session at the latest (full details on the PopGroup⁵¹ website).

PopGroup⁵¹ will also feature a presentation and Q&A by a member of the BBC Natural History Unit, and will explore the relationship between scientific research and factual broadcasting. This takes place in Room LT1 at 4.10pm on **Friday 5th** January.

We are encouraging delegates to use the hashtag #PGG51 to tweet about the conference, as well as our facebook page. If you do **NOT** wish delegates to tweet or photograph slides during your talk, please make this clear at the start of your talk.

Posters

Posters should be in A0 portrait format and will be displayed in the main atrium of the LSB during a drinks reception on **Thursday 4th** from 6–8 pm. There will also be a second opportunity to view posters with drinks on **Friday 5th** between 5–6.30 pm.

Please bring your poster as you register. During the poster sessions please stand near to your poster. Drinks receptions are kindly sponsored by *Heredity* on Thursday and *Proceedings of the Royal Society B* and *Genes* on Friday. Please note student posters will be marked with a coloured sticker. Take this opportunity to view and discuss posters!

Prizes for talk/poster

The prizes for this year's best student poster and best student talk are generously sponsored by *Frontiers* and will be presented at the conference dinner at the M-shed. Voting slips will be included in the welcome bag at registration. Student talks/posters will be marked with an **(S)** in the programme. Please remember to post your voting slips to either of the two boxes in Chemistry or LSB by 5 pm on **Friday 5th**.

Business meeting

There will be a PopGroup business meeting on **Friday 5th** during the lunch break. This meeting will discuss the management and venues of future PopGroup meetings. Everyone is welcome and encouraged to attend. It will be held in Chemistry LT2 at 13.20.

Student volunteers

Our wonderful student volunteers are all wearing T-shirts resplendent with our PopGroup⁵¹ logo. Please feel free to ask any of them for any help or advice you may need (many thanks to them for their efforts!).

Other useful information

Left luggage will be available in Life Sciences on the last day of the meeting (full details on the website).

Important telephone numbers:

UK emergency number 999

University of Bristol Security Office 0117-9287848

Childcare facilities will also be available.

Full information is available on the PopGroup⁵¹ website.

