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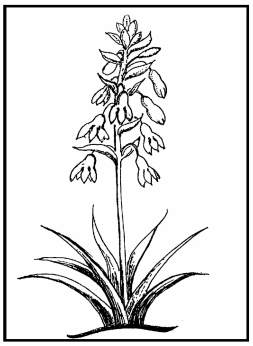

*Galtonia candicans*

# The Galton Institute

# NEWSLETTER

Issue Number 79

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## Contents



## EDITORIAL

The most important event of the year for the Institute is the annual conference and the last was a triumph for all who contributed to it. There is a report in this issue by two Council members of a calibre that made me feel redundant.

The Institute is dependent upon donations and one generous anonymous donor has been giving a healthy sum annually and continues to do so even though he is not a member of the Institute. Thank you, it is much appreciated and is an excellent example for others.

### Obituary
### Madeleine Simms

6 September 1930 - 3 October 2011

Madeleine Simms was a fine and effective campaigner whose formidable methods have since been adopted by professional lobbying firms. She championed a number of social issues but her greatest achievement was her contribution to the Abortion Act 1967.

Madeleine discovered that abortion was illegal after the birth of her first child in 1959 and she felt this to be wrong. Her main motivation was the suffering of unwanted children although the injustice of private abortions sometimes being available to those who paid also appalled her. By 1961 when the birth defects from the anti-nausea drug Thalidomide became apparent she was already active in the Abortion Law Reform Association. Her passion and persistence eventually found David Steel to sponsor the Bill; he worked with her and her fellow campaigners to produce a Bill which was less radical than she wished, but she was sufficiently pragmatic to realise that it was a workable start.

Soon after her birth in Vienna as Madeleine Zimmerman, her politically-aware family moved to London where she was educated at St Paul's Girl's School and Aberdeen University where she read Moral Philosophy and English Literature.

She married Dennis Simms whom she met through the Jewish Graduates Association, of which he was Chairman, and had two children to whom she was devoted.

In the early 1970's she read Medical Sociology at Bedford College, London and subsequently worked at the Institute for Social Studies in Medical Care and as a trustee of various population and birth control trusts. She served on the Council of The Galton Institute in the 1990s.

Her main published work was Abortion Law Reform which she wrote with Keith Hindell in 1971 and some of her reports are of use today. Her zeal, single-mindedness and manner did not always endear her to those around her but her campaign for the reform of the abortion legislation was a prelude to the so-called women's movement and without her drive these changes would have been greatly delayed in this country.

**Geoffrey Vevers**

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# Galton Institute

# Conference 2012:

## Human Genetic Diversity

***Report by***
***Dr Elena G Bochukova***
***and***
***Dr Branwen Hennig***

The 2012 Galton Institute Conference was held on 14th November at the Royal Society, London The topic of the meeting was human genetic diversity and comprised eight high calibre presentations by distinguished speakers. The general theme throughout this year's conference could be summarised as 'Migrate and Mate'.

The first session started with **Professor Mark Stoneking** (Max Planck Institute, Leipzig, Germany) who presented the concepts of population spreading, and the utilization of modern genetic techniques to detect '**Archaic Admixture in Modern Human Populations'**. Introducing the topic of evolution of modern humans in its natural context of existing fossil evidence, he also emphasized the key contribution of factors such as migration and mating, and how these could be inferred by genetic evidence. He demonstrated the power of genetic tools to address controversies stemming from fossil data with regard to the origin of modern humans (e.g. multiregional evolution versus recent African origin). Using methods such as mitochondrial DNA (mtDNA) and Y-chromosome analysis, and genome-wide data, the genetics has spoken in support to a recent African origin of modern humans (~100, 000 yrs). Further exploration into the population admixture was aided by recent developments of the whole-genome sequencing techniques. Accumulating sequencing data from modern humans alongside ancient DNAs such as the Neanderthal has been generated over the past several years and is quickly shaping our current understanding of population mixing and spreading. In the latter part of his talk, Professor Stoneking focused on an intriguing story of the genomic sequencing of another ancient DNA specimen found in the Siberia's Denisova cave in 2010. The Denisovans genome revealed admixture with populations as far as South East Asia and Australia. A picture of multiple dispersals from Africa emerged as an overarching theme from this fascinating talk.

