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Veterinary & Life Sciences

Institute of Biodiversity, Animal Health & Comparative Medicine

#POPGROUP46

GLASGOW

18-21 DEC 2012



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Conference Details and Logistics

Conference Support: Welcome to PopGroup 46. We are delighted to welcome you to Glasgow. This year's meeting is hosted by the Institute of Biodiversity, Animal Health & Comparative Medicine (IBAHCM), College of Medical, Veterinary & Life Sciences. The meeting is sponsored annually by the Genetics Society (who also publish the journal *Heredity*) and discounts are offered to Genetics Society members. This year we had a large number of applicants who were not Genetics Society members. If you would like to join the Genetics Society to receive a discount for next year's meeting, please use the following link: <https://services.portlandpress.com/gts/apply.htm>.

This year, we have also obtained generous support for social activities from the Glasgow City Marketing Board, the Royal Society, and IBAHCM. Prizes for the talk and poster competitions have been generously donated by Nature Reviews Genetics, Oxford University Press, and Roberts & Company.

The conference bags are officially called "Charlesworth tote bags" (<http://www.promotionalgifts.org/charlesworth-cotton-tote-bags-p7279.htm>). Many thanks to Martin Muir for designing the logo and providing assistance with website design.

Conference Venue: Registration will be available at the Jurys Inn in Central Glasgow from 16:00-23:00 on Tuesday, 18th December. This is also where the NERC Biomolecular Analysis Facility information session (17:00-18:00) and the opening reception (18:00-23:00) will be held. The rest of the conference will take place at the Gilmore Hill campus of the University of Glasgow. Registration will be available in the Atrium of the Wolfson Medical School Building (WMSB; C8 on the campus map) from 8:30-17:00 on Dec. 19 and 20. Plenary sessions will be held in Lecture Theatre 2 of the Boyd Orr Building (BOB; D1 on the campus map) and contributed talks, coffee breaks and lunch on Dec. 21 will be held in the WMSB. Lunches on Dec. 19 and 20 and the poster session on Dec. 19 will be held in the Glasgow University Union (GUU; E8 on the campus map), which is about a 7 minute walk from where the talks will take place. From the WMSB, turn right on University Avenue, walk up the hill, then down and follow the curve around to the left. The GUU is on the left hand side. Dinner on Dec. 19 will be off-campus. The Civic reception, conference dinner and ceilidh on Dec. 20 will be held at the Hunter Halls (HH; A12 on the campus map), in the main quad of the University.

Oral Presentations: Contributed sessions will take place in the West Medical School Building (C8 on the UG map), in one of three rooms located to the right of the open atrium area (where the coffee breaks will take place). Talks will last 19 minutes (including questions), to allow 1 minute to change rooms and change over speakers. The standard option will be PC computers but if you wish to use a Mac laptop or Ipad, please check with the AV attendant before your session to make sure that a smooth transition will work. Please upload your talks in the break before your session at the latest.

Session Chairs: The last speaker in the session will be assigned as the session chair. If you are not able to act as chair, please contact the conference organisers. Chairs should signal to the speakers when 15 minutes has passed, then again at 17 minutes, and then stand up at 18 minutes to let the speaker know that the room changeovers will be in one minute. Questions should be finished by 19 minutes.

Posters: Posters will be displayed in the Glasgow University Union (GUU), which is at the bottom of University Avenue (just before Gibson Street, E8 on the campus map). The size of the display boards is A0 portrait, so please ensure that your poster will fit that space. Posters can be put up at the beginning of the lunch session on Wednesday and should be taken down

at the end of the lunch session on Thursday. There will be a storage area available in the GUU; posters can be picked up on Friday morning if you don't want to carry them around on Thursday evening.

Prizes: Following the tradition started in Nottingham last year, there will be prizes for the best student talks, the best student posters, and the best nonstudent talk. In addition, since we have scheduled some student talks on the last day, there will be separate prizes as a reward for those presenting at the end. Cash prizes (and journal subscriptions) have been generously donated by Nature Reviews Genetics and books have been donated by Oxford University Press and Roberts & Company (the books will be on display in the area where coffee is served). All delegates will be asked to vote; you will receive a hard copy in your registration package or you can download an electronic version from the conference website. Please return your voting forms by hard copy at the registration desk or by email to: Barbara.mable@glasgow.ac.uk by 17:30 on Thursday, Dec. 20. Awards will be presented at the conference dinner. For the last day, awards will be presented at lunch on Dec. 21st so please return your voting forms by 12:15.

Wireless Access: Wireless access has been arranged at the hotel; please check with the desk for a password. At the University, there will be two options available for Wi-Fi access. 1) Eduroam: we strongly suggest that you use this option if it is available to you. You should be able to obtain a password from your own University before attempting to log in to wireless at Glasgow. 2) The conference will be assigned a guest password for wireless using the GU Visitor system. However, it is necessary to access this using Cisco Clean Access ActiveX web client or Cisco Clean Access Java Applet web client for authentication. Currently many devices including iPhones, iPads and Blackberries are unable to operate this. The University also uses a proxy server, which can sometimes be problematic. If you are having difficulties with internet access, please check the instructions provided in the appendix at the back of the conference booklet. Since most people now have their own computers, we haven't booked a computer cluster for the conference; however, if you require internet access and don't have a laptop, please contact the conference organisers.

Transportation

Getting to Glasgow (directions to Jury's Inn, 80 Jamaica Street, G1 4QG): Jurys Inn is only 2 minutes from Central Station and 15 minutes from Queen Street Station, with direct rail links to all parts of the UK. The airports of Glasgow International and Glasgow Prestwick are both easily accessible, the former by bus or taxi and the latter by train.

From Glasgow Central Station – 0.1 km: Three minute walk. Exit Glasgow Central Station from the Union Street exit (east side). Turn right and keep walking down past MacDonalds. Jurys Inn Glasgow is situated at the end of this street (Jamaica Street) on the right hand (west) side

From Glasgow Queen Street Station – 0.2 km: From Queen Street station take the George Square exit. Turn right onto St Vincent St and then left onto Buchanan St. (a closed pedestrian shopping district). Continue down to the end of Buchanan St, turn right onto Argyle St and take an immediate left onto Jamaica St. Jurys Inn is across the road on the right hand (west) side.

From Glasgow International Airport – 15 km: There is a bus (First 500) available at the airport, which will take you to Central Station. The bus is available every 15 minutes and will take approximately 20-30 minutes, depending on traffic. Once at Central Station please see directions above.

A taxi to Jury's Inn will take about 15 minutes and will cost £16 when booked with Glasgow Taxi's, quoting code **CM7**. To book, call 0141 429 7070. You can also catch a black cab directly outside of the terminal buildings but the price will be higher (£20).

From Glasgow Prestwick Airport – 48 km: There is a train service available at Prestwick airport, which will take you to Central Station. These trains are available every half hour and will take approximately 30-40 minutes.

By car: Jury's Inn have discounted rates in the car park immediately opposite the hotel. The rate for 24 hours parking is £7.00.

Getting between the city centre (Jury's Inn, train stations and bus terminal) and the west end (University of Glasgow G12 8QQ): Glasgow has good public transport and is a safe place to walk.

Subway: The easiest way to travel between the west end and central Glasgow is via the subway. It is one of the oldest in the UK and is small but functional. It has an inner and an outer circle, so that you can get to any stops in either direction; however, choose the direction that has your destination as the closest stop. Tickets cost £1.40 for a single, £2.60 for a return and £3.80 for an all day discovery ticket. The Jurys Inn is close to St. Enoch's subway station. To get to St. Enoch's station from the Jurys Inn, leave the hotel on Jamaica street and cross the street at the intersection; turn left (north) and take the first right. Walk down one block and then turn left into a courtyard, where the subway station is located (three minute walk). Take the inner circle of the subway to Hillhead to get to the University; take the outer circle on the return journey. Once you arrive in Hillhead, turn left (south) as you come out of the subway, walk along Byres Road until you reach the crossroads, then turn left up University Avenue; the Boyd Orr Building (where the plenary lectures will be held) will be on your left (tall 60s building). The Wolfson Medical Building, where most of the talks will take place and where the registration desk will be located Wednesday-Friday, is across the road (more modern building with lots of glass and a bike rack out front). Walking between the subway and the University will take about 5 minutes; you should allow 30 minutes in total to get from Jurys Inn to the University. The last subway train from Hillhead to the Centre is at 11:10 pm; trains run every 8 minutes at nonpeak times. There are also buses, but more difficult to predict schedules and not any cheaper than the subway.

[Glasgow Subway map and information](#)

Taxis: There are taxi ranks at the train stations at Queen Street and Central Station (in the centre) and outside the Hillhead subway station (in the west end). A taxi between the west end and the centre takes 10-15 outside of rush hour, will cost £5-7 and can work out cheaper than the subway if split between a number of people. If travelling to the University, the best point to be dropped off is at the Botany Gates (University Place Car Park) on University Avenue. The last train to Edinburgh is at 11:30 pm and it is best to leave 30 minutes to get to Queen Street from the West End (20 minutes minimum). Taxi queues can be long late at night. Walking will take about 45 minutes. Taxis to Edinburgh are expensive but can be cheaper than the train if you have a large group.

On Foot: If walking from the Jurys to the west end, the best route to take will depend on the time of day. Although Glasgow is a very safe place to walk in general, it is always recommended (as for any big city) to avoid walking through the parks after dark and the University locks its back gates at night. Walking will take about 45 minutes. From the Jurys Inn, there are lots of routes (google maps will likely suggest a more convoluted route) but the easiest to navigate is to walk directly up to Sauchiehall Street (turn left out of the hotel on Jamaica street and walk north for 10 minutes), then turn left (west) and walk to the motorway (M8). Cross over the motorway and continue walking along Sauchiehall Street, which will turn into Argyll Street. After about 15 minutes, the University will be visible up the hill on the right (north). To walk through the park, turn right at Clifton Street and follow the main path through the park, past the fountain, the duck pond and child's play area, and then cross the river. The path will come out on Kelvin Way. Cross the road and turn right (north). From here you can take one of two routes: 1) Turn left just below the hill to the University and walk up a steep staircase up to the University, turn left,

walk past the main buildings and down the hill, turn right by the Zoology (Graham Kerr Building), then walk straight towards the Botany Gate. Walk through the gate and the Wolfson Medical school building will be on your left (beside a car park); the Boyd Orr Building is the large 60's building across the road on University Avenue. 2) Continue walking north on Kelvin Way to the corner of University Avenue, turn left and walk up the hill and then down; the Wolfson Medical School Building will be on your left and the Boyd Orr Building on your right. At night, you would need to take the University Avenue route back to Kelvin Way (because the gates will be locked) and you can walk along Kelvin Way to Sauchiehall street. Alternatively, you can turn left at the bottom of University Avenue (by the GUU) and turn immediately right onto Gibson Street, then walk east towards the motorway (it will turn into Woodlands Road). Cross the multi-lane road by the motorway (Charing Cross), turn right and then left onto Sauchiehall street.

By car. It is difficult (and expensive) to park in the west end of Glasgow so we would recommend that you take public transport. If you are commuting and need to park your car in the west end please contact ppg@populationgeneticsgroup.org in advance.

Social Events

All social events are included in the registration package, as most have had at least partial sponsorship from various organisations.

December 18: NERC Biomolecular Analysis Facility (NBAF) Information Session; Opening reception at the Jurys Inn (sponsored by the Genetics Society)

Registration: 16:00-23:00

NBAF Information session: 17:00-18:00

Reception: open from 18:00

Finger food buffet: available from 19:00-21:00

First drink free and then cash bar

The hotel also has a bar that will stay open as long as required and there are many pubs in the area.

December 19: Poster Reception at the Glasgow University Union; Dinner off campus

The poster session will take place from 17:30-19:15 on the Wednesday evening. There will be a mulled wine and mince pies reception in conjunction with this. There will also be a cash bar available and there are other bars in the building with a wider selection of beers.

Following the reception there will be two options for dinner (sponsored by the Glasgow City Marketing Board and Royal Society Publishing):

A/ Buffet meal at a local pub (Curler's Rest). It will be crowded and cosy but they have a good selection of beers and wines available. The meal will include one drink and then there will be a cash bar. The buffet will start at 20:00 (drinks from 19:30) and the bar has late opening for Christmas until 1 am. The pub is located on Byres Road, in the block north of the Hillhead subway station (right/east side of road).

B/ If you selected a sit-down meal at a restaurant instead of the buffet, it will be held at La Vita Spuntini's, which is an Italian tapas style restaurant. The restaurant is booked for 17:30 and you should proceed there after the poster session. There will be a fixed two-course menu (the Festa menu WEBLINK), which includes one drink. Additional courses and drinks will be charged extra. The restaurant is located on Byres Road, in the first block on the northwest corner of University Avenue (beside the Tennents pub).

December 20: Civic Drinks reception, Conference Dinner & Ceilidh at the Hunter Halls, University of Glasgow

19:00: Civic Drinks Reception, with Prosecco and canapés (sponsored by the Lord Provost's office)

Canapés

Savoury shortbread with tomato and feta cheese (v)

Parmesan and rosemary shortbread rounds, topped with cherry tomato and feta cheese

Scottish smoked salmon on a mini oatcake

Fine Scottish smoked salmon on a mini oatcake with cream cheese

Carpaccio of venison with rocket and pear chutney

Thinly sliced fillet of venison with a rocket and pear chutney

20:00: Conference Dinner (catered by Saltire). Please note that number of vegetarian options will be calculated based on food preferences indicated on the registration form. If you do not want the fish soup or duck main course, please let the conference organisers know as soon as possible.

Starters

Sweet potato and red onion with parmesan crouton soup (vegetarian option)

or

Smoked haddock chowder (Cullen skink)

Main

Duck leg confit with apple and rocket, parmentier potatoes and a cider jus

or

Leek and fennel tart with smoked apple wood cheese, poached egg and hollandaise sauce (vegetarian option)

Dessert

DIY Cranachan (to be explained at the dinner)

Coffee and Chocolates

21:30-1:00: Conference Ceilidh (sponsored by IBAHCM)

'Coila Ceilidh Band' (one of the members is himself a population geneticist, Willie Weir). Wine will be available through the evening but there will be a cash bar for other options.

Glasgow's West End

The University is located on the corner of Byres Road and University Avenue. Byres Road (one block from the conference venue) has many shops, pubs, restaurants and coffee shops. [There are also an increasing number of ice cream shops, but not likely the right time of year.] Some recommendations are provided below but Pat's guide to the west end (<http://www.glasgowwestend.co.uk/>) and The List (<http://www.list.co.uk/>) are both good for assessing options. The main tourist part of the west end is a cobblestone lane called Ashton Lane. It runs parallel to Byres Road and can be accessed from the west side of the Boyd Orr Building on University Avenue or a small lane off of Byres Road by the Iceland store (close to Hillhead).

Pubs: In the west end, we would recommend that Curler's Rest be the default pub conference venue, as it is large and has good beer, wine and whisky (right next to Hillhead subway station on Byres Road). Other recommended pubs in the area are: The Ubiquitous Chip (three different pubs of varying sizes; Ashton Lane); Brel (good selection of Belgian beers; Ashton Lane); Tennents (classic Glaswegian sports bar with good selection of beers, despite the name; corner of University Avenue and Byres Road); Oran Mor (former church; corner of Byres Road and Great Western Road); The Three Judges (classic pub with live music at times; corner of Dumbarton Road and Byres Road); Brewdog (brew pub with dangerously strong beer; Argyll street, across from the Kelvingrove Museum); The Ben Nevis (classic pub with live music at times; Argyll street, halfway between the University and the hotel); and Dram (large, specialises in whisky; Woodlands Rd, between the University and the hotel). These pubs all have a good selection of beers and whiskies but there are also many other pubs to choose from in the area, particularly if you like Tennents and lagers. A local friendly pub that we like (but that doesn't have a good beer selection) is The Dolphin (Dumbarton Road, west of Byres Road). Oran Mor stays open until 2 am (3 am from Thursday to Sunday) but most of the others close at 23:00 or 00:00 (unpredictable, as some will have late opening licenses until 1 am for the Christmas season). The closest club to the University is Viper (corner of Great Western Road and Bank Street), which is technically an under 25 venue but that doesn't usually stop people from going. There are also a number of clubs in the city centre.

Coffee: Unfortunately, something we can't control is the quality of coffee at the University. There are, however, lots of coffee options nearby for those who need a latte fix and there is a Costa coffee on the ground floor of the Jurys hotel. On Byres Road, some options are: Starbuck's (right next to the Hillhead subway station); TinderBox (good strong coffee and desserts; corner of Byres Road and University Avenue); Kember and Jones (excellent deli with good baking; between University Avenue and University Place); Heart and Buchanan (traditional deli that has been somewhat compromised by Waitrose moving in across the road; close to Great Western Road on the eastern side of Byres Road); Avenue G (good coffee and food but not always very quick service; on the western side of Byres Road, about halfway between University Avenue and Great Western Road).

Restaurants: There are many restaurants in the west end, with a rather high turnover. It is best to check websites for menus and prices. At Christmas, it is always best to book but there are often good deals available. Some of our favourites that have been around for at least a few years are listed by category below:

Indian: Ashoka's (classic Glaswegian chain; Ashton Lane); Wee Curry Shop (very small but includes Haggis pakoras; Ashton Lane); Wee Curry shop (not the same owners as the one on Ashton lane and different food; Byres Road, close to Dumbarton Road); Balbir's (large, specialises in large groups and banquet menus; Church Street, which runs parallel to Byres Road, close to Dumbarton Road).

Italian: Una Storia (formerly Mimmo's, small and friendly; Ashton Lane); Zizzi (wood-fired pizzas and pastas; Cresswell lane, which is a northern extension of Ashton Lane, past Great George

Street); Paperino's (chain of pizza places but large; Byres Road, across from Hillhead); Little Italy (small, but better than it looks from the outside – authentic Italian ingredients and good coffee; western side of Byres Road, close to University Avenue); La Vita Spuntini (Italian tapas; Byres Road, across from Hillhead).

Scottish/Bistro: Cail Bruich (Scottish bistro – worth the full price but often have good pre-theatre deals midweek; Great Western Road, just east of Byres Road); The Bothy (Scottish bistro cuisine – classic Scottish cuisine; Ruthven Lane, which is just off of Byres road across from Hillhead); Number 16 (Scottish bistro; Byres Road, near Dumbarton Road); Stravaigin (Scottish; Gibson Street, which is very close to the Glasgow University Union).

Other: La Vallée Blanche (French, Byres Road, midway between Hillhead and Great Western Road); Bovine (as the name implies, specialise in steaks but usually quite good vegetarian options; western side of Byres Road near Great Western Road); Two Fat Ladies (the original famous fish restaurant, at 88 Dumbarton Road – just east of Byres Road).

SCHEDULE AT A GLANCE

Wednesday 19 December, 2012

Time			
09.00-09.10	Welcome and introduction (Boyd Orr Lecture Theatre 2)		
09.10-10:00	PLENARY (Boyd Orr Lecture Theatre 2) Mike Arnold <i>University of Georgia</i> Reproductive Isolation and Introgression: lessons learned (and being learned) from the Louisiana Irises		
10.00-10:40	COFFEE BREAK (Wolfson Medical School Atrium)		
Contributed Sessions	Hugh Fraser	Gannochy	Yudowitz
10:40-11:00	Kanapathy Gajapathy S <i>University of Jaffna</i> Morphological complexity and speciation in <i>Phlebotomus argentipes</i> species complex: A need for a molecular tool to discriminate vector populations	James L Kitchen <i>University of Warwick</i> Agrisims: Simulating crop domestication using individual based modeling	Austin Burt <i>Imperial College London</i> Engineered endonucleases for control of pest populations
11:00-11:20	Tim Downing <i>National University of Ireland Galway</i> Ancient and recent origins of drug resistance of a Leishmania parasite epidemic	Jenny Hagenblad <i>Linköping University</i> Nutrient content in wheat and the NAM-B1 gene – A story of domestication and plant improvement	Ravinder Kanda <i>Imperial College London</i> A model for the dynamics of endogenous retroviruses
11:20-11:40	Matthew Hartfield <i>MiVEGEC, IRD, Montpellier</i> Determining the effect of Hepatitis C genotype on virus outcome	Kirsten Wolff <i>Newcastle University</i> Genetic diversity and hybridisation in ancient lime trees (<i>Tilia</i>)	Elizabeth HB Hellen <i>University of Nottingham</i> Prediction of ancient transposon proliferation processes through phylogenetic analysis of modern elements
11:40-12:00	Hannah Trewby S <i>University of Glasgow</i> Using bacterial population genomics to investigate the spread of bovine tuberculosis	Aline Finger <i>Royal Botanic Garden Edinburgh</i> Forest fragmentation genetics in a formerly widespread island endemic tree: <i>Vateriopsis seychellarum</i> (Dipterocarpaceae)	Samuel H Lewis S <i>University of Edinburgh</i> The population genetics of recent antiviral gene duplicates in <i>Drosophila</i>
12.10-14.00	LUNCH (Glasgow University Union)		
14:00-14:20	Alina K Niskanen S <i>University of Oulu</i> Immune gene diversity in canines	Paris Veltsos <i>University of St Andrews</i> QTLs for behavioural variation within populations are different than between populations	Daniel Weissman <i>IST Austria</i> Patterns of diversity in adapting, spatially extended populations
14:20-14:40	Marie Kidd S <i>University of New South Wales</i> The inference of phased haplotypes for the immunoglobulin heavy chain variable region gene loci by high-throughput analysis of VDJ gene rearrangements	Rodrigo Cogni <i>University of Cambridge/ Stony Brook University</i> Strong selection acting on the couch potato gene: spatial-temporal variation in a diapause cline	Simon Aeschbacher <i>University of Vienna</i> Limits to local adaptation and consequences for its genetic architecture
14:40-15:00	Thorsten Stefan S <i>University of Glasgow</i> Modelling the generation and maintenance of diversity at the MHC	Jose L Campos <i>University of Edinburgh</i> Molecular evolution and variation in regions of the <i>Drosophila melanogaster</i> genome that lack crossing over	Jitka Polechová <i>IST Austria</i> When does genetic drift prevent expansion of a species' range?
15:00-15:20	Joaquin Prada J de Cisneros S <i>University of Glasgow</i> Modelling resistance against gastrointestinal nematodes in sheep	Gilbert Smith S <i>University of St Andrews</i> Transcriptome-wide expression variation associated with environmental plasticity and mating success in the cactophilic <i>Drosophila mojavensis</i>	John Brookfield <i>University of Nottingham</i> Population genetic change and species co-existence
15.20-15.50	COFFEE BREAK (Wolfson Medical School Atrium)		
15:50-16:10	Samantha Lycett <i>University of Edinburgh</i> Pandemic expansion and seasonal oscillations in influenza viral diversity	Paul M Richards S <i>University of Nottingham</i> Unwinding the chiral evolution of Japanese snails using RAD-seq	Jens Nullmeier S <i>MPI Göttingen</i> The coalescent in boundary-limited range expansions
16:10-16:30	Chris Illingworth <i>Wellcome Trust Sanger Institute</i> Components of selection in the evolution of the influenza virus: linkage effects beat inherent selection	Angus Davison <i>University of Nottingham</i> A RAD-Seq phylogeny of Mandarin snails from the Japanese Ogasawara archipelago	Sebastian Novak S <i>IST Austria</i> Type-dependent migration in continuous space and time
16:30-16:50	Gytis Dudas S <i>University of Edinburgh</i> Antagonistic interactions between co-circulating subtypes of human influenza viruses	Anja M Westram <i>University of Sheffield</i> Genetic basis and geographical patterns of adaptive divergence in an intertidal snail	Jerome Kelleher <i>University of Edinburgh</i> Coalescent simulation in continuous space
16:50-17:10	Lu Lu S <i>University of Edinburgh</i> Diverse reassortment patterns of avian influenza viruses among different subtypes in internal segments	Quentin Jossart S <i>Université Libre de Bruxelles</i> Weak differentiation according to host species and small spatial scale in a parasite crab	David Marcelo Schneider S <i>Universidade Estadual de Campinas</i> Robustness against extinction by stochastic sex determination in small populations
17:10-17:30	Fiona Savory <i>National Centre for Bio. Sci., Bangalore</i> Evolutionary dynamics of a multipartite plant virus in a heterogeneous mountain landscape	Katy Morgan <i>Max Planck Institute</i> Island biogeography of <i>Pristionchus pacificus</i> reveals dispersal limited by environment rather than sea barriers	Valeria Montano <i>University of Veterinary Medicine Vienna</i> Using a human model to reproduce the variability of a human parasite
17:45-19:15	POSTER SESSION AND MULLED WINE RECEPTION (Glasgow University Union)		
19:30	DRINKS AND DINNER (BUFFET AT CURLER'S REST OR SIT-DOWN DINNER AT LA VITA SPUNTINI, BOTH ON BYRES ROAD)		