PopGroup⁵¹ team

Organising Committee

Jon Bridle

Mark Beaumont

Rupert Collins

Carlos Gracida Juarez

Martin Genner

Eleanor O'Brien

Rita Rasteiro

Andy Saxon

Conference co-ordinator

Helen Chadwick

Additional support

Alan Beavan

Xiaoyang Dai

Sinead English

Jo Howard-McCombe

Alex Jansen van Rensburg

Student Volunteers

Guy Burstein

Celine Clark

Laura Denton

Dunia Gonzales

Calabryn Lester

Millie Mark

Cameron Matthews

Maddy McCarthy

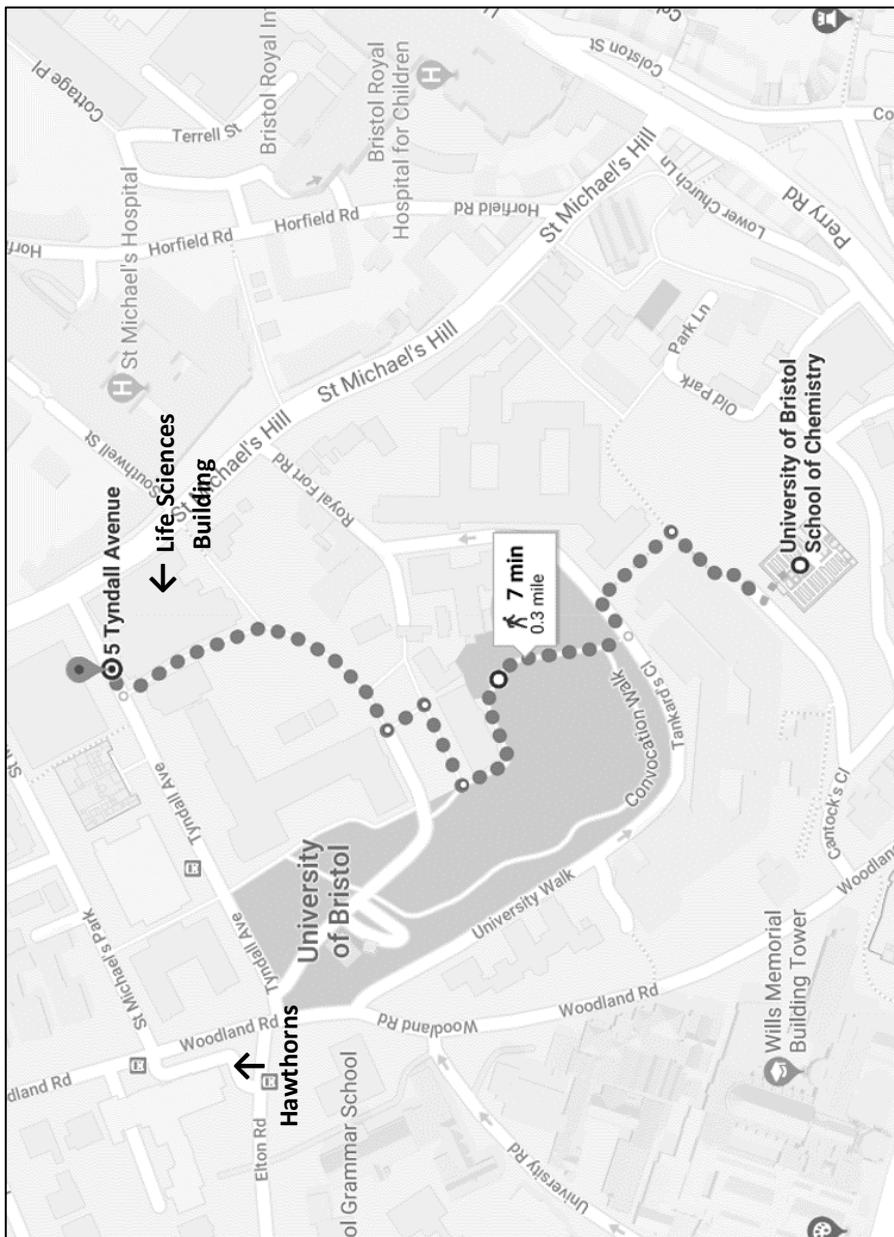
Oliver Soutar

Daniel Ward

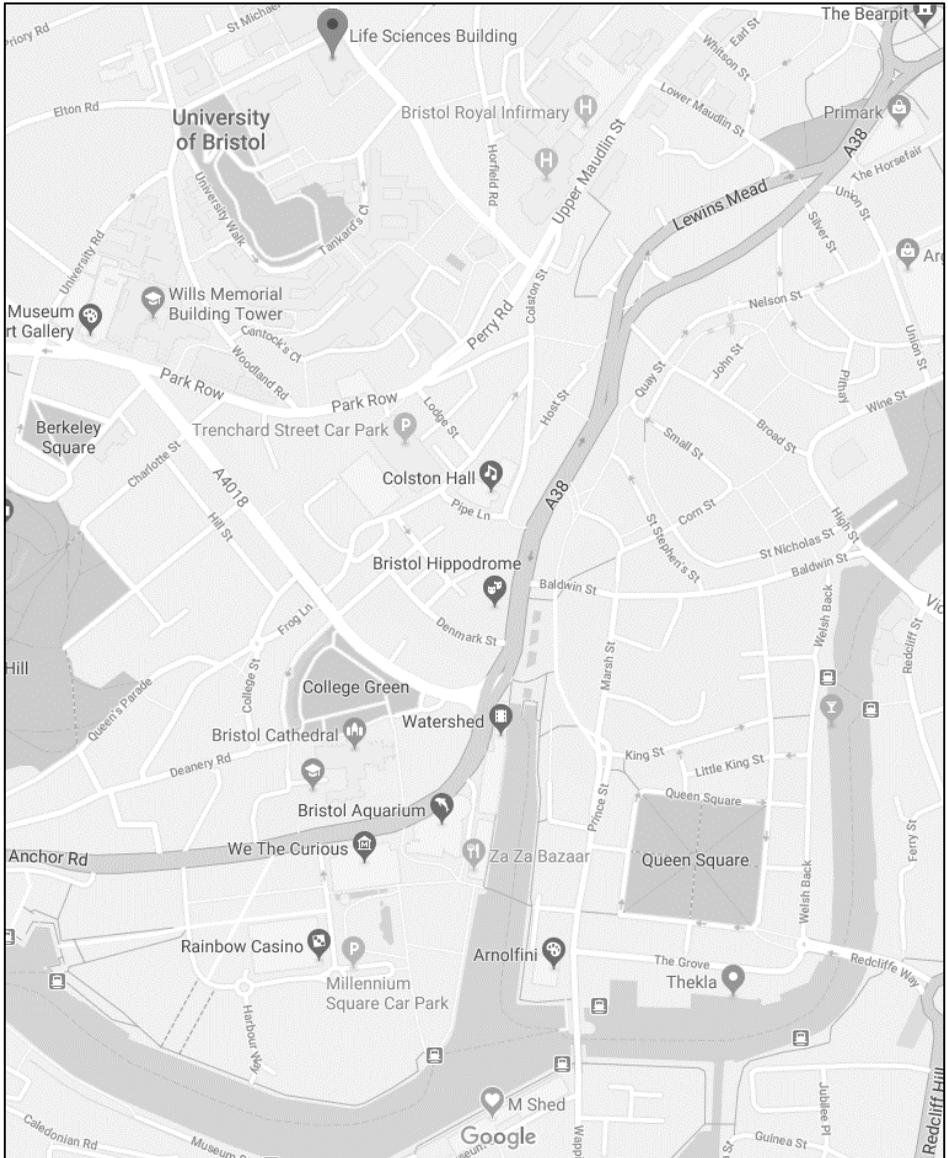
Nathan Williams

Megan Whatty

Venue locations



Walking route between Life Sciences Building (LSB) and School of Chemistry



Route from LSB to M-shed museum (for conference dinner). Please enter by the main (waterside) entrance, by the cranes

Plenary talks abstracts

Mike Brockhurst

Professor of Microbial Evolution, University of Sheffield

Taking a dip in the mobile gene pool

Horizontal gene transfer (HGT) allows evolution to proceed by adaptive leaps via gain of new functional traits, such as antibiotic resistance. Bacterial comparative genomics reveals extensive horizontal gene transfer facilitated by mobile genetic elements (MGE) but little is known about how the ecology of microbial communities and their environments affects HGT dynamics. Moreover, intragenomic conflict between MGEs and their bacterial hosts is common and impedes HGT. I will present data from experimental evolution of environmental *Pseudomonas* species showing that gene mobilisation and transfer is most likely when the MGE is useless, and that conflicts between chromosomes and MGEs can be rapidly resolved by diverse mechanisms of compensatory evolution of the MGE or the host, which ameliorates the cost of the MGE allowing its survival.

Joe Felstenstein (Fisher Memorial Trust Lecture via live video link)

Professor of Genome Sciences, University of Washington

Is there a more fundamental theorem of natural selection?

R.A. Fisher's Fundamental Theorem of Natural Selection has intrigued evolutionary biologists, who wondered whether it could be the basis of a general maximum principle for mean fitness of the population. Subsequent work by Warren Ewens, Anthony Edwards, and George Price showed that a reasonable version of the FTNS is true, but only if the quantity being increased by natural selection is not the mean fitness of the population but a more indirectly defined quantity. That leaves us in an unsatisfactory state. In spite of Fisher's assertion that the theorem "hold[s] the

supreme position among the biological sciences”, the Fundamental Theorem is, alas, not-so-fundamental. There is also the problem that the additive genetic variances involved do not change in an easily predictable way. Nevertheless, the FTNS is an early, and imaginative, attempt at formulating macro-scale laws from population-genetic principles. I will not attempt to revive the FTNS, but instead am trying to extend a 1978 model of mine, put forth in what may be my least-cited paper. This attempts to make a “toy” model of an evolving population in which we can bookkeep energy flows through an evolving population, and derive a long-term prediction for change of the energy content of the system. It may be possible to connect these predictions to the rate of increase of the adaptive information (the “specified information”) embodied in the genetic information in the organisms. The models are somewhat absurdly oversimple, but I argue that models like this at least can give us some results, which decades of more handwavy papers on the general connection between evolution, entropy, and information have not.

Tracey Chapman

Professor of Evolutionary Genetics, University of East Anglia

Sexual conflict: mechanisms and emerging themes

The potential for sexual conflict is pervasive. It can generate and maintain abundant genetic variation in diverse reproductive adaptations. Thus the selective pressures arising from sexual conflict and co-operation can drive diversification within and between species. Mechanistic studies have been important in gaining direct evidence for the existence of sexual conflict. The mechanisms involved range from the use of genital spines, claspers, songs, smells to ejaculate molecules. I'll focus on one well-studied example, sexual conflict over the effects of seminal fluid proteins in the fruit fly *Drosophila melanogaster*. I'll discuss how the rich diversity and complexity of traits subject to sexually antagonistic selection could arise due to the deployment of

sexually antagonistic adaptations in a manner that lessens the probability of resistance evolution. In this I will draw upon research into the evolution of resistance to insecticides, antimicrobials and vaccines and hence discuss whether male manipulative traits could be 'resistance-proofed'.