**Professor Himla Soodyall** (National Health Laboratory Service, Johannesburg, South Africa) continued the theme of genetic diversity in relation to Africa, but focused on '**Population Genetic Studies in Africa**' rather than those without. She highlighted the benefits of employing a varied number of tools, including linguistic, climatic, archaeological and genetic methods to reconstruct the past. Of these, genetics gives us the least biased information. Findings from several past and ongoing studies in Africa and particular Southern Africa were described. Many of these used both mtDNA and Y chromosome markers as means to determine the matrilineal and patrilineal history of population ethnic groups, thus continuing on the 'migrate and mate' theme. Such studies have identified the Karretjie people to relate to the oldest branches in the phylogenetic tree of (African) populations and corroborated the oral history of white ancestors (presumably from shipwrecks in the late 18th century) in family clans residing along the wild coast of South Africa. More recently, genome-wide screening of single-nucleotide polymorphisms (SNPs) is used for dissecting the genetic structure of African populations and their subgroups. Professor Soodyall finished emphasising the importance of public engagement with the community as basis for genetic studies in any setting, and gave examples of educational material used as part of her work.

'**Population Genetics of Admixture in the Americas'** was the original title of the next talk, but this was changed to **Population Genetics in the Personal Genome Era** by **Professor Carlos Bustamante** (Stanford School of Medicine, USA) who delivered it. His research focuses on the fine-scale genetic structure of human populations and its implication for genomic medicine. In a time when majority of the genome-wide association studies use European ancestry samples, he argued the point that expanding our knowledge of common disease genetics could benefit greatly from investigation of rare disease alleles contributed by multi-ethnic samples. Furthermore, modern human population substructure and ancestry reconstruction has a direct relevance for the design of genetic studies. As clear illustration of the power of high-throughput sequencing technologies to identify precise genetic origin of a specimen was the story of 'Ötzi' (found in the Alps and likely >5,000 years old), whose genetic ancestry analysis identified as Sardinian man. More recently, modern inhabitants of the Americas have been the subjects of Professor Bustamante's work, and their genetic diversity was viewed in the context of historical circumstances. When genetic information from African Americans and Hispanic/Latino individuals is analysed, and matched with the history of the Americas (African slave trade and colonial history), then these mass migrations could be traced as genetic signatures. Utilizing this information when designing further genetic

studies could become a powerful tool to uncovering more disease-contributing alleles in complex disorders.

A shift closer to home for most conference attendants was made in the presentation on '**A Genetic Map of the People of the British Isles'** by **Professor Sir Walter Bodmer** (Department of Oncology, Weatherall Institute, Oxford and The Galton Institute). This collaborative project generated a genetic map based on data on >600,000 SNPs from just over 2000 individuals from rural areas of the UK who's four grandparents are from the same area. Professor Bodmer stressed how crucial it is to take account of correlations between genetic markers (so called linkage disequilibrium) to avoid skewing of a genetic map. The analysis of these data demonstrated in an elegant manner that the British population can be subdivided into several groups based on their genetic make-up, e.g. distinct subpopulations clusters in the Orkneys, the tips of Wales, Cornwall, Devon, the Welsh borders and so forth. These groups correlate well with geographic regions, surnames and historic events. In parallel a genetic study on a number of European populations was carried out. This helped to determine the origin of different population groups on the British Isles. For instance the ancestry of present day residents of the Orkney Islands can be shown to go back to the Vikings. Similarly, the genetics indicate that historic Anglo-Saxon invasions have contributed a component of Danish and German ancestry to population sub-groups living further south in the United Kingdom.

Professor Bodmer concluded on the note that underlying population genetics needs to be considered in the context of genetics of health and disease, with different genetic backgrounds affecting the detection of causal genetic variation and downstream diagnostic or treatment options.

