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THE ROYAL SOCIETY

# DISCUSSION MEETING ON
# Human evolution, migration and history revealed by genetics, immunity and infection

Monday 6 and Tuesday 7 June 2011

Organised by Professor Danny Altmann, Dr Francois Balloux and Dr Rosemary Boyton

## Programme and abstracts
## Speaker biographies
## Participant list
## Notes
## Publication order form

*The abstracts and biographies which follow are provided by the presenters and the Royal Society takes no responsibility for their content.*

| DAY 1 | | | | DAY 2 | | | |
|---|---|---|---|---|---|---|---|
| **SESSION 1**<br>Human genetics, evolution and migration<br>**Chair: Marc Feldmann** | | **SESSION 2**<br>Human leukocyte antigens (HLA) as markers of human population and their history<br>**Chair: Danny Altman** | | **SESSION 3**<br>Epidemics, evolution and human history<br>**Chair: Alice Roberts** | | **SESSION 4**<br>Pathogen selection pressure<br>**Chair: Francois Balloux** | |
| **09.30** | Welcome by Peter Cotgreave Royal Society | **13.30** | **Peter Parham**<br>Primate-specific evolution of NK cell receptor recognition of MHC class 1 | **09.00** | **Adrian Hill**<br>Case-control studies of infectious disease susceptibility | **13.30** | **Mark Achtman**<br>Insights from genomic comparisons of genetically monomorphic bacterial pathogens |
| **09.35** | **Danny Altmann**<br>Introduction to Human evolution, migration and history revealed by genetics, immunity and infection | **14.00** | Discussion | **09.30** | Discussion | **14.00** | Discussion |
| **9.50** | **Stephen Oppenheimer**<br>Out-of-Africa, the peopling of continents & islands: tracing uniparental gene trees across the map | **14.15** | **Marcelo Fernández-Viña**<br>Tracking of human migrations by the analysis of the distribution of HLA alleles, lineages and haplotypes in closed and open populations | **09.45** | **Sebastien Gagneux**<br>Evolutionary forces in human tuberculosis | **14.15** | **John Novembre**<br>Human population structure and the adaptive response to pathogen-induced selection pressures |
| **10.20** | Discussion | **14.45** | Discussion | **10.15** | Discussion | **14.45** | Discussion |
| **10.35** | Coffee | **15.00** | Tea | **10.30** | Coffee | **15.00** | Tea |
| **11.00** | **Mark Jobling**<br>Identifying genetic traces of historical expansions | **15.30** | **Erik Thorsby**<br>The Polynesian gene pool: An early contribution by Amerindians to Easter Island | **11.00** | **Kristian Andersen**<br>Pinpointing signals of natural selection to investigate causal variants in selective sweeps | **15.30** | **Nina Jablonski**<br>Human skin pigmentation, migration, and disease susceptibility |
| **11.30** | Discussion | **16.00** | Discussion | **11.30** | Discussion | **16.00** | Discussion |
| **11.45** | **Marta Lahr**<br>African origins - the morphological and behavioural evidence of early humans in Africa | **16.15** | **Alicia Sanchez-Mazas**<br>Role of migration, demography and natural selection in the molecular evolution of the HLA polymorphism in human populations | **11.45** | **Eske Willerslev**<br>Early peopling of the new world | **16.15** | **Sarah Williams-Blangero**<br>Host genetics and population structure effects on parasitic diseases |
| **12.15** | Discussion | **16.45** | Discussion | **12.15** | Discussion | **16.45** | Discussion |
| **12.30** | LUNCH | **17.00** | CLOSE | **12.30** | LUNCH | **17.00** | CLOSE |

# Human evolution, migration and history revealed by genetics, immunity and infection

**Monday 6 June and Tuesday 7 June 2011**

Organised by Professor Danny Altmann, Dr Francois Balloux and Dr Rosemary Boyton

**Synopsis**

This meeting offers a journey from molecules to history, bringing together geneticists, immunologists, anthropologists and historians. Infection has been the most potent evolutionary force in human history, eliminating genes offering poor resistance and selecting for new mutations conferring protection against a threat. Can genetics help us understand natural selection, human evolution and migration over the past 70,000 years?