Thursday 20 December, 2012

Time			
09.00-09.10	Welcome and introduction (Boyd Orr Lecture Theatre 2)		
09.10-10:00	PLENARY (Boyd Orr Lecture Theatre 2) Charlie Baer <i>University of Florida</i> Exploring the mutational landscape of <i>Caenorhabditis</i>		
10.00-10:40	COFFEE BREAK (Wolfson Medical School Atrium)		
Contributed Sessions	Hugh Fraser	Gannochy	Yudowitz
10:40-11:00	Darren J Obbard <i>University of Edinburgh</i> The discovery and population genetics of <i>Drosophila</i> viruses	David Shuker <i>University of St Andrews</i> Challenges to the gene's eye view of evolution: hot air or hot water?	Ignacio Gallo <i>Freelance</i> Population genetics of gene function
11:00-11:20	Catalina Gonzalez Quevedo S <i>University of East Anglia</i> Spatial variation in avian malaria infection in a wild population of Berthelot's pipit (<i>Anthus berthelotii</i>)	Richard Nichols <i>Queen Mary University of London</i> Variation in speciation time for different parts of the genome	Lukas Geyrhofer S <i>MPI Göttingen</i> Noisy evolutionary waves
11:20-11:40	Danielle Gilroy S <i>University of East Anglia</i> Functional variation at immune loci in the Seychelles warbler	Martin Carr <i>University of Huddersfield</i> Evolutionary trends in the Choanoflagellates: insights into the origin of metazoa	Harold P de Vladar <i>IST Austria</i> Stabilizing selection on polygenic traits: stability and response under unequal effects
11:40-12:00	Michael J Stear <i>University of Glasgow</i> Breeding parasite resistant sheep	Toni I. Gossmann <i>University of Hohenheim</i> The embryogenic hourglass in plants	Duncan Palmer <i>University of Oxford</i> Integrating genealogical and dynamical modelling to infer escape and reversion rates in HIV epitopes
12.10-14.00	LUNCH (Glasgow University Union)		
14:00-14:20	Torsten Guenther S <i>University of Hohenheim</i> Nitrogen content of the <i>Arabidopsis thaliana</i> transcriptome is shaped by mutational bias and GC-biased gene conversion	Jon Bride <i>University of Bristol</i> Evolution on the move: adaptation in the UK Brown Argus butterfly in response to climate change	Kai Zeng <i>University of Sheffield</i> A coalescent model of background selection with recombination, demography and variation in selection coefficients
14:20-14:40	Kathryn Elmer <i>University of Glasgow</i> Comparative genomics and transcriptomics of extremely young species of crater lake cichlid fishes	Nicola Nadeau <i>University of Cambridge</i> Genome-wide patterns of divergence and gene flow across a butterfly radiation	Brian Charlesworth <i>University of Edinburgh</i> Stabilising selection and mutational bias in finite populations
14:40-15:00	John Stainton S <i>Roslin Institute</i> To evaluate and apply novel statistical techniques for diversity based gene-mapping	Krzysztof M Kozak S <i>Zoology, University of Cambridge</i> Conflicting signals in the phylogeny of Heliconiini butterflies	Kavita Jain <i>J. Nehru Centre for Adv. Sci. Res., Bangalore, India</i> Fixation of mutators in asexual populations: the role of genetic drift and epistasis
15:00-15:20	Christian Schlötterer <i>Vetmeduni Vienna</i> Pool-GWAS: a general and cost-effective method for fine-mapping natural phenotypic variation	Catharine Bruce S <i>University of East Anglia</i> Linking landscape genetics to metacommunity ecology: spatial genetic structure provides meaningful insight to dispersal characteristics in a tropical ant-plant system	Pam Wiener <i>The Roslin Institute, University of Edinburgh</i> A regression approach to selection mapping
15.20-15.50	COFFEE BREAK (Wolfson Medical School Atrium)		
15:50-16:10	Victoria Avila <i>University of Edinburgh</i> Testing for faster-X effects in two lineages of the genus <i>Drosophila</i>	Jonathan Ellis <i>Manchester Metropolitan University</i> Finding candidate markers of adaptive variation in social insects	Sozos Michaelides S <i>University of Oxford</i> Phylogeography and population genetic structure of an alien lizard
16:10-16:30	Darren J Parker S <i>University of St. Andrews</i> Do closely related species use the same genes to adapt to fluctuating environmental conditions?	Faye Willman S <i>University of Kent</i> Spatial and temporal population genetics of the Mauritian Pink Pigeon (<i>Columba mayeri</i>)	Jen Swanstrom S <i>University of Bristol</i> Uncovering hidden genetic diversity in a cryptic species of African river catfishes, <i>Chiloglanis</i>
16:30-16:50	Colin McClure S <i>University of Bath</i> A genetic dissection of hormesis	Kathrin Theissingner <i>University of Koblenz-Landau</i> First large-scale genetic analysis of the vulnerable noble crayfish <i>Astacus astacus</i> in Europe	Heidi Aisala S <i>University of Oulu</i> Sex and clonality: the evolutionarily successful strategies of a parasitic flatworm
16:50-17:10	James Hutchison S <i>University of Sheffield</i> Searching for 'speciation genes': A candidate gene approach	Orly Razgour S <i>University of Bristol</i> The shaping of genetic variation in edge populations under past and future climate change: the grey long-eared bat as a case study	David Tarkhnishvili <i>Iliia State University</i> Parthenogenesis – dead end in the evolution of reptiles?
17:15-18:15	GENERAL MEETING (YUDOVITZ)		
19:00-20:00	CIVIC RECEPTION (HUNTER HALLS)		
20:00-21:30	CONFERENCE DINNER (HUNTER HALLS)		
21:30-1:00	CEILIDH (HUNTER HALLS)		

Friday 21 December, 2012

Time			
09.00-09.10	Welcome and introduction (Boyd Orr Lecture Theatre 2)		
09.10-10:00	PLENARY (Boyd Orr Lecture Theatre 2) Rod Page <i>University of Glasgow</i> Why I blog instead of writing papers		
10.00-10:40	COFFEE BREAK (Wolfson Medical School Atrium)		
Contributed Sessions	Hugh Fraser	Gannochy	Yudowitz
10:40-11:00	Clare Marsden <i>University of California, Davis</i> Temporal and spatial mosaic of hybridisation between the M and S molecular forms of <i>Anopheles gambiae</i>	Alex Ball S <i>University of Bath</i> The evolution of sexual dimorphism in a diverse avian family, the Penduline tits (Remizidae)	Sonia Consuegra <i>Aberystwyth University</i> Inbred and furious: genetic diversity, parasites and behaviour in a highly inbred fish
11:00-11:20	Konrad Lohse <i>University of Edinburgh</i> Population genomics of the oak gall wasp <i>Biorhiza pallida</i>	Anna Santure <i>University of Sheffield</i> Molecular dissection of clutch size and egg mass in a wild great tit (<i>Parus major</i>) population indicates polygenic genetic architectures and no evolutionary constraint	J Arvid Ågren S <i>University of Toronto</i> Mating system shifts and transposable element evolution
11:20-11:40	Toby Fountain S <i>University of Sheffield</i> Estimating the size and genetic composition of founding groups in a re-emerging pest, the common bed bug	Clemens Kuepper <i>University of Sheffield</i> High gene flow in two polyandrous plover species	Deborah Charlesworth <i>University of Edinburgh</i> Breakdown of dioecy and high female frequencies
11:40-12:00	Ludovic Duvaux <i>University of Sheffield</i> Speciation in pea aphid host plant races: insights from chemosensory gene divergence	Daniel Jeffares <i>University College London</i> Genomic diversity in the model fission yeast species <i>Schizosaccharomyces pombe</i>	Richard Ennos <i>University of Edinburgh</i> Patterns of mating and generation of diversity in a <i>Geum</i> hybrid swarm
12.00-13.00	LUNCH (Wolfson Medical School Atrium)		
13:00	Departure/Optional Excursion to SCENE		

Abstracts-Plenary Lectures

Plenary 1: December 19

Reproductive Isolation and Introgression: Lessons learned (and being learned) from the Louisiana Irises

Michael Arnold

University of Georgia

In this talk, I will illustrate the development of one plant species complex, the Louisiana Irises, into a 'model system' for investigating hybrid fitness and the role of genetic exchange in adaptive evolution and diversification. In particular, I will argue that a multitude of approaches, involving both experimental and natural environments, and incorporating both manipulative analyses and surveys of natural populations, are necessary to adequately test for the evolutionary significance of introgressive hybridization. An appreciation of the variability of hybrid fitness leads to the conclusion that certain genetic signatures reflect adaptive evolution. Finally, I will discuss some of the newer experiments our group is establishing using a variety of genomic and transcriptomic approaches to decipher the basis of reproductive isolation and adaptation.

Plenary 2: December 20

*Exploring the mutational landscape of *Caenorhabditis**

Charlie Baer

University of Florida

Evolution is directed and ultimately (maybe) constrained by the input of genetic variation by mutation. "Mutation accumulation" (MA) experiments, in which replicate populations of initially genetically identical organisms are allowed to evolve at very small effective population size, have been productively used to characterize the input of genetic variance by mutation in numerous model systems, and several seemingly general results have emerged. Comparison of mutational variation to the standing genetic variation for the same trait provides (quantitative) insight into the nature of natural selection on the trait. Here I report new data from several studies in *Caenorhabditis* nematodes in which a much broader set of traits are investigated than have been previously investigated in similar studies, including pathogen resistance, metabolite concentrations, and meiotic spindle morphology and dynamics. The intriguing preliminary conclusion drawn from a handful of life history and adult morphological traits that the average strength of selection against new mutations is "always" around a few per-cent appears not to generally hold for other types of traits. Further, mutational heritabilities of many features of the meiotic spindle defy the classical generalization that mutational heritabilities are "always" around 0.1% per generation, and that result appears to be due to low (but consistent) genetic variance rather than large residual variance. In contrast, the conclusion that mutation accumulation generally increases microenvironmental sensitivity is largely reinforced.

Plenary 3: December 21

Why I blog instead of writing papers

Rod Page

University of Glasgow

The ease with which we can now publish and distribute information, essentially for free, has major implications for science publishing, and is prompting people to rethink notions of access, peer review, and publication. If one of the goals of science is to disseminate knowledge then it's not clear that the traditional model of publication is best suited to meeting this goal. This

talk explores other approaches to publication, such as blogging, the role of post-publication review, alternatives to journal impact factor, social media, and the rise of "open science".

Abstracts-Oral Presentations

Limits to local adaptation and consequences for its genetic architecture

Simon Aeschbacher and Reinhard Burger

University of Vienna

Adaptation to a new environment requires the presence of locally beneficial alleles, either as standing or de-novo variation. In the latter case, even beneficial mutations must overcome an initial phase of stochastic loss. Influx of maladapted alleles via immigration poses another limit. Beneficial alleles can become established only if immigration is below a critical value codetermined by the selective advantage. The genetic background of a beneficial mutation is also important. If linked to a beneficial background, such a mutation will profit from a hitchhiking-like effect. If occurring on a deleterious background, it is doomed to extinction unless it recombines away. Therefore, recombination plays an ambiguous role. We study the invasion properties of a weakly beneficial mutation occurring in proximity to a second locus at which a beneficial and a deleterious allele are in migration-selection balance. Using the theory of branching processes, we obtain exact numerical and approximate analytical results for the invasion probability as a function of the migration and the recombination rate. We derive predictions for the genetic architecture of traits undergoing local adaptation, such as the degree of genomic clustering and the distribution of fitness effects, and study sojourn times of beneficial mutations. We extend our results to include epistasis by non-neutral Dobzhansky-Muller incompatibilities and a migrant pool that is polymorphic for the background locus. Our results have a direct bearing on the interpretation of genomic patterns of adaptation and our perspective of discovering footprints of selection in DNA sequence data.

Mating system shifts and transposable element evolution **S**

J Arvid Ågren, Robert J Williamson and Stephen I Wright

University of Toronto

Despite having overwhelmingly deleterious fitness effects, self-replicating transposable elements (TEs) are the major contributor to genomes of eukaryotes in general and plants in particular. Under several theoretical models, mating system plays an important role in governing their evolutionary dynamic. Selfing may be associated with a reduction in TE abundance because the lack of outcrossing means that a particularly virulent transposon cannot spread to other individuals in the population. Furthermore, self-regulation of transposition is expected to evolve to be higher in selfers. Here, we present tentative results from computer simulations suggesting that host-mediated silencing reducing the genome wide transposition rate may evolve to be more efficient in selfing compared to outcrossing genomes. We then use genome sequences from selfing and outcrossing species in the plant genera *Capsella* (selfing *C. rubella* and outcrossing *C. grandiflora*, divergence time < 200 kya) and *Arabidopsis* (selfing *A. thaliana* and outcrossing *A. lyrata*, divergence time ~ 10 mya) to make inferences about the effects, and timeframe of those effects, of mating system on TE evolution. First, by aligning the reference genomes of *C. rubella*, *A. thaliana*, and *A. lyrata* we find orthologous regions to be consistently larger in *A. lyrata* compared to *C. rubella* and *A. thaliana* and that these regions also often harbour relatively more TEs, suggesting TE-driven genome expansion in the outcrosser. Second, by using paired-end Illumina sequences we compared TE abundance in the two recently diverged *Capsella* species, finding no clear evidence for consistent copy number differences.

Sex and clonality: the evolutionarily successful strategies of a parasitic flatworm S**Heidi Aisala**, Haakon Hansen and Jaakko Lumme

Department of Biology, University of Oulu, Finland

At ecological time scale, clonality is reproductively advantageous, because it allows the population to grow exponentially in favourable conditions. However, asexual lineages are often short-lived at evolutionary time scale, as the lack of recombination leads to accumulation of deleterious mutations. Our study focuses on the species-rich genus *Gyrodactylus* (Platyhelminthes, Monogenea), which consists of small host specific fish parasites. In this genus, a combination of clonality and sexuality has proved to be an ideal strategy to be successful at both time scales. Mainly parthenogenetic reproduction maintains the adaptive allelic combinations and provides superior colonisation ability, as only one individual is enough to found a new population. In spite of strict host specificity, host switching has occurred frequently at evolutionary time scale. These switches seem to be tightly connected to occasional sexual reproduction, which has led to adaptive radiation and has thus provided a way out of the otherwise inescapable evolutionary dead-end.

Testing for faster-X effects in two lineages of the genus *Drosophila***Victoria Avila**, Sophie Marion de Proce and Brian Charlesworth

University of Edinburgh

Theory predicts that, under certain circumstances, DNA sequences on X chromosomes should have a faster rate of adaptive evolution when compared to similar loci on the autosomes. We have analysed the evolutionary rates of coding sequences in 2 clades of *Drosophila*: *melanogaster* and *pseudoobscura*. These clades differ by a centric fusion between Muller's A and D elements that characterises *D. pseudoobscura* and its relatives. Element A element is part of the X chromosome in both subgroups, but Muller's D element is part of an autosome in the *melanogaster* group (3L), and part of the X chromosome in the *pseudoobscura* clade (XR). By comparing the evolutionary rates of gene coding sequences among the 3 categories of genes: the ones that are on autosomes in both subgroups, the ones that are on the X chromosome in both subgroups, and the ones that are on the autosomes in the *melanogaster* clade but on the X chromosome in the *pseudoobscura* clade, we can investigate if the faster-X effect has taken place during the evolution and divergence of these subgroups. We found evidence for a faster-X effect for nonsynonymous substitutions in the *melanogaster* clade, but little clear for this in the *pseudoobscura* clade.

The evolution of sexual dimorphism in a diverse avian family, the Penduline tits (Remizidae) S**Alex Ball**, René E. van Dijk, Steve Dorus and Tamás Székely

University of Bath

Sexual selection is a potent evolutionary force that has been invoked to explain rapid diversification in morphological and behavioural traits. In this study we focus on a family of passerine birds most notable for their diverse array of reproductive strategies. The Penduline tits (Remizidae) are a small passerine family distributed widely throughout Eurasia and Africa. The European species (*Remiz pendulinus*) is known to be highly promiscuous, with both males and females able to obtain up to 6 mates sequentially in a single season. This is only possible with constant desertion of their current partner, leading to uni-parental care by either parent or bi-parental desertion in 30% of nests. However within an African species (*Anthoscopus minutus*), monogamous pair-bonds are formed and bi-parental care is the norm. Recently we have produced the first molecular phylogeny of this family and begun to reconstruct the evolution of key sexually selected traits.

*Evolution on the move: adaptation in the UK Brown Argus butterfly in response to climate change***Jon Bridle** and James Buckley

University of Bristol

A species' geographical ranges typically consists of many populations differently adapted to local ecological conditions, such as the availability of particular hosts or prey. However, specialization on localized resources could prevent species from colonizing new sites where the same resources are not available, limiting their capacity to track climatic changes. In contrast, we find that recent temperature-related ecological release of the Brown Argus butterfly, *Aricia agestis*, in Britain has facilitated rapid evolution of altered inter-specific adaptations, as well as morphology related to increased dispersal. Female butterflies in long-established parts of their range exhibit local adaptation, usually showing increased preference for laying their eggs on the locally most abundant host plants. However, butterflies in recently-colonized areas show a consistent preference for a host plant species (*Geranium molle*) that is geographically widespread in the region of expansion. These recent colonists also appear to have lost local adaptations present in the established part of the range. Our data suggest that future anthropogenic warming can be expected to bring about a major restructuring of patterns of local adaptation, and may potentially limit continuing evolution.

*Population genetic change and species co-existence***John Brookfield**

University of Nottingham

The process of adaptive evolution occurs through high fitness alleles increasing their frequency in populations. In a formal sense, the mean fitness of a species is thereby increased. Population genetics is typically silent about whether such a fitness increase has any consequence for a species' interactions with other species in its ecological community. Indeed, it is generally assumed that adaptive evolution leaves the community interactions unchanged. Here, through a modelling approach, I investigate the relationship between the stable coexistence of species and adaptive evolutionary changes within these species. By creating a diverse environment, and allowing species to evolve different ecological niches, it is possible to compare expected rates of speciation and rates of adaptive evolution. The models explore the relationship between environmental diversity and species diversity, and the impact of environmental unpredictability on species coexistence.

Linking landscape genetics to metacommunity ecology: spatial genetic structure provides meaningful insight to dispersal characteristics in a tropical ant-plant system **S****Catharine Bruce** and Douglas Yu

University of East Anglia

Landscape genetics can provide insight into dispersal characteristics that are fundamental to understanding the functioning of metacommunities. We present data based on an ant-plant system in the Peruvian Amazon where stable regional coexistence between multiple species of ants is thought to be facilitated by a trade-off between fecundity and dispersal ability. In order to describe the dispersal characteristics of these ants for parameterisation of a coexistence model, worker collections were made at three pairs of sites and genotyped at 10-11 microsatellite loci. Results show that the dispersal ability of coexisting species differs in line with predictions. This is supported by (1) levels of between-site population differentiation, and (2) the relative strength of within-site isolation-by-distance. The latter can be used to generate dispersal parameters and is sufficiently sensitive that we detect a consistent effect of hostplant density on dispersal distance. Finally we use genetic structure to estimate a dispersal kernel for the poorest disperser through identifying full-sib pairs among newly-dispersed ant queens, and using the rate at which probability of sibship decreases with increasing geographic distance to infer the distribution of dispersal distances and provide an additional measure of dispersal scale. Comparing estimates of average dispersal distance yielded from (1) a previous empirical study,

(2) fine-scale isolation-by-distance and (3) the distribution of inter-sib distances indicates that population genetic structure can provide accurate and meaningful dispersal data for parameterising ecological models without requiring exhaustive sampling methods that are labour-intensive and impractical in many landscapes.

Engineered endonucleases for control of pest populations

Austin Burt and Anne Deredec

Imperial College London

Enzymes that recognise and cut a particular sequence of DNA could be used to control pest populations. For example, a homing endonuclease that targets a gene needed for survival or reproduction could be used to impose a genetic load upon a population, or a Y-linked enzyme that targets the X at male meiosis could be used to produce a male-biased sex ratio. We have investigated the potential efficacy of these approaches using population genetic and population dynamic models, focused in particular on the malaria-transmitting mosquito *Anopheles gambiae*. Models of self-sustaining genetic constructs are able to spread through a population from a single inoculative release show that population elimination is possible, and have helped define the molecular genetic requirements for this to occur. We have also investigated models of self-limiting variants of these strategies, those that are not expected to persist indefinitely without recurrent releases. These models contribute to our understanding of how engineered endonucleases could be used as reagents for genetically engineering natural populations.

*Molecular evolution and variation in regions of the *Drosophila melanogaster* genome that lack crossing over*

Jose L. Campos and Jose L. Campos, Daniel L. Halligan, Peter D. Keightley, Brian Charlesworth, Penelope R. Haddrill

Institute of Evolutionary Biology, University of Edinburgh

The frequency of genetic recombination is expected to affect the efficiency of natural selection. This can be studied by comparing patterns of DNA sequence variability and evolution in regions with no crossing over versus regions where crossing over occurs. We have analysed more than 200 genes in the heterochromatin of *D. melanogaster* that lack crossing over and are located in 5 independent non-crossover regions. Using polymorphism data from an African population from the *Drosophila* Polymorphism Genome Project (DPGP), there is a 3 to 15 fold reduction in synonymous diversity, consistent with a reduction in N_e because of interference due to selection at linked sites; this reduction is proportional to the number of closely linked sites. There are also increased values of the ratios of nonsynonymous to synonymous diversities and divergence, consistent with relaxed purifying selection on nonsynonymous mutations. The proportion of adaptive nonsynonymous substitutions (α) and the ratio of the rate of adaptive to neutral divergence per basepair ($\omega\alpha$) were lower for the non-crossover genes. Coalescent simulations show that a single "catastrophic" sweep in the noncrossover regions is not compatible with the data. The results suggest that both positive selection and purifying selection are compromised when recombination is rare or absent, due to greater effects of Hill-Robertson interference compared with the rest of the genome.

Evolutionary trends In the Choanoflagellates: insights into the origin of Metazoa

Martin Carr

University of Huddersfield

The protistan choanoflagellates have recently been shown to be the sister-group to Metazoa and therefore have been recognized as an important group in determining how metazoans evolved from their unicellular ancestors. Presented here is a taxon-broad, multi-gene phylogenetic tree of the choanoflagellates, upon which morphological and ecological traits have been mapped. The tree highlights a number of previously unsuspected innovations in

choanoflagellate evolution and also points to characteristics of the last common ancestor of the choanoflagellates and Metazoa. Furthermore whole genome data from choanoflagellates and their protistan relatives highlight the antiquity of gene families previously considered metazoan specific.

Stabilising selection and mutational bias in finite populations

Brian Charlesworth

University of Edinburgh

Theoretical investigations of stabilising selection on a quantitative trait in an infinite population have shown that the trait mean is likely to be maintained close to the optimal value in the face of mutational bias. It is known from the theory of mutation, drift and directional selection that mutational bias can cause the equilibrium value of a trait to depart from the optimal value in a finite population. The extent to which happens under stabilising selection is investigated using a matrix method for the numerical modelling of the probability distribution of variant frequencies at a large number of sites affecting a trait subject to selection, mutation and drift. Analytical approximations for the trait mean and genetic variance are derived, which provide insights into the numerical results. The main conclusion is that the scaled intensity of selection acting on individual variants is nearly independent of the effective population size over a wide range of parameter space, and is approximately equal to the logarithm of the mutational bias parameter, even when there is a very small departure of the mean from the optimum. This implies that studies of the frequency spectra of DNA sequence variants may find it impossible to distinguish stabilising selection from directional selection. The potential for applying this theory to polymorphism data is explored with data on insertion/deletions in noncoding sequences of *Drosophila*.

Breakdown of dioecy and high female frequencies

Deborah Charlesworth and Allan Crossman

University of Edinburgh

Loss of separate sexes (breakdown of dioecy) is probably common in angiosperms, and could potentially occur in two different ways (i) through females acquiring some male function, conferring reproductive assurance if the density of pollinators or conspecifics is low, and leading to androdioecious populations (consisting of males and coexes — the 'modified' males), or (ii) through males acquiring some female function, again allowing them to reproduce by self-fertilisation and leading to gynodioecious populations (females plus cosexes). We modelled the second form of breakdown, which may be common, to study female frequencies, and show that these can be high in breakdown populations if the ancestral dioecious population has excess females, as is common in dioecious plants.

Strong selection acting on the couch potato gene: Spatial-Temporal variation in a diapause cline

Rodrigo Cogni, Kate Kuczynski, Spencer Koury, Erik Lavington, Emily L. Behrman, Katherine R. O'Brien, Paul S. Schmidt, and Walter F. Eanes

University of Cambridge/ Stony Brook University

In the colonization of temperate regions of the world, *Drosophila melanogaster* has co-opted a form of reproductive diapause to meet the challenges associated with overwintering in northern populations. The couch potato gene and its polymorphisms are strongly associated with the genetic variation for expression of this diapause trait in North American populations. In this study, we examine the geographic variation for 14 SNPs in the *cpo* gene across the eastern seaboard of the US over 13 years. We find that the polymorphism in Ile/Lys at residue 462 is tightly correlated with latitude and its frequencies are directly predicted by the incidence of diapause trait. We find that the geographic patterns for *cpo* SNPs sampled in 1997 are very similar to those same SNPs sampled in 2009-2010. Furthermore, SNPs that show apparent associations with *cpo* expression are also clinal with the low expression allele increasing in

frequency with latitude, as would be predicted from functional knockout studies of *cpo*. Finally, we observe that the frequency of the diapause-associated *Lys* allele (is at elevated frequency following the winter season but subsequently declines) during the summer as the local populations expand, consistent with the previously documented decrease in diapause incidence over seasonal time. We estimate the selection required to drive this response to be very large, on the order of 30 to 50% per generation.

Inbred and furious: genetic diversity, parasites and behaviour in a highly inbred fish

Sonia Consuegra and Amy Ellison

Aberystwyth University

Mixed-mating (i.e. intermediate levels of self-fertilization and outcrossing in hermaphrodites) is relatively common in plants and animals, but why self-fertilization (selfing) rates vary so much in nature has proved difficult to explain. We have investigated the maintenance of mixed-mating in a partially selfing vertebrate, the androdioecious fish (*Kryptolebias marmoratus*). Populations of *K. marmoratus* are composed mainly by highly homozygous selfing females and a low proportion of males that can outcross with them. We found that outcrossing with males increases genetic diversity in this highly inbred species and explored how this genetic diversity can influence parasite resistance and behaviour (aggression and mate choice) in selfing species, potentially playing an important role for the persistence of mixed-mating.

A RAD-Seq phylogeny of Mandarina snails from the Japanese Ogasawara archipelago

Angus Davison, M. Maureen Liu and Satoshi Chiba

University of Nottingham

Progress in understanding the speciation and adaptive radiation of snails has been limited in recent years, principally because of a lack genomic resources. This has meant that the vast majority of studies have been restricted to using mtDNA, nuclear ribosomal RNA and a very limited selection of other genes. In the past, we have used mtDNA and microsatellites to investigate the adaptive radiation of *Mandarina* snails, but the conclusions have been limited, because of a lack of power and the ability of mtDNA to introgress between species. I will illustrate how we have used a single RAD-Seq run to generate thousands of markers and produce a first multilocus phylogeny of the genus.