The **2012 Galton Lecture** was delivered by **Professor Hugh Montgomery** (University College London) and entitled '**Rock, Blue Genes and Getting High. How we cope when oxygen is scarce?**'. He gave an overview of the earth's development to an oxygen-dependent environment with evolution of most living forms of life along the way. Several examples highlighted the adaptation to (temporarily) hypoxic situations, such as carps in anoxic lakes frozen over during winter or humans living at high altitude. Genetic work on Tibetans indicates that variation in the EPAS1 and the ADAM17 genes are associated with low haemoglobin levels in blood. Both these genes are biological plausible candidates in oxygen metabolism, for example EPAS1 encodes the transcription factor HIF2a, which stimulates production of red blood cells and thus increases the concentration of haemoglobin, but this does not explain the whole picture of adaptation to hypoxic conditions. However, evidence from epidemiological studies can aide to further our understanding. For instance, leptin and ghrelin hormonal regulation of appetite leads to the well documented weight loss at high altitude. This may lead to reduced maintenance costs through a reduction of protein synthesis and a switch of the metabolic pathways from anabolism to catabolism. Professor Montgomery concluded that adaptation to a hypoxic environment is unlikely to be based on an increase in oxygen delivery, and more likely to be due to reduced use or need for oxygen.

**Dr Simon Myers** (Department of Statistics, Oxford) delivered a captivating talk on '**The Interplay of Recombination and Human** Genetic Diversity'. Dr Myers intro-

***Professor Hugh Montgomery with the silver Galton Plate, presented in recognition of the delivery of the 96th Galton Lecture at the 2012 conference***

duced recombination as an essential part of reproduction: a motor for generation of diverse haplotypes in the populations. The factors controlling this process have been investigated in large-scale population data including the international HapMap project. When subjected to systematic analysis the patterns of recombination in humans show non-random narrow 'hotspots' in both sexes, occurring not uniformly throughout the human genome, most of these have a short lifespan and are not shared with closely related primates such as the chimpanzee.

What determines where the recombination takes place and the very existence of recombination hotspots? This research has a direct relevance to the so called 'genomic disorders' where recombination goes wrong – e.g. mechanisms such as non-homologous allelic recombination (NAHR) lead to gross genomic defects and copy-number variation. Bioinformatic analysis of the sequences around the hotspots characterized the first sequence motifs associated with hotspot activity, and produced evidence that these same motifs mark sites of recurrent disease-causing

genomic rearrangements in humans. Further bioinformatic interrogation led to the identification of a fast evolving zinc-finger protein, PRDM9, as binding to these hotspot motifs. Genome-wide comparison of recombination patterns across populations reveals population-specific hotspots, and the dynamics of their appearance and disappearance will be the next challenge in this line of research.

This year's Fisher Memorial Lecturer was **Professor Peter Donnelly** (Department of Statistics, Oxford and Wellcome Trust Centre for Human Genetics, Oxford). His talk was entitled '**Genetic Variation in Human Health and Disease'.** Although Fisher's Infinitesimal model, which in essence says that many SNPs of small effect act on disease (and are thus not useful in risk prediction), rings true in the context of genome-wide association studies (GWAS), such studies have been successful in shedding light on the underlying mechanisms and pathways that lead to disease. For example, joint effects of protective alleles in IL23R, ERAP1 and the HLA-B loci have been shown to reduce the risk of ankylosing spondylitis by about a 10-fold. Other studies using a model comparison framework have demonstrated that different subtypes of ischaemic stroke appear to have a different genetic substructure. Another example where GWAS has been successful in informing about the underlying disease pathways has been the identification of the *BCL11A* gene (transcriptional master regulator of the haemoglobin switch) in sickle cell disease and malaria protection. This discovery also offers a potential new route for clinical intervention and switching to a higher protective level of foetal haemoglobin HbF in adults. Genome-wide approaches provide us both with advantages, e.g. identifying new genes, new phenotypes, causal variation, as well as challenges, e.g. variant calling is still difficult and the genome annotation far from perfect, are being used more and more frequently in part due to becoming more affordable over time. Professor Donnelly focused on the clinical utility of whole-genome sequencing describing the progress on the WGS500 project currently running in Oxford, where 500 clinical samples with various rare genetic defects are being sequenced and already succeeding in uncovering novel aetiology of disease. He gave an example of a collaborative work which has recently identified a brain glutamate channel gene mutated in a family with mental retardation and specific defect in sleep architecture.

The final part of Professor Donnelly's talk explained the principle behind the maintenance of variation in the gene pool due to a selective advantage, and presented data from a comparison of human and chimpanzee DNA, indicating the presence of ancient balancing selection that has occurred before the separation of these species.