Katie Peichel

Professor and Head of Division, Evolutionary Ecology, University of Bern

Genetics of adaptation in sticklebacks: the roles of pleiotropy and linkage

Despite recent progress, relatively little is known about the specific genetic and molecular changes that underlie adaptation to new environments. Stickleback fish have been at the forefront of research to uncover the genetic and molecular architecture that underlies adaptation and speciation. A wealth of quantitative trait locus (QTL) mapping studies in sticklebacks has provided insight into the distribution of effect sizes during adaptation and has also revealed that several regions of the genome contain more loci than expected for traits involved in adaptation. It is unknown whether these trait clusters result from tight physical linkage of multiple genetic changes responsible for different traits, or from a single genetic change with pleiotropic effects. I will discuss recent research in my group that is focused on disentangling the roles of pleiotropy and linkage in adaptation, using both genome-wide approaches and more focused studies of specific loci with a major effect on adaptation.

Daven Presgraves

Professor in Evolutionary Genetics and Genomics, University of Rochester

The evolution, genetics, and consequences of species differences in meiotic recombination

Crossing over between homologous chromosomes during meiosis repairs programmed DNA double-strand breaks, ensures proper segregation, shapes the genomic distribution of nucleotide variability in populations, and enhances the efficacy of natural selection among linked sites. Differences in the rate and chromosomal distribution of crossing over have evolved between species, but little is known about how or why. I will show that a single meiosis gene with a history of recurrent adaptive evolution acts as a global, *trans*-acting modifier of the rate and distribution of crossing over between closely-related *Drosophila* species. We speculate that adaptive evolution of our recombination gene occurred to mitigate species-specific risks of ectopic exchange between transposon insertions and gave rise, incidentally, to species differences in the chromosomal distribution of nucleotide variability. We also investigate the deeper history, causes, and consequences of evolution of our recombination gene over the *Drosophila* phylogeny.

Programme: Thursday 4th January

8:30	Registration (School of Chemistry)			
8:50	Welcome and Information (LT1)			
9:00	Plenary lecture (LT1) Mike Brockhurst Taking a dip in the mobile gene pool			
9:50	Coffee Break			
	Room LT1	Room LT2	Room LT3	Room LT4
10:30	Daniel Falush Admixture of <i>Helicobacter pylori</i> driven by deleterious mutation load	John Turner The flexible lek: a bundle of evolutionary puzzles	Jennifer James (S) Investigating the life history and demographic traits that are Predictive of N_e	Helena Batalha (S) Genetic diversity and divergence in the endangered Cape Verde warbler
10:50	Tim Downing Bacterial genomes from the UK and Ireland highlight transposable elements as drivers of antibiotic resistance	Eniko Szep (S) Does migration help or hinder local adaptation?	Reuben Nowell Comparative genomics of desiccating and non-desiccating bdelloid rotifer species	Toni Gossmann Severe loss of genetic diversity in the alpine marmot genome as a long-term consequence of cold temperature adaptation in a warming climate
11:10	Ana Zhu Strain variation in gut microbiota	Claire Armstrong (S) Genomic associations with bill length and disease reveal drift and selection across island bird populations	Casper Lumby (S) Inference of viral transmission events	Ellika Faust (S) Cleaner fish escape salmon farms and hybridise with local wrasse populations
11:30	Henry Barton (S) The strength of GC biased gene conversion is conserved across two passerine species	Thomas Mathers Evolutionary genomics of host range expansion in the green peach aphid	Bjarki Eldon Modelling gene genealogies in highly fecund populations	Pirita Paaanen Arabidopsis arenosa and its cousins, autotetraploid <i>A. arenosa</i> and allotetraploid <i>A. suecica</i>
11:50	Jane Charlesworth Do bacterial pathogens have smaller genomes than their non-pathogenic relatives?	Jitka Polechová Is the sky the limit? On the expansion threshold of a species' range	Peter Keightley Can you say which is the derived or ancestral allele at a polymorphic site?	Andrew Helmstetter Population genetics of wild and domesticated hazelnut (<i>Corylus avellana</i>) in Turkey
12:10	Lunch (Life Sciences Building)			

	Room LT1	Room LT2	Room LT3	Room LT4
14:00	Tom Booker (S) Estimating the parameters of selective sweeps	Maria Cuenca Cambronero (S) Evolution of thermal tolerance in	Andrew Pomiankowski Sexual conflict explains the	Hanja Pisa (S) The Pitfalls of Adaptation to the Better Niche

	from patterns of diversity around functional elements in wild house mice	multifarious environments over five decades of global change	extraordinary diversity of mechanisms regulating mitochondrial inheritance	
14:20	Leo Speidel (S) A method for estimating genome-wide genealogies for thousands of samples	Sheng-Kai Hsu (S) Sexually antagonistic gene expression evolution in <i>Drosophila simulans</i> populations adapting to a novel thermal environment	Homa Papoli Yazdi (S) A genetic map of ostrich Z chromosome allows for the inference of inversions in avian sex chromosome evolution	Levi Yant A genus-wide view of gene flow and selection in outcrossing <i>Arabidopsis</i> species
14:40	Josiah Seaman (S) Genome assembly and alignment using maps-style visualisation	Sian Bray A possible role in adaptation to low calcium serpentine soils by Two Pore Channel 1	Steven Van Belleghem Patterns of Z chromosome divergence among <i>Heliconius</i> species highlight the importance of accounting for demography	Joel Peck What is adaptation and how should it be measured?
15:00	Kevin Dawson Using population genetic methods to infer the demographic parameters of an in vivo population of human stem cells from a combination of NGS data and single cell genomes	Joe Colgan Signatures of selection in a wild pollinator revealed through population genomics	Deborah Charlesworth Associations of SNPs with the sex-determining locus of the young guppy sex chromosome	Bruno Nevado Adaptive evolution during evolutionary radiations in plants
15:20	Coffee Break			