Stabilizing selection on polygenic traits: stability and response under unequal effects

Harold P. de Vladar and Nick Barton

IST Austria

When polygenic traits are under stabilizing selection, many different combinations of alleles allow close adaptation to the optimum. If alleles have equal effects, all combinations of alleles that result in the same deviation from the optimum are equivalent. Furthermore, the genetic variance that is maintained by mutation-selection balance is close to that of Turelli's House of Cards model. In reality, alleles vary in their effects, making the fitness landscape asymmetric, and complicating analysis of the equilibria. For this case, we show that that the resulting genetic variance is a fraction under the House of Cards approximation. The precise value depends on the fraction of fixed alleles and on the total mutational effects of polymorphic alleles. The interplay between stabilizing selection (of strength β) and mutation (rate μ) leads to a sharp transition: alleles with effects smaller than a threshold value of $\sqrt{4\mu/\beta}$ remain polymorphic, whereas those with larger effects are fixed. Thus there can be an arbitrary number of polymorphic alleles, in as long as they have small effects. This last result is in contrast to an original observation by Wright, where he showed that under stabilizing selection and no mutation at most one polymorphic allele can be maintained. We find that if the optimum is displaced, alleles with effects close to the threshold value sweep first, and their rate of

increase is bounded by $\sqrt{\frac{\beta}{\mu}}$. We discuss the relationship between the House of Cards and Lande's Gaussian model from the perspective of our analyses.

Ancient and recent origins of drug resistance of a Leishmania parasite epidemic

Tim Downing, Hideo Imamura, Julien Longchamp, Mandy Sanders, Craig Shaw, An Mannaert, Manu Vanaerschot, Suman Rijal, Katharine Carter, Graham Coombs, Gabriele Schonian, Jean-Claude Dujardin, James Cotton and Matthew Berriman

National University of Ireland, Galway

Leishmaniasis is a fatal disease endemic to tropical and sub-tropical regions. Over 51,000 people die annually from the visceral form and consequently comprehensive biological characterisation of ongoing epidemics is needed to track their origin and transmission. We used the high-quality reference genome of a Nepalese clinical strain to detect variation by mapping Illumina HiSeq DNA reads with a median genome-wide coverage of over 40-fold for each of 208 samples isolated from leishmaniasis patients in India and Nepal with documented treatment regimes and outcomes. 192 of these belong to a genetically monomorphic but phenotypically variable epidemic spanning two distinct drug treatment eras during 2002-2010. Placing clinical diversity in an evolutionary context showed that the majority of epidemic strains originated after a population crash during the Indian anti-parasite spraying campaigns in the 1960s, but also identified two divergent lineages with the same region. By comparing patient treatment backgrounds with the spatial and temporal distribution of the sample, different drug-susceptibility mutations were discovered. In addition, parallel experiments on the mechanisms of experimentally-induced drug resistance in the lab environment contrasted with those observed here, indicating that epistasis, gene dosage and clonality may provide further insights into continued persistence of this agile pathogen. A key challenge for tackling this infectious disease is to distinguish endemic from epidemic evolutionary phases so that the sources of modern infections can be resolved. This study provides a foundation for continuous monitoring of novel and drug-resistant outbreaks that act as a threat to public health by deep sequencing in zones of endemic disease.

Antagonistic interactions between co-circulating subtypes of human influenza viruses **S**

Gytis Dudas and Andrew Rambaut

University of Edinburgh

Antagonistic interactions between subtypes of influenza viruses are known to take place in the human population, and are at their extreme during influenza pandemics, for example all 20th century influenza pandemics have resulted in the extinction of previously circulating seasonal influenza strains. In this study we reconstruct the demographic history of 5 human influenza A and B virus subtypes: seasonal A(H3N2) and A(H1N1), A(H1N1pdm09) responsible for the swine flu pandemic, as well as B(Victoria) and B(Yamagata), between 2006 and 2011 in order to study the interactions between these subtypes before, during and after the 2009 swine flu pandemic.

Methods: 700-1200 sequences for each of the 5 subtypes from 2006-2011 were downloaded from EpiFlu-GISAID, and a non-parametric coalescent-based method, the GMRF skyride, was used to infer fluctuations in the effective viral population size over time whilst accommodating for uncertainty in tree topology, substitution model parameters and variation in molecular clock rate using BEAST.

Results: Between 2006 and 2009, peaks in H3N2 diversity corresponded with troughs in H1N1 diversity (and vice versa), and the peaks coincided with antigenic innovations in one or the other subtype. Furthermore in 2009/2010 the effective viral population size of the H1N1pdm09 pandemic subtype was at its peak, but the diversity in H3N2 and H1N1 seasonal strains was very low. We show that these bottlenecks can be traced to localised lineage extinctions which coincide with the arrival of antigenically novel influenza A viruses. However, influenza B virus subtypes show little, if any, interactions between themselves or with influenza A viruses.

*Speciation in pea aphid host plant races: insights from chemosensory gene divergence***Ludovic Duvaux**, Carole Smadja, Julia Ferrari, Jing-Jiang Zhou and Roger Butlin

University of Sheffield

Differentiation between incipient species is expected to be variable across the genome. This is notably true when gene flow opposes both drift and divergent selection in shaping such a pattern, forming 'islands of differentiation' around selected loci contributing to reproductive isolation. We argue that, beyond population genomics and QTL mapping, a candidate gene approach can advance detection of such loci even further. Many insects use chemical cues to recognise host plants and because divergence in host plant recognition is an essential step in race formation, chemosensory genes seems good candidates to play a key role in prezygotic isolation. To address this prediction, the pea aphid system is unique in having multiple races at different levels of divergence. Here, we used SureSelect capture and Solexa sequencing to study patterns of divergence for about 200 chemosensory genes and 200 control genes in 8 aphid races. We observed that the proportion of genes with Copy Number Variation (CNV) was quite high both within and between races, notably for chemosensory genes, and tried to link this pattern to differential expression between races. By removing genes with CNV, we analysed sequence diversity within and between races in an Approximate Bayesian Computation framework in order to detect loci experiencing significantly less effective gene flow than expected under various demographic scenarios. Such genes are expected to evolve under positive selection and/or to contribute to reproductive isolation, and are good candidates to study the genetic basis of adaptation underlying the high degree of ecological specialisation of these races.

*Finding candidate markers of adaptive variation in social insects***Jonathan Ellis**, Lucy Turner and Mairi Knight

Manchester Metropolitan University

In response to on-going biodiversity loss, conservation genetics has established itself as an important branch of biology. Historically concentrating on assessing stochastic processes using neutral loci, there has been a recent surge of interest in understanding and quantifying variation at loci underlying ecologically important traits. To this end, patterns of selection and polymorphism at these loci must be characterized. Here we present data regarding patterns of selection and estimates of polymorphism for innate immune loci and metabolic loci (phosphoglucose isomerase, phosphoglycerate mutase) in bumblebees. Bumblebees are ecologically and economically important as pollinators of crops and wildflowers yet many species are undergoing declines in range and abundance. For the gene regions studied, we found very little polymorphism. Possible explanations will be discussed as will alternative loci and methods for assaying adaptive variation in a conservation genetics context.

*Comparative genomics and transcriptomics of extremely young species of crater lake cichlid fishes***Kathryn Elmer**, Shaohua Fan, Andreas Kautt and Axel Meyer

University of Glasgow

Because colonizations occur independently, crater lakes are natural laboratories in which to study replicate speciation of fishes by ecological divergence. Up to now, there has been a dearth of transcriptomic and genomic information that would aid in understanding the molecular basis of the phenotypic differentiation and parallel evolution. We characterized the diversity of expressed sequences (transcriptomes) between ecologically divergent, endemic species of Nicaraguan crater lake Midas cichlid fishes in allopatry and sympatry. Based on the ratio of non-synonymous to synonymous mutations in orthologous sequences, we infer positive selection in the diversification of sympatric sister species at fewer than 15 genes. In a complementary analysis, genomic polymorphism also reflected signals of selection on genome evolution, though these patterns differed between sympatric radiations across crater lakes. However,

some patterns were general, such as a limnetic ecomorph being the first sympatric divergence within each flock and a correlation between loci responding to selection and the time since divergence. Genome-wide analyses are allowing us to identify the rare variation that distinguishes young species with much greater scope than has been previously possible.

Patterns of mating and generation of diversity in a Geum hybrid swarm

Richard Ennos, Markus Ruhsam and Pete Hollingsworth

University of Edinburgh

Self-pollination is considered an 'evolutionary dead-end'. However, recent studies demonstrate that selfing species can contribute to the evolutionary process via introgressive hybridisation with outcrossers; such introgression is usually asymmetrical from the selfer to the outcrosser. Here we test whether observed asymmetrical introgression is solely attributable to mating patterns, or whether it is driven by differential selection on the progeny. We studied a hybrid swarm between the outcrossing *Geum rivale* (Rosaceae) and the selfing *G. urbanum*. 30 samples representing the morphological range in the hybrid swarm and five of their open pollinated offspring were screened for AFLPs, microsatellites and morphological traits. Progeny performance was quantified in a common garden and fitness measures taken. Our results show elevated selfing in *G. rivale* indicating that introgression from the inbreeder alters its breeding system. The range of genotypes and phenotypes in the progeny far exceeds that in the established adults in the hybrid swarm. The common garden experiment revealed that ecological selection rather than intrinsic genetic problems best explains this difference. Overall this suggests there is a wide range of potential evolutionary outcomes depending on the selective forces in the hybrid swarm, and that mating patterns alone do not explain the observed asymmetrical introgression.

*Forest fragmentation genetics in a formerly widespread island endemic tree: *Vateriopsis seychellarum* (Dipterocarpaceae)*

Aline Finger, Chris Kettle, Chris Kaiser-Bunbury, Terence Valentin, James Mougale and Jaboury Ghazoul

Royal Botanic Garden Edinburgh

Habitat fragmentation and changed land use have seriously reduced population size in many tropical forest tree species. Formerly widespread species with limited gene flow may be particularly vulnerable to the negative genetic effects of forest fragmentation and small population size. *Vateriopsis seychellarum* (Dipterocarpaceae) is a formerly widespread canopy tree of the Seychelles, but is now reduced to 132 adult individuals distributed in eleven sites. Using ten microsatellite loci, a genetic inventory of all adult trees and a sample of 317 progeny we demonstrate that despite its restricted range, overall genetic diversity was relatively high (H_E : 0.56). The juvenile cohort, however, had significantly lower allelic richness (adults RS : 3.91; juveniles RS : 2.83) and observed heterozygosity than adult trees (adults H_o : 0.62; juveniles H_o : 0.48). Rare alleles were fewer and kinship between individuals was stronger in juveniles. Significant fine-scale spatial genetic structure (FSGS) was observed in remnant adults, and parentage analysis indicated that more than 90% of sampled seeds disperse < 25 m and pollen dispersed < 50 m. The molecular data confirmed that two populations were derived entirely from self-fertilised offspring from a single surviving mother tree. These populations produce viable offspring. Despite this extreme genetic bottleneck, self-compatibility may provide *V. seychellarum* with some resistance to the genetic consequences of habitat fragmentation, at least in the short term. We discuss our findings in the context of other rare and threatened dipterocarp species which are vulnerable to mis-management of genetic resources and population fragmentation.

Estimating the size and genetic composition of founding groups in a re-emerging pest, the common bed bug **S**

Toby Fountain, Gavin Horsburgh, Ludovic Duvaux, Klaus Reinhardt and Roger Butlin
University of Sheffield

The number and demographic background of colonists can have dramatic consequences on the genetic diversity and success of new populations. Founder events often result in drastic reductions in diversity and genetic drift can lead to rapid population differentiation. Knowledge of the size and genetic composition of propagules is therefore crucial in understanding patterns of diversity and dispersal in natural populations. The common bed bug (*Cimex lectularius*) is re-emerging as a significant economic and public health pest, precipitated by a sudden global resurgence in its populations. Much of their recent success has been attributed to human facilitated passive dispersal, allowing rapid movement of individuals across vast distances. It is therefore expected that limited numbers found infestations. This in combination with frequent extinctions and a strong insecticide selective pressure is predicted to drastically reduce levels of variation within infested properties. We used 21 newly designed microsatellite markers to estimate the number and genetic composition of bed bug founders, and the subsequent effects on population structure at two hierarchical levels. We found very limited diversity within infestations but high degrees of structuring across the city of London, with extreme levels of genetic differentiation between infestations ($F_{ST} = 0.59$). This, coupled with modelling estimates, is suggestive of a very small group of related passively dispersing founders. As localised extinction events are common due to pest control, we propose that bed bugs follow metapopulation dynamics of frequent extinction and recolonisation. These results also provide a valuable resource for future targeted control of bed bug infestations.

Morphological complexity and speciation in Phlebotomus argentipes species complex: A need for a molecular tool to discriminate vector populations **S**

Kanapathy Gajapathy, Sara Goodacre, and Sinnathamby Noble Surendran
University of Jaffna, Sri Lanka and University of Nottingham, UK

The sandfly, *Phlebotomus (Euphlebotomus) argentipes* (Diptera; Psychodidae: Phlebotominae) species complex, is believed to be the potential vector for leishmaniasis in Sri Lanka. It is a mixture of morphologically distinct three sibling (morpho) species, namely Ph. (Eup.) *argentipes* sensu stricto, Ph. (Eup.) *annandalei* and Ph. (Eup.) *glaucus*. The existence of this complex in Sri Lanka has been recorded since the 1940's. A recent study based on samples collected from endemic localities for cutaneous leishmaniasis in the country, revealed evidence for the presence of a new morphologically distinct sibling species. Molecular characterization of the members of the sibling species from the species complex, using DNA sequence of 28S region of nuclear ribosomal DNA (rDNA), 18S rRNA gene, and cytochrome oxidase I (COI) region of mitochondrial DNA, was carried out. Sequence analysis for 28S and 18S genes showed no variation among the members of the Argentipes complex. The most parsimonious, neighbour joining and maximum likelihood trees (1000 bootstrap), deduced with the COI data, have produced a separate clade for the newly described species from the endemic regions. The isolation of Leishmania minicircle kinetoplast DNA from this new morpho species provides further evidence that this could be a potential vector for leishmaniasis in the country. Further molecular characterization based on ITS2 and CO1 gene sequence analysis is warranted to establish a diagnostic molecular assay, and the population structure and genetic diversity of the members of the Argentipes complex in Sri Lanka.

*Population genetics of gene function***Ignacio Gallo**

Freelance

This talk presents a simple toy model which uses ideas from population genetics and statistical mechanics to gain insights on how the distribution of a gene throughout a population may reflect the function that the gene serves within an organism. At the coarse level of description chosen for this model, function is decomposed only in the two biological dimensions of survival and reproduction.

*Noisy evolutionary waves S***Lukas Geyrhofer** and Oskar Hallatschek

MPI for Dynamics and Self-Organization, Biophysics and Evolutionary Dynamics Group, Göttingen, Germany

Adaptation is a central process in evolution, in which the fitness of a population is increased by accumulating beneficial mutations. One of the challenges of modeling adaptation in large, but finite, populations is to simultaneously treat both, natural selection for mutations and genetic drift. Even in very large populations the latter cannot be neglected: genetic drift can drive even very fit clones to extinction as long as they are small. In recent years considerable progress has been made to describe the mean behavior of adapting asexual populations. Here, we present an exact approach to fluctuations in the process of adaptation, which is beyond the scope of most current theories. Mutation, reproduction and selection is modeled by a branching random walk process. Competition for a finite amount of resources is accounted for by a constraint on the population density in fitness space. This constraint is designed to close the hierarchy of moments at any arbitrary level. As a consequence we obtain access not only to the mean (first moment), but also to the fluctuations (higher moments) of the fitness distribution. This noise induced by genetic drift crucially influences the dynamics of high-fitness low-frequency clones in the tip of the wave, which ultimately drive the adaptation process. Utilizing this framework we might be able to unravel universal features inherent to many stochastic adaptive wave models. Predictions from our theoretical approach could be compared to long term evolution experiments, where microbial populations are grown long enough to observe the continual fitness increase.

*Functional variation at immune loci in the Seychelles warbler***Danielle Gilroy S**

University of East Anglia

Infectious disease is a major demographic and evolutionary driver of natural populations. Pathogen-mediated selection is thought to generate genetic diversity through a number of possible mechanisms. We need to understand the relative importance of these mechanisms in wild systems, particularly in non-model vertebrate species that have undergone a genetic bottleneck. The Seychelles warbler (*Acrocephalus sechellensis*) world population has recovered from an ancient bottleneck of 26 individuals and has consequently lost much genetic diversity. Since allelic richness throughout the genome has been reduced, it presents a more tractable system for molecular ecology studies. However, allelic diversity is crucial for adaptive potential, which is the ability for a population to adapt to challenges such as disease infection. By investigating functional variation that exists at key immune loci in a population, we can infer their genetic health and determine the relationship between variation at adaptive immune loci and the hosts host ability to resist or tolerate pathogens. The Major Histocompatibility Complex (MHC) is the most polymorphic gene cluster in vertebrates, with a pivotal role in immune defence. Whilst a plethora of studies into functional MHC variation exist, there is now a need to go beyond the MHC and study other immune-genes of key to the innate immune defence. Taking a candidate gene approach, we will use the malaria strain GRW1 in the Seychelles warbler system, to investigate patterns of pathogen-mediated selection. Specifically, we will assess the

relationship between functional genetic variation, host resistance and susceptibility to pathogen infection, and its effects on fitness.

Spatial variation in avian malaria infection in a wild population of Berthelot's pipit (Anthus berthelotii) **S**

Catalina Gonzalez Quevedo, David S Richardson and Richard G Davies

University of East Anglia

Understanding how the environment influences transmission and maintenance of disease in wild host populations is a key aspect of disease ecology and for understanding host-pathogen coevolution. Spatial heterogeneity in environmental factors plays an important role in disease dynamics and transmission, and this has been well studied at large spatial scales. However, despite considerable understanding of how environmental variables vary at fine spatial scales, the effect of environmental parameters on host-pathogen dynamics at such scales is poorly known. Here, we used a combination of molecular screening and GIS-based analysis to investigate how a range of environmental factors determine the landscape-wide distribution of malaria in a population of Berthelot's pipit (*Anthus berthelotii*) in Tenerife. We found spatial structure in malaria infection, with higher than expected prevalence in the south and the north of the island. Anthropogenic factors were found to be better predictors of malaria distribution than natural factors, with proximity to water reservoirs and poultry farms being major determinants of infection probability. In contrast, stark climatic differences across the landscape did not appear to influence the prevalence of malaria. These results suggest that current levels of infection in this species are artificially elevated by human-induced impacts. We found no genetic structure at neutral loci in this population, giving a good background against which to assess whether the spatial heterogeneity of malaria-promoting environmental factors are translated into differential selection pressures on host immune genes, thus giving insight into host-pathogen coevolution.

The embryogenic hourglass in plants

Toni I. Gossmann and Karl J. Schmid

University of Hohenheim

In animals a morphological hourglass is observed across taxa. Embryos appear divergent in early stages, converge to a very similar form during mid-embryogenesis - the phylotypic stage - and diverge again with further development. There is also evidence from *Drosophila* and zebrafish that this is reflected in molecular patterns, ancient and conserved genes are predominantly expressed during the phylotypic stage. Surprisingly a molecular hourglass has been recently described in plants even though there is no observation of a morphological hourglass across plant taxa. However, the underlying mechanisms responsible for multicellularity evolution in plants are not well understood. Here we investigate the selective forces currently acting on genes expressed during embryogenesis using whole genome sequence data of *Arabidopsis thaliana*. We contrast our results to phylotranscriptomic patterns during prezygotic cell development.

Nitrogen content of the Arabidopsis thaliana transcriptome is shaped by mutational bias and GC-biased gene conversion **S**

Torsten Guenther, Christian Lampei and Karl J Schmid

University of Hohenheim

Many plant species live under a persistent ecological nitrogen limitation and need to cope with that situation. The nitrogen content of the transcriptome and proteome of the model *Arabidopsis thaliana* and other plant species is reduced in comparison to other taxa. This might be the direct result of a long-term selection for reduced nitrogen usage (Acquisti et al., MBE, 2009). To test if such selection is currently ongoing in *A. thaliana*, we analyzed the natural variation of nitrogen content in the transcriptome of 80 recently sequenced accessions. In contrast to our

expectations, the overall nitrogen content of the transcriptome is increased due to the fact that nitrogen increasing alleles segregate at higher derived allele frequencies. We also find that this pattern is even stronger in populations with larger effective population sizes, which should be exactly opposite if there was ongoing selection to reduce nitrogen content. Our observations let us reject the hypothesis to of a currently ongoing reduction of nitrogen content in the transcriptome of *A. thaliana*. We show that this pattern is instead the result of an interplay between different processes that influence base composition. These forces include a biased mutational spectrum, purifying selection against functionally deleterious mutations and GC-biased gene conversion. We also present strong evidence that the recombination-associated process of GC-biased gene conversion plays an important role in shaping the base composition of *A. thaliana*.

Nutrient content in wheat and the NAM-B1 gene – A story of domestication and plant improvement

Jenny Hagenblad

Linköping University

The transition of domestic crop species from wild progenitor to high-yielding modern varieties is characterized by two major events both involving the introduction of new and strong selection pressures acting on the species. The first, the domestication, occurred some 10,000 years ago while the second, modern plant improvement, has taken place during the past 150 years. A few genes have been tied to selection during domestication and plant improvement, most notably the *tb1* gene in maize. One suggested domestication gene is NAM-B1 in wheat. It has antagonistic effects with the wildtype allele giving faster maturation time and higher nutrient content in the seed. Two null alleles instead lead to slower maturation time causing larger yield, but with a lower nutrient content. Although originally suggested to be a domestication gene we could show, using historical collections of 19th century seeds that the wildtype allele was still present in widely cultivated wheats during the latter half of the 19th century. Screening extant wheats from across the world pointed to environmental components being important in preserving the wildtype allele in bread wheats. Sequence data from accessions from different species of extant wheats in and around the NAM-B1 region further paints a picture of the evolutionary history of this gene and the interacting roles of natural and artificial selection.

Determining the effect of Hepatitis C genotype on virus outcome

Matthew Hartfield, Fabio Luciani and Samuel Alizon

MiVEGEC, IRD, Montpellier

Infection by hepatitis C virus (HCV) leads to one of two outcomes, which varies amongst patients. Either the infection resolves itself within a matter of weeks, or it can persist over several years. It is difficult to ascertain to what extent this outcome is determined by the virus genotype itself using transmission networks, as these tend to be poorly known. Recently, phylogenetic methods have been created to estimate the proportion of set-point viral load that is inherited from one HIV-infected patient to the next. Studies found that up to half the variance in this trait is determined by the virus genotype. Here, we aim to investigate whether we can detect a similar signal in HCV infections. We first simulate inheritance of a binary trait outcome along a given phylogenetic tree to predict how traits gather in groups, and explain how these simulations are used to ascertain the virus effect on the infection outcome. Finally, we apply our method to HCV cohort data from Australia to try and detect an effect of virus genotype on whether hosts will clear the virus rapidly or develop a chronic infection. We also investigate whether key host SNPs, which are known to affect HCV infection outcome, affect this measure of inheritance.

Prediction of ancient transposon proliferation processes through phylogenetic analysis of modern elements

Elizabeth HB Hellen and John FY Brookfield

University of Nottingham

A family of transposable elements from modern organisms includes elements that differ from each other to varying degrees, as they have, over time, undergone mutation. They can be treated as alleles in a genetic population. Using these differences we can reconstruct their process of proliferation through transposition, over millions of years, and have done this for mammalian class II transposon families. The date of origin of a family was predicted using two methods. Firstly, we identified the most recent common ancestor species which contained elements from the family, and estimated how long ago this species existed. Secondly, we used molecular dating to date the most common recent ancestor element (MRCA) of all modern elements. We observed whether the MRCA of modern elements existed at the same time that the family first occupied the host genome, or whether it was much later. We used the data to resolve between two hypothetical proliferation processes. A “turnover” process is where transposition, inactivation and loss of elements happen continuously. Here, modern elements are likely to originate from a sub-branch of the original tree, with the molecular dating predicting an MRCA that was more recent than the origin date predicted from the host species that now share the element. The second is a “life cycle” process, where elements are created and subsequently inactivated in a discontinuous process. This will result in the prediction of a similar date using each of our two methods. It is this “life cycle” hypothesis that is favoured by the data.

Searching for ‘speciation genes’: a candidate gene approach **S**

James Hutchison and Roger K Butlin

University of Sheffield

Identifying incompatibilities which prevent gene flow between divergent lineages is a central theme in current speciation research. By identifying the functional classes of genes and the specific forces driving their divergence across species, we can gain an understanding of their contribution to the evolution of new species. Two sub-species of the meadow grasshopper *Chorthippus parallelus* come into contact and hybridise in the Pyrenees Mountains. Tension zones, maintained by a balance of selection against hybrid genotypes and the inward migration of pure individuals, are found in mountain passes below an altitude of roughly 2000 metres. While crosses between the sub-species produce fertile females, heterogametic F1 males are sterile. Within the hybrid zones sterile individuals are absent and grasshoppers display intermediate phenotypes. Clines for sterility, along with an array of morphological, electrophoretic and behavioural characteristics, have previously been mapped across several Pyrenean hybrid zones. Revealing the loci involved in hybrid sterility will allow us to discover the nature of their divergence, the incompatibilities between them and their historical spread within subspecies. The incompatibility underlying sterility is widely thought to result from negative epistatic interactions (Bateson-Dobzhansky-Muller model). In the hybrid zones, genes which are involved in the incompatibilities should experience strong negative selection and display a steep allelic transition between subspecies. Using a range of techniques including crossing experiments, expression analysis, sequence comparisons and genomic cline mapping I identify candidate sterility loci and explore the dynamics of gene flow within the Pyrenean hybrid zones.