***Professor Peter Donnelly, FRS with the Fisher Memorial silver dish presented in recognition of the delivery of the 31st Fisher Memorial Lecture***

**Professor Luca Cavalli-Sforza** was unfortunately unable to attend and conclude the conference. The day thus ended with **Professor Alberto Piazza** (University of Torino and Human Genetic Foundation, Torino, Italy) who spoke about '**The Italian Genome Project**'. The research described shows many parallels to the 'Genetic map of the British Isles' study in its design and analysis methods. Interesting anecdotes based on the genetic data, e.g. the strong Greek influences in Sicily and Anatolian connections in the origin of the Etruscans, were presented. The final point made about the inaccuracy of classical phylogenetic trees, where changes in one branch are not independent from those in another due to 'migration and mating' between branches nicely rounded off this most stimulating day.

The conference was organized and chaired by Professor Sir Walter Bodmer, Professor Adam Eyre-Walker and Professor Philippa Talmud, with help from Betty Nixon and many thanks to the Royal Society for hosting this event.

**Elena G. Bochukova**,
University of Cambridge

**Branwen J. Hennig,**
London School of Hygiene and Tropical Medicine

**THE GALTON INSTITUTE CONFERENCE 2013**

**To be held at The Royal Society on Wednesday 6 November, 2013**

## Insect and zoonose genomes and human health

Admission:
free but strictly by ticket

# British Society for Population Studies

## Annual Conference 2012

The 2012 British Society for Population Studies Conference, held at the University of Nottingham from 10-12 September, was the best-attended annual conference for many years, with over 250 participating and with 128 submitted papers presented.

In addition to the two plenary sessions reported on below, there were training events. One was on sex ratios, population pyramids and accessing the data of the Office of National Statistics led by Piers Elias. Others include the calculation of healthy life expectancies, by Pia Wohland, on quantitative methods by Jo Sage and Elspeth Graham, and on event history analysis (also known as survival analysis) by Ben Wilson and Valeria Cetorelli. There was also a fringe meeting on social media and population studies.

The full Conference programme and all abstracts can be viewed at the BSPS website at: http://www2.lse.ac.uk/socialPolicy/BSPS/annualConference/2012/Home.aspx

**Plenary 1:**
**Professor Peter McDonald**
(Australian National University and President of the International Union for the Scientific Study of Population)

***A century of population studies, Society and Population Studies' Societies.***

Professor McDonald provided a comprehensive history of the International Union for the Scientific Study of Population (IUSSP) and the Population Association of America (PAA).

He began by examining the influence of notable characters in laying the foundations for the first population associations. In addition to esteemed demographers like Frank Lorimer, there were surprise benefactors like Edward Willis Scripps, a media mogul in the mould of William Randolph Hearst (or Citizen Kane). He emphasised the tension between advocacy and the history of population associations and then highlighted three historical paradigms. Each is related to birth control and show the thinking of many advocates and academics in the 1920s and 30s. The Neo-Malthusians saw population growth as a potential threat to capitalism and economic growth; Eugenicists were primarily concerned with the quality of a population and spent much time considering fertility differentials.

Professor McDonald then highlighted three historical paradigms, each related to birth control, which show the thinking of many advocates and academics at the time. Although far from novel, the ideas of the Neo-Malthusians saw population growth as a potential threat to capitalism and economic growth. Eugenicists on the other hand, were primarily concerned with population "quality", and spent much time considering fertility differentials.

More controversial than either of these, at the time, was the issue of access to contraception, which was the primary concern of many feminists and those supporting women's rights, including Margaret Sanger. She was the main organiser of the first international population conference (held in Geneva in 1927), which led to the formation of the first international population association, the Assembly of the International union for the Scientific Investigation of Population Problems (IUSIPP), in 1928. She received little credit for this at the time, and despite the will of advocates, this first association refused to make a statement on population policy. This international association continued to operate as a consortium of national committees, with various degrees of success, and after a gap during the Second World War, it was restarted in 1947 and became the IUSSP.

