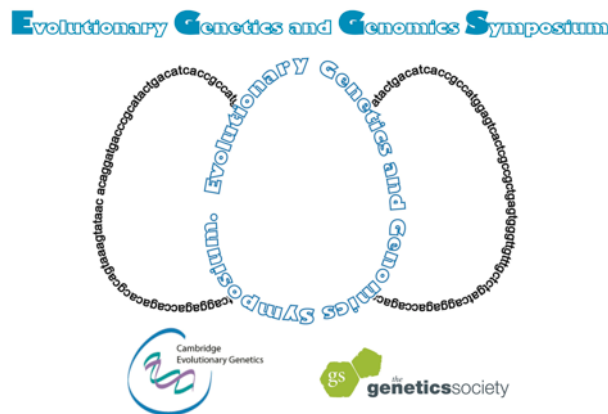


EGGS Meeting Report



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Attracting generous help from the Genetics Society, this year the small Cambridge Evolutionary Genetics meeting or 'CEG' mutated into 'EGGS': *The Evolutionary Genetics and Genomics Symposium*, and was held in the historic location of Cambridge University's Genetics Department on the 18th of March.

Coordinated by Ben Longdon and Richard Merrill (University of Cambridge), the meeting attracted close to one hundred participants from across Europe. Speakers were drawn from a broad range of expertise, giving the meeting an eclectic and stimulating air as talks spanned the full range of the discipline: plants to animals, bacteria to trypanosomes, symbionts to pathogens, field studies to theoretical models, and genes to genomes. If there were themes unifying the day, they were surely the relevance and power of an evolutionary genetics approach in all manner of biological systems, and the pervasive march of next-generation sequencing technologies into mostly every walk of evolutionary biology.

The day-long meeting was split into three fast paced sessions, giving invited speakers forty-five minutes and everyone else fifteen. Following the opening remarks, Diethard Tautz (Max-Planck-Institut für Evolutions biologie) took to the floor and delivered a wide-ranging invited talk, setting a diverse tone for the conference. Initially, he covered the search for signatures of selection in European mice, including the finding that populations with non-functional copies of the alpha-amylase gene may recover a functioning allele with introgression from neighbouring populations - a process he likened to "natural gene therapy". Diethard went on to discuss morphological trait mapping and how selective sweeps seen in wild populations of fat island mice are recapitulated in experimental selection lines. Finally he discussed the origins of new genes, making the case for de-novo birth from cryptic sites as an underappreciated force as compared to gene duplication. The latter proved a particularly popular topic in the subsequent Q&A.

Next up, Julien Martinez (Department of Genetics, University of Cambridge) described his work on the endosymbiont *Wolbachia*, and its ability to protect *Drosophila* from viruses. This anti-viral effect has many researchers championing deliberate infection with the bacterium as a way to reduce the

spread of insect vectored diseases. Encouragingly, Julien reported that Wolbachia strains conferring protection against the natural fly pathogen DCV, also do so against the distantly related Flock House Virus. Subsequently Ian Henderson (Department of Plant Sciences, University of Cambridge) drew the first session to a close with his talk on recombination hotspots in *Arabidopsis*. Using crossover sequencing he found that many plant immunity genes or 'R-Genes' are in regions of extraordinarily high recombination rates, concluding that selection may be acting to increase recombination around these genes.

The second session started with Jessica Stapley (University of Sheffield/Smithsonian Tropical



Research Institute) on the evolution of the colourful dewlap of Anolis lizards. In her Panamanian field site, Jessica reported strong experimental evidence for female mate choice in the size if not colour of male neck-flaps, and showed preliminary RAD-tag data suggesting that genetically populations are still divided geographically despite hybridisation. Following on, Jordi Paps (University of Oxford) delivered a lively summary of his comparative-genomics approach for finding the ancestral gene complement of bilateral animals using many whole genomes. The talk was clearly a winner with the crowds, netting Jordi the much coveted EGGs 2014 best-talk-chocolate-egg (pictured).