	Room LT1	Room LT2	Room LT3	Room LT4
15:50	Mechthild Lütge (S) Speciation events in functional co-occurrence networks across pan-genomes	Matthew Ackerman Quantitative genetics in structured populations	Jörg Bachmann (S) Genetic basis and timing of the transition to selfing in <i>Capsella orientalis</i>	Melanie Brien (S) Comparing the genetic basis of structural colour in <i>Heliconius</i> butterflies
16:10	Katharina Böndel Mutation accumulation in <i>Chlamydomonas</i>	Bonnie Fraser Genomic basis of convergent evolution in the Trinidadian guppy	Samuel Perini (S) The contribution of size and ecotype variation to sexual isolation in <i>Littorina saxatilis</i>	Hans Recknagel (S) Support for a reversal to oviparity in <i>Zootoca vivipara</i> from genome-wide SNP phylogenomics
16:30		James Buckley RAD-genotyping at multiple spatial scales in <i>Arabidopsis lyrata</i> reveals signatures of pathogen-mediated selection	Victor Soria-Carrasco Demographic patterns and processes in <i>Timema</i> stick insects	Kathryn Elmer Synteny and co-localization of ecologically relevant quantitative trait loci across salmonid species
17:00	Fisher Memorial Lecture (LT1) Joe Felsenstein Is there a more fundamental theorem of natural selection?			
18:00 20:00	Posters & drinks reception (Life Sciences Building)			

Programme: Friday 5th January

8:50	Welcome and Information (LT1)			
9:00	Plenary lecture (LT1) Tracey Chapman Sexual conflict: mechanisms and emerging themes			
9:50	Kenneth Mather Prize (LT1) Jessica King The evolution of phenotypic plasticity when environments fluctuate in time and space			
10:10	Coffee Break			
	Room LT1	Room LT2	Room LT3	Room LT4
10:50	Nick Priest Alcohol medicates against STIs: evidence that non-immunological costs are justified	Simon Segar Speciation in figs and their pollinating wasps along the slopes of a New Guinean mountain	Waldir Berbel-Filho (S) Is epigenetic variation related to genetic background in a selfing species?	Daniel Crouch The genetics of the human face
11:10	Joanna Hagen (S) The genetic and developmental basis of male genitalia evolution between <i>Drosophila</i> species	Emma Curran (S) Population genomics of parallel clines in iridescent structural colour in <i>Heliconius</i> butterflies	Kang-Wook Kim Spatio-temporal heterogeneity of transcriptome evolution in <i>Drosophila melanogaster</i>	Reto Burri Interpreting differentiation landscapes in the light of long-term linked selection
11:30	Filip Ruzicka (S) Sexual antagonism maintains genetic variation across the <i>Drosophila melanogaster</i> distribution range	Tom Hill Adaptation of baculoviruses and nudiviruses in <i>Drosophila</i> and other arthropods	Darren Parker Convergent gene expression changes across independent transitions to asexuality: insights from stick insects	Nick Barton Establishment in a new habitat by polygenic adaptation
11:50	Stuart Wigby Quantitative proteomics reveals seminal fluid plasticity in <i>Drosophila melanogaster</i>	Josie Paris Brown trout and toxic metals: adaptation to the legacy of Britain's mining history	Samuel Lewis The evolution of DNA methylation across non-insect arthropods	Susan Johnston Are individual recombination rates under selection in contemporary populations
12:10	Lunch (Life Sciences Building)			
13.20	Business Meeting (LT2)			

13:50	Plenary lecture (LT1) Katie Peichel Genetics of adaptation in sticklebacks: the roles of pleiotropy and linkage			
14:40	Coffee Break			
	Room LT1	Room LT2	Room LT3	Room LT4
15:10	Markus Möst The landscape of selection across major colour pattern loci in mimetic <i>Heliconius</i> butterflies	TBC	James Horton (S) Evolutionary trade-offs and innovation in evolving gene regulatory networks	Falk Hildebrand SNP calling in metagenomic datasets
15:30	Hannes Becher (S) Targeted resequencing of hundreds of loci to detect genetic differentiation across a chromosomal hybrid zone in the grasshopper <i>Podisma pedestris</i>	Carlos Martinez Ruiz (S) Has social conflict led to selection for a social supergene and initiated the degeneration of a social chromosome?	Christian Schlötterer Evolution of gene expression in <i>Drosophila</i>	Petri Kempainen Chromosome partitioning analyses and inferences of genetic architecture (in natural populations)
15:50	Sara Goodacre Arachnoglobbia: Long-distance dispersal- gene flow and the potential for localised adaptation in linyphiid spiders	Lewis Spurgin Genome-wide association studies in natural populations: managing expectations and avoiding error	Agnieszka Lipinska Generation-biased gene expression in brown algae	Jerome Kelleher Inferring ARGs for millions of chromosomes
16:10	BBC Natural History Unit Q&A (LT1)			
17:00	Posters & drinks reception (Life Sciences Building)			
18:30				
19:00	Conference dinner & Ceilidh (M-Shed)			
01:00				

Programme: Saturday 6th January

8:50	Welcome and Information (LT1)			
9:00	Plenary lecture (LT1) Daven Presgraves The evolution, genetics, and consequences of species differences in meiotic recombination			
9:50	Coffee Break			
	Room LT1	Room LT2	Room LT3	Room LT4
10:30	Laurence Hurst Why recombine? Evidence against the hypothesis that gene conversion corrects mutations	Anja Marie Westram Understanding the genomic basis of parallel evolution using hybrid zone analysis	John Brookfield Expected dynamics of preference alleles in the context of cytoplasmic incompatibility	Matthew Hartfield Signatures of selective sweeps with arbitrary dominance and self-fertilisation
10:50	Simon Aeschbacher Distinguishing between primary and secondary gene flow based on pairwise sequence differences	Rui Faria Detection of chromosomal rearrangements in <i>Littorina saxatilis</i> : insights from a hybrid zone	Emma Berdan The population genomics of cuticular hydrocarbons in an inversion system	Konrad Lohse Modelling the genomic landscape of divergence and gene flow
11:10	Mario dos Reis Population genetics of codon substitution	Hernan Morales Genomics of parallel ecotype local adaptation in <i>Littorina saxatilis</i>	Rodrigo Pracana The evolution of the social chromosome supergene across fire ant populations	Zhangyi He A numerical solution of the Wright-Fisher SDE with application to transition probability density approximation"
11:30	Kai Zeng New methods for inferring the distribution of fitness effects for INDELS and SNPs	Sean Stankowski Patterns of genome-wide variation across temporal, spatial and ecological axes of the bush monkeyflower radiation	Diala Abu Awad Effects of partial selfing on the equilibrium genetic variance, mutation load and inbreeding depression under stabilising selection	Stuart Baird Compression population genomics
11:50	Adam Eyre-Walker Does evolution proceed by large or small steps at the molecular level	Mark McMullan The population genetics of the ash dieback invasion of Europe highlights	Bram Kuijper Sexual conflict over phenotypic plasticity	Wolfram Moebius Range expansions in heterogeneous environments: population front