Professor McDonald discussed the influence of these two associations on later events; these include the IUSIPP's committee in America (imaginatively named the American National Committee), organised the first meeting of The Population Association of America (PAA). As with the IUSSP, the PAA's dilemma from its inception was the extent to which it should 'follow the money' or 'maintain the purity of scientific endeavour'. The first President of the PAA, Henry Pratt Fairchild, and several subsequent Presidents (Louis Dublin, Frederick Osborne, and Warren Thompson) met in 1931 at the Town Hall Club in New York City. Also at this meeting of 38 people, was Margaret Sanger. Osborne suggested that she should not be put forward as an officer of the organiSation because he felt the PAA should have a scientific focus, rather than an activist orientation.

In the final section of his lecture, Professor McDonald followed the birth of these two associations forward in time, and discussed their influence upon more recent events. These included the formation of the Population Investigation Committee (1936), UN population division (1946), Institut National d'études Démographiques (1946) and Population Council (1953), alongside other organisations that came to be firmly involved in population issues, such as United States Agency for International Development.

He summarized the current situation with the wide range of existing associations cooperating with each other and that the discipline of populations studies had never been in a healthier state.

**Plenary 2:**
**Professor Danny Dorling**
(University of Sheffield) and

**Glen Watson**
(Office for National Statistics)

***The 2011 Census*.**

With the first UK census results still hot off the press, conference gave an extended plenary session to two excellent and knowledgeable speakers. Danny Dorling of Sheffield University focused on the headline results of population growth, and how sure we could be of them. Glen Watson, Director of the Census and soon to become ONS Director General, focused on taking the census. Their presentations are available on the BSPS conference website. All in all, the 2011 Census can be described as the best since 1981, and perhaps the best ever.

Danny Dorling started by noting that the census estimate of 56.1m residents in England and Wales was half a million more than had previously been estimated. It was 3.7m more than in 2001, and 5.3m more than in 1991. The figures tell of an accelerating growth with largest increases in London Boroughs such as Newham and Tower Hamlets, but also elsewhere such as Manchester, and in the 18-29 age group. Can we believe it? The difference with the previous estimates is mainly an increase of women in their late twenties and thirties, perhaps uncounted immigrants from the 'good' times earlier in the 2000's. The Office for National Statistics' own final reconciliation report will not be delivered until December. Danny suggested that there are more people who are resident in more than one country, particularly other countries of Western Europe, which may increasingly lead to duplicate but correct counting.

While Danny was not critical of the numbers counted as residents, he does believe that the 95% confidence limits over-estimate the certainty of the estimates for each area. The published 95% confidence estimates vary from 0.6% for some Districts including in Norfolk, to between 3% and 4% for Liverpool, Hammersmith & Fulham, Camden, Plymouth, and Kensington & Chelsea. He did not think that the models of non-response could be good enough to capture all the human reasons that might affect Census results in one direction or another.

England and Wales' accelerating population is unique in Europe. Danny speculated that this may be related to the way each government was dealing with the recession in the years before 2011, noting the stronger cuts in public expenditure in the UK.

He finally made a plea to consider the benefits of the census and the alternatives, since Francis Maude the Cabinet Office Minister had declared himself for change. Danny felt that the census could only be replaced by personal microchips, of which he was not in favour. In discussion Danny was upbeat about the possibility of persuading politicians to change their minds, if their individual passions, ambitions and differences within the government were all considered.

Glen Watson explained how the census was planned and executed and its subsequent processing and validation. Key features had changed to improve the fieldwork: an up-to-date address register with methodology to improve and validate it; online enumeration of substantial numbers of residents; and on-street collection focused on areas with lowest return rates, measured by a questionnaire tracking system. There were protests in particular over the use of arms manufacturer Lockheed Martin for the data processing, but none that significantly disrupted the collection.

70% of the forms were returned by post before enumerators started on those who had not. The emphasis on areas with lowest return rates meant that some easier areas did not reach as high a response as they would have in earlier censuses, but no Local Authority had less than an 80% response rate in 2011, compared with 13 such areas in 2001. This reduced range of response rates helped to improve confidence in the results.

The post-enumeration Census Coverage Survey estimates non-response in each Local Authority and provides the details required to 'fill up' the census database with records to represent missed residents. It achieved a minimum 70% response rate in every authority, equal to the 2001 experience, also a good achievement given that in 2011 it was more focused on the worst-to-enumerate areas, and social attitudes to door-to-door interviewers have not improved. Forms were taken to Trafford, at its peak nearing 40 articulated lorries-full in a day, and after scanning there was the biggest paper shredding operation in UK history. And finally, as discussed in detail in other sessions of the conference, the age-sex structures of each local authority were subject to detailed validation through 'deep dives' in comparisons with other data sources and demographic analysis.