**Monday 6 June 2011**

**9.30 Welcome by Dr Peter Cotgreave**, Director of Public Affairs, Royal Society

**9.35 Introduction by Professor Danny Altmann,** Lead Organiser

**Session 1 – Human genetics, evolution and migration**
**Chair Professor Mark Feldmann FRS, Imperial College London, UK**

**9.50 Out-of-Africa, the peopling of continents & islands: tracing uniparental gene trees across the map**
Professor Dr Stephen Oppenheimer, University of Oxford, UK

Genetic relationships between human groups were first studied by comparisons of relative allele frequency at multiple loci. Geographic study of detailed, highly-resolved trees of single non-recombining uniparental loci (mitochondrial DNA: mtDNA and Y chromosome: NRY), following lineages rather than populations, then revolutionised knowledge of the peopling of the world; although, curiously, use of geographically highly specific mutations that protect against malaria, found on individual *autosomal* globin genes, were first in this single-locus trend. MtDNA, with its high SNP mutation rates and relative ease of dating, joined the fray and gave stronger proof of the recent replacement of all human species by Anatomically Modern Humans, who left Africa via a single southern exit about 70,000 years ago and rapidly spread round the Indian Ocean towards the Antipodes, long before a small branch left a South Asian colony, earlier on the trail, to populate Europe. The worldwide phylogeny of mtDNA is now near-fully resolved, but regional analysis will continue to illuminate subsequent migrations. The NRY with a lower SNP mutation rate, still has dating problems; but validated the mtDNA results, and with more geographic specificity and genomic size, as with the autosomal human genome, has much more detail to offer for the future.

**10.20 Discussion**

**10.35 Tea/coffee**

**11.00 Identifying genetic traces of historical expansions**
Professor Mark Jobling, University of Leicester, UK

The historical record tells us stories of population expansions in the last few thousand years, but what was their demographic impact? Genetics can throw light on this issue, and has mostly done so through the maternally inherited mitochondrial DNA (mtDNA) and the male-specific Y chromosome, despite a number of problems, including marker ascertainment bias, possible influences of natural selection, and the obscuring layers of the palimpsest of historical and prehistorical events. Y-chromosomal lineages are particularly affected by drift, which can be accentuated by recent social selection, but examples of the latter are scarce, and more ancient expansions appear to predominate, for example in Asia. A diversity of approaches to expansions in Europe is yielding insights into the histories of Phoenicians, Roma, Jewish populations, Anglo-Saxons and Vikings, but the field would benefit from more consensus on appropriate methods, and better communication between geneticists and experts in other disciplines.

**11.30 Discussion**

**11.45 African origins - the morphological and behavioural evidence of early humans in Africa**
Dr Marta Mirazon Lahr, University of Cambridge, UK

Studying the origins of our own species, *Homo sapiens*, should be straightforward - we know what we look like and how we behave, and it should be simply a matter of pinpointing the moment in time when these human biological and cultural characteristics are in place. In practice, this is not the case. Evolution is a relentless process, and the characteristics that make us so obviously human today neither appeared at the same time, or had similar expression. To complicate matters further, circumstances can make evolutionary change happen faster and more haphazard, and at least two of these - sharp demographic fluctuations and exposure to new environments - characterise the context of late human evolution. The inevitable outcome is that the last population ancestral to all humans - that to whom we can trace our origins, did not look or behave like anyone alive today. This paper explores what we can learn from the fossil and archaeological records about the early phases of modern human evolution in Africa.

**12.15 Discussion**

**12.30 Lunch**

**Session 2 – Human leukocyte antigens (HLA) as markers of human population and their history**

**Chair Professor Danny Altmann, Imperial College London, UK**

**13.30 Primate-specific evolution of NK cell receptor recognition of MHC class I**
Professor Peter Parham FRS, Stanford University, USA

Natural killer (NK) cells are lymphocytes that function in both immune defence and the process of embryo implantation in placental reproduction. These distinctive functions are both controlled and varied through the action of NK cell receptors that recognise polymorphic major histocompatibility complex (MHC) class I molecules. These ligand-receptor systems co-evolve rapidly and can become unstable, as seen from the independent evolution of analogous systems in different species of placental mammal, notably human patients and their murine models. The system of killer cell immunoglobulin-like receptors (KIR) and HLA-A, B and C (human MHC class I) ligands that controls human NK cells has counterparts only in simian primates and exhibits considerable species-specific character. In particular, the human and chimpanzee systems are distinguished by an array of qualitative and quantitative traits. KIR and HLA class I are candidates for being the

most polymorphic human genes, and because they segregate on different chromosomes, their combined genotype individualizes human immune systems. A broad spectrum of human diseases is associated with HLA and KIR factors, including infection, autoimmunity, complications of pregnancy and transplantation. A synthesis of these data with knowledge of the genetics and population biology of KIR and HLA class I, support a model in which competing pressures from immunity and reproduction have shaped the unique characteristics of the human KIR-HLA system.