*Components of selection in the evolution of the influenza virus: linkage effects beat inherent selection***Chris Illingworth** and Ville Mustonen

Wellcome Trust Sanger Institute

The influenza virus is an important human pathogen, with a rapid rate of evolution. The rate of homologous recombination within genes of influenza is essentially zero. As such, where two alleles within the same gene are in linkage disequilibrium, interference between alleles will occur, whereby selection acting upon one allele has an influence upon the frequency of the other. We here measured the relative importance of selection and interference effects upon the evolution of influenza. We considered time-resolved allele frequency data from the global evolutionary history of the haemagglutinin gene of human influenza A/H3N2. Using a model that accounts for selection-caused interference between alleles in linkage disequilibrium, we estimated the inherent selective benefit of individual polymorphisms in the viral population. These selection coefficients were in turn used to calculate the total selective effect of interference acting upon each polymorphism, considering the effect of the initial background upon which a mutation arose, and the subsequent effect of interference from other alleles that were under selection. Viewing events in retrospect, we estimated the influence of each of these components in determining whether a mutant allele eventually fixed or died in the global viral population. Alleles going on to fix in the global population tended to be under more positive selection, to arise on more beneficial backgrounds, and to avoid strong negative interference from other alleles under selection. However, on average, the fate of a polymorphism was determined more by the combined influence of interference effects than by its inherent selection coefficient.

*Fixation of mutators in asexual populations: the role of genetic drift and epistasis***Kavita Jain** and Apoorva Nagar

J. Nehru Centre for Advanced Scientific Research, Bangalore, India

We study the evolutionary dynamics of an asexual population of nonmutators and mutators on a class of epistatic fitness landscapes. We consider the situation in which all mutations are deleterious and mutators are produced from nonmutators continually at a constant rate. We find that in an infinitely large population, a minimum nonmutator-to-mutator conversion rate is required to fix the mutators but an arbitrarily small conversion rate results in the fixation of mutators in a finite population. We calculate analytical expressions for the mutator fraction at mutation-selection balance and fixation time for mutators in a finite population when the difference between the mutation rate for mutator and nonmutator is smaller (regime I) and larger (regime II) than the selection coefficient. Our main result is that in regime I, the mutator fraction and the fixation time are independent of epistasis but in regime II, mutators are rarer and take longer to fix when the decrease in fitness with the number of deleterious mutations occurs at an accelerating rate (synergistic epistasis) than at a diminishing rate (antagonistic epistasis).

*Genomic diversity in the model fission yeast species *Schizosaccharomyces pombe*.***Daniel Jeffares**, Sendu Bala, Jared Simpson, Zamin Iqbal, Babis Rallis, Francesc Xavier Marsellach Castellví, Charalampos Rallis, Theodora Sideri, Nikolas Maniatis, Garrett Hellenthal, Jacqueline Hayles, William Brown, Francois Balloux, Richard Durbin and Jürg Bähler

University College London

The fission yeast *Schizosaccharomyces pombe* is an important model for cellular processes, particularly cell division, DNA damage, replication and transcription. However almost nothing is known about the natural habitat, diversity or ecology of this species. As a step towards describing the diversity of this species more fully, we have sequenced all 161 strains that were available in stock centers. These strains are derived from all continents, and have been collected from cultivated fruits or from various fermentations (eg: Brazilian Cachaça, wine must). We find a species that is genetically diverse. I will describe our initial analysis of the genetic

diversity of the species and mention the other analysis that is ongoing and planned: structural variant discovery, phenotyping, and descriptions of cell morphology.

Weak differentiation according to host species and small spatial scale in a parasite crab **S**

Quentin Jossart, Bruno David, Colin De Bruyn, Chantal De Ridder, Thierry Rigaud and Rémi Wattier

Université Libre de Bruxelles; Université de Bourgogne

The pinnotherid crab *Dissodactylus primitivus* lives parasitically on two burrowing echinoids (*Meoma ventricosa* and *Plagiobrissus grandis*). *D. primitivus* asymmetrically uses its sympatric hosts: all post-metamorphic stages (juveniles, adults) are present on *M. ventricosa* while only adults are found on *P. grandis*. The fecundity of female crabs varies between hosts: being higher on *P. grandis* than on *M. ventricosa*. Furthermore, crabs living on *M. ventricosa* are more chemically attracted by this host than by *P. grandis*. Finally, the hosts present great variations in morphology and behavior. Altogether, these characteristics are leading toward a potential differentiation of crabs according to host species. We investigated the genetic (microsatellites) and morphometric (outline analysis) differentiation of this parasite crab between two host species at one Jamaican site (Western Lagoon, Discovery Bay), and compared it with geographic differentiation among four sites along the north coast of Jamaica. A stronger genetic structure between the two sympatric hosts than between different geographic locations would be a good marker of host-differentiation. Results from genetic analyzes (FST, AMOVA, Fisher tests of differentiation, Bayesian approaches) showed an absence of spatial differentiation, probably related to the local hydrography. Moreover, no genetic differentiation according to host species was evident. This lack of host-differentiation could be notably explained by mobility of adult crabs between hosts. However, a small morphological differentiation (MANOVA, Discriminant Analysis) was observed between crabs issued from the two hosts, but only for females. The morphological difference may result from several mechanisms including plasticity related to host morphology.

A model for the dynamics of endogenous retroviruses

Ravinder Kanda, Mike Tristem and Tim Coulson

Imperial College London

Mammalian DNA is littered with the signatures of past retroviral infections. For example, at least 8% of the human genome can be attributed to endogenous retroviruses. Many of the more recent genotypes attributable to past retroviral insertions show little or no presence/absence polymorphism, suggesting that the endogenous retrovirus spread through the human population potentially quite rapidly. We develop a simple susceptible-infected-recovered (SIR) model to investigate the circumstances under which a retrovirus that causes disease can become incorporated into the host population, before it, or its LTR signature once the inserted virus is no longer functional, spreads through a host population. We conclude that signatures of no longer active endogenous retroviruses are only likely to go to fixation within a population if (a) the LTR provides a host fitness benefit or, (b) more interestingly, when the probability of evolving immunity to a related exogenous version of the virus is extremely small. Our results reveal the parameter space under which incorporation of exogenous retroviruses into a host genome may be beneficial to the host.

Coalescent simulation in continuous space

Jerome Kelleher, Nicholas H Barton and Alison M Etheridge

University of Edinburgh

Coalescent simulation is an essential tool in modern population genetics, and the basic algorithm has been extended to incorporate many different evolutionary scenarios over the past thirty years. Despite this long term interest in coalescent algorithms, there are no available

methods to simulate the ancestry of a sample of lineages that occupy a spatial continuum, mostly due to the severe technical difficulties experienced by the classical models of isolation by distance. The extinction/recolonisation model solves these technical problems and provides a consistent and rigorous framework for the study of populations evolving in continuous space. The basic algorithm to simulate the coalescent in this model is straightforward, and proceeds backwards in time event-by-event until the sample has coalesced. More sophisticated approaches are possible, however. We may use a power tessellation, for example, to calculate the exact distribution of the time between two events that can potentially affect lineages, greatly reducing the number of events that must be generated. This is offset, however, by the computational effort required to maintain this tessellation and it is not obvious when (or if) this leads to faster execution times. We use asymptotic results from the model to analyse these algorithms, allowing us to make informed decisions about which algorithm to deploy in a particular situation.

The inference of phased haplotypes for the immunoglobulin heavy chain variable region gene loci by high-throughput analysis of VDJ gene rearrangements **S**

Marie Kidd, Yan Wang, Katherine Jackson and Andrew Collins

University of New South Wales

Genetic variation within and between populations at the immunoglobulin gene loci is likely to be of clinical significance, but is extremely difficult to investigate. The variable region of the antibody is encoded by 7 sets of highly similar genes, interspersed between numerous repetitive elements over three chromosomes. However, the application of high-throughput sequencing to V(D)J rearrangements allows the inference of phased haplotypes if commonly rearranged genes are heterozygous, as V(D)J recombination is an intrachromosomal event. We have assembled 42 immunoglobulin heavy chain variable region gene haplotypes, and each one is unique. Deletion polymorphisms were observed involving both multiple IGHV and IGHD genes, several of which have been confirmed by whole-genome shotgun sequencing. Duplications were observed where two sequences previously recognized as allelic variants of a single gene were found to lie on the same chromosome. We also detected numerous allelic variants not currently listed in the ImMunoGenetics databases. A recent analysis of 10 individuals from Papua New Guinea identified a new heavy chain variable gene and 16 novel allelic variants. Almost half of these variants had been previously reported to the dbSNP, and exist in well-studied populations. However, allele frequency data in the dbSNP is not suitable for population-based studies of the immunoglobulin loci. This is due to their repetitive nature and also because the V(D)J rearrangement process has already taken place in lymphoblastoid cell lines used by the 1000 Genomes and HapMap projects. Genetic variation at these loci remains a major gap in our knowledge of the human genome.

Agrisims: Simulating crop domestication using individual based modeling

James L Kitchen, Dorian Fuller, Terrence Brown and Robin G Allaby

University of Warwick

Since cultivation practices began, our crops have acquired a number of traits making them better suited to farming processes: these traits include the tough rachis (non-shattering) phenotype and larger seed sizes. This process is known as domestication. We aim to better understand the process of domestication and therefore seek to determine which factors have given rise to patterns of domestication that are consistent with those in the archaeological record. To this end we have developed a spatial individual based simulation model called Agrisims. We have used Agrisims to study the spread of the tough rachis mutant in a regularly harvested crop field surrounded by wild plants: here we analyzed the effects of varying the proportion of dispersed seeds that are predated, the proportion of harvested seeds that are sown for the next year and the proportion of seeds that are retained by non-mutant crops at harvest. We have also varied the amounts of gene flow between the surrounding wild plants and the field crops. Higher proportions of dispersed seeds predated and harvested seeds sown increases selection for the tough rachis mutant, whereas more seeds retained by non-mutants

(earlier harvesting) decreases selection. Moderate to high levels of gene flow from surrounding wild plants allows the mutant to reach high levels within the field (approximately 90%), yet plateau and never fixate. We have used approximate Bayesian computation to assess which combinations of these parameters may have given rise to summary data from the archaeological record.

Conflicting signals in the phylogeny of Heliconiini butterflies **S**

Krzysztof M. Kozak, Chris D. Jiggins and Niklas Wahlberg

Department of Zoology, University of Cambridge

The Neotropical butterfly genus *Heliconius* is notorious for instances of hybrid speciation and widespread gene flow. The unusual biology makes this clade an intriguing test case for multispecies coalescent methods in phylogenetics. To understand the relations of over 60 species of *Heliconius* and allies we combine Sanger sequencing, ancient DNA techniques and a novel approach based on de novo assembly of whole genome resequencing data. Our dataset comprises 16.5 kbp in 22 loci sampled from multiple individuals, balancing alignment length with taxonomic representation. We also present a whole mitochondrial alignment for select species. Although the histories of individual loci are highly incongruent, MP, ML and Bayesian phylogenies based on nuclear and whole-mitochondrial supermatrices show nearly identical, well-supported topologies. In contrast, multispecies coalescent methods (*BEAST, BUCKY, MDC, MP-EST) produce the same general topology, but with much lower support values. The inherent incongruence is demonstrated further by a good fit to a highly reticulate network. The observed patterns have likely resulted from both gene flow and from Incomplete Lineage Sorting during recent bursts of speciation. Our study provides a robust phylogenetic hypothesis for an emerging model system and demonstrates how different phylogenetic techniques can either obscure or highlight heterogeneous signal in the data.

High gene flow in two polyandrous plover species

Clemens Kuepper

University of Sheffield

Gene flow promotes genetic homogeneity of species in time and space by preventing genetic differentiation. We investigated gene flow and genetic differentiation in two widely distributed wader species: Kentish plover *Charadrius alexandrinus* and snowy plover *C. nivosus*. Both species exhibit unusually flexible mating system with high female breeding dispersal. We analysed genetic structure and gene flow using mitochondrial DNA, 21 autosomal microsatellites a Z microsatellite marker and 1253 polymorphic RAD markers (for snowy plovers only). We found no structure or isolation-by-distance over the continental range using microsatellites and mtDNA although the RAD markers showed a weak differentiation in snowy plovers. In Kentish plovers isolated populations such as oceanic islands were moderately differentiated from the continental locations. Genetic differentiation based on autosomal markers was positively correlated with distance between mainland and oceanic islands. In Kentish plovers comparisons of uniparentally and biparentally inherited markers were consistent with female-biased gene flow. Maternally inherited mtDNA was less structured, whereas the Z-chromosomal marker was more structured than autosomal microsatellites. Adult males were more related than females within genetic clusters. Taken together our study provided two main outcomes: First, in species with high gene flow analyses of genetic differentiation are greatly helped by employing more markers. Second, polyandrous females may play a prominent role in maintaining genetic homogeneity across large geographic distances.

The population genetics of recent antiviral gene duplicates in Drosophila **S****Samuel H. Lewis**, Claire L. Webster and Darren J. Obbard

University of Edinburgh

RNAi is a major invertebrate defensive pathway, in which small RNAs are derived from a target RNA and guide an Argonaute-family protein to cleave and subsequently degrade the target. This mechanism defends against both viruses and transposable elements. These contrasting and potentially conflicting selective pressures may have driven the rapid adaptive evolution documented in Argonaute-family genes, which places them among the top 3% of fastest evolving *D. melanogaster* genes. It has been hypothesised that this rapid evolution is driven by an arms race between viral suppressors of RNAi (VSRs) and the RNAi mechanism. In *Drosophila*, siRNA-mediated antiviral and anti-TE defence are mediated by Argonaute2 (Ago2). The majority of insects possess a single Ago2; however, duplication has occurred in several Dipteran taxa including Phoridae, Glossina and *Drosophila*. Ago2 has undergone numerous recent duplications in the obscura group of *Drosophila*, producing three paralogues in *D. obscura* and five in *D. pseudoobscura*. We present population genetic data for the Ago2 paralogues in *D. obscura* and *D. pseudoobscura*. We find that all *D. pseudoobscura* paralogues have remarkably low genetic diversity, possibly resulting from recent selective sweeps. Additionally, we detect the action of positive selection on some paralogues, and an excess of rare variants at others. We also find strong evidence for codon usage bias in the oldest paralogue, potentially due to changes in expression pattern. These results suggest that the Ago2 paralogues in the obscura group have each evolved under different selection pressures, possibly imposed by functional specialization in an evolutionary arms race.

*Population genomics of the oak gall wasp Biorhiza pallida***Konrad Lohse**, Jack Hearn, Nick Barton and Graham Stone

University of Edinburgh

We investigate the historical relationships between three major refugial populations in the oak gall wasp *Biorhiza pallida* using de novo genome assemblies from a small number of haploid individuals. We use a recently developed maximum likelihood method to numerically fit a range of models of population divergence with and without secondary admixture to genome-wide samples of sequence blocks. Despite a signal of strong (up to 90%) and recent admixture between populations in the Balkans and the Middle East, we are able to resolve the initial order of population divergence, which suggests that *B. pallida* colonised Europe from the Middle East. We consider the effects of linkage and mutational heterogeneity on such analyses.

Diverse reassortment patterns of avian influenza viruses among different subtypes in internal segments **S****Lu Lu**, Samantha Lycett and Andrew J. Leigh Brown

University of Edinburgh

The segmented RNA genome of Avian influenza viruses (AIV) allows for genetic reassortment between co-infecting viruses, providing an evolutionary pathway to generate genetic innovation. The genetic diversity (16 HA and 9 NA subtypes) of AIV indicates that an extensive reservoir of influenza viruses is potentially circulating in wild bird populations. Reassortment events that occur in birds can spill over to humans and may be the cause of human pandemics. In this study, we quantify the reassortment patterns among Eurasian subtypes, using three subsets, each with 344 Eurasian sequences which were subsampled from over 3000 well-formed AIV sequences in the NCBI database and represented the original subtype proportions. Time-scaled phylogenies of the internal protein coding segments were constructed and the ancestral states of the subtypes were reconstructed upon the trees. Reassortment rates of certain subtypes were estimated using Bayesian and maximum likelihood methods. Rates showed significant diversity among subtypes. Specifically, H5 and H9 HA subtypes present lower reassortment rates than those of H1 to H4, and N1 and N2 NA subtypes present lower reassortment rates compared to those of N3 to N9. For H5N1 and H9N2 the reassortment rates are significantly

lower than the other subtypes which may be explained by the large proportion of domestic poultry populations. In contrast, the H1N1, H3N8, H4N6 subtypes exhibit high reassortment rates which could be due to the infection of wild bird hosts with multiple low pathogenicity strains in the avian reservoir.

Pandemic Expansion and Seasonal Oscillations in Influenza Viral Diversity

Samantha Lycett, J. A. Hedge, A. J. Leigh Brown and A. Rambaut

University of Edinburgh

In 2009 a new H1N1 influenza A strain invaded the human population, and was rapidly distributed around the world causing a pandemic. It subsequently replaced the old A(H1N1) human strain but not A(H3N2). In this study we investigate the fate of the variants generated in the initial expansion and track the emergence of seasonal population size oscillations.

Methods: 700 A(H1N1pdm09) genomes and 150 A(H3N2) genomes sampled from 2009-2012 were downloaded from the EpiFlu-GISAID and NCBI Influenza databases, and used to infer the distribution of phylogenetic trees and model the variation in viral effective population size through time with BEAST (Bayesian Evolutionary Analysis by Sampling Trees). Using isolate location as a discrete trait, we estimated transition rates between continents and the times at which lineages changed continents.

Results: H1N1 viral diversity revealed that a population bottleneck occurred mid 2010 coinciding with summer in the northern hemisphere. In the early part of the pandemic North America acted as a source transmitting to Europe and Asia, however Asia also became an important source particularly for Oceania. In contrast, H3N2 diversity decreased during the early part of the H1N1 pandemic, but increased in 2010 reflecting the importance of Asia as a source of diversity. During 2010 north-south shifts in diversity corresponding to the respective winter seasons were observed, indicative of a return to seasonal oscillations in both strains. Together these results imply that population immunity drove a return to seasonal dynamics within two years from the start of the pandemic.

Temporal and spatial mosaic of hybridisation between the M and S molecular forms of Anopheles gambiae s.s.

Clare Marsden, Y Lee, MR Sanford, CC Neiman, LC Norris, A Weakley, AJ Cornel and GC Lanzaro

University of California-Davis

The malaria vector, *Anopheles gambiae*, is widely regarded as consisting of two incipient species, the M and S molecular forms. However, there has been much debate about the extent of reproductive isolation between the M and S forms, with one view positing that M and S are diverging in the presence of gene flow, and the other proposing a more advanced stage of the speciation process with little realized gene flow due to low hybrid fitness. These hypotheses have been difficult to assess because hybrids are typically identified based on a single SNP assay which does not identify all hybrids and cannot distinguish between F1 and backcrossed hybrids. Here we employed a new hybrid diagnostic method which is based on a panel of 15 SNPs that are known to be fixed between M and S forms and which are located within the centromeric regions of all three *A. gambiae* chromosomes. We show that while frequencies of F1 hybrids and backcrosses were rare or absent in some sites, they were common in others, indicating that hybrids are often viable, fecund and result in introgression. However, our data also highlighted that hybrid frequencies within a site are variable over time, indicating that hybrid fitness is temporally dynamic possibly in response to changes in ecological conditions.

A genetic dissection of hormesis* S*Colin McClure** and Nick Priest

University of Bath

What doesn't kill you, makes you stronger. This statement from existential philosophy captures the essence of hormesis, a phenomenon which occurs when organisms receive fitness benefits from exposure to mild levels of stress. Although hormesis is observed through the application of many treatments and across multiple taxa, we do not know how it occurs or even whether it enhances Darwinian fitness. My research focuses on resolving these questions using empirical studies in the model genus *Drosophila*. In this talk, I will present recent work I have completed to identify the genetic basis of hormesis in natural and laboratory populations.

Phylogeography and population genetic structure of an alien lizard* S*Sozos Michaelides**

University of Oxford

Human activities are increasingly modifying the abundance and distribution of species and the ecological and economic consequences of invasive species have been long recognised. Identifying the phylogeographic origin of introduced populations is an important task to further test the causes and consequences of human-mediated translocations. The common wall lizard (*Podarcis muralis*) covers a wide range in western and southern Europe with several genetically and geographically distinct populations. The species was introduced, through multiple introductions, in the UK where it has established more than 25 populations. In order to resolve the origin of these populations we used a phylogenetic tree approach where we combined unique haplotypes (using a 655bp region of the mtDNA cytB gene), from 500 individuals from 23 non native populations, with published sequences from the native range. We identified 12 unique haplotypes in the introduced populations that were nested into five native, geographically distinct clades. Multiple clade origin was common within populations, with a maximum of three different haplotype clades being represented within a single population. These results show that human introductions have created substantial opportunities for hybridization between genetically and phenotypically distinct lineages, which may have important consequences for the establishment success and long-term viability of introduced wall lizard populations. Furthermore, we genotyped 800 individuals from 23 introduced and 15 native populations at 9 microsatellite loci to infer the genetic variation in the introduced range and how is affected by their origin and admixture.

Using a human model to reproduce the variability of a human parasite* S*Valeria Montano**, Anders Eriksson, Andrea Manica and Yoshan Moodley

University of Veterinary Medicine Vienna

The ancient association of *Helicobacter pylori* with its human host has led both species to very similar evolutionary histories as mirrored by the worldwide phylogeography of the bacterium. Our model assumes that one human host corresponds approximately to a single bacterial strain, since the intra-host genetic variation in *H. pylori* was shown to be low enough to have a negligible effect over a long time scale. Using estimates of human carrying capacities and migration rates among spatial demes, we simulated coalescent genealogies for the human host over a range of demographic scenarios and tested if those are able to reproduce the current observed variation of *Helicobacter pylori* in the Asian continent.

*Island biogeography of *Pristionchus pacificus* reveals dispersal limited by environment rather than sea barriers*

Katy Morgan

Max Planck Institute

Volcanic island chains such as the Mascareignes are frequently associated with adaptive radiations, in which dispersal and the colonisation of new islands are followed by the rapid divergence of populations isolated by sea barriers. The limited distribution of the nematode species *Pristionchus pacificus* within the Indian Ocean Islands, which is restricted to the Mascareigne islands of Mauritius and La Réunion, suggests that sea barriers have limited dispersal, prevented the colonisation of neighbouring islands and are likely to have restrained migration between Mauritius and La Réunion since their initial colonisation. Considerable differences between these islands in topography and the diversity of ecotypes are likely to result in differences in the selective pressures experienced by populations on either island, potentially driving adaptive divergence. *Pristionchus pacificus* is found in association with a number of host beetle species, and the assemblage of host species also differs between Mauritius and La Réunion. However, in contrast to the hypothesis of limited dispersal and a low probability of island colonisation, we find evidence for multiple independent colonisations of both islands by distinct and highly differentiated genetic lineages, suggesting high genetic diversity may have been influenced colonisation success. In addition, extensive migration between Mauritius and La Réunion is supported, despite their isolation and the apparent lack of beetle movements between them. The apparent restriction of specific genetic lineages to certain ecozones within both of the islands, despite extensive migration across ocean barriers, suggests that the dispersal of *P. pacificus* is strongly limited by environmental, rather than geographical factors.

Genome-wide patterns of divergence and gene flow across a butterfly radiation

Nicola Nadeau, Simon H. Martin, Krzysztof M. Kozak, Patricio Salazar, Camilo Salazar, Mayte Ruiz, Kanchon K. Dasmahapatra, John W. Davey, Simon W. Baxter, Mark L. Blaxter, Riccardo Papa, James Mallet and Chris D. Jiggins

University of Cambridge

The *Heliconius* butterflies are a diverse recent radiation comprising multiple levels of divergence with ongoing gene flow between species. The recently sequenced genome of *Heliconius melpomene* allowed us to investigate the genomic evolution of this group using dense RAD marker sequencing. Phylogenetic analysis of 54 individuals robustly supported reciprocal monophyly of *H. melpomene* and *H. cydno* and refuted previous phylogenetic hypotheses that *H. melpomene* may be paraphyletic with respect to *H. cydno*. *H. timareta* also formed a monophyletic clade closely related but distinct from *H. cydno* with *H. heurippa* falling within this clade. We find evidence for genetic admixture between sympatric populations of the sister clades *H. melpomene* and *H. cydno/timareta*, particularly between *H. cydno* and *H. melpomene* from Central America and between *H. timareta* and *H. melpomene* from the eastern slopes of the Andes. Between races, divergence is primarily explained by isolation-by-distance, with little race-specific structure. Detailed analyses across two racial hybrid zones, in Peru and Ecuador, show that genomic divergence is highest around loci controlling colour pattern. However, the two hybrid zones show very different background levels of divergence, suggesting different evolutionary histories or selective regimes.

Variation in speciation time for different parts of the genome

Richard Nichols, James Cotton and Veronica Comper

Queen Mary University of London

After alignment of thousands of genes across vertebrate genomes, we use the number of substitutions to estimate the relative time back to a common ancestor for different parts of the genome. The expected variation between loci will be affected by the ancestral population size, hence it is possible to use the data to estimate the ancestral population size. For the human

chimp ancestor this estimate is of the same order as the number of generations back to human-chimp speciation; we ask if that estimate is plausible. Estimates for individual chromosomes vary much more than would be predicted. Did some chromosomes undergo earlier speciation than the rest of the genome? We argue that this pattern is better explained by the effects of gene conversion among members of multi-gene families.