		huge adaptive potential of the causal fungus <i>Hymenoscyphus fraxineus</i>		perturbations and their effect on genetic diversity
12:10	Brian Charlesworth Genetic load and heterosis in subdivided populations	Jamie Stevens Contrasting patterns of population structure, gene flow and connectivity in octocorals: implications for MPA designation	Elizabeth Duxbury The causes of genetic variation in susceptibility to infectious disease in natural populations	Anne Kupczok Homogeneous rates of molecular evolution in dairy phage genomes over three decades
12:30	Lunch (Life Sciences Building)			
14:00	End of the meeting			

Posters

Hande Acar	The role of the environment in HGT
Einar Arnason	Phenotypic variation among genotypes of an inversion polymorphism defining behavioral ecotypes in Atlantic cod
Helena Batalha (S)	Genetic diversity and divergence in the endangered Cape Verde warbler
Laurence Belcher (S)	Savvy investment in a microbe
Max Brown (S)	Hybrid speciation in British Euphrasia
Emily Burdfield Steel	Shiny happy bugs: Investigating colour variation in an aposematic species
Silvia Busoms	Role of the Na transporter AtHKT1;1 in <i>A. thaliana</i> populations well-adapted to coastal habitats
Clarissa Carvalho (S)	Spatial epigenetic variation in <i>Timema cristinae</i>
Jobran Chebib (S)	Structure of genotype-phenotype map affects evolvability of a population
Gemma Clucas	Genome-wide differentiation and adaptation of Atlantic cod ecotypes in the Gulf of Maine
Rory Craig (S)	Genome re-sequencing reveals patterns of local and continental population structure in the unicellular green alga <i>Chlamydomonas reinhardtii</i>
Daniel Crouch	Short term advantage of sexual reproduction under natural selection in finite populations
Helena Dahlberg (S)	Genetic diversity in wild and domesticated stands of Norway spruce
Xiaoyang Dai (S)	Likelihood-free inference of natural selection and genetic recombination from temporal changes in allele frequencies: Selection strength inferences via Approximation Bayesian Computation-framework
Rishi De-Kayne (S)	Constructing a linkage map for Swiss Alpine whitefish
Pablo Deschepper (S)	Analysis of spatial genetic variation reveals genetic divergence among populations of <i>Primula veris</i> associated to contrasting habitats
Tim Downing	Genome structure and gene content evolution in the Leishmania parasite Viannia subgenus
Jamie Dunning (S)	Global phylogeny of a fragmented finch species
Elizabeth Duxbury	The causes of genetic variation in susceptibility to infectious disease in natural populations
Isobel Eyres	Experimental adaptation and speciation in rotifers
Kirsten Farncombe (S)	Is haplodiploidy superior to diploidy?
Varvara Fazalova	Post-mating pre-zygotic reproductive isolation in pea aphids
Susana Freitas	Sexual healing
Joelle Gouy de Bellocq	The importance of the host phylogeographic structure in the spatial spread of viruses: <i>Mastomys natalensis</i> arenaviruses in Tanzania

Joanna Hagen (S)	The genetic and developmental basis of male genitalia evolution between <i>Drosophila</i> species
Christoph Hahn	Impacts of climate-driven evolution on plant-soil interactions and ecosystem functioning
Katrín Halldórsdóttir	Variance and heteroplasmy of length variation in mtDNA over a single generation transition in Atlantic cod <i>Gadus morhua</i>
Zhangyi He	Effects of the ordering of natural selection and population regulation mechanisms on Wright-Fisher models
Laura Hebberecht López (S)	Probing the developmental regulation of <i>Heliconius</i> wing patterns
Andrew Helmstetter	Investigating the role of human colonisation on population decline in Madagascar's highland flora
Tom Hill	Divergence in TE activity across the <i>Drosophila</i> phylogeny
Tin-Yu Hui	An alternative approach to estimate contemporary effective population size using linkage disequilibrium information
Michał Izydorczyk (S)	Human endogenous retroviruses and cancer
Jack Kamm	Inferring history from the joint SFS of ancient DNA
Carolin Kosiol	Polymorphism-aware phylogenetic models and their applications
Rebecca Lewis (S)	Genetic rescue of maladapted populations
Philip Madgwick (S)	When the 'invisible hand' leads selfish individuals to act for the good of the group
Lucas Marie-Orleach	Social plasticity and sexual isolation: How does the social environment affect fruit fly courtship song?
Claudia Martin (S)	Genomic signatures of adaptation in an island bird
Richard Merrill	Genetics of visual mate recognition in <i>Heliconius</i> butterflies
Pablo Orozco Ter Wengel	Jersey and Guernsey cattle genetics reveal the Viking colonisation of the English Channel Islands
Alex Papadopoulos	Poster title TBC
Elisabet Peedu (S)	Genetic structure in <i>Silene dioica</i> metapopulations
Lucy Peters (S)	Genomic approaches to understanding the genetic architecture of antler morphology in red deer
Barret Phillips	X-Y differentiation is lineage-specific in Swiss populations of <i>Rana temporaria</i>
Hanja Pisa (S)	The pitfalls of adaptation to the better niche
Michael Pointer (S)	A genetic approach to conserving the critically endangered Malagasy day-gecko, <i>Phelsuma antanosy</i>
Roddy Pracana	The evolution of the social chromosome supergene across fire ant population
Matteo Rossi (S)	Neurotranscriptomic divergence between sympatric <i>Heliconius</i> species
Josiah Seaman (S)	Genome assembly and alignment using Maps-style visualization
Jiyeong Shin (S)	Population genetic structures of <i>Armadillidium vulgare</i> from South Korea using the mitochondrial COI gene
Victor Soria-Carrasco	Demographic patterns and processes in <i>Timema</i> stick insects
Evelyn Taylor-Cox (S)	Evolutionary genetics and demography of population range expansion in two species of British Lepidoptera