**14.00 Discussion**

**14.15 Tracking of Human Migrations by the analysis of the distribution of HLA alleles, lineages and haplotypes in closed and open populations**

Professor Marcelo Fernández-Viña, Stanford University, USA

The HLA system shows extensive variation in the number and function of loci and the number of alleles present at any one locus. Allele distribution has been analyzed in many populations through the course of several decades and the implementation of molecular typing has significantly increased the level of diversity revealing that many serotypes have multiple functional variants. While the degree of diversity in many populations is equivalent and may result from functional polymorphism in peptide presentation, outbred and inbred populations present contrasting numbers of alleles and lineages at the loci with high density expression products. In spite of these differences, the homozygosity levels in almost all of them are comparable. The balanced distribution of HLA alleles is consistent with overdominant selection. The genetic distances between outbred populations correlate with their geographical locations; the formal genetic distance measurements are larger than expected between inbred populations of the same region. The latter present many unique alleles grouped in a few lineages consistent with limited founder polymorphism in which any novel allele may have been positively selected to enlarge the communal peptide binding repertoire of a given population. On the other hand, it has been observed that some alleles are found in multiple populations with distinctive haplotypic associations suggesting that convergent evolution events may have taken place as well. Likely due to its fundamental role in varying immune responses, it appears that the HLA system has been under strong selection. Therefore, allelic diversity in HLA should be analyzed in conjunction with other genetic markers to accurately track the migrations of modern humans.

**14.45 Discussion**

**15.00 Tea/coffee**

**15.30 The Polynesian gene pool: An early contribution by Amerindians to Easter Island**

Professor Erik Thorsby, University of Oslo, Norway

It is now generally accepted that Polynesia was settled by peoples from Southeast Asia, who after reaching Tonga and finally Samoa migrated by inter-island water crossings to the many islands of this archipelago, arriving at Easter Island around AD 1000. An alternative that eastern parts of Polynesia was first inhabited by Amerindians has found little support. There are, however, many indications of a prehistoric (i.e. before Polynesia was discovered by Europeans) contact between Polynesia and the Americas, but no genetic proof of a prehistoric Amerindian contribution to the Polynesian gene pool. To further address this issue, we recently carried out genomic HLA typing as well as typing for mtDNA and Y chromosome markers of blood samples collected in 1971 and 2008 from reputedly non-admixed Easter Islanders. All individuals carried HLA alleles and mtDNA types previously found in Polynesia, and most of the males carried Y chromosome markers of Polynesian origin (a few had European Y chromosome markers) , further supporting an initial

Polynesian population on Easter Island. The HLA investigations revealed, however, that some individuals also carried HLA alleles which have previously almost only been found in Amerindians. Further, our studies strongly suggest that these Amerindian alleles were introduced in prehistoric time. Our results demonstrate an early Amerindian contribution to the Polynesian gene pool on Easter Island, and illustrate the usefulness of typing for immunogenetic markers such as HLA to complement mtDNA and Y chromosome analyses in anthropological investigations.

**16.00 Discussion**

**16.15 Role of migration, demography and natural selection in the molecular evolution of the HLA polymorphism in human populations**

Professor Alicia Sanchez-Mazas, University of Geneva, Switzerland

The major histocompatibility complex (MHC) in humans, HLA, has a complex evolution where both stochastic (e.g. genetic drift) and deterministic (natural selection) evolutionary forces are involved. Due to their very high level of polymorphism, and because numerous population samples have been typed for HLA during several decades for anthropological and transplantation purposes, HLA genes are among the most studied genetic markers for reconstructing human settlement history. However, previous studies have shown that some HLA genetic patterns deviate significantly from those obtained for neutral markers, and a model of Pathogen-Driven Balancing Selection (PDBS) has been proposed.
In this study, we investigate the PDBS model by analysing HLA allelic diversity on a large database of 535 populations in relation to pathogen richness and prevalence. Our results confirm that geographic distances are excellent predictors of HLA genetic differentiations among populations. We also find a positive correlation between genetic diversity and pathogen richness at two HLA class I loci, as predicted by the PDBS model, and a negative correlation at one class II locus. However, such effects are reduced when small-sized populations submitted to rapid genetic drift are removed, indicating a significant demographic effect. The precise mechanisms of the PDBS hypothesis thus remain uncertain.

**16.45 Discussion**

**17.00 Close**

**Tuesday 7 June 2011**

**Session 3 – Epidemics, evolution and human history**

**Chair Dr Alice Roberts, University of Bristol, UK**

**9.00 Case-control studies of infectious disease susceptibility**
Professor Adrian Hill, University of Oxford, UK

Infectious pathogens have long been recognised as potentially powerful agents impacting on human genetic diversity. Analysis of large-scale case-control studies provides one of the most direct means of identifying human genetic variants that currently impact on susceptibility to particular infectious diseases. For over 50 years candidate gene studies have been used to identify loci for many major causes of human infectious mortality, including malaria, tuberculosis, HIV/AIDS, bacterial pneumonia and hepatitis. But with the advent of genome-wide approaches many new loci have been identified in diverse populations. Genome-wide linkage studies identified a few loci, but genome-wide association studies are proving more successful and exome sequencing now offers even greater power. Review of findings to date suggests that the genetic architecture of infectious disease susceptibility may be importantly different from non-infectious diseases and it is suggested that natural selection may be the driving force underlying this difference.