Immune gene diversity in canines **S**

Alina K Niskanen, Lorna Kennedy, Marco Apollonio, Massimo Scandura, Ilpo Kojola, Hannes Lohi, Minna Ruokonen and Jouni Aspi

University of Oulu

Maintaining adaptive genetic variation is one of the key factors in the conservation of small populations. Major histocompatibility complex (MHC) includes substantial numbers of immune genes. Lowered genetic variation in MHC loci can lead to lowered immunity against pathogens which may increase the risk of extinction of the population. Humans have recently caused both wolves and domestic dogs to go through major population bottlenecks. We studied the amount of genetic variation and natural selection in MHC loci of both species. We sequenced the highly variable second exon from three MHC class II loci; DLA-DRB1, DLA-DQA1 and DLA-DQB1 among 446 European and North-American wolves and 1020 dogs from 11 different breeds. We also studied the association of MHC class II loci to *Echinococcus granulosus* and *Trichinella* spp. infections among the Finnish wolf individuals. Our results show that the MHC haplotypes in European and North-American wolf populations are highly differentiated. Altogether 43 three locus haplotypes were found, of which old and new world wolves shared only 5. The allele frequencies in the North-American and two European wolf populations were more equal than expected; Tajima's D and Fu & Li D* and F* tests also gave significantly positive values, implying balancing selection. We also found that homozygosity increased the risk of *Trichinella* spp. infection among Finnish wolves. Dog breeds differed substantially in their MHC diversities. The breeds with highest MHC polymorphism were as diverse as wolf populations.

Type-dependent migration in continuous space and time **S**

Sebastian Novak

IST Austria

We derive a general model of type-dependent migration in space that contains many previous models as special cases. One result is that type-dependent migration can lead to similar phenomena as selection and might therefore distort our predictions from spatial clines maintained by selection. Qualitatively, we show how different migration patterns deform spatial frequency profiles and assert that, according to our model, increased mobility implies an advantage in out-competing otherwise identical opponents. Furthermore, we perform an approximation in the limit of weak migration differences that allows to study the invasion of alleles modifying migration patterns such that dispersal can be seen as an evolving trait. Apart from its application to questions concerning the evolution of dispersal or of habitat preference, our model can serve as a basis to be specialized to various applications of type-dependent migration and to put future studies on common ground.

The coalescent in boundary-limited range expansions **S**

Jens Nullmeier and Oskar Hallatschek

Max-Planck-Institute for Dynamics and Self-Organization - Biological Physics and Evolutionary Dynamics

Habitat ranges of most species shift over time, for instance due to climate change, human intervention, or adaptation. These demographic changes often have drastic effects on the genetic composition of the population, such as a stochastic resampling of the gene pool through the "surfing" phenomenon. Most models assume that the speed of range expansions is only limited by the dispersal ability of the colonizing species and its reproductive potential. While

such models of “phenotype-limited” expansions apply for instance to species invasions, it is clear that many range expansions are limited rather by the slow motion of habitat boundaries, as driven for instance by global warming. Here, we develop a coalescent model to study the genetic impact of such “boundary-limited” range expansions. Our simulations and analytical calculations show that the resulting loss of genetic diversity is markedly lower than in species invasions if large carrying capacities can be maintained up to the habitat frontier. Counterintuitively, we find that the total loss of diversity does not depend on the speed of the range expansion: Slower expansions have a smaller rate of loss, but also last longer. Based on our results, we conclude that boundary-limited range expansions have a characteristic genetic footprint and should be distinguished from range expansions limited only by intrinsic characteristics of the species.

*The discovery and population genetics of *Drosophila* viruses*

Darren J. Obbard, Claire Webster, Shaun Robertson, Giada Ferrari and Daisy Crowson
University of Edinburgh

Several groups have used population-genetic and phylogenetic approaches to show that some antiviral immune genes in *Drosophila* (notably the antiviral RNAi pathway) display highly elevated rates of adaptive evolution. However, although this is consistent with a host-virus arms race, the evolutionary genetics of *Drosophila* viruses are almost unstudied. In an attempt to understand the evolutionary genetics of viruses in *Drosophila*, we have sequenced both rRNA-depleted RNAseq, and small-RNA, libraries from large pooled samples of wild-caught *D. melanogaster*, identifying several new RNA viruses (including viruses with sequence-similarity to Sacbrood Virus, Slow Bee Paralysis Virus, Chronic Bee paralysis virus, Acyrthosiphon Pisum Virus, Brevicoryne brassicae picorna-like Virus, Flaviviruses, and Cypoviruses) and a DNA virus (Nudivirus). Following a wider geographic survey of *D. melanogaster* using RT-PCR, we find that the previously known viruses of *D. melanogaster* (including DAV, Sigma and Nora) are widespread at low to intermediate prevalence, but that the new viruses vary widely in prevalence and distribution. None of the viruses shows high rates of adaptive evolution, and in general (despite substantial synonymous divergence) protein sequences are very highly conserved. However, while this may indicate that these viruses are not engaged in ‘arms race’-like coevolution, we suspect that the short timescale of viral co-ancestry (tens to hundreds, rather than thousands, of years) makes this process extremely difficult to detect. This is in sharp contrast to viral evolution in response to vertebrate adaptive immunity, which adapts plastically on the same timescale as viral evolution.

Integrating genealogical and dynamical modelling to infer escape and reversion rates in HIV epitopes **S**

Duncan Palmer, Gil McVean and Angela McLean
University of Oxford

The rates of escape and reversion in response to selection pressure arising from the host immune system, notably the cytotoxic T-lymphocyte (CTL) response, are key factors determining the evolution of HIV. Existing methods for estimating these parameters from cross-sectional population data using ordinary differential equations (ODE) ignore information about the genealogy of sampled HIV sequences, which has the potential to cause systematic bias and over-estimate certainty. Here, we describe an integrated approach, validated through extensive simulations, which combines genealogical inference and epidemiological modelling, to estimate rates of CTL escape and reversion in HIV epitopes. We show that there is substantial uncertainty about rates of viral escape and reversion from cross-sectional data, which arises from the inherent stochasticity in the evolutionary process. By application to empirical data, we find that point estimates of rates from a previously published ODE model and the integrated approach presented here are often similar, but can also differ several-fold depending on the structure of the genealogy. The model-based approach we apply provides a framework for the statistical analysis of escape and reversion in population data and highlights the need for

longitudinal and denser cross-sectional sampling to enable accurate estimate of these key parameters.

Do closely related species use the same genes to adapt to fluctuating environmental conditions? **S**

Darren J. Parker, Laura Vesala, Michael G. Ritchie, Asta Laiho, Anneli Hoikkala and Maaria Kankare

University of St. Andrews

For insects, seasonal fluctuating temperature conditions require the ability to acclimate to lower than optimal temperatures in order to remain active. Cold tolerance in insects has been shown to have a genetic basis in numerous groups; however it is not clear if the underlying genetic architecture producing this phenotype is the same across species. We used the SOLiD platform to sequence the transcriptomes of two *Drosophila* species that diverged approximately 9 Myr ago, *D. montana* and *D. virilis*, from both cold acclimated and non-cold acclimated individuals. We established the genes which were differentially expressed between the treatments, allowing us to a) identify the genes and pathways involved in cold acclimation in each of the species and b) test whether they are conserved between the two species. Approximately 150 genes were differentially expressed between cold acclimated and non-cold acclimated treatments in *D. virilis* and *D. montana*. The biological processes associated with these genes were broadly similar in both species and included circadian clock regulation and metabolism. Only 9 genes were found to be differentially expressed in both species. They included the clock genes *period* and *vrille*, which are transcription factors that regulate a large number of downstream genes, (input-output genes). The results suggest that downstream genes involved in cold acclimation are different between the two species, but the changes in gene expression may be orchestrated in part by the same genes.

When does genetic drift prevent expansion of a species' range?

Jitka Polechová and Nick Barton

IST Austria

Genetic drift reduces local genetic variance, which is crucial for adaptation-driven range expansion. When do low population numbers limit further expansion of a species' range? We employed the understanding of i) the deterministic dynamics of the joint change in population density and evolution of a quantitative trait and ii) the effect of genetic drift on a cline, to find a threshold where a finite population ceases to adapt to an environment changing in space. In the talk, I will aim to explain the robustness and the meaning of the threshold, which combines dispersal load, neighbourhood size, strength of selection per locus and strength of density regulation. The threshold is a single dimensionless parameter. In general, it is clear that in finite populations, even a small increase in the perceived gradient of the optimum across space can lead to a sudden inability of a species to continuously adapt to gradually changing environments, and drive a sharp range margin or range fragmentation.

Modelling resistance against gastrointestinal nematodes in sheep **S**

Joaquin Prada J. de Cisneros, Louise Matthews, Thorsten Stefan, Colette Mair and Michael J. Stear

University of Glasgow

Gastrointestinal nematode infections have a huge impact on livestock production. Selective breeding for nematode resistance could improve the resistance of livestock. However, the response to selection cannot be predicted from genetic theory alone because culling susceptible animals reduces environmental contamination and lowers the transmission of infective stages. An individual-based, immunologically-explicit model of nematode infection was created to predict the response to selection using parameters obtained from a long-term study of natural and deliberate infections in Scottish sheep. The response to selection was modelled

over 10 generations. We compared the response to selection for improved immunity (parasite-specific IgA) against selection for reduced nematode egg output. Selection based on IgA was more effective at reducing egg output than direct selection on reduced faecal egg output.

The shaping of genetic variation in edge populations under past and future climate change: the grey long-eared bat as a case study **S**

Orly Razgour, Javier Juste, Carlos Ibáñez, Andreas Kiefer, Hugo Rebelo, Sébastien Puechmille, Raphael Arlettaz, Terry Burke, Deborah A. Dawson, Mark Beaumont and Gareth Jones

University of Bristol

With rates of climate change exceeding the rate at which many species are able to shift their range and limited evidence of genetic adaptation, it is important to understand how future climatic changes are likely to affect biodiversity at all levels of organisation. The effect of Quaternary climatic fluctuations on the distribution of species and patterns of genetic variation across their range may provide a clue to some potential future consequences. We studied the genetic consequences of past and future climatic changes on the grey long-eared bat, *Plecotus austriacus*, a species with relatively limited dispersal ability and a high sensitivity to climate change. We combined predictive ecological niche modelling across temporal scales with genetic data and model-based inference of demographic history. Concordance between the location of glacial refugia identified through genetic analysis and ecological niche modelling indicates that the climatic niche of *P. austriacus* is likely to be conserved and therefore can be projected into the future. Areas identified as potential glacial refugia and source populations at the rear-edge of the species' range (Iberia) contained disproportionately high levels of genetic diversity, but were also most at risk from future climate change. Niche conservatism, predicted shifts in suitable areas and limited contemporary migration rates all suggest that climate change is likely to result in extensive losses of genetic diversity. We demonstrate the importance of edge-of-range populations both as stable reservoirs of genetic diversity (refugial populations) and as the source of future spread of genetic variability (leading-edge populations).

Unwinding the chiral evolution of Japanese snails using RAD-seq **S**

Paul M Richards, Satoshi Chiba and Angus Davison

University of Nottingham

In some chirally dimorphic snails, such as Japanese *Euhadra*, dextral (right-coiling) and sinistral snails (left-coiling) are unable to mate with one another. Although the shell morphs are in theory reproductively isolated, there is still the potential for gene flow, because of a delay in the expression of the coiling phenotype that is caused by the maternal inheritance of the chirality locus. A remaining question is to understand how new chiral morphs become established because there should be strong frequency dependent selection against the novel type. Geographic isolation (founder effect), character displacement and predation are all implicated. In *Euhadra*, we identified contact zones between dextral and sinistral snails. Very similar mitochondrial DNA haplotypes were discovered in sinistrals and dextrals from the same location, with most differences occurring between regions, implying recent chiral evolution or else introgression. To resolve this issue, we used Restriction Site Associated DNA sequencing (RAD-seq) to rapidly produce a genome wide set of SNPS from fifteen individuals, comprising both dextrals and sinistrals. The analysis of this data will be used to understand the geographic scale over which chiral evolution has taken place.

*Molecular dissection of clutch size and egg mass in a wild great tit (*Parus major*) population indicates polygenic genetic architectures and no evolutionary constraint*

Anna Santure, Isabelle De Cauwer, Matthew R. Robinson, Jocelyn Poissant, Ben C. Sheldon and Jon Slate

University of Sheffield

Clutch size and egg mass are life history traits that are extensively studied in wild bird populations, as classic life history theory predicts a negative trade-off between them, either at the phenotypic or genetic level. Here, we analyse the genetic architectures of clutch size and egg mass in a wild great tit (*Parus major*) population from Wytham Woods, Oxford. Using three different marker-based approaches, chromosome partitioning, quantitative trait locus (QTL) mapping and a genome wide association study (GWAS), both traits reveal a polygenic basis. The variance explained by each great tit chromosome scales with predicted chromosome size, no location in the genome contains genome-wide significant quantitative trait loci, despite both traits having moderately high heritabilities, and no individual SNPs are associated with large proportions of variation in clutch size or egg mass. A bivariate scan of the genome fails to identify any regions contributing to the small, non-significant negative genetic covariance between the traits, suggesting that there are no genetic constraints between the two traits that could prevent either evolving in the face of directional selection. In summary, the results explain why clutch size and egg mass are not usually negatively correlated within populations, despite their being a trade-off between them at the between-species level. Our findings also support the hypothesis that variation in key life history traits in natural populations is likely to be determined by many loci of small effect spread throughout the genome, which are subject to continued input of variation by mutation and migration.

Evolutionary dynamics of a multipartite plant virus in a heterogeneous mountain landscape

Fiona Savory and Uma Ramakrishnan

National Centre for Biological Sciences, Bangalore

Genetic exchange plays a key role in plant virus evolution, and can have important epidemiological implications. For instance, by generating novel combinations of nucleotide polymorphisms, recombination or reassortment events may lead to the emergence of highly virulent strains, or facilitate adaptation to different hosts, vectors or environments. Genetic exchange also confounds the reconstruction of viral phylogenies, which can be used to infer spatial transmission dynamics and inform the development of management strategies. We investigated the occurrence of recombination and reassortment among natural isolates of Cardamom Bushy Dwarf Virus (CBDV), a multipartite, single-stranded DNA nanovirus which infects large cardamom, *Amomum subulatum*. This important cash-crop is cultivated across a range of altitudes in sub-Himalayan regions of Northeast India, Nepal and Bhutan. Our analyses demonstrate that frequencies of recombination vary considerably among different genome components and that reassortment plays a major role in the evolution of CBDV. We will discuss our findings with reference to the relative roles of deterministic (selection) versus stochastic (drift) evolutionary forces acting on the fate of recombinant and reassortant genotypes across multiple spatial scales.

Pool-GWAS: a general and cost-effective method for fine-mapping natural phenotypic variation

Christian Schlötterer, Héloïse Bastide, Andrea Betancourt, Viola Nolte, Raymond Tobler, Petra Stoebe and Andreas Futschik

Vetmeduni Vienna

Various approaches can be applied to uncover the genetic basis of complex traits, each with their specific strengths and limitations. Here, we introduce a replicated Pool-GWAS approach, which combines the advantages of Genome Wide Association Studies (GWAS) and QTL mapping. Rather than genotyping individuals, as in classic GWAS studies, Pool-GWAS contrasts allele frequencies between pools of individuals with different phenotypes. As it enjoys about a 200-fold cost advantage over typical GWAS studies, it can be used for any outcrossing species with a sequenced reference genome. As a proof of principle, we apply this technique to study variation in one of the best characterized morphological traits in *Drosophila*, female abdominal pigmentation. In a joint analysis of two European populations of *D. melanogaster*, SNPs with the strongest associations with pigmentation mapped to cis-regulatory modules of tan and bric-à-brac, genes having a central role in pigmentation.

Robustness against extinction by stochastic sex determination in small populations **S**

David Marcelo Schneider, Eduardo do Carmo, Yaneer Bar-Yam and Marcus A. M. de Aguiar
Universidade Estadual de Campinas

Sexually reproducing populations with a small number of individuals may go extinct by stochastic fluctuations in sex determination, causing all their members to become male or female in a generation. In this work we calculate the time to extinction of isolated populations with fixed number N of individuals that are updated according to the Moran birth and death process. At each time step, one individual is randomly selected and replaced by its offspring resulting from mating with another individual of the opposite sex; the offspring can be male or female with equal probability. A set of N time steps is called a generation, the average time it takes for the entire population to be replaced. The number k of females fluctuates in time, similarly to a random walk, and extinction, which is the only asymptotic possibility, occurs when $k = 0$ or $k = N$. We show that it takes only one generation for an arbitrary initial distribution of males and females to approach the binomial distribution. This distribution, however, is unstable and the population eventually goes extinct in $2N/N$ generations. We also discuss the robustness of these results against bias in the determination of the sex of the offspring, a characteristic promoted by infection by the bacteria *Wolbachia* in some arthropod species or by temperature in reptiles.

Challenges to the gene's eye view of evolution: hot air or hot water?

David Shuker

University of St Andrews

In recent years a growing and diverse body of literature has challenged the gene's eye view of evolution encapsulated by the Modern Synthesis and central to modern population genetic theory. This literature has voiced the need for a "New Synthesis" and highlighted "missing" processes in evolution. Various research programmes have contributed (deliberately or otherwise) to this challenge, including the fields of evo-devo, phenotypic plasticity, niche construction and epigenetics. In this talk I will review this challenge to our traditional population-genetic view of evolution, exploring recent and not so recent attempts to expand what we think of as evolutionary "processes". I will argue that we need to appreciate the difference between "things" that generate phenotypic variation, genetic variation, and those that then sort genetic variation. Many, if not all, of the processes considered to be missing from the traditional view, fall into the first category rather than the latter two.

*Transcriptome-wide expression variation associated with environmental plasticity and mating success in the cactophilic *Drosophila mojavensis** **S**

Gilbert Smith, Yongxiang Fang, Xuan Lui, John Kenny, Andrew Cossins, Cassia de Oliveira, William J Etges and Michael G Ritchie

University of St Andrews

Ecological speciation occurs with the adaptation of populations to different environments and concurrent evolution of reproductive isolation. The role of phenotypic plasticity might influence both ecological adaptation and reproductive traits. We examined environment-specific gene expression and male mating success in a cactophilic *Drosophila* using high throughput transcriptome sequencing. *Drosophila mojavensis* exhibits cactus-dependent mating success across different species of host plants, with genotype-by-environment interactions for numerous traits. We cultured flies from egg to eclosion on two natural cactus hosts and surveyed gene expression in adult males that were either successful or unsuccessful in achieving copulation in courtship trials. We identified gene expression differences which included functions involved with metabolism, most likely related to chemical differences between host cactus species. Several epigenetic related functions were identified that might play a role in modulating gene expression in adults due to host cactus effects on larvae. Cactus-dependent mating success implicated expression differences of genes involved in translation, transcription and nervous system development. This suggests a role of neurological function genes in the mating success of *D. mojavensis* males. Together, these results suggest that the influence of environmental variation on mating success via regulation of gene expression might be an important aspect of ecological speciation.

To evaluate and apply novel statistical techniques for diversity based gene-mapping **S**

John Stainton, Pamela Wiener, Brian Charlesworth, Chris Haley, Andreas Kranis and Kellie Watson

Roslin Institute

The hitchhiking effect reduces genetic variation at sites linked to those under positive selection. Statistical methods can be used to find significant areas of low genetic variation which can then be investigated to find potential genes of interest. Due to strong human driven selection, farm animals are well suited to these methods. A study on genetic variation in domesticated animals may find important regions for further study and allow the evaluation of the power and performance of these statistical methods in a way data from other species does not. Broiler chickens are selected for a variety of traits, including growth rate, feed conversion ratio, yield, reproduction, health and welfare. Broiler SNP data was provided by an industrial partner. This data includes 9 broiler lines genotyped using a 12k SNP chip and 1 line genotyped with a 42k chip. Genetic differentiation (Weir and Cockerham's F_{ST}) and heterozygosity (Nei's unbiased estimator of gene diversity) tests were applied to detect signatures of selection. Patterns of selection signals across the 9 lines were explored. Regions showing strong evidence of selection were further investigated for possible candidate genes.

Breeding parasite resistant sheep

Michael J. Stear, Thorsten Stefan, Joaquin Prada and Louise Matthews

University of Glasgow

The heritability of resistance in lambs to natural, predominantly *Teladorsagia circumcincta* nematode infection is remarkably high. There are several immunological and parasitological measures of resistance and several traits have heritabilities over 0.5. The reasons for the high heritability are unclear. We therefore investigated whether there was a trade-off between reduced growth and protection in 1000 naturally infected Scottish Blackface lambs and over 200 naturally infected Texel lambs. Protection was associated with increased parasite-specific IgA and IgE activity. Reduced growth in heavily infected animals was associated with increased IgE but not increased IgA activity. The genetic correlation between resistance and growth was positive; resistant lambs with low egg counts grew more quickly than susceptible lambs.

Therefore a simple trade-off between immunity and growth does not exist in these lambs. Selective breeding for high IgA responses to improve parasite resistance is an attractive possibility. Mathematical modelling indicates that the response to selection will be relatively rapid.

Modelling the generation and maintenance of diversity at the MHC **S**

Thorsten Stefan

University of Glasgow

Genes of the Major Histocompatibility Complex (MHC) are unusually polymorphic. The reason for this diversity has been debated for more than four decades, without any consensus being reached. While balancing selection is assumed to be essential for maintaining the polymorphism, the main evolutionary mechanisms and their relative importance within a host-pathogen system, or across systems, remain incompletely understood. Because of the important role MHC molecules play in the immune system of vertebrates, pathogen mediated-processes are assumed to be strong drivers of balancing selection, with heterozygote advantage being one of the popular explanations for the mechanism. We examine whether, or to what extent, heterozygote advantage can account for the observed polymorphism by comparing different established theoretical models that relate fitness contributions of MHC alleles to the genotypic fitness of a host. By running stochastic simulations over evolutionary time scales we model the evolution of alleles in the MHC in species of the Bovidae family. We compare features of the different models and extract a model that best reflects biological observations.

Uncovering hidden genetic diversity in a cryptic species flock of African river catfishes, *Chiloglanis* **S**

Jen Swanstrom, John P. Friel, Denis Tweddle and Martin Genner

University of Bristol

Rivers appear to contain low species diversity due to narrow niche range and comparatively more disturbance compared with lakes. Rivers flowing into Lake Malawi contain an order of magnitude fewer species than the lake, however such low diversity could be obscured by cryptic morphology. A genus of African river catfishes, *Chiloglanis*, provides an example of this. Currently two species are known in Malawi, yet descriptions were based solely on morphology with no genetic information. Individuals were sampled from populations across the Malawi catchment and all major surrounding catchments to reconstruct *Chiloglanis* evolutionary history. Approximately 350 individuals from 47 populations were sequenced at two loci, the control region and S7 intron 1, to look for congruence across genes. Morphometric measurements were taken from a subset of samples from each clade to determine whether they are true cryptic species. Results show well-supported congruence across two loci, suggesting that lineages are evolving independently, with 10 distinct clades in Malawi. Across East Africa, 17 clades were found, most were allopatric, but two clades were sympatric in Zambia, a new finding for this genus. Morphometric results suggest that differences are too subtle to be detected easily; in practice clades are indistinguishable in the field, providing further evidence for a cryptic species flock. The *Chiloglanis* genus shows the utility of integrative taxonomic methods, and how stabilizing selection acts to constrain morphology and obscure a hidden level of diversity. *Chiloglanis* catfishes comprise a cryptic species flock, and perhaps the most species rich catfish genus known.

*Parthenogenesis – dead end in the evolution of reptiles?***David Tarkhnishvili** and Mari Murtskhvaladze

Ilia State University

The genus *Darevskia* is one of the most speciose reptile groups of non-tropical Eurasia. The group is comprised of 25 described species, including eight parthenogenetic clones of hybrid origin. Previous molecular genetic studies suggest that (1) all parthenogenetic forms descend from hybridization among representatives of two distinct clades of bisexual *Darevskia*, (2) the level of mitochondrial DNA divergence of the parthenogens and their maternal species is low, which suggests their recent origins. Parthenogenetic forms of the genus are found throughout large mountain areas with a limited accessibility for bisexual congeneric lizards. The relative analysis of spatial distribution and abundances of two parthenogenetic lizards and their daughter unisexual forms suggests that the unisexuals are stronger competitors and they influence the extent of spatial niche of the paternal and maternal species, which causes geographic separation of their ranges. The expansion of the parthenogens excludes contacts between the parental forms and repeated development of new parthenogenetic clones. This view is supported by the analysis of microsatellite loci in the lizards, which suggests that all unisexual individuals descend from a single hybrid pair.

*First large-scale genetic analysis of the vulnerable noble crayfish *Astacus astacus* in Europe***Kathrin Theissing** and Anne Schrimpf, Lucian Pârvolescu, Ivana Maguire, Holger Schulz and Ralf Schulz

University of Koblenz-Landau, Institute for Environmental Sciences

Global changes, human impact and climatic oscillations had a severe impact onto the distribution and diversity of the vulnerable European noble crayfish *Astacus astacus*. The main aim of this study was to resolve the natural genetic structure of European noble crayfish populations and to estimate to what degree human translocations dissolved the natural genetic make-up. We sampled 500 individuals from 120 populations across Europe. We sequenced a 350 base pair (bp) fragment of the mitochondrial cytochrome oxidase subunit I (COI) and a 500 bp fragment of 16s rRNA (16S). Furthermore, for 24 populations a microsatellite analysis was performed based on six polymorphic loci. Twenty-two COI-haplotypes and sixteen 16S-haplotypes were identified. Both genes exhibited one common haplotype across the whole study area. High numbers of private haplotypes suggested two separate glacial refugia on the western and central Balkan. In contrast, very low haplotype diversities in central Europe were detected, which could result from human translocations and/or founder effects due to postglacial re-colonization. Microsatellites exhibited strong genetic differentiation between central and eastern Europe as well as between the central and western Balkan, but little among central European populations. Despite human translocations a differentiation of noble crayfish populations in all major catchment areas was detectable. Our data thus support the establishment of distinct evolutionary significant units to protect the present-day genetic diversity of *A. astacus* in Europe.