Mijke van der Zee (S)	Genetics of local adaptation and convergent evolution in the Trinidadian guppy (<i>Poecilia reticulata</i>) using new introduction experiments
Ben Whittaker (S)	Population genetics of the lumpfish (<i>Cyclopterus lumpus</i>) across the species range
Johannes Wirtz (S)	The evolving moran genealogy
Edgar Wong (S)	Genomic consequences of gene flow between <i>Senecio</i> species on Mount Etna
Kai Zeng	The effects of GC-biased gene conversion (gBGC) on the study of natural selection: empirical evidence and theoretical modelling
Ana Zhu	Strain variation in gut microbiota

Delegate list

ABU AWAD DIALA	Station Biologique de Roscoff	diala.a@gmail.com
ACAR Hande	University of Liverpool	hndacar@gmail.com
ACKERMAN Matthew	Wellcome Trust Sanger Institute	matthew.s.ackerman@gmail.com
AESCHBACHER Simon	University of Zurich	saeschbacher@mac.com
ANDRES Aida	University College London	a.andres@ucl.ac.uk
ARMSTRONG Claire	University of East Anglia	c.armstrong@uea.ac.uk
ARNASON Einar	University of Iceland	einararn@gmail.com
ASPINALL Paigan	University of Bath	pjpa20@bath.ac.uk
BACHMANN Jörg	Stockholm University	jorg.bachmann@su.se
BAIRD Stuart	Czech Academy of Sciences	Stuart.J.E.Baird@gmail.com
BARTON Henry	University of Sheffield	hbarton2@sheffield.ac.uk
BARTON Nick	IST Austria	nick.barton@ist.ac.at
BATALHA Helena	University of East Anglia	h.batalha@uea.ac.uk
BEAUMONT Mark	University of Bristol	m.beaumont@bristol.ac.uk
BEAVAN Alan	University of Bristol	alan.beavan@bristol.ac.uk
BECHER Hannes	Queen Mary London	h.becher@qmul.ac.uk
BELCHER Laurence	University of Bath	lb780@bath.ac.uk
BERBEL-FILHO Waldir	Swansea University	809027@swansea.ac.uk
BERDAN Emma	University of Gothenburg	emma.berdan@gu.se
BETANCOURT Andrea	University of Liverpool	A.Betancourt@liverpool.ac.uk
BHATIA Rama	University of Liverpool	rama.bhatia@liverpool.ac.uk
BOLLBACK Jonathan	University of Liverpool	bollback@liverpool.ac.uk
BÖNDEL Katharina	University of Edinburgh	Katharina.Boendel@ed.ac.uk
BOOKER Tom	University of Edinburgh	t.r.booker@sms.ed.ac.uk
BRAY Sian	John Innes Centre	sian.bray@jic.ac.uk
BRIDLE Jon	University of Bristol	jon.bridle@bristol.ac.uk
BRIEN Melanie	University of Sheffield	mnbrien1@sheffield.ac.uk
BROCKHURST Mike	University of Sheffield	m.brockhurst@sheffield.ac.uk
BROOKFIELD John	University of Nottingham	john.brookfield@nottingham.ac.uk
BROWN Max	University of Edinburgh	max.brown@ed.ac.uk
BUCKLEY James	ETH Zürich	james.buckley@env.ethz.ch
BUGGS Richard	Queen Mary London	r.buggs@qmul.ac.uk
BURDFIELD STEEL Emily	Macquarie University	emily.burdfield-steel@mq.edu.au
BURRI Reto	FSU Jena	reto.burri@uni-jena.de
BURT Austin	Imperial College London	a.burt@imperial.ac.uk
BUSOMS Silvia	John Innes Centre	silvia.busoms@jic.ac.uk
BUTLER George	University of Reading	george.butler@pgr.reading.ac.uk
BUTLIN Roger	Universities of Sheffield and Gothenburg	r.k.butlin@shef.ac.uk
CARR Martin	University of Huddersfield	M.Carr@hud.ac.uk
CARVALHO Clarissa	University of Sheffield	cferreiradecarvalho1@sheffield.ac.uk
CHAPMAN Tracey	University of East Anglia	tracey.chapman@uea.ac.uk
CHARLESWORTH Brian	University of Edinburgh	Brian.Charlesworth@ed.ac.uk
CHARLESWORTH Deborah	University of Edinburgh	Deborah.Charlesworth@ed.ac.uk
CHARLESWORTH Jane	University of Cambridge, EMBL-EBI	jc988@cam.ac.uk
CHEBIB Jobran	University of Zurich	jobran.chebib@ieu.uzh.ch
CLUCAS Gemma	University of New Hampshire	gemma.clucas@unh.edu
COELHO Susana	CNRS	coelho@sb-roscoff.fr
COLGAN Joe	Queen Mary London	t.colgan@qmul.ac.uk
COLLINS Rupert	University of Bristol	rc16041@bristol.ac.uk