Matteo Fumagalli (UCL, UC Berkeley) brought proceedings back to the population level by discussing the recent sequencing of both brown and polar bears. He reported evidence for more adaptive evolution in the polar bear lineage, perhaps linked to rapid change in the species as it adapted to more Northerly climes. Supporting this finding, the team found signatures of positive selection in adipose, cardiovascular and pigment related genes – perhaps charting the transition of a brown-bear like ancestor into the colourless, seal-decimating top predator of the Arctic we know today.

Simon Martin (Department of Zoology, University of Cambridge) delivered an informative talk on tracking introgression in *Heliconius* butterflies of Central and South America, showing how true races still exist, despite millions of generations of extensive hybridisation. He also discussed techniques for dating ancient hybridisation events, including the tracking of large introgressed blocks as they are gradually broken down by recombination. Sean Meaden (University of Exeter) ended the morning by tackling the question of how fitness costs vary between differing environments. Using a bacteria/phage model system, he showed that resistance mutations exhibiting little cost in lab-media, may in fact be highly costly in a more natural settings such as a leaf. Further to this he identified the causative resistance SNPs using MiSeq sequence data.

The afternoon session began with an entertaining and insightful invited talk from Virpi Lummaa (University of Sheffield) on the evolutionary benefits of human menopause. Blending sociology and genetics, Virpi asked the challenging question "Why do women bother living beyond the menopause?" pointing to the fact that a post-reproduction life stage is extremely rare amongst mammals. She then set about answering the question with a revealing insight into the history of

Finland by way of its detailed church records. Looking at the historical success of children under different sociological conditions, she concluded that having a menopausal granny in the attic may in fact be the secret to success in humans.

Switching tack from wild humans to lab reared *Drosophila*, Alethea Wang (ZSL, Toronto) talked about the fitness effects of a panel of *Drosophila* mutations. Utilising a small army of undergraduates to genotype almost two million flies, she showed how the distribution of selective effects differed between environments. Martijn Timmermans (NHM) followed up with the hunt for the locus controlling wing patterning in *Papilio* butterflies, once again using next-generation sequencing data. With a combination of GWAS, FST outlier and linkage disequilibrium data, he suggested that the key gene may be in fact be the famous transcription-factor *Engrailed*.

Following a leisurely lunch, Richard Durbin (Wellcome Trust Sanger Institute) used his invited spot to talk about the latest findings from next-generation sequencing studies of the classic Rift-lake cichlid system. Perhaps most astonishingly, he reports that despite the amazing phenotypic variation seen in Rift-lake fish, genetic diversity is in fact incredibly low. He also talked about the pairwise sequentially Markovian coalescent approach for inferring demographic history, and how it is shedding light on human migration out of Africa.

In the penultimate talk of the day, Seth Barribeau (ETH) laid to bed to any claims that the insect immune system is simple or primitive, using RNA-seq and transcriptomics to highlight expression differences between lab colonies of bumblebees. Despite the immune system's complexity, he found that the most successful trypanosome parasites may actually suppress host immunity rather than simply evade it. Seth's clear and colourful presentation won him runner-up in the competition for best talk, and the second of the day's prestigious chocolate eggs. Following Seth, the final slot of the afternoon fell to Fabrice Eroukhanoff (Oslo), who talked about genotyping of Italian sparrows and how widespread linkage persists and selection still favours homozygotes.

The day closed with discussions over drinks in the department, including a keg of local beer, and a trip to a nearby microbrewing pub for dinner. All-in-all this highly enjoyable meeting served to showcase how diverse, stimulating and relevant evolutionary genetics still remains, some eighty years on from the start of the modern synthesis. In the future we hope that the EGGS meeting will continue to grow and attract a broad range of researchers from across Europe working on Evolutionary Genetics and Genomics.