*Using bacterial population genomics to investigate the spread of bovine tuberculosis***Hannah Trewby**, Roman Biek, Anthony O'Hare, David Wright, Tom Mallon, Carl McCormick, Richard J. Orton, Stanley McDowell, Robin A. Skuce, Rowland R. Kao

University of Glasgow

Current sequencing technologies have made it possible to study population processes at unprecedented scales. Here, we describe how bacterial whole genome sequencing provides new insights into processes driving the persistence and spread of an important veterinary pathogen. Bovine tuberculosis (bTB) is caused by the bacterium *Mycobacterium bovis*. In addition to its economic importance it is also believed to pose a major health problem in many areas of the world. It is primarily a disease of cattle, but in Britain and Ireland failure to eradicate bTB in the cattle population has been linked to infection in the Eurasian badger. Despite extensive research effort involving laboratory and field studies, the exact roles of badgers and

cattle in bTB in the Britain and Ireland remains not only unclear but also mired in controversy. Using isolates from Northern Ireland, we sequenced all samples available for a recently emerged *M. bovis* molecular strain type (n=146) (including six badger samples). Combining these molecular data with detailed demographic information on the cattle population, we are able to investigate the fine-scale processes involved in transmission of the pathogen, untangling the relative roles played by movements of infected cattle between farms compared to local spatial processes. Our results indicate a predominance of local transmission, the existence of core areas seeding most new infections, and minimal divergence among *M. bovis* genomes isolated from cattle and badgers. The approach described here shows great promise for understanding and quantifying the mechanisms involved in persistence and spread of bTB in Britain and Ireland.

QTLs for behavioural variation within populations are different than between populations

Paris Veltsos, Barbara Morrissey, Emma Gregson, Claude Wicker-Thomas, Roger K Butlin, Jon Slate, Anneli Hoikkala and Michael G Ritchie

University of St Andrews

We present QTL analysis for traits under sexual selection (courtship song and cuticular hydrocarbons) in two isolated populations of *Drosophila montana*. Limited reproductive isolation exists between the populations which have evolved separately for about 0.5 MY. The traits were scored from three generations raised in the lab from wild-collected isofemale lines, and their effect on courtship success was measured from the same individuals.

Results: Few significant QTLs were detected for within population variation. Any detected were different to QTL identified previously by crossing divergent populations. Genomic regions containing candidate genes previously associated with those traits, such as *per* and *fru*, were not associated with within population variation.

Discussion: The general lack of QTL combined with their small effect and large proportion of variance explained, is compatible with polygenic determination of traits that are important in sexual selection within populations. The genes associated with divergence between phylogenetically distant populations appear to be different to those associated with sexual selection within populations.

Patterns of diversity in adapting, spatially extended populations

Daniel Weissman and Nick Barton

IST Austria

Models of spatially extended populations often assume for convenience that the population's range is perfectly symmetric, with all locations equivalent. While this is unrealistic, the hope is that it is approximately true for large ranges. However, we find that this is often not the case for populations undergoing recurrent adaptation. In such populations, reproductive value can depend strongly on position, even far from the boundaries of the range. In such populations, traditional statistics such as F_{st} can give a misleading picture of the actual migration patterns. Paradoxically, the effect tends to be strongest in regions of the genome far from the genes undergoing selection, and can be stronger in populations with larger ranges, where boundary effects are expected to be less important. These results suggest that the classic circular and toroidal toy models for spatial structure may be inappropriate for many adapting populations.

Genetic basis and geographical patterns of adaptive divergence in an intertidal snail

Anja M. Westram, Juan Galindo and Roger K. Butlin

University of Sheffield

Understanding the genetic basis of speciation is a major goal of speciation research and requires the identification of loci affected by divergent selection between incipient species. These loci, and those closely linked to them, are expected to show increased divergence (e.g.

FST) compared to neutral loci. Next-generation sequencing allows for the analysis of large sets of loci simultaneously, so that the base line level of divergence can be established and loci with an elevated degree of divergence identified. Additionally, these methods may also reveal previously inaccessible geographical patterns of speciation if multiple populations are sampled. We use this approach to study incipient speciation in the marine snail *Littorina saxatilis*. *L. saxatilis* is split into two ecotypes (adapted to crab predation vs. wave exposure) on rocky shores across Europe. While morphological patterns of divergence are similar, it is not clear yet whether the ecotypes have a common origin (and therefore the same genetic basis) across large geographical scales, or evolved several times in parallel (with a potentially different genetic basis). Here, we ask this question using RNA-sequencing. We generated 150M short read sequences (Illumina) of the transcriptomes of snails from Spain, Sweden and the United Kingdom. After assembling the transcriptome, we identified SNPs/contigs showing increased divergence between ecotypes, potentially reflecting divergent selection. Outlier SNPs/contigs identified in multiple geographical locations may indicate a common origin of divergence. We present results on the degree of overlap between geographical regions and discuss these findings in the light of geographical patterns of speciation.

A regression approach to selection mapping

Pam Wiener, Ricardo Pong-Wong and Beatriz Gutierrez Gil

The Roslin Institute, University of Edinburgh

Selection mapping applies the population genetics theory of hitchhiking to the localization of genomic regions containing genes under selection. This approach predicts that neutral loci linked to genes under positive selection will have reduced diversity due to their shared history with a selected locus and thus, genome scans of diversity levels can be used to identify regions containing selected loci. Unlike most other methods, the regression-based approach presented here takes into account the expected pattern of decreasing genetic diversity with increased proximity to a selected locus. Simulated data is used to examine the patterns of diversity under different scenarios, in order to assess the power of a regression-based approach to the identification of regions under selection. Application of the regression method to both simulated data and data from genomic regions known to have been under selection demonstrates its potential to detect selection. Results suggest this approach may give more precise estimates of the location of the selected locus than alternative methods, although the power may be slightly lower. Applications of the method to genome-wide SNP data from livestock are presented.

Spatial and temporal population genetics of the Mauritian Pink Pigeon (Columba mayeri)

Faye Willman, Lauren Ward and Jim Groombridge

University of Kent

The Mauritius pink pigeon (*Columba mayeri*) is an endemic species that has undergone significant recovery, from a population of approximately 9 individuals in 1990 to over 400 individuals to date. Based on a pilot study carried out at DICE, this project uses 21 species-specific microsatellite markers to investigate the population genetic structure of the pink pigeon in response to over 30 years of management. Despite high levels of translocation and reintroduction, subpopulation structure is maintained. Significant F_{st} values can be seen between 5 of the 6 populations on Mauritius. Furthermore, the vast demographic data set held for the pink pigeon explains subtle features of subpopulation structure across a spatial and temporal scale. In addition to free-living birds, captive pink pigeons have been genotyped to ascertain to what extent their alleles are represented in the wild population on Mauritius. This project attempts a comprehensive genetic analysis that integrates nuclear DNA markers, more traditional studbook/pedigree information from the global metapopulations, and data from field monitoring programmes to best inform future species management strategies.

Genetic diversity and hybridisation in ancient lime trees (Tilia)

Kirsten Wolff, Prattana Phuekvilai, Samuel Logan, Carl Barker and Paul Ashton
Newcastle University

Hybridisation and introgression between species affect both speciation and adaptation, to varying degrees. Studies in, for example, oak and poplar have shown genomic regions that reveal high differentiation between species for regions with reproductive isolation genes and other regions with lower differentiation, containing adaptive genes. *Tilia cordata* (small leaved lime) and *T. platyphyllos* (large leaved lime) are endemic in Europe and they can hybridize (*T. x europea*). Although commercially not important, they play important roles in their ecosystems. A cooler climate and human impact has reduced sexual regeneration and the number of trees, especially in the north. However, genotypes can survive for many hundreds of years and individuals may therefore be ancient. Microsatellite markers confirm that the species are diploid with high diversity and a predominantly outbreeding mating system. It is unclear what the extent and direction of hybridisation and introgression are in the wild. There are some morphological differences, but in the absence of flowers it is often difficult to identify the species or the hybrid with certainty. Here we present preliminary studies investigating hybridisation in *Tilia*. The individuals clearly grouped by species, confirming their genetic differences. We found a significant number of hybrid individuals in some populations, confirming morphological classification in most cases. In subsequent studies we aim to use NGS technologies to understand better the genomics of speciation.

A coalescent model of background selection with recombination, demography and variation in selection coefficients

Kai Zeng

University of Sheffield

There is increasing evidence that background selection, the effects of the elimination of recurring deleterious mutations by natural selection on variability at linked sites, may be a major factor shaping genome-wide patterns of genetic diversity. To accurately quantify the importance of background selection, it is vital to have computationally efficient models that include essential biological features. To this end, a coalescent model of background selection that takes into account the effects of genetic recombination, recent changes in population size and variation in selection coefficients against deleterious mutations across sites has been constructed. The accuracy of the model is verified by checking against the results of forward simulations. These simulations also reveal several patterns of diversity that are in qualitative agreement with observations reported in recent studies of DNA sequence polymorphisms. These results suggest that the model should be useful for data analysis.

Abstracts-Poster Presentations

Genetic relationships between the local pear cultivars of Georgia and their progenitor species Pyrus caucasica Fed. S

Zeza Asanidze

Iliia State University, Tbilisi, Georgia (zezva.asanidze.1@iliauni.edu.ge)

Wild endemic species of pear – *Pyrus caucasica* is considered as progenitor of local cultivars. However, so far there are no strong evidences supported by molecular studies to confirm genetic relationship between wild populations of this species and local cultivars. With *P. caucasica* population sampled in territory of Georgia also have been analyzed 6 wild pears as an out-group. As an out-group were also used a group of introduced cultivars from European and Asian countries. The data based on study of 11 microsatellites (GD12, GD96, GD142, GD147, CH01d08, CH01d09, CH01f07a, CH02b10, CH02d12, NH015a, CH01h01) were analyzed by multivariate statistic. The results have shown close genetic relationship between population of Caucasian wild pear and some of the sampled local pear cultivars of Georgia. Involvement of out-groups revealed high level of divergence between *P. caucasica* and European progenitor wild pears - *P. pyraster* and *P. nivalis*. The cluster analysis revealed high level of diversity between studied cultivated pears. Thus, the results confirm that the most of the studied local cultivars are in close genetic relationship with Caucasian wild pear.

Investigating evidence for positive selection in selected candidate innate immune genes in livestock

Ilori Babatunde Moses, Joram Mwacharo and Olivier Hanotte

University of Nottingham

Migration of livestock to new environments from the wild following the process of domestication expose them to new challenges in terms of tolerance or susceptibility to different infectious diseases. The resulting population genetic adaptation has an important impact in shaping the genetic diversity of genes. Genes in the first line of defence against pathogens (Toll-like receptors, cytokines, cell surface proteins and other receptors) might be subject to frequent positive or balanced selection due to coevolutionary dynamics with pathogens. Screening innate immune genes for selective signatures associated with disease immunity or susceptibility would allow for identification of important genes critical for disease resistance or the evolution of differential disease susceptibilities. Here, we report the comparison of the relative fixation rates of synonymous (silent) and nonsynonymous (amino acid-altering mutations) substitutions at 27 candidate genes for innate immunity in East African shorthorn zebu cattle (EASZ) and other livestock species. Gene diversity in EASZ was determined after screening full genome sequencing data of a pool of 10 individuals, while sequences from other livestock species were obtained from NCBI. Using codon-based likelihood ratio test approaches, Hyphy package implemented in Data Monkey Web Server and Codeml (PAML, version 4.6), some of the selected genes show evidences of positive selection both within and between species. Out of the 27 selected genes, results at 10 genes were compatible with purifying selection while the remaining 17 showed evidence of positive selection, with the selected codon ratio ranging from one to ten. Our result shows that the selection pressure is not uniform across the innate immune genes.

Detecting signature of selection in West Kenyan Small East African Shorthorn Zebu cattle **S****Hussain Bahbahani**, Martin Blythe, Harry Clifford, Mary Nadila, David Wragg and Olivier Hanotte

University of Nottingham

The humped *Bos taurus indicus* zebu were domesticated, about 10,000 years B.P., on the Indian subcontinent (Chen et al., 2010). These cattle were introduced to the Horn of Africa via two independent waves, and their dispersion across the continent was likely favoured by the rinderpest epidemics (Hanotte et al., 2002). Zebu introduction was associated with genetic introgression with the local African taurine *Bos taurus taurus*. Small East African Shorthorn Zebu (SEASZ) are found in East Africa. They are adapted to the tropical sub-humid environment, and their crossbreed nature (Asian zebu x African taurine) has recently been revealed (Ndila, PhD thesis). The main purpose of this study is to identify genetic signature of positive and balance selection associated with tropical adaptation in SEASZ using genome-wide SNPs genotyping and full-genome sequencing. We report the results of genome wide scans using two FST-based (inter-population genetic differentiation (FST) and intra-population Bayesian analysis) and two Extended Haplotype Homozygosity (EHH)-based (intra-population iHs analysis and inter-population Rsb analysis) approaches. The full genome sequence of SEASZ has been used to measure the pooled heterozygosity of 1 Mbp windows along the zebu genome. We identify several candidate genomic regions for positive and balance selection, including genes which function may be associated with tropical adaptation (e.g, male reproduction-related and immunological-related genes, heat shock proteins).

Population genetic analysis of highly polymorphic species *Ciona savignyi* using high-throughput sequencing data**Georgii Bazykin**, Maria Baranova and Alexey S. Kondrashov

Moscow State University

Ciona savignyi is a marine ascidian which has the highest confirmed nucleotide diversity among multicellular organisms, probably due to an exceptionally large effective population size. The average genome-wide heterozygosity is 4.5%, while the heterozygosity at 4-fold degenerate synonymous sites is 8%. We investigated the action of negative and positive selection in this highly polymorphic population. The pn/ps ratio and minor allele frequency spectra indicate strong negative selection; conversely, negative correlation between dN and Ps and strong footprint of sweeps indicate a high rate of recurrent positive selection in the genome.

Facultative parthenogenesis discovered in wild vertebrates**Warren Booth**, Charles F. Smith., Pamela H. Eskridge., Shannon K. Hoss., Joseph R. Mendelson III. and Gordon W. Schuett

The University of Tulsa

Facultative parthenogenesis (FP)—asexual reproduction by bisexual species—has been documented in a variety of multi-cellular organisms but only recently in snakes, varanid lizards, birds and sharks. Unlike the approximately 80 taxa of unisexual reptiles, amphibians and fishes that exist in nature, FP has yet to be documented in the wild. Based on captive documentation, it appears that FP is widespread in squamate reptiles (snakes, lizards and amphisbaenians), and its occurrence in nature seems inevitable, yet the task of detecting FP in wild individuals has been deemed formidable. Here we show, using microsatellite DNA genotyping and litter characteristics, the first cases of FP in wild-collected pregnant females and their offspring of two closely related species of North American pitviper snakes—the copperhead and cottonmouth. Our findings support the view that non-hybrid origins of parthenogenesis, such as FP, are more common in squamates than previously thought. With this confirmation, FP can no longer be viewed as a rare curiosity outside the mainstream of vertebrate evolution. Future research on FP in squamate reptiles related to proximate control of induction, reproductive competence of parthenogens and population genetics modelling is warranted.

Cause and Consequence: genomic divergence between molecular forms of Anopheles gambiae
S

Chris Clarkson, Martin Donnelly, David Weetman, Dominic Kwiatkowski, Bronwyn MacInnis, Gareth Maslen and Magnus Manske

Liverpool School of Tropical Medicine

The primary malaria vector *Anopheles gambiae* exists as a species complex within which 'molecular forms' exhibit only partial reproductive isolation. To investigate possible causes and consequences of divergence for medically-important phenotypes we compared genome sequences of sympatric M and S molecular forms. Introgression and strong selection of a known insecticide resistance mutation has led to conversion of a large 'genomic island' area from the genetic background of one form to the other, with potential impact on reproductive isolation. By contrast strong differentiation was found close to, but not centred upon, other insecticide- and Plasmodium-resistance genes, suggesting their divergence by hitchhiking, rather than direct selection. These results suggest an interplay between speciation and selection of medically-important phenotypes and potential for unstable evolutionary dynamics.

The NERC Biomolecular Analysis Facility at Sheffield

Deborah Dawson, Coordinator: Dr Deborah Dawson (D.A.Dawson@Sheffield.ac.uk)

Director: Prof Terry Burke (T.A.Burke@Sheffield.ac.uk)

University of Sheffield

The NERC Biomolecular Analysis Facility comprises five nodes (Sheffield, Edinburgh, Liverpool, Birmingham and Wallingford) which collectively provide a range of biomolecular support. The Facility is supported by the Natural Environment Research Council (NERC) and was established in 1998. The node at Sheffield has successfully supported 189 projects and 108 PhD students. Our users have published over 200 publications from Facility-supported studies, including large numbers in high-ranking journals such as Nature and Science. At Sheffield we provide state-of-the-art molecular genetics facilities and training to the UK community in the science areas that fall under the remit of NERC. The application process is straightforward and applicants do not need to be NERC-funded. We support studies of genes, individuals, behaviour, mating strategies, populations and phylogeny:

Genes and chromosomes: QTL identification, linkage mapping, evolutionary genetics;
individuals: individual identification, abundance and distribution, species and hybrid identification;

Behaviour: behavioural ecology, mating strategies, mate choice, reproductive behavior, dispersal, kin and sexual selection;

Populations: effective population size, genetic bottlenecks, population structure, landscape genetics (e.g. habitat fragmentation), spatial ecology;

Phylogeny: molecular systematics, biodiversity, conservation biology.

The service is based on a well-proven arrangement in which, usually, a researcher (often a PhD student) visits the laboratory at Sheffield to complete their own analyses under the supervision of our experienced staff. Training and consumables are provided. For more details please visit our homepage (<http://www.shef.ac.uk/nbaf-s/>) or if you wish to make informal enquiries regarding the feasibility of applying for access to the Facility please contact Deborah Dawson (D.A.Dawson@Sheffield.ac.uk).

Genetic disconnectedness in indigenous village chickens S**Takele Teye Desta**, David Wragg, Joram Mwacharo and Olivier Hanotte

University of Nottingham

Non-descript village chicken populations are characterized by extensive phenotypic diversity. This diversity makes it impossible to classify them into distinct breeds or strains and as a result they are often referred to as ecotypes. In this study, we genotyped 94 village chickens from eight countries across Africa, Asia and Latin America using the 60K Illumina SNP chip and we aimed at dissecting their genetic structure. Though STRUCTURE analysis revealed the highest optimal number of ancestral populations to be eight, principal component analysis clustered the populations into three groups: Ethiopian, Burkinabe and the remaining populations. We found extensive genetic admixture within a population. Pairwise F_{ST} values revealed low (0.0248, Kenyan vs Sri Lankan chickens) to moderate (0.1776, Burkinabe vs Cambodian chickens) levels of genetic differentiation whereas both F_{IS} and F_{IT} values show mild levels of inbreeding within and across populations. Burkinabe chickens were the most closely related, whereas genetic relatedness was the lowest in Sri Lankan chickens. The high number of ancestral populations and the presence of wide genetic variation within a population possibly reflect historical and on-going uncontrolled breeding, and the influence of local founder, dispersion and adaptation events.

Tracking rhino horns: validation of a forensic STR marker set for black rhinos S**Kara Dicks**, Ian McDowall, Paul O'Donoghue and Lucy Webster

University of Chester

Both African and Asian rhinoceros are threatened by over-exploitation, and as such trade in their horns is banned under CITES (Convention on International Trade in Endangered Species of Wild Flora and Fauna). Despite this international treaty, use of rhino horns in traditional Asian medicine has increased dramatically in recent years, and there has been a corresponding increase in poaching of wild rhinos as well as thefts of horns from museums, auctioneers and other private collections across Europe. As such, there is an increasing need to employ DNA forensic techniques to track the trade in rhino horn. Individual genetic profiles can be generated using short tandem repeat loci, matching a recovered specimen to a specific crime. This study validates a set of 16 markers for forensic use on Kenyan black rhinoceros (*D. bicornis michaeli*). The markers were tested to demonstrate their sensitivity to template DNA concentration, reproducibility and robustness under various PCR conditions. Population data was generated to investigate allele frequencies and calculate match probabilities. Fourteen markers were shown to be robust, reliable and reproducible, and profiles generated from blood and horn samples of the same individual showed consistent genotypes. Average probability of identity ranges from 1.41×10^{-8} to 3.15×10^{-10} when accounting for different levels of population structure and relatedness. This marker set can be used with confidence for forensic identity testing of black rhinoceros horns.

Explaining selection on flower colour in a snapdragon hybrid zone S**Tom Ellis**, David Field, Nick Barton, Enrico Coen, Desmond Bradley and Xana Rebocho

IST Austria

Flower colour is a useful model for relating genetic changes to reproductive success because traits typically have a simple, well understood genetic basis with a conspicuous effect on an ecologically relevant phenotype. We study two subspecies of the snapdragon *Antirrhinum majus* in the Spanish Pyrenees that differ at two loci controlling floral pigmentation, but with negligible post-zygotic barriers. These subspecies form a narrow and apparently stable hybrid zone with sharp clines at colour loci, indicating a role for floral colour in maintenance of pre-zygotic barriers. To investigate the role of pollinator preference for colour morphs we used cellophane tags lodged in the 'mouth' of the flowers to infer pollinator visitation to plants of different genotypes across three years within the core of the hybrid zone. Pollination rates varied

strongly from year to year, but no overall pattern of preference for particular colours is clear. We are currently looking to extend this work by examining pollinator behaviour in the regions flanking the hybrid zone, and to use paternity analysis to infer patterns of gene flow within and among colour morphs to better elucidate the effect of pollinator behaviour on gene flow.

Molecular evolution in the genus Begonia S

Katie Emelianova and Catherine Kidner

Royal Botanic Gardens Edinburgh

Begonia is one of the most speciose plant genera, comprising over 1,500 species spanning multiple biomes. The genera's large size and diversification has been attributed to poor dispersal leading to low levels of drift, high endemism and extensive population differentiation. However, indications that the genus underwent a genome duplication early in its history has prompted investigation into the impact of this duplication on *Begonia* diversity. Large sequence datasets have been generated from two South American species (*B. conchifolia* and *B. plebeja*) and one South East Asian species (*B. venusta*) to represent genus-wide diversity. A draft genome of *B. conchifolia* and transcriptomes of *B. conchifolia*, *B. plebeja* and *B. venusta* will be used to analyse differential retention and/or expression of ortholog duplicates, elevated nonsynonymous substitution and species specific regulatory network evolution. The anthocyanin biosynthetic pathway will be the preliminary focus of the project, based on the hypothesis that duplication of either regulators or biosynthetic enzymes facilitated the wide variation seen in anthocyanin pigmentation in *Begonia*. Identification of copy number for each gene in the pathway in the draft genome will be followed by sequence and expression analysis using de novo sequencing and RT-PCR to identify patterns of variation across *Begonia*. Based on this preliminary analysis, a bioinformatics pipeline will be devised to analyse global patterns of variation in copy number and sequence using the draft genome and transcriptomes. Results showing patterns of positive selection may support a hypothesis implying genome duplication as a key player in the diversification of *Begonia*.

Why are there so many Laparocerus (Curculionidae) species in the Canary Islands? S

Christiana Faria, Antonio Machado, Isabel Amorim, Paulo A.V. Borges and Brent C. Emerson
University of East Anglia

The weevil genus *Laparocerus* (Coleoptera, Curculionidae, Entiminae) is the most diverse genus in the Canary Islands, with 128 species endemic to the archipelago described so far, but little is understood as to why the genus has radiated so extensively. As a first approach to understand what factors may have promoted diversification within the genus we sampled mitochondrial (COII) and nuclear (ITS2) DNA sequence variation within the *Laparocerus tessellatus* complex. The questions we focus on are: (i) to what extent does geography structure genetic diversity within species? (ii) what have been the relative roles of diversification within islands and colonization between islands? Phylogenetic trees, haplotype networks and genotypes were used to analyze the data. MtDNA data reveals a more complex evolutionary history than ITS2 data, with the greater variation among mtDNA sequences revealing a substantial role for geography in structuring genetic diversity within species. Among the remaining species, ITS2 data suggests that the common ancestor of the group inhabited Gran Canaria, and that the species of Gran Canaria evolved in situ. MtDNA data suggests a complex colonization history among other islands, with each of the single species on La Palma (*Laparocerus* sp.1) and El Hierro (*L. bimbache*) being the product of more than a single colonization event. Within some sampling locations genotypes present evidence for linkage disequilibrium, indicating non-random mating. Further investigation would help to establish whether this is a consequence of fine scale genetic structuring, or the existence of cryptic species.

Looking for positive selection in recently duplicated genes

Iris Fischer, Jean-François Dufayard, Vincent Ranwez and Nathalie Chantret
SupAgro INRA, Montpellier

Whole genome duplications (WGDs) as well as small-scale duplications (SSDs) occurred frequently in the course of plant evolution. In combination with a relatively high retention rate of novel genes, duplication events seem to be an important factor in plant genome evolution. Indeed, a large fraction of angiosperm diversity was suggested to stem from duplications followed by adaptive specialization of paralogous gene copies. Thanks to recent progress in genome sequencing, we can now address the question whether positive selection is a driving force in the evolution of duplicated genes. We searched in a database containing phylogenies of plant gene families for cases where recent successive duplication events followed by retention resulted in at least six gene copies. Those ultra-paralogous gene clusters were tested for positive selection using codon substitution models implemented in PAML. We found that choosing the appropriate alignment and cleaning method is crucial as the codeml site-model is highly sensitive to alignment errors. Overall, 5-10% of all clusters showed evidence for positive selection. The banana genome shows very little evidence for selection at ultra-paralogs, whereas duplicated genes in rice and *Brachypodium* seem to have undergone positive selection more frequently than the average. However, these preliminary results have to be interpreted carefully due to discrepancies for genome coverage and annotation quality between species.