COOK Nicola	University of St Andrews	nc52@st-andrews.ac.uk
CRAIG Rory	University of Edinburgh	rory.craig@ed.ac.uk
CRAZE Paul	Trends in Ecology and Evolution	p.craze@elsevier.com
CROUCH Daniel	University of Oxford	daniel.crouch@oncology.ox.ac.uk
CUENCA CAMBRONERO Maria	University of Birmingham	mxc331@bham.ac.uk
CUNNINGHAM Christopher	Swansea University	c.b.cunningham@swansea.ac.uk
CURRAN Emma	University of Sheffield	evcurran1@sheffield.ac.uk
DAHLBERG Helena	Umeå University	helena.dahlberg@umu.se
DAI Xiaoyang	University of Bristol	356728156@qq.com
DAVIES Charli	University of East Anglia	charlotte.s.davies@uea.ac.uk
DAWSON Kevin	Wellcome Trust Sanger Institute	kevinjdawson1@gmail.com
DE-KAYNE Rishi	EAWAG	rishi.de-kayne@eawag.ch
DESCHÉPPER Pablo	KU Leuven	pablo.deschepper@kuleuven.be
DOS REIS Mario	Queen Mary London	m.dosreisbarros@qmul.ac.uk
DOWNING Tim	Dublin City University	downingtimgmail.com
DUNNING Jamie	University of Nottingham	jamiedunning8@googlemail.com
DURBIN Richard	University of Cambridge	rd109@cam.ac.uk
DUXBURY Elizabeth	University of Cambridge	emd55@cam.ac.uk
ELDON Bjarki	MFN Berlin	bjarki.eldon@mfn-berlin.de
ELMER Kathryn	University of Glasgow	kathryn.elmer@glasgow.ac.uk
ENGLISH Sinead	University of Bristol	sinead.english@bristol.ac.uk
EYRES Isobel	University of Sheffield	i.eyres@sheffield.ac.uk
EYRE-WALKER Adam	University of Sussex	a.c.eyre-walker@sussex.ac.uk
FALUSH Daniel	University of Bath	danielfalush@googlemail.com
FARIA Rui	University of Sheffield	r.macieiradefaria@sheffield.ac.uk
FARNCOMBE Kirsten	University of Reading	k.m.farncombe@pgr.reading.ac.uk
FAUST Ellika	University of Gothenburg	ellika.faust@gu.se
FAVREAU Emeline	Queen Mary London	emeline.favreau@qmul.ac.uk
FAZALOVA Varvara	University of Oxford	varvara.fazalova@zoo.ox.ac.uk
FITZPATRICK Jack	University of Liverpool	hjffitz2@liv.ac.uk
FOOTE Andrew	Bangor University	FooteAD@gmail.com
FRASER Bonnie	University of Sussex	b.fraser@sussex.ac.uk
FREITAS Susana	University of Lausanne	freitas.sn@gmail.com
GENNER Martin	University of Bristol	m.genner@bristol.ac.uk
GIBSON Beth	University of Sussex	b.gibson@sussex.ac.uk
GOODACRE Sara	University of Nottingham	sara.goodacre@nottingham.ac.uk
GOSSMANN Toni	University of Sheffield	t.gossmann@sheffield.ac.uk
GOUY DE BELLOQC Joelle	Czech Academy of Sciences	joellegouy@gmail.com
GRACIDA JUAREZ Carlos	University of Bristol	cj16551@bristol.ac.uk
HAGEN Joanna	Oxford Brookes University	15058474@brookes.ac.uk
HAHN Christoph	University of Liverpool	c.z.hahn@liverpool.ac.uk
HAILER Frank	University of Cardiff	hailerf@cardiff.ac.uk
HALLDÓRSDÓTTIR Katrín	University of Iceland	katrinhalldorsdottir@gmail.com
HAMMOND Robert	University of Leicester	rh225@le.ac.uk
HARTFIELD Matthew	Aarhus University	matthew.hartfield@birc.au.dk
HE Zhangyi	University of Oxford	jefferyhe@outlook.com
HEBBERECHT LÓPEZ Laura	University of Cambridge	lh588@cam.ac.uk
HELMSTETTER Andrew	Royal Botanic Gardens Kew	a.helmstetter@kew.org
HILDEBRAND Falk	EMBL	falk.hildebrand@gmail.com
HILL Tom	University of Kansas	tom.hill@ku.edu
HORTON James	University of Bath	jsh51@bath.ac.uk
HOU Xian	Beijing Forestry University	bhqhouxian@163.com
HOWARD-MCCOMBE Jo	University of Bristol	j.howard-mccombe@bristol.ac.uk

HSU Sheng-Kai	Vetmeduni Vienna	kevin6a2156@gmail.com
HUANG Wei	University of Edinburgh	s1755246@sms.ed.ac.uk
HUETTENBUEGEL Sandra	Heredity	sandra.huettenbuegel@glasgow.ac.uk
HUI Tin-Yu	Imperial College London	tin-yu.hui11@imperial.ac.uk
HURST Laurence	University of Bath	l.d.hurst@bath.ac.uk
IZYDORCZYK Michal	Oxford Brookes University	17020478@brookes.ac.uk
JAMES Jennifer	University of Sussex	j.e.james@sussex.ac.uk
JANSEN VAN RENSBURG Alex	University of Bristol	alexjvr@gmail.com
JARDINE Michael	University College London	michael.jardine.17@ucl.ac.uk
JEFFRIES Daniel	University of Lausanne	dljeffries86@gmail.com
JIGGINS Chris	University of Cambridge	c.jiggins@zoo.cam.ac.uk
JOHANNESSON Kerstin	University of Gothenburg	Kerstin.Johannesson@gu.se
JOHN Max	University of Leicester	mwhj1@le.ac.uk
JOHNSON Louise	University of Reading	l.j.johnson@reading.ac.uk
JOHNSTON Susan	University of Edinburgh	Susan.Johnston@ed.ac.uk
KAMM Jack	Wellcome Trust Sanger Institute	jk21@sanger.ac.uk
KANDA Ravinder	Oxford Brookes University	Rkanda@brookes.ac.uk
KEIGHTLEY Peter	University of Edinburgh	peter.keightley@ed.ac.uk
KELLEHER Jerome	University of Oxford	jerome.kelleher@well.ox.ac.uk
KEMPPAINEN Petri	University of Helsinki	petri.kemppainen@helsinki.fi
KIM Kang-Wook	University of Sheffield	k.kim@sheffield.ac.uk
KIMBELL Helen	Frontiers	helen.kimbell@frontiersin.org
KING Andrew	University of Exeter	r.a.king@exeter.ac.uk
KING Jessica	University of Edinburgh	jessica.king@ed.ac.uk
KOSIOL Carolin	University of St Andrews	ck202@st-andrews.ac.uk
KOUFOPANOOU Vassiliki	Imperial College London	v.koufopanou@imperial.ac.uk
KUIJPER Bram	University of Exeter	a.l.w.kuijper@exeter.ac.uk
KUPCZOK Anne	Kiel University	akupczok@ifam.uni-kiel.de
LAWSON Daniel	University of Bristol	dan.lawson@bristol.ac.uk
LEWIS Rebecca	University of East Anglia	becky.lewis@uea.ac.uk
LEWIS Samuel	University of Cambridge	sam.lewis@gen.cam.ac.uk
LIPINSKA Agnieszka	CNRS UPMC	alipinska@sb-roscoff.fr
LOHSE Konrad	University of Edinburgh	konrad.lohse@gmail.com
LUMBY Casper	University of Cambridge	ckl35@cam.ac.uk
LÜTGE Mechthild	EMBL	mechthild.luetge@embl.de
MADGWICK Philip	University of Bath	pgm29@bath.ac.uk
MARIE-ORLEACH Lucas	University of St Andrews	lmo2@st-andrews.ac.uk
MARTIN Claudia	University of East Anglia	claudia.martin@uea.ac.uk
MARTINEZ RUIZ Carlos	Queen Mary London	c.martinezruiz@qmul.ac.uk
MATHERS Thomas	John Innes Centre	thomas.mathers@jic.ac.uk
MCGREGOR Alistair	Oxford Brookes University	amcgregor@brookes.ac.uk
MCMULLAN Mark	Earlham Institute	mark.mcmullan@earlham.ac.uk
MENNELL Holly	University of Bristol	holly.mennell@bristol.ac.uk
MERRILL Richard	LMU Munich	merrill@bio.lmu.de
METHERINGHAM Carey	Queen Mary University of London	clm79@student.le.ac.uk
MOEBIUS Wolfram	University of Exeter	w.moebius@exeter.ac.uk
MORALES Hernan	University of Gothenburg	hern.moral@gmail.com
MÖST Markus	University of Innsbruck	Markus.Moest@uibk.ac.at
NADEAU Nicola	University of Sheffield	n.nadeau@sheffield.ac.uk
NEVADO Bruno	University of Oxford	bruno.nevado@plants.ox.ac.uk
NICHOLS Richard	Queen Mary University of London	r.a.nichols@qmul.ac.uk
NOWELL Reuben	Imperial College London	reubennowell@gmail.com
O'BRIEN Eleanor	University of Bristol	eleanor.obrien@bristol.ac.uk