The results have been generally well-received. ONS provided graphical interfaces to the results at http://www.ons.gov.uk/ons/guide-method/census/2011/index.html, highlighting both a time series approach over the past century, and a comparison facility of population pyramids for any two local authorities. These were also syndicated to media websites which were particularly successful: ONS hits were only 10% of all the hits on the 100 years animation, for example, most of them being on the BBC website. Glen finished with "Enjoy the results so far: and believe them – I know I do".

By the time of the next BSPS conference in 2013, we will know of

challenges to census results if any materialise. But we will also hear of extensive analysis of the results which will be released with increasing detail of population characteristics during the intervening twelve months.

Plenary reports:
**Ben Wilson and Ludi Simpson**

**BSPS** would like to take this opportunity to thank **The Galton Institute** for their generous financial support towards Conference costs, particularly student bursaries.

## WALES GENE PARK SIXTH FORM CONFERENCE

The Wales Gene Park has organised a Sixth Form Conference on alternate years since 2004 when about 250 pupils attended the event in Cardiff. Since then it has grown and this year over 850 students attended the Wrexham event at the William Aston Hall, Glyndwr University and nearly 1500 attended the Cardiff event at St David's Hall in the city centre.

Topics are chosen for their relevance to the A/S and A level syllabi but they also have to be interesting and entertaining in order to keep the students engaged. The speakers each give us 3 questions which will be answered in their talks and we produced quiz sheets based on this information. The students were encouraged to listen for the answers by offering prizes for correctly completed sheets. The evaluation sheets for staff are used in the planning of future events to ensure they are relevant.

This year we were joined by eight speakers who were all received enthusiastically and evaluated well. The following abstracts were sent to schools prior to the event.

### Wrexham:

**Dr Sue Assinder, Director of Education, Liverpool School of Tropical Medicine**

**The ABC of DNA**

Knowing about the fundamental structure and function of DNA is critical if we want to understand modern advances such as genetic engineering and DNA fingerprinting. This talk will take a historical perspective to the story of DNA, beginning with its discovery in the shadow of the Crimean War and concluding with the elucidation of the human genome sequence. It will describe the key experiments through which scientists worked out the structure of DNA, established its organisation within chromosomes and painstakingly dissected the cellular processes involved in replication and protein synthesis. The focus will be on highlighting the experimental approach to scientific discovery and the way in which collective scientific knowledge builds gradually on the work of generations of individual scientists.

**Matthew Watts, Regulatory Policy Manager, HFEA**

**Debating Mitochondria Replacement**

Researchers are working on new medical techniques that could allow women to avoid passing on genetically inherited mitochondrial diseases to their children. These techniques, which are IVF based, offer options for affected families. However they are also at the cutting edge, both of science and of ethics. The HFEA is the UK regulator of assisted reproductive techniques, and has launched a consultation to seek the publics' view on the social and ethical impact of making these techniques available to patients.**http:mitochondria.hfea.gov.uk/mitochondria/**

**Dr. Pablo Orozco-Terwengel, Research Scientist, Cardiff University**

**Conservation of Endangered Species and Wildlife Forensics**

Planet earth presents an astonishing diversity of organisms. This diversity has taken millions of years to form through the process of evolution. However, while there have been several mass extinctions in the past, the last couple of hundreds of years have experienced a dramatic decline in diversity paralleled by an increase in human population size. Developments in molecular biology and genetics have opened new windows to understand species diversity. Furthermore, molecular genetics has become a tool of utmost importance for scientists to understand the nature of population's genetic variation in relation to species distribution, demography and adaptation. In this presentation I will discuss the value of molecular genetics for wildlife and the impact it has on the field of conservation genetics.