A population genetics model of the evolution of gene regulatory networks **S**

Lisa French, Elizabeth HB Hellen and John FY Brookfield
University of Nottingham

Phenotypic differences between individuals and species can be caused by differences in levels of gene expression. Transcription factors are one of the mechanisms controlling gene expression, and they often interact together in networks to promote or repress protein production. Computational models of gene regulatory networks can help us understand how the interactions between transcription factors evolved. An individual-based evolutionary simulation has been developed allowing the evolution of transcription factor networks to be investigated in a population genetics context. The model consists of a population of individuals each with a haploid genotype containing n transcription factors. Each transcription factor is described by a number of parameter values which determine how it interacts with other genes in the network. Individuals are assigned fitness values, based upon how close the gene network is to producing an optimum protein concentration of one or more of the genes. The reproductive chances of an individual are dependent upon its fitness. Mutations can occur during the reproductive process, altering the parameters of the transcription factors in the offspring, which can result in a change in the output of the network and therefore affect fitness. Recombination is also built into the model. The model is run over a number of generations, and allows investigation of the effects of selection and genetic drift.

Short-term variations in gene flow in a cyclic common vole population

Bertrand Gauffre, Bertrand Gauffre, Karine Berthier, Pablo Inchausti, Yannick Chaval, Jean-François Cosson and Vincent Bretagnolle
INRA CEBC-CNRS (Centre d'Etudes Biologiques de Chizé)

In fluctuating populations, genetic structure is expected to vary as the result of an unstable balance between the competing processes of genetic drift and migration. The influence of genetic drift would predominate over migration during low numbers while the reverse would occur during high numbers. Cyclic rodent populations are extreme examples of high demographic instability and thus good candidates to test for these general predictions. In this study, we analyzed the multiannual genetic structure of a cyclic rodent using a sample of 875 common voles trapped over three complete cycles (from 1999 to 2007) and genotyped at 10 microsatellite loci. We tested the predictions that genetic diversity and gene flow were

temporally variable, and whether these variations were related with vole densities. Genetic diversity was expected to decrease and genetic structure to increase during low numbers, and the reverse was expected during high numbers. Overall, these predictions were verified in our dataset with slight but significant temporal variation in genetic diversity and gene flow. We evidenced that gene flow is higher during high numbers, thus allowing for the recovery of genetic diversity and slowly erase genetic differentiation. Investigation of sex-specific relatedness patterns using spatial autocorrelation analyses revealed that males dispersal distances are lengthened during high numbers which could be a mechanism explaining the observed temporal variations in gene flow.

*Using phylogenetics to inform conservation strategies for the endangered Neotropical River otter (*Lontra longicaudis*) in Mexico* **S**

Jimena Guerrero, Roman Biek and Juan Pablo Gallo

University of Glasgow

Otter populations have suffered from human activities throughout history, causing them to decline or disappear from many areas. Although the Neotropical river otter (*Lontra longicaudis*) is classified as data deficient by the IUCN, its populations are suspected to be declining. In Mexico, the species reaches the northern limit of its range in marginal, arid habitats, which lead us to hypothesise the species may be particularly vulnerable to fragmentation in this area. Therefore, we conducted a genetic population study of river otters in Mexico to address three aims: First, to estimate genetic diversity in Mexican otters and compare it to estimates from other species and populations. Secondly, to examine the phylogenetic relationships between Mexican and South American populations, which have been proposed to belong to different subspecies. Thirdly, to determine whether Mexican populations exhibit genetic structure. Based on non-invasive sampling throughout Mexico, we amplified part of the mitochondrial control region for 50 individuals and combined our data set with published sequences. Our results show that Mexican populations are phylogenetically distinct and have lower genetic diversity than populations in South America. Analyses within Mexico retrieved eight haplotypes, which provided some indication of genetic structure. In particular, all individuals within the arid, northern part of Mexico carried the same unique haplotype, suggesting potential genetic isolation. While further work to verify these findings based on autosomal markers is still in progress, our results provide important preliminary guidance for developing a conservation strategy for river otters in Mexico and other parts of the species range.

*Does introgression cause the high genetic diversity of pseudoautosomal (PAR) genes in the plant *Silene latifolia**

Sara Guirao-Rico

Institute of Evolutionary Biology, University of Edinburgh

DNA sequence diversity in genes in the partially sex-linked pseudoautosomal region (PAR) of the evolving sex chromosomes of the plant *Silene latifolia* is higher than expected from within-species diversity of other genes. This suggests some form of balancing selection, and an interesting possibility is that this is the footprint of sexually antagonistic alleles that are maintained polymorphic in PAR genes, which is predicted to occur during sex chromosome evolution. However, it is important to test the alternative possibility that the high PAR region sequence diversity is due to introgression from *S. dioica*. *S. latifolia* and *S. dioica* both have wide geographical distributions across Eurasia and viable hybrids occur naturally in the wild. Comparison of raw divergence estimates between *S. latifolia* and *S. dioica* with within-species diversity indicate that most diversity is within the species, not between them. Although there is no formal test to distinguish between introgression and ancestral polymorphisms, examining whether haplotypes are shared between two species, and quantifying ancestral polymorphisms could help to disentangle them, and help test whether the observed high diversity in PAR genes can be explained by introgression.

Exploring the architecture of wing color pattern genes within the silvaniform clade of Heliconius butterflies: a linkage mapping approach **S**

Bárbara Huber, Annabel Whibley, Mathieu Joron

CNRS, Muséum National d'Histoire Naturelle

Understanding the origins and maintenance of phenotypic diversity is one of the main aims of evolutionary biology. To disentangle the genetic basis of adaptive traits in a given clade is an important starting point to understand the role of evolutionary processes such as selection in evolution. Butterflies in the *Heliconius* genus have become a model of choice to answer questions related to the origins of species. They show a spectacular adaptive radiation of wing colour patterns across the Neotropics. Such visual signals are used by the butterflies to warn predators about their toxicity and are involved in mimicry between coexisting species. The genetic basis underlying wing coloration diversity in this clade is limited to few homologous loci across the species, ranging from a multilocus architecture in *H. melpomene*, *H. erato* and *H. cydno*, to a single supergene in *H. numata*. Is the supergene restricted to the *H. numata* species or present in other species in the numata clade? We have been exploring the architecture of colour loci in two species in the numata clade, namely *H. hecale* and *H. ismenius*, by using a linkage mapping approach based in crosses between different geographic races. We have found that several independent loci are responsible for colour variation in these two species, pointing to the fact that the supergene may have evolved from an ancestral multilocus architecture. By using RAD-sequencing and by genotyping candidate loci identified in other species of *Heliconius*, we have shown once again that the same toolkit of genes is shared among different species in the genus to control for both geographic divergence of coloration and convergence for mimicry.

Comparative transcriptomics in the pond snail Lymnaea stagnalis **S**

Harriet F Johnson, Maureen (Mengning) Liu and Angus Davison

University of Nottingham

It has long been known that coiling direction (left right asymmetry or chirality) in snails is determined by a single locus of maternal effect. As part of a larger effort to characterise the chirality locus in the pond snail *Lymnaea stagnalis*, I am comparing the use of RNA-Seq with another emerging technique, expression RAD Seq (eRAD), by trialling the effectiveness of both methods in qualitatively and quantitatively describing the maternal gonad tissue. As eRAD may provide increased depth of sequencing with reduced representation, then it may be ideal for use with organisms that lack a completed genome or transcriptomic resources.

Genealogy of seasonal human influenza virus (H3N2) under complex demographic dynamics and positive selection **S**

KangChon Kim and Yuseob Kim

Ewha Womans University

H3N2 strains of human influenza virus A circulates globally and periodically recurs during the influenza seasons, causing severe disease and hundreds of thousands of deaths annually. Migration and periodicity are distinctive aspects of influenza dynamics. We developed a population genetic model in which viruses migrate between demes (subpopulations corresponding to geographic regions) and the population size of a deme oscillates seasonally. Then, using computer simulation, we tested if this demographic dynamics can shape the structure of evolutionary tree similar to that of human influenza virus A H3N2. Under a neutral model that assumes no fitness effect of new mutations, genetic distance and outbreak time difference for a pair of viral sequences are not correlated as high as in the real influenza data. The topology of evolutionary tree quantified by such a correlation and also by Tajima's D become more similar to the actual data as recurrent directional selection, which models the antigenic drift of viruses by host immune pressure, is added to the simulation especially when

relative fitness of mutants of different locus is not equal. This result suggests the fundamental role of strong positive selection in determining the evolutionary trajectory of seasonal influenza viruses. At the same time, it demonstrates the importance of modeling correct demography for understanding adaptive evolution in this virus.

Mutation rate and plasticity and fitness in Escherichia coli

Rok Krašovec, Roman V. Belavkin, John Aston, Alastair Channon and Christopher G. Knight
University of Manchester

Knowing mutation rate is vital for understanding evolutionary processes. It is fully appreciated that mutation rates vary between genotypes and locally over the genome, but how plastic mutation rate can be for a particular site in a particular genotype is far less clear. Mathematical theory and numerical simulations suggest that, if the fitness of an organism is high, mutation rate will be minimised but if the fitness is low, the mutation rate for that same genotype will be increased. In order to identify variation in mutation rate with fitness we performed fluctuation tests with *Escherichia coli* MG1665 varying absolute fitness w_{abs} and assaying mutation to rifampicin resistance (RIF^R). We observed a reduction in mutation rate with increasing w_{abs} and then tested hypotheses explaining this effect. We tested relative fitness (w_{rel}) by using *E. coli* B strains experimentally evolved by Richard Lenski. We performed more than a hundred fluctuation tests growing strains in the presence of competitors with different w_{rel} . Despite w_{rel} differences of 70% and assaying both wild type strains and mutators, we found no dependence of mutation rate to RIF^R on w_{rel} . However, final culture density *does* show a strong relationship in the expected direction with RIF^R mutation rates. We are now testing the dependence of the observed mutation-rate plasticity on the quorum sensing system. Our observations demonstrate that mutation rate is a plastic trait that may be controlled by social interactions within microbial populations. Whether this mutation rate plasticity can be adaptive remains to be tested.

Host phylogeny determines viral persistence and replication in novel hosts

Ben Longdon, Jarrod D. Hadfield, Claire L. Webster, Darren J. Obbard and Francis M. Jiggins
University of Cambridge

Pathogens switching to new hosts can result in the emergence of new infectious diseases, and determining which species are likely to be sources of such host shifts is essential to understanding disease threats to both humans and wildlife. However, the factors that determine whether a pathogen can infect a novel host are poorly understood. We have examined the ability of three host-specific RNA-viruses (Drosophila sigma viruses from the family Rhabdoviridae) to persist and replicate in 51 different species of Drosophilidae. Using a novel analytical approach we found that the host phylogeny could explain most of the variation in viral replication and persistence between different host species. This effect is partly driven by viruses reaching a higher titre in those novel hosts most closely related to the original host. However, there is also a strong effect of host phylogeny that is independent of the distance from the original host, with viral titres being similar in groups of related hosts. Most of this effect could be explained by variation in general susceptibility to all three sigma viruses, as there is a strong phylogenetic correlation in the titres of the three viruses. These results suggest that the source of new emerging diseases may often be predictable from the host phylogeny, but that the effect may be more complex than simply causing most host shifts to occur between closely related hosts.

Population genetic history and phylogeography of Aristeus antennatus in the Central and Eastern Mediterranean Sea. S

Annamaria Marra, Stefano Mona and Porzia Maiorano
University of Bari

The red shrimp *Aristeus antennatus* is an ecologically and economically important deep-water species in the Mediterranean Sea. In this study we investigated the genetic variability of A.

antennatus sampled from ten localities in the Central Eastern Mediterranean and compared it to available data from the Western area. We analyzed two regions of mitochondrial DNA in 319 individuals, namely the cytochrome c oxidase subunit I (500 bp) and ribosomal 16S subunit (447 bp). We found two main results: i) low diversity and genetic homogeneity within the Mediterranean Sea (no genetic barriers to gene flow were detected between western and central-eastern basins); ii) a constant long-term effective population size in almost all demes but a strong signature of population expansion around 50,000 years B. P. in the pooled sample (in agreement with the most recent expansion time found for some benthic species). Our results suggest that Eastern and Western Mediterranean are part of a genetically homogeneous unit which experienced an historical expansion. We explained these findings through the existence of deeper-dwelling stocks which expanded in the Mediterranean around 50,000 years B.P. The continuous movements of individuals from “virgin” dwelling deeper grounds to fishing areas could support an effective ‘rescue effect’ contributing to the recovery of the exploited stocks. Management decisions for *A. antennatus* will therefore require careful consideration of the metapopulation dynamic of all stocks in the Mediterranean Sea, particularly those inhabiting higher depth.

Genomic signatures of speciation with gene flow in Heliconius butterflies **S**

Simon H Martin, Kanchoon K Dasmahapatra, Nicola J Nadeau, Camilo Salazar, James R Walters, Mark Blaxter, Andrea Manica, James Mallet and Chris D Jiggins
University of Cambridge

Most speciation events probably involve some degree of ongoing gene flow during divergence, but this has rarely been characterized on a genome-wide scale. Documenting the extent and timing of admixture between diverging species will directly address the longstanding question of the extent to which geographic isolation plays a role in speciation. We have quantified differentiation and admixture genome-wide at different stages of divergence in the neotropical butterfly genus *Heliconius*, by sequencing the whole genomes of 31 individuals. Races of *Heliconius melpomene* with adjacent ranges but distinct wing colour patterns showed clear islands of divergence at colour pattern loci, with minimal background differentiation. In contrast, between hybridizing sister species *H. melpomene* and members of the *H. cydno/timareta* group, there was widespread and highly heterogeneous divergence throughout the genome. Comparisons between sympatric and allopatric populations revealed a genome-wide trend of reduced divergence in sympatry, especially at derived sites, indicative of pervasive interspecific gene flow. Up to 40% of 100 kb genomic windows clustered by geography rather than by species membership, proving that a very substantial fraction of the genome flows between sympatric species. Gene flow was significantly reduced around loci controlling divergent wing patterns, as well as throughout the Z chromosome, consistent with theoretical expectations and known Z-linked incompatibility. Estimation of introgression at different levels of phylogenetic divergence indicated that gene flow between these species has continued since early in speciation. Overall these results show that ecologically divergent species can emerge and persist despite ongoing gene flow affecting a surprisingly large proportion of the genome.

Wolbachia infection in the Podisma pedestris hybrid zone **S**

Paloma Martinez-Rodriguez, JL Bella and RA Nichols
Universidad Autónoma Madrid

We provide evidence that Wolbachia bacterial sequences have become integrated into *Podisma*'s insect chromosomes. The Wolbachia sequences obtained from the gonads putatively include current Wolbachia infections, which may contribute to hybrid inviability. Compared to known Wolbachia genomes, the sequences from leg muscle include matches to two divergent clades, they have multiple indels and mis-sense mutations, strongly suggesting multiple ancient integrations.

Ecological coherence in marine reserve network design: an empirical evaluation of sequential site selection using genetic structure.

Caitríona E. McInerney, A. Louise Allcock, Mark P. Johnson and Paulo A. Prodöhl

University of Sheffield

Networks of marine protected areas (MPAs) are key components to protect marine biodiversity. Thus, for every EU member state, the establishment of 'ecologically coherent' MPA networks is a legal requirement by 2020. A general definition for ecological coherence does not exist, but it is accepted that this is a multifaceted conservation objective that includes some potentially conflicting concepts. For example, the most genetically distinctive site to complement an existing network is likely to be at some distance from currently protected sites, but a closer site is likely to be better placed to improve network connectivity. Conflicting concepts include the extent to which the MPA network maximises diversity (including genetic diversity) and the extent to which protected areas interact with non-reserve locations (genetic connectivity). In this study, the preferred location to complement protected sites in an MPA network was estimated using genetic structure of three intertidal mollusc species with different dispersal capacities. Samples were analysed using microsatellite markers from sites inside and at four locations around each of two marine protected areas: Strangford Lough and Lough Hyne, Ireland. Three different measures of genetic distance: F_{ST} , D_{est} and a measure of allelic dissimilarity, along with a direct assessment of the total number of alleles in different candidate networks were compared as standardized site scores across different methods and selection criteria. Results indicate that apparently conflicting criteria for 'ecological coherence' could be reconciled using genetic measures, leading to a clear choice of site in the region with the strongest genetic structuring. Similar patterns were found across species with different dispersal capacities. This suggests that it will be possible to make quantitative statements about the ecological coherence of different networks with relatively straightforward genetic information.

Suppressors of RNAi from plant viruses are subject to episodic positive selection

Gemma Murray, Darren Obbard and Sergei Kosakovsky Pond

University of Cambridge

Viral Suppressors of RNAi (VSRs) are proteins that actively inhibit the antiviral RNA interference (RNAi) immune response, providing an immune evasion route for viruses. It has been hypothesised that VSRs are engaged in a molecular 'arms race' with RNAi-pathway genes. Two lines of evidence support this. First, VSRs from plant viruses display high sequence diversity and are frequently gained and lost over evolutionary timescales. Second, *Drosophila* antiviral RNAi genes show high rates of adaptive evolution. Here I consider whether VSRs diversify faster than other genes, and if so, whether this is a result of positive selection, as might be expected in an arms race. Through analysis of 12 plant RNA viruses, I show that the relative rate of protein evolution is higher for VSRs than for other genes, but that this is not attributable to pervasive positive selection. I argue that, because evolutionary timescales are extremely different for viruses and eukaryotes, it is unlikely that viral adaptation will be dominated by one-to-one coevolution with eukaryotes. Instead, for plant virus VSRs, I find strong evidence of episodic selection—diversifying selection that acts on a subset of lineages—which might be attributable to frequent shifts between different host genotypes or species.

Examining the genetic basis of craniofacial shape in an adaptive radiation

Kevin Parsons and R. Craig Albertson

University of Glasgow

Divergence in craniofacial characteristics is a hallmark of many adaptive radiations, and can play a determining role in resource use. The African rift-lake cichlids offer one of the most dramatic examples of adaptive radiations in vertebrates, and display a plethora of craniofacial phenotypes. The ability to hybridize these recently derived species provides a unique opportunity to determine the genetic basis of craniofacial phenotypes. We created hybrids for genetic mapping by crossing species displaying 1) an exceptionally wide jaw for scraping algae,

to 2) a species with a narrow jaw for 'plucking' filamentous algae. Using next-gen sequencing we created a high density linkage map and identified a number of candidate genes related to jaw width. In tandem we also performed a population genomic comparison between wide and narrow jaw species collected from the wild. Cross referencing between data sets shows that loci related to jaw width are also under the influence of natural selection. These findings provide an important inroad into the genetic basis of adaptive craniofacial divergence, which may also have relevance for analogous human syndromes.

A hybrid genetic linkage map of two ecologically and morphologically divergent Midas cichlid fishes (Amphilophus spp.) **S**

Hans Recknagel, Kathryn R Elmer and Axel Meyer

University of Glasgow

Cichlid fishes are an excellent model system for studying speciation and adaptive radiations due to their tremendous species richness and phenotypic variability. Research, so far, has mostly focused on African rift lake cichlids, but the Neotropical Midas cichlid species flock (*Amphilophus spp.*) also offers a tractable model system with a variety of rather distinct phenotypes. Here we apply double-digest restriction-site associated DNA sequencing (ddRADSeq) in order to obtain a high-density linkage map of an interspecific cross between the benthic *A. astorquii* and the limnetic *A. zaliosus*, both endemic to Lake Apoyo, Nicaragua. 343 F2-hybrids were genotyped for a total of 755 RAD markers. 25 linkage groups span over a distance of 1427 cM with an average marker spacing distance of 1.95 cM, almost matching the total number of chromosomes ($n=24$). Regions of segregation distortion were identified in five linkage groups. The genetic map will facilitate the detection of eco-morphologically relevant adaptive traits in Midas cichlids. We performed comparative genomic analyses in teleosts and found highly conserved synteny between African cichlids and Neotropical cichlids, and less conserved synteny between cichlids and other teleosts. These results suggest that the cichlid's phenotypic variability does not correlate with a high degree of chromosomal rearrangements, neither do Midas cichlids exhibit a higher mutation rate compared to other teleosts. Our linkage mapping analysis shows that ddRADSeq is an appropriate method to develop hundreds of markers and to construct high-density linkage maps even in genetically very young populations.

Applied evolution: an experimental approach to investigating how the interaction between parasite life history strategies and control measures affects rates of resistance evolution **S**

Alan Reynolds

University of Glasgow

The problem of overcoming resistance involves finding methods of drug use such that parasite populations are kept at low numbers and the evolution of resistance is minimised. Several factors are known to affect the rate at which parasites can evolve resistance, including the type of drug, dosage, timing of application, migration rates between susceptible and resistant populations, the standing frequency of resistance alleles in the population and the specific mechanisms of resistance. In addition, life history characteristics of the parasites and their reproductive strategies could influence the rate at which resistance develops. Current research to date on parasitic organisms has considered many of these factors in isolation but there has been little attempt to explore interactions between life-history traits, mating systems and other factors affecting the rate of resistance. This study will take an experimental evolutionary approach to understanding the influence of such interactions, using free-living *Caenorhabditis remanei* as a model. The rate of resistance evolution will be evaluated by treating nematodes with anthelmintics, applied at different dosages and rates, under experimentally varied reproductive modes and population demographics.

Using neutral cline decay to estimate contemporary dispersal: a generic tool and its application to a major crop pathogen

Adrien Rieux, T. Lenormand , J. Carlier , L. De Lapeyre, De Bellaire and V. Ravigne

University College London

Dispersal is a key parameter of adaptation, invasion and persistence. Yet standard population genetics inference methods hardly distinguish it from drift and many species cannot be studied by direct mark-recapture methods. Here we introduce a method using rates of change in neutral markers cline shapes to estimate contemporary dispersal. We apply it to the devastating banana pest *Mycosphaerella fijiensis*, a wind-dispersed fungus for which a secondary contact zone had previously been detected using landscape genetics tools. By tracking the spatio-temporal frequency change of 15 microsatellite markers, we find that σ , the standard deviation of parent-offspring dispersal distances, is 1.2 km/generation^{1/2}. The analysis is further shown robust to a large range of dispersal kernels. We conclude that combining landscape genetics approaches to detect breaks in allelic frequencies with analyses of changes in neutral genetic clines offers a powerful way to obtain ecologically relevant estimates of dispersal in many species.

*Genetic diversity and structure of *Puccinellia maritima*: An important saltmarsh engineer species* **S**

Romuald Rouger and Alistair S Jump

University of Stirling

Saltmarshes in the U.K. have reduced considerably notably because of land claiming. To counteract this loss, restoration programs have been implemented throughout the country. But they heavily rely on species ability to recolonize a site. One important saltmarsh species is *Puccinellia maritima*. By accreting sediments, this species helps to create suitable habitats for other species to develop on. Its colonizing ability is then an important pre-requisite for restoration success. Colonization of a site can be decomposed into two phases: arrival on site and development on site. In this poster, we study the ability of *P. maritima* to complete these two phases by looking at population genetic diversity across the U.K. and how genetic structure compare between reference and newly restored saltmarshes. Our figures show small pairwise F_{st} values between populations of *P. maritima*. That indicates that gene flow occurs between populations even if they are distant. *P. maritima* asexually spreads by stolons, therefore a strong genetic structure was expected in the reference saltmarsh where individuals had time to develop over relatively large spatial scale. Nevertheless, no genetic structure was found in neither restored or reference saltmarshes. Different reasons could explain this pattern but none can be selected before adding more statistical power to the analysis. This work, if confirmed by further results, would indicate that *P. maritima* could quickly recolonize sites even in areas where saltmarshes have almost disappeared.

Wolf population expansion in Georgia: the recolonization of the Colchis lowland **S**

Maia Shaqarashvili, Natia Kopaliani and Zurab Gurielidze

Ilia State University, Institute of Ecology, Tbilisi, Georgia.

Until 1950s, grey wolf was widespread throughout Georgia. Later on, human persecution and presence of a bounty system caused severe decrease of the wolf population and its total annihilation in some parts of the country (specifically, lowlands of West Georgia, historical Colchis). Our research executed in 2009-2010 suggested recent expansion of wolves into densely populated areas and agricultural lands of the Colchis Lowland and its outskirts, where it had not appeared for the past 50-60 years. Forest landscape of Colchis Lowland is highly fragmented and patchy. Until recent times, wolves have been concentrated in mountainous and remote regions. Our aim was to study interpack connectivity between the wolves found in new territories and source populations in order to detect the dispersal routes using molecular tracking. Eight micro-satellite loci were genotyped. The origin of the dispersed wolves was determined.

Genetic consequences of prolonged vegetative regeneration in traditionally managed forests in Europe

M Jennifer Sjölund and Alistair S Jump

University of Stirling

The traditional forest management practice of coppicing was historically very common, yet the persistence of these systems is under threat as coppicing has declined due to socio-economic changes. Trees were cut close to ground level to produce shoots, which were harvested for multiple uses. Habitats created from historic coppicing are recognised as areas of high conservation value as they are frequently highly species-rich, however, the impact of coppicing on intraspecific diversity remains poorly understood. It is predicted that coppicing will impact population genetic diversity and structure because it alters the regeneration mechanism within a population, changing it from sexual to vegetative reproduction. This is the first study that has looked at the intraspecific effects of traditional management in the Beech tree (*Fagus sylvatica*), the most common forest tree species in mainland Europe and with a significant proportion being managed as coppice. Sampling was done over a regional scale giving it a wider European context than previous studies. Paired sites of coppice and un-coppiced forest were compared in Germany, France, and Italy, using 13 microsatellite markers. Differences in spatial genetic structure were found between sites. The diversity and richness of private alleles was higher in coppiced forests, making ancient coppices valuable candidates for gene reserve forests. Understanding the impacts of management on genetic diversity and population genetic structure can help us to prioritise conservation effort.