OOSTRA Vicencio	University College London	v.oostr@ucl.ac.uk
OROZCO TER WENGEL Pablo	University of Cardiff	sbipao@cf.ac.uk
ORR David	University of Leeds	bds@leeds.ac.uk
PAAJANEN Pirta	John Innes Centre	pirta.paajanen@jic.ac.uk
PAPADOPULOS Alex	Bangor University	a.papadopoulos@bangor.ac.uk
PAPOLI YAZDI Homa	Uppsala University	hpapoli@gmail.com
PARIS Josie	University of Sussex	j.paris@sussex.ac.uk
PARKER Darren	University of Lausanne	DarrenJames.Parker@unil.ch
PATERSON Steve	University of Liverpool	s.paterson@liverpool.ac.uk
PAYNE Pavel	University of Liverpool	pavel.payne@liverpool.ac.uk
PECK Joel	University of Cambridge	jp564@cam.ac.uk
PEEDU Elisabet	Umeå University	elisabet.peedu@umu.se
PEICHEL Katie	University of Bern	catherine.peichel@iee.unibe.ch
PERINI Samuel	University of Gothenburg	samuel.perini@gu.se
PERRY William	Bangor University	w.perry@bangor.ac.uk
PETERS Lucy	University of Edinburgh	Lucy.Peters@ed.ac.uk
PHILLIPS Barret	University of Lausanne	barret.phillips@unil.ch
PISA Hanja	University of Vienna	hanja.pisa@univie.ac.at
POINTER Michael	University of East Anglia	mdpointer@gmail.com
POLECHOVÁ Jitka	University of Vienna	jitka@univie.ac.at
POMIANKOWSKI Andrew	University College London	uchbpom@ucl.ac.uk
PRACANA Roddy	Queen Mary London	rodrigopracana@gmail.com
PRESGRAVES Daven	University of Rochester	daven.presgraves@rochester.edu
PRIEST Nick	University of Bath	n.priest@bath.ac.uk
RASTEIRO Rita	University of Bristol	rita.rasteiro@bristol.ac.uk
RAZGOUR Orly	University of Southampton	Orly.Razgour@soton.ac.uk
RECKNAGEL Hans	University of Glasgow	hans.recknagel@glasgow.ac.uk
REUTER Max	University College London	M.reuter@ucl.ac.uk
RITCHIE Michael	University of St Andrews	mgr@st-andrews.ac.uk
ROSE Saloni	IISER Mohali	salonirose.95@gmail.com
ROSSI Matteo	LMU Munich	rossi@bio.lmu.de
ROZE Denis	CNRS	roze@sb-roscoff.fr
RUZICKA Filip	University College London	filip.ruzicka.09@ucl.ac.uk
SACCHERI Ilik	University of Liverpool	saccheri@liv.ac.uk
SAXON Andy	University of Bristol	andy.saxon@bristol.ac.uk
SCHLÖTTERER Christian	Vetmeduni Vienna	christian.schloetterer@vetmeduni.ac.at
SEAMAN Josiah	Queen Mary London	josiah.seaman@gmail.com
SEGAR Simon	Czech Academy of Sciences	simon.t.segar@gmail.com
SHIN Jiyeong	EHWA	wldud0915ek@gmail.com
SONI Viv	University of Sussex	v.soni@sussex.ac.uk
SORIA-CARRASCO Victor	University of Sheffield	v.soria-carrasco@sheffield.ac.uk
SPEIDEL Leo	University of Oxford	leo.speidel@outlook.com
SPURGIN Lewis	University of East Anglia	l.spurgin@uea.ac.uk
STANKOWSKI Sean	University of Sheffield	s.stankowski@sheffield.ac.uk
STEVENS Jamie	University of Exeter	j.r.stevens@ex.ac.uk
SZEP Eniko	IST Austria	eniko@ist.ac.at
TAYLOR Tiffany	University of Bath	t.b.taylor@bath.ac.uk
TAYLOR-COX Evelyn	University of Liverpool	e.taylorcox@hotmail.co.uk
THOMPSON Kirsten	University of Exeter	k.f.thompson@exeter.ac.uk
TURNER John RG	University of Leeds	j.r.g.turner@leeds.ac.uk
TURNER Leslie	University of Bath	l.m.turner@bath.ac.uk
VAN BELLEGHEM Steven	University of Cambridge	vanbelleghemsteven@hotmail.com
VAN DER ZEE Mijke	University of Sussex	mv250@sussex.ac.uk

WESTRAM Anja Marie	University of Sheffield	a.westram@sheffield.ac.uk
WHITE Nathan	University of Sheffield	nwhite3@sheffield.ac.uk
WHITTAKER Ben	Swansea University	909937@swansea.ac.uk
WIGBY Stuart	University of Oxford	stuart.wigby@zoo.ox.ac.uk
WILLIS Katie	Imperial College London	KW1016@ic.ac.uk
WIRTZ Johannes	University of Cologne	wirtzj0@uni-koeln.de
WONG Edgar	University of Oxford	edgarwly@gmail.com
WOUTERS Roland	John Innes Centre	roland.wouters@jic.ac.uk
WURM Yannick	Queen Mary London	y.wurm@qmul.ac.uk
YANT Levi	John Innes Centre	Levi.Yant@jic.ac.uk
ZENG Kai	University of Sheffield	k.zeng@sheffield.ac.uk
ZHAN Xiangjiang	IOZ Chinese Academy of Sciences	zhanxj@ioz.ac.cn
ZHAO Lei	University of Cambridge	zhaolei325@gmail.com
ZHU Ana	Wellcome Trust Sanger Institute	ana.zhu@sanger.ac.uk

Notes:

