30 years of The Selfish Gene

"They are in you and me; they created us, body and mind; and their preservation is the ultimate rationale for our existence. They have come a long way, those replicators. Now they go by the name of genes, and we are their survival machines."

This wonderful quote from *The Selfish Gene* by Richard Dawkins formed the opening remarks of an extraordinary meeting: 'The Selfish Gene: Thirty Years On'. The event was organised by Helena Cronin and was held at the London School of Economics on 23rd March 2006, to mark the 30th anniversary of this landmark book.

There was a formidable array of speakers: Daniel C Dennett (Tufts), Sir John Krebs, FRS (Zoology, Oxford), Matt Ridley, Ian McEwan, Richard Dawkins, FRS (Oxford) and in the chair was Melvyn Bragg. If, like many, you were unable to get a ticket, then you may be interested in the full details and transcripts which can be found at the following 'Edge' website: (http://www.edge.org/documents/archive/edge178.html).

Population Genetics Group

14th – 16th December 2005, University of Edinburgh

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The 39th annual meeting of the Population Genetics Group was held last December in the beautiful but blustery parkland of Heriot-Watt University, west of Scotland's capital city. It was hosted by the School of Biological Sciences at the University of Edinburgh and was organised by Deborah and Brian Charlesworth. Pop Group has always been an informal meeting, bringing together scientists working on population genetics and evolutionary biology, and over the years, the mainland European visitors have made up a growing proportion of the attendees (this year, 40%), with a small number of scientists travelling from outside Europe (8%). Furthermore, the meeting is increasingly appealing to an audience of molecular evolutionary biologists and genome analysts. This was reflected in two of the three plenary talks that examined large-scale genotype data for signatures of adaptation (Wolfgang Stephan, University of Munich) and recombination (Gil McVean, University of Oxford).

Wolfgang Stephan opened the first day by talking about the population genetics of adaptation. He discussed his work on detecting selection across the genome in *Drosophila melanogaster* and reviewed attempts to estimate the frequency and intensity of selective events that have occurred in its recent history. Gil McVean discussed the application of population genetic methods to large-scale genotype data and described recent progress in the construction of whole-genome maps of recombination rates. Using his coalescent-based method for estimating recombination rate variation at fine (kilobase) scales, he identified more than 30,000 recombination hotspots in the human genome, most of which occur in non-coding sequence. By making comparisons with chimpanzees, he showed that although hotspots themselves evolve very fast, and although their positioning and intensity is largely responsible for recombination rate variation over fine scales, recombination rates over large (megabase) genomic distances are well conserved. He also described several sequence motifs ('recombination tags') that he found are associated with recombination hotspots and coldspots, and discussed the possible influence of these sequences on recombination activity.

Arcadi Navarro (Universitat Pompeu Fabra, Barcelona) continued the theme of human genome analysis, and demonstrated how a large-scale sequencing project could shed light on the evolutionary history of disease. Navarro examined the world-wide pattern of variation in the prion-encoding gene PRNP. He analysed sequences from 174 humans and found two main haplotypes associated with a nonsynonymous substitution at a single codon. The excess of low-frequency variants between these two haplotypes indicates that positive or purifying selection has acted on this gene (in contrast to the previously accepted hypothesis of an ancient, stable, balanced polymorphism).

Douda Bensasson (Manchester University) presented an example of genome analysis on yeast. Thanks to the availability of a whole genome sequence she examined the third chromosome of *Saccharomyces paradoxus* for patterns of molecular population genetic variation. Her most compelling discovery was the

high level of divergence at the centromere between European and Asian populations, showing that centromeres diverge nearly three times faster than sites expected to be under only slight selective constraint. Why are these centromeres evolving so quickly? The 'centromeric drive' hypothesis (where a centromere biases segregation, giving itself a greater chance of reaching the egg) cannot explain the high level of divergence among *Saccharomyces* species, because in yeast both the centromeres present in the diploid progenitor cell are represented in the four equally sized spores (unlike animals and seed plants where each meiotic division generates a single egg with only one of the centromeres of the diploid cell). Instead, Douda proposed that centromeres might be subject to particularly high mutation rates, which she will test in future experiments.

While many talks used existing datasets, others drew on new empirical data, and several examined the quantitative genetics of wild populations. In his plenary, Patrice David (Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier) discussed his work identifying the traits that affect selfing and outcrossing hermaphroditic snails, and the degree of genetic and environmental influences on selfing. In another talk, Jon Slate (University of Sheffield) illustrated the merits of genetic markers used to estimate the impact of past bottlenecks on population heterozygosity. He used a population of Père David's deer, known to have been isolated 1500 years ago and to have subsequently undergone a number of severe population bottlenecks, and compared estimates of effective population size, based on molecular markers with historical records of a past bottleneck. Brian McEvoy (Trinity College, Dublin) tracked Viking ancestry in modern Ireland by looking at Y-chromosome in a cohort of Irish men who bear surnames of Viking origin. Many talks revealed the growing use of new software — such as the program 'Structure' (distributed free, for using multi-locus genotype data to investigate population structure) — and showed broad applications in the study of population history, structure and the impact of landscape on genetics. Some delegates noted that there were fewer quantitative genetic talks than past years, and even fewer of these were theoretical studies, which may reflect a move by quantitative geneticists to attend other meetings.

In one of the few behavioural studies presented at the meeting, John True (Stony Brook, State University of New York) investigated the consequences of geographic isolation in *Drosophila melanogaster*. He found heritable differences in pigmentation, body size and male courtship repertoires between mainland America and Bahamas populations, and discussed what this might tell us about when these areas were colonized by *D. melanogaster*, and where the colonizers came from.

Many talks discussed the population genetics of selfish genetic elements — Casey Bergman (University of Manchester) discussed the insertion of transposable elements into coding regions in *Drosophila*. He discussed the frequency with which transposable elements are found in the protein coding regions of eukaryotes and their potential role in creating genetic novelty. Martin Carr (University of York) discussed the discovery of the first transposable element in stalk-eyed flies; a system better known for the study of sexual selection. Kelly Dyer (University of Edinburgh) considered a different type of selfish element — a rare driving X chromosome in the mycophagus (mushroom-eating) fruit fly *Drosophila recens*. Is this driving X chromosome recent or ancient, and what is its likely outcome? Sampling from populations of *D. recens* across the USA, she found that individuals harbouring the rare driving X possess a single haplotype on the X. She showed that the extensive linkage disequilibrium on this X is likely to be due to a complicated system of chromosomal inversions that prevents recombination around the driving locus. She explained that this lack of recombination will prevent the purging of deleterious mutations and prevent the fixation of beneficial mutations, and predicted that in time the driving X will degrade.

There were, of course, numerous interesting talks that there is unfortunately no room to discuss here; suffice to say that the range of presentations reflected the shift among evolutionary biologists towards whole genome analysis, bioinformatics and large-scale human sequencing projects. It is possible that this is partly why the value of population genetics in modern biology is becoming more widely appreciated, not least for its importance for understanding genetic variation underlying disease. We thank Deborah and Brian Charlesworth and their band of helpers for a stimulating and enjoyable three days and thank the sponsors, in particular the Genetics Society and *Trends in Ecology and Evolution*, for their continued support for the Pop Group meeting.