Contrasting population genetic structures in sympatric Daphnia species

Anne Thielsch, Robert H. S. Kraus and Klaus Schwenk

University of Koblenz-Landau

Cyclic parthenogens, such as many zooplankton organisms, display an alternation of asexual and sexual reproduction. During favourable conditions amictic individuals reproduce asexually, while deteriorating environmental cues induce sexual reproduction which results in dormant stages that enable dispersal through time and space. Although many zooplankton species are good dispersers through their sexually produced dormant stages, the influence of gene flow is assumed to be negligible, as the local populations usually monopolize the available resources, preventing immigration of new genotypes. To evaluate the importance of different factors influencing population genetic structure, we studied European populations of three widely distributed and ecologically plastic species of the genus *Daphnia*, *D. galeata*, *D. longispina* and *D. cucullata*, using microsatellite and mitochondrial DNA markers. Although all taxa may co-occur they show contrasting population genetic structures. While *D. longispina* and *D. cucullata* populations are highly differentiated across localities, *D. galeata* populations are genetically quite homogenous. This indicates historical diversification in *D. longispina* and *D. cucullata* resulting in the development of mature populations with restricted gene flow possibly due to monopolization of local resources. In contrast, *D. galeata* expanded probably very recently and populations may still be connected through gene flow. The population genetic structure of the taxa was most likely influenced by different historical events. *D. longispina*, for example, may have expanded its range after the last ice age, while recent expansion of *D. galeata* might be facilitated by anthropogenic alteration of freshwater habitats (e.g., eutrophication) which enabled multiple successful invasions by this taxon.

The role of male sex pheromones in reproductive isolation of Heliconius butterflies **S****Sohini Vanjari**

University of Cambridge

Pheromones play an important role in butterfly courtship, but little is known about them in *Heliconius*, the neotropical genus famous for müllerian mimicry. We postulate that reproductive isolation between sympatric related species of *Heliconius* must involve olfactory communication, especially where such species are closely related to each other or share wing patterns due to mimicry. Using the GC-MS technique we identified potential pheromone compounds localized in hind wing androconia of 10 day old males of *Heliconius melpomene*, which were absent in any female or newly emerged male wing extracts. Furthermore, comparison between Electroantennagram (EAG) responses elicited by extracts of different wing parts shows that the hind wing androconia wing extract gives the most consistent and long lasting response. These results collectively indicate that biologically essential compounds are mainly confined to the androconial region on the hind wing in males and are produced after eclosion. Behavioural assays carried out to determine the role of putative male sex pheromones in mating behavior exhibited a significant difference in female response to scented paper models of *Heliconius* over the control model. Females responded positively to synthetic blends and negatively to control compound (hexane). Competition experiments and mate choice experiments will be performed using *Heliconius melpomene* and *Heliconius cydno* as a base model system, to understand the importance of chemical communication in *Heliconius* speciation. Defining the exact effect of pheromones on *Heliconius* speciation will help us to understand how reproductive isolation drives evolutionary processes.

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- The network access method is IEEE 802.1x using your "home" institution username and password.

Connecting: Visitors will need to use their home institutions instructions and user name/password.

Important security note: It is **your responsibility** to take steps to ensure that you maintain your own data protection and privacy. You should discuss this with and receive guidance from your home site.

Depending on the facilities offered by your home network, you perhaps may use a VPN to secure traffic; alternatively you may already deploy secure methods such as HTTPS (SSL) VPNs or secure web pages for email (or perhaps other secure protocols such as SSH). You should be aware that any data traffic which is 'in the clear' is potentially visible to others with the right kind of software unless you take precautions.

The JRS wireless network use WPA security with TKIP encryption.

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 - your home institution's Computing Regulations
 - and by the [JANET Acceptable Use Policy](#) (to which your institution is a signatory).

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- HTTP, HTTPS, web proxy, ICMP (Echo, Echo-reply, Source-quench, Time-exceeded)
- SSH, Cisco VPN, Microsoft VPN, BGMP, Lotus Note, PPTP, GRE, AHP, ESP

How to configure your browser on the wireless network

All Web browsers are required to use the local Web Cache. This conserves Internet bandwidth and reduces costs.

- To use the local wireless Web Cache, please find your browser type and version below and follow the configuration instructions.
- If you experience difficulties please contact the IT services [Help desk](#) (Tel : X 4800 - Email : IThelpdesk@glasgow.ac.uk)

Browser	Instructions
Microsoft Internet Explorer version 9, 8, 7 (PC)	<p>Proxy Configuration</p> <ol style="list-style-type: none"> 1. select Tools, Internet options, Connections 2. select LAN Settings 3. select Automatically detect settings 4. select OK 5. select OK <p>Note you will not need to configure another browser if you do this</p> <p>Clearing Local Cache</p> <ol style="list-style-type: none"> 1. select Tools, Internet Options, General 2. select Delete Files from the Temporary Internet files section of the dialogue box 3. select Clear History from the History section of the dialogue box 4. select OK
Macintosh Safari	<ol style="list-style-type: none"> 1. select Safari, Preferences 2. select Advanced button 3. select Change Settings button 4. under Select Proxy to configure select automatic proxy configuration 5. under Proxy Configuration File enter address http://wwwcache.gla.ac.uk/dialin.pac 6. select Apply now
Firefox	<ol style="list-style-type: none"> 1. select Tools, Options (in Firefox 4 select the Alt key to bring up menus) 2. select the Advanced button 3. select the Network tab 4. under connection select Settings 5. select Automatic proxy configuration URL: 6. enter address http://wwwcache.gla.ac.uk/dialin.pac 7. select OK
Google Chrome	<ol style="list-style-type: none"> 1. select Spanner icon then Options 2. select the Under the bonnet tab 3. select Change proxy settings

	<ol style="list-style-type: none"> 4. select LAN Settings 5. select Use automatic configuration script 6. enter address http://wwwcache.gla.ac.uk/dialin.pac 7. select OK 8. select OK 9. select Close
Opera	<ol style="list-style-type: none"> 1. select Tools, Preferences 2. select Advanced 3. select Network 4. select Proxy servers 5. elect Use automatic proxy configuration 6. enter address http://wwwcache.gla.ac.uk/dialin.pac 7. select OK
All other browsers	<p>Update to one of the browsers listed above. If this is not possible, then see generalised configuration settings for non-recommended browsers</p> <ol style="list-style-type: none"> 1. select Tools/Options/Connection (or equivalent) 2. select Connect through proxy server (or equivalent) 3. enter address http://wwwcache.gla.ac.uk/dialin.pac

TIP: You can use IE for both VPN and personal use if you follow the instructions below. If you do not use IE You may need to configure one browser for VPN use and another for use elsewhere.

Guest Internet access wireless connection instructions*

Note

This service has an inactivity time out of 20 minutes, which begins either when your machine hibernates or closes down.

*Please note: **a Java capable browser or device is required to use this service.** **If the browser you use in the operating systems described above has a lower version of Java installed than is required you will be redirected to a webpage where you can update your Java.

Windows 7

- Click once on the Wireless network connection icon usually on the bottom right taskbar.
- You will see a list of available wireless networks.
- Double-click or click '**Connect**' to **GUvisitor connection**. (You may need to tell Windows 7 that this is a **public** network)
- When GUvisitor is connected open your web browser.**
- A welcome screen for **University of Glasgow Guest Internet Access** service should appear
- Type the **Username and Password** you received via email and click continue or press return key.
- You will see a "login successful" window. You may want to keep this available when you want to log out.
 - If you have allowed popups a new window will also appear with your home page.
 - If you have popups disabled open a new browser window to begin browsing.
- To Log out return to the original window and select Log out.

Windows XP

- Click on **Start** button. (Usually bottom left of screen)
- Click on **Control Panel**.
- Double Click **Network and Internet Connections**.
- Click on **Network Connections**.
- Double-click on **Wireless Network Connection**.
- Click **View Wireless Networks**.
- Double click on **GUvisitor**.
- When GUvisitor is connected open your web browser.**
- A welcome screen for **University of Glasgow Guest Internet Access** service should appear.
- Type the **Username and Password** you received via email and click continue or press return key.
- You will see a "login successful" window. You may want to keep this available when you want to log out.
 - If you have allowed popups a new window will also appear with your home page.
 - If you have popups disabled open a new browser window to begin browsing.
- To Log out return to the original window and select Log out.

Windows Vista

- Click on **Start** button. (Bottom left of screen).
- Click on **Control Panel**.
- Click on **Network and Internet**.
- Under **Network and Sharing Centre** click on **Connect to a network**.
- Double-click on GUvisitor wireless connection
- A Windows warning message will show – click **Connect Anyway**
- Click **Close**
- When GUvisitor is connected open your web browser.**
- A welcome screen for **University of Glasgow Guest Internet Access** service should appear
- Type the **Username and Password** you received via email and click continue or press return key.
- You will see a "login successful" window. You may want to keep this available when you want to log out.
 - If you have allowed popups a new window will also appear with your home page.
 - If you have popups disabled open a new browser window to begin browsing.
- To Log out return to the original window and select Log out.

Mac OS X

- From **System Preferences**, select **Network** and ensure that **Show Airport status in menu bar** is ticked
- Quit **System Preferences**
- From **Airport menu** select **GUvisitor**
- Open **Safari** **
- A welcome screen for **University of Glasgow Guest Internet Access** service should appear
- Type the **Username and Password** you received via email and click continue or press return key.
- A new window will appear with your home page
- To Log out return to the original window and select Log out

Participants

Abuomwan, Nichola	National Centre For Marine Sciences and Biotechnology, Nigeria	elusibus@gmail.com
Aeschbacher, Simon	University of Vienna, Austria	simon.aeschbacher@univie.ac.at
Agren, Arvid	University of Toronto, Canada	arvid.agren@utoronto.ca
Ahmed, Sophia	Algal Genetics Group, Roscoff, France	sophia.ahmed@sb-roscoff.fr
Aisala, Heidi	University of Oulu, Finland	heidi.aisala@oulu.fi
Arias, Monica	CNRS - UMR 7205 - BCDiv, France	monica.arias@mnhn.fr
Arnold, Michael	University of Georgia, USA	arnold@plantbio.uga.edu
Avila, Victoria	University of Edinburgh, UK	victoria.avila@ed.ac.uk
Azubike, Izuchukwu	NMSB, Nigeria	elusibus@gmail.com
Babatunde, Ilori	University of Nottingham, UK	plxbi@nottingham.ac.uk
Baer, Charles	University of Florida, USA	cbaer@ufl.edu
Bahbahani, Hussain	University of Nottingham, UK	plxhb1@nottingham.ac.uk
Ball, Alex	University of Bath, UK	a.d.ball@bath.ac.uk
Bardacki, Fezvi	Adnan Menderes University, Turkey	fbardacki@adu.edu.tr
Bazykin, Georgii	IITP RAS, Russian Federation	gbazykin@iitp.ru
Beaumont, Mark	University of Bristol, UK	m.beaumont@bristol.ac.uk
Berdan, Emma	Museum für Naturkunde, Germany	emma.berdan@mfn-berlin.de
Biek, Roman	University of Glasgow, UK	roman.biek@glasgow.ac.uk
Blaxter, Mark	University of Edinburgh, UK	mark.blaxter@ed.ac.uk
Booth, Warren	University of Tulsa, USA	warren-booth@utulsa.edu
Bothwell, John	Queen's University Belfast, UK	j.bothwell@qub.ac.uk
Bridle, Jon	University of Bristol, UK	jon.bridle@bristol.ac.uk
Brookfield, John	University of Nottingham, UK	john.brookfield@nottingham.ac.uk
Bruce, Catharine	University of East Anglia, UK	catharine.bruce@gmail.com
Buckley, James	University of Glasgow, UK	James.Buckley@glasgow.ac.uk
Burdfield-Steel, Emily	University of St Andrews, UK	erb28@st-andrews.ac.uk
Burke, Terry	University of Sheffield, UK	t.a.burke@shef.ac.uk
Burt, Austin	Imperial College London, UK	a.burt@imperial.ac.uk
Butlin, Roger	University of Sheffield, UK	r.k.butlin@sheffield.ac.uk
Campos, Jose	University of Edinburgh, UK	j.campos@ed.ac.uk
Carr, Martin	University of Huddersfield, UK	martcarr74@gmail.com
Charlesworth, Deborah	University of Edinburgh, UK	deborah.charlesworth@ed.ac.uk
Charlesworth, Brian	University of Edinburgh, UK	Brian.Charlesworth@ed.ac.uk
Charlesworth, Jane	ARK-Genomics, UK	chieko.kontani@roslin.ed.ac.uk
Clarkson, Chris	Liverpool School of Tropical Medicine, UK	c.clarkson@liverpool.ac.uk
Cogni, Rodrigo	Cambridge University, UK	rodrigocogni@gmail.com
Consuegra, Sofia	Aberystwyth University, UK	skc@aber.ac.uk
Davison, Angus	University of Nottingham, UK	angus.davison@nottingham.ac.uk
Dawson, Deborah	University of Sheffield, UK	D.A.Dawson@Sheffield.ac.uk
Dawson, Kevin	Wellcome Trust Sanger Institute, UK	kevin.dawson@sanger.ac.uk
de Vladar, Harold P.	IST Austria, Austria	hpvladar@ist.ac.at
Desta, Takele	University of Nottingham, UK	plxtd@nottingham.ac.uk
Dicks, Kara	University of Chester, UK	kara_10_17@hotmail.com
Downing, Tim	NUI Galway, Ireland	tim.downing@nuigalway.ie
Dudas, Gytis	University of Edinburgh, UK	g.dudas@sms.ed.ac.uk

Duvaux, Ludovic	University of Sheffield, UK	l.duvaux@sheffield.ac.uk
Ellis, Tom	IST Austria, Austria	tom.ellis@ist.ac.at
Ellis, Jonathan	Manchester Metropolitan University, UK	j.ellis@mmu.ac.uk
Elmer, Kathryn	University of Glasgow, UK	kathryn.elmer@glasgow.ac.uk
Emelianova, Katie	Royal Botanic Gardens Edinburgh, UK	k.emelianova@rbge.ac.uk
Ennos, Richard	University of Edinburgh, UK	rennos@ed.ac.uk
Ernst, Julja	University of Edinburgh, UK	juljaernst@gmail.com
Faria, Christiana	University of East Anglia, UK	christiana.faria@uea.ac.uk
Finger, Aline	RBGE, UK	a.finger@rbge.ac.uk
Fischer, Iris	INRA UMR AGAP, France	iris.fischer@supagro.inra.fr
Fountain, Toby	University of Sheffield, UK	t.fountain@sheffield.ac.uk
French, Lisa	University of Nottingham, UK	plxlf@nottingham.ac.uk
Gajapathy, Kanapathy	University of Jaffna, Sri Lanka	gayan156@gmail.com
Gallo, Ignacio	Freelance, UK	ignacio@cantab.net
Gauffre, Bertrand	INRA - USC1339 (CEBC-CNRS), France	gauffre@cebc.cnrs.fr
Geyrhofer, Lukas	MPI for Dynamics and Self-Organization, Göttingen, Germany	lukas.geyrhofer@ds.mpg.de
Gilroy, Danielle	University of East Anglia, UK	D.Gilroy@uea.ac.uk
Gonzalez Quevedo, Catalina	University of East Anglia, UK	c.gonzalez-quevedo@uea.ac.uk
Gossmann, Toni	University of Hohenheim, Germany	toni.gossmann@googlemail.com
Guenther, Torsten	University of Hohenheim, Germany	torsten.guenther@uni-hohenheim.de
Guerrero, Jimena	University of Glasgow, UK	j.guerrero-flores.1@research.gla.ac.uk
Guirao, Sara	University of Edinburgh, UK	sara.guirao@ed.ac.uk
Hagenblad, Jenny	Linköping University, Sweden	Jenny.Hagenblad@liu.se
Hartfield, Matthew	MiVEGEC, IRD, Montpellier, France	matthew.hartfield@ird.fr
Hatlen, Andrea	Queen Mary University of London, UK	andreapanda8@yahoo.com
Hellen, Elizabeth	University of Nottingham, UK	elizabeth.hellen@nottingham.ac.uk
Hodcroft, Emma	University of Edinburgh, UK	emmahodcroft@gmail.com
Hopkins, David	University of Sheffield, UK	boa07dph@sheffield.ac.uk
Huber, Barbara	Museum National d'Histoire Naturelle, France	babahuber@gmail.com
Hutchison, James	University of Sheffield, UK	j.hutchison@shef.ac.uk
Illingworth, Christopher	Wellcome Trust Sanger Institute, UK	ci3@sanger.ac.uk
Iyoriohe, Williams	NCMSB, Nigeria	elusibus@gmail.com
Jackson, Ben	University of Sheffield, UK	b.jackson@sheffield.ac.uk
Jain, Kavita	J Nehru Centre for Advanced Scientific Research, India	jain@jncasr.ac.in
Jamie, Gabriel	University of Cambridge, UK	gabrieljamie@gmail.com
Jeffares, Daniel	University College London, UK	d.jeffares@ucl.ac.uk
Jiggins, Chris	University of Cambridge, UK	c.jiggins@zoo.cam.ac.uk
Johnson, Harriet	University of Nottingham, UK	plxhfj@nottingham.ac.uk
Johnson, Louise	University of Reading, UK	l.j.johnson@reading.ac.uk
Jossart, Quentin	Université Libre de Bruxelles	qjossart@ulb.ac.be
Kanda, Ravinder	Imperial College London, UK	r.kanda@imperial.ac.uk

Keightley, Peter	University of Edinburgh, UK	peter.keightley@ed.ac.uk
Kelleher, Jerome	University of Edinburgh, UK	jerome.kelleher@ed.ac.uk
Kidd, Marie	University of New South Wales, Australia	m.kidd@unsw.edu.au
Kim, KangChon	Ewha Womans University, Korea, Republic of	kangchonsara@hanmail.net
Kim, Kang-Wook	The University of Sheffield, UK	k.kim@sheffield.ac.uk
Kitchen, James	University of Warwick, UK	j.l.kitchen@warwick.ac.uk
Knight, Mairi	Plymouth University, UK	mairi.knight@plymouth.ac.uk
Kozak, Chris	University of Cambridge, UK	kmkozak87@gmail.com
Krasovec, Rok	University of Manchester, UK	rok.krasovec@manchester.ac.uk
Kuepper, Clemens	University of Sheffield, UK	c.kuepper@sheffield.ac.uk
Levsen, Nicholas	Newcastle University, UK	nicholas.levsen@ttu.edu
Lewis, Samuel	University of Edinburgh, UK	s1066244@sms.ed.ac.uk
Lohse, Konrad	University of Edinburgh, UK	konrad.lohse@gmail.com
Longdon, Ben	Department of Genetics, UK	b.longdon@gen.cam.ac.uk
Lu, Lu	University of Edinburgh, UK	lulu_biochina@hotmail.com
Lunt, Dave	University of Hull, UK	dave.lunt@gmail.com
Lycett, Samantha	University of Edinburgh, UK	samantha.lycett@ed.ac.uk
Mable, Barbara	University of Glasgow, UK	barbara.mable@glasgow.ac.uk
Marquardt, Jeannine	Natural History Museum London, UK	jeannine.marquardt@gmx.de
Marra, Annamaria	University of Bari, Italy	annamaria_marra@libero.it
Marsden, Clare	University of California - Davis, USA	cdmarsden@ucdavis.edu
Martin, Simon	University of Cambridge, UK	shm45@cam.ac.uk
Matthews, Louise	University of Glasgow, UK	louise.matthews@glasgow.ac.uk
McClure, Colin	University Of Bath, UK	cdm28@bath.ac.uk
McInerney, Caitriona	University of Sheffield, UK	c.mcinerney@ulster.ac.uk
McTaggart, Seanna	University of Edinburgh, UK	smctagga@staffmail.ed.ac.uk
Michaelides, Sozos	Oxford University, UK	sozos.michaelides@zoo.ox.ac.uk
Mlynski, David	University of Bath, UK	dtm21@bath.ac.uk
Montano, Valeria	University of Veterinary Medicine Vienna, Austria	valeria.montano@vetmeduni.ac.at
Moran, Peter	University of St. Andrews, UK	pm74@st-andrews.ac.uk
Morgan, Katy	Max Planck Institute, Tübingen, Germany	katy.morgan@tuebingen.mpg.de
Muir, Anna	University of Glasgow, UK	a.muir.2@research.gla.ac.uk
Murray, Gemma	University of Cambridge, UK	ggm2@cam.ac.uk
Murtskhvaladz, Marine	Ilia State University, Georgia	david_tarkhishvili@iliauni.edu.ge
Musselle, Chris	University of Bristol, UK	chris.j.musselle@gmail.com
Mwacharo, Joram	University of Nottingham, UK	joram.mwacharo@nottingham.ac.uk
Nadeau, Nicola	University of Cambridge, UK	njn27@cam.ac.uk
Nicholls, James	University of Edinburgh, UK	james.nicholls@ed.ac.uk
Nichols, Richard	QMUL, UK	r.a.nichols@qmul.ac.uk
Niskanen, Alina	University of Oulu, Finland	alina.niskanen@oulu.fi
Novak, Sebastian	IST Austria, Austria	sebastian.novak@ist.ac.at
Nullmeier, Jens	MPI, Göttingen, Germany	jens@nld.ds.mpg.de
Obbard, Darren	University of Edinburgh, UK	darren.obbard@ed.ac.uk
Page, Rod	University of Glasgow, UK	roderic.page@glasgow.ac.uk
Palmer, Duncan	University of Oxford, UK	duncan.palmer@stx.ox.ac.uk
Parker, Darren J.	University of St. Andrews, UK	djp39@st-andrews.ac.uk
Parsons, Kevin	University of Glasgow, UK	Kevin.Parsons@glasgow.ac.uk
Paterson, Steve	University of Liverpool, UK	S.Paterson@liverpool.ac.uk
Pemberton, Josephine	University of Edinburgh, UK	j.pemberton@ed.ac.uk

Perry, Richard	University of Edinburgh, UK	r.h.j.perry@ed.ac.uk
Razali, Haslina	University of Sheffield, UK	haslina.razali@gmail.com
Polechova, Jitka	IST Austria, UK	jitka@ist.ac.at
Prada, Joaquin	University of Glasgow, UK	joaquinprada@glasgow.ac.uk
Razgour, Orly	University of Bristol, UK	Orly.Razgour@bristol.ac.uk
Recknagel, Hans	University of Glasgow, UK	Hans.Recknagel@glasgow.ac.uk
Reynolds, Alan	University of Glasgow, UK	1109149R@student.gla.ac.uk
Richards, Paul	University of Nottingham, UK	plxpr5@nottingham.ac.uk
RIEUX, Adrien	University Collee London, UK	a.rieux@ucl.ac.uk
Ritchie, Mike	University of St Andrews, UK	mgr@st-andrews.ac.uk
Rouger, Romuald	University of Stirling, UK	romuald.rouger@stir.ac.uk
Santure, Anna	University of Sheffield, UK	asanture@gmail.com
Savory, Fiona	National Centre for Biological Sciences, India	fionars@ncbs.res.in
Schloetterer, Christian	Institut für Populationsgenetik, Austria	christian.schloetterer@vetmeduni.ac.at
Schneider, David	Universidade Estadual de Campinas, Brazil	davidmarsc@gmail.com
Shakarashvili, Maia	Ilia State University, Georgia	david_tarkhnishvili@iliauni.edu.ge
Shuker, David	University of St Andrews, UK	david.shuker@st-andrews.ac.uk
Sjolund, Jennifer	University of Stirling, UK	m.j.sjolund@stir.ac.uk
Smith, Gilbert	University of St Andrews, UK	gs70@st-andrews.ac.uk
Stainton, John	Roslin Institute, UK	John.Stainton@roslin.ed.ac.uk
Stear, Michael	University of Glasgow, UK	Michael.stear@glasgow.ac.uk
Stefan, Thorsten	University of Glasgow, UK	thorsten.stefan@glasgow.ac.uk
Stone, Graham	University of Edinburgh, UK	graham.stone@ed.ac.uk
Swanstrom, Jen	University of Bristol, UK	jen.swanstrom@bristol.ac.uk
Tarkhnishvili, David	Ilia State University, Georgia	david_tarkhnishvili@iliauni.edu.ge
Theissinger, Kathrin	University of Koblenz-Landau, Germany	theissinger@uni-landau.de
Thielsch, Anne	University Koblenz-Landau, Germany	thielsch@uni-landau.de
Thompson, Martin	University of Cambridge, UK	mjt68@cam.ac.uk
Trewby, Hannah	University of Glasgow, UK	h.trewby.1@research.gla.ac.uk
Vanjari, sohini	University of Cambridge, UK	sv329@cam.ac.uk
Veltsos, Paris	University of St Andrews, UK	parisveltsos@gmail.com
Verity, Robert	QMUL, UK	r.verity@qmul.ac.uk
Verspoor, Eric	Inverness College UHI, UK	Eric.Verspoor.ic@uhi.ac.uk
Webster, Lucy	Science and Advice for Scottish Agriculture, UK	lucy.webster@sasa.gsi.gov.uk
Weissman, Daniel	IST Austria, Austria	dbw@ist.ac.at
Welch, John	University of Cambridge, UK	jjw23@cam.ac.uk
Wesche, Philipp	University of Johannesburg, UK	mail@philippwesche.org
Westram, Anja Marie	University of Sheffield, UK	a.westram@sheffield.ac.uk
Wiener, Pamela	Roslin Institute, UK	pam.wiener@roslin.ed.ac.uk
Willman, Faye	University of Kent, UK	faye.willman@gmail.com
Wolff, Kirsten	Newcastle University, UK	kirsten.wolff@ncl.ac.uk
Zeng, Kai	University of Sheffield, UK	k.zeng@sheffield.ac.uk
Zhang, Hanyuan	University of Sheffield, UK	bop10hz@sheffield.ac.uk
Zhong, Weihao	University of Bath, UK	wz230@bath.ac.uk
Zohren, Jasmin	QMUL, UK	j.zohren@qmul.ac.uk

Notes