**Dr Natasha De Vere, Head Of Science And Research, National Botanic Garden of Wales**

**Barcode Wales: Dna Barcoding the Nation's Native Flowering Plants for Biodiversity Conservation and Human Health**

DNA barcoding uses specific regions of DNA to act as unique identifier for species. First a reference database of DNA barcodes is created using known samples and then unknown DNA sequences can be compared to these to allow an identification to be made. Species can be identified from pollen grains, fragments of seeds or roots, wood, dung, stomach contents or environmental samples collected from the air, soil or water. Projects are underway throughout the world to DNA barcode all living things and ensure that these barcodes are freely available online as a global resource. The scientific community have agreed on sections of two genes called rbcL and matK to act as the DNA barcode for

plants. These genes can be used to catalogue plant life as they have a slightly different code between species but are very similar within a species.

Over the last four years the Barcode Wales project has created a reference database of DNA barcodes based on the 1143 native flowering plants and conifers of Wales. The project has assembled 5723 DNA barcodes for the rbcL and matK genes, giving the most complete coverage of plant DNA barcodes for any nation in the world.

Now that this phase of the project is complete we are working on a wide range of applications that use our DNA barcodes for biodiversity conservation and human health. We are using our DNA barcodes to track pollinators by identifying the pollen carried on their bodies. We are finding out more about our Welsh plants by creating a phylogenetic tree that shows their evolutionary relationships. We are also investigating the medicinal properties of honey. We are collecting honey from beekeepers throughout the UK and testing its ability to kill the hospital infection, MRSA. We are then DNA barcoding the honey to find out whether the plants the bees visit to make the honey affects its antibacterial properties.

**Dr Annie M Procter, Clinical Director of The All Wales Medical Genetics Service**

**Advances in Medical Genetics: Why Genetic Tests are Different**

Advances in science are increasingly enabling us to investigate and analyse ourselves in minute detail. This is facilitating the diagnosis of disease and the prediction of ill health in individuals who, at the time of testing, are fit, well and apparently 'disease free'. Whilst our scientific knowledge is vast and still expanding, our ability to translate the scientific data we are collecting into useful information for patients, families and the public in general is an enormous challenge. Questions such as 'who should perform the tests?'; 'who should give the results?'; 'where can people go to discuss and understand the implications of the information they receive?'; 'who owns the genetic information?' 'where should genetic information be stored and who should have access to it as many genetic tests have implications for individuals way beyond the person who has had the test (for example children, parents and members of the family they do not even know)?'. These are questions to ponder on while we consider new developments in medical genetics.

**Professor David Cove, Professor of Genetics Emeritus, University of Leeds, UK , Visiting Professor, Washington University In St. Louis, USA**

**Is there a Gene for Happiness**

As a geneticist, I am often asked "Is it caused by the genes or by the environment?" In my talk, I will explain how for most attributes, this is not only an impossible question to answer, but is not even a valid question. Both our genes and the environment input into how we end up, but it is their interaction together that is often the most important factor.

**Cardiff:**

In Cardiff two of the speakers were different from those in Wrexham.

**Dr Pete Kille , Bio-Initiatives Director, Cardiff School of Biosciences**

**Next Generation Sequencing: Opening Pandora's Box**

Pete Kille will cover a timeline of discoveries relating to DNA and the people behind them from the revelations made by Mendel in relation to heredity, through to the sequencing of the Human Genome and the controversy surrounding the commercial funded project headed by Professor J. Craig Venter. Pete will talk about what it means to have your own genome sequenced and present some of the technologies that allow this to be done in days or weeks and only for a few thousand pounds.

**The Right Reverend Dr Lee Rayfield, Bishop of Swindon**

**Does 'We Can' Mean 'We Should'? Advances in Genetic Medicine and The Ethical Dilemmas They Pose**

Advances in our understanding of genetics and cell biology at the molecular level have led to incredible breakthroughs in medical treatment in recent decades. In Vitro Fertilisation (IVF) has not only provided treatment for infertility but given birth to a host of other techniques known as Assisted Reproductive Technologies (ARTs). Clinics can now help parents at risk of having children with a serious inherited disease to have healthy children, or to have a child whose cord blood cells might be used as a life-saving transplant for a brother or sister. In laboratories human genes are regularly being transferred to bacteria, yeast, plants and animals and the range of applications for therapeutic purposes seems endless. Human beings can now do so much. But how do we decide what should - or should not - be done and who makes those decisions in the UK?

The Wales Gene Park gratefully acknowledges the support received from **The Galton Institute** in staging this year's event. The feedback from the evaluations has been extremely encouraging with many schools already expressing their support for the next event in 2014.