**9.30 Discussion**

**9.45 Evolutionary forces in human tuberculosis**
Dr Sebastien Gagneux, Swiss Tropical and Public Health Institute, Switzerland

Human tuberculosis (TB) is caused by a group of closely related mycobacteria, collectively known as the *Mycobacterium tuberculosis* complex (MTBC). MTBC harbours limited genetic diversity compared to other bacteria. However, our findings based on comparative genome hybridization and large-scale DNA sequencing indicate that the amount of strain-to-strain variation in MTBC is more pronounced than previously believed. In particular, MTBC exhibits a phylogeographical population structure with particular lineages associated with different geographic regions and human populations. Current evidence further suggests that MTBC originated in Africa, and subsequently spread around the world first accompanying the ancient Out-of-Africa migrations of modern humans, followed by more recent waves of exploration, trade and conquest. Consistent with this long-term association between MTBC and its human host, epidemiological data suggest that different MTBC lineages might have adapted to different human populations. However, recent population genomic analyses show that the known human T-cell epitopes in MTBC are evolutionarily hyper-conserved. Taken together, these data suggest a model in which these conserved antigens elicit immune-pathological mechanisms that contribute to the transmission of MTBC, e.g. by promoting lung-cavities, whiles other, as yet unknown and more variable antigens might help modulate or evade protective immune responses in a human population-specific manner.

**10.15 Discussion**

**10.30 Tea/coffee**

**11.00 Pinpointing signals of natural selection to investigate causal variants in selective sweeps**
Dr Kristian Andersen, Harvard University, USA

Human genomes contain hundreds of regions with evidence of positive natural selection, yet, for all but a handful of cases, the underlying advantageous mutation remains unknown.

We have developed a method, the Composite of Multiple Signals (CMS), which combines tests for multiple signals and is capable of pinpointing variants under selection. With human sequence data now available for the 1000 Genomes Project, we have localized several hundred signals of selection to ~50-100kb regions, identifying potential polymorphism that were targets of selection.

Many of these regions contain genes known to be important for pathogen infectivity. Lassa haemorrhagic fever, a severe illness caused by the Arenavirus Lassa virus is endemic in West Africa and estimated to infect more than 300,000 individuals and cause thousands of deaths each year. Interestingly, in the West African population we have identified positive selection of two genes: i) LARGE that modifies the Lassa entry receptor alpha-dystroglycan and is required for infectivity and ii) IL21 that plays a crucial role in Arenavirus immunity.

We hypothesize that allelic variants of these genes may have conferred an evolutionary advantage providing this population with genetic resistance to Lassa fever. Having pin-pointed likely variants using CMS we are now at a stage where we can initiate experimental studies in order to test such hypotheses.

**11.30 Discussion**

**11.45 Early peopling of the New World**
Professor Eske Willerslev, Natural History Museum of Denmark, Denmark

Abstract not available at time of press

**12.15 Discussion**

**12.30 Lunch**

**Session 4 – Pathogen selection pressure**
**Chair Dr Francois Balloux , Imperial College London, UK**

**13.30 Insights from genomic comparisons of genetically monomorphic bacterial pathogens**
Professor Mark Achtman, University College Cork, Ireland

Some of the most deadly bacterial diseases, including leprosy, anthrax and plague, are caused by bacterial lineages with extremely low levels of genetic diversity, so-called 'genetically monomorphic bacteria'. It has only become possible to analyze the population genetic analysis of such bacteria since the recent advent of high-throughput comparative genomics. The genomes of genetically monomorphic lineages contain very few polymorphic sites, which often reflect unambiguous clonal genealogies. Some genetically monomorphic lineages have evolved in the last decades, e.g. antibiotic resistant *Staphyloccus aureus*, whereas others have evolved over several millennia, e.g. the cause of plague, *Yersinia pestis*. Based on recent results, it is now possible to reconstruct the sources and the history of pandemic waves of plague by a combined analysis of phylogeogr aphic signals in *Y. pestis* plus polymorphisms found in ancient DNA. Different from historical accounts based exclusively on human disease, *Y. pestis* evolved in China, or the vicinity, and has spread globally on multiple occasions. These routes of transmission can be reconstructed from the genealogy, most precisely for the most recent pandemic that was spread from Hong Kong in multiple independent waves in 1894.

**14.00 Discussion**

**14.15 Human population structure and the adaptive response to pathogen-induced selection pressures**
Professor John Novembre, University of California, Los Angeles, USA

The past few years of research in human evolutionary genetics have provided novels insights and questions regarding how human adaptations to recent selective pressures have taken place. Here I review the advances most relevant to understanding human evolution in response to pathogen-induced selective pressures. Key insights come from empirical studies of human population structure and demography, genomic signatures of recent human adaptive evolution, and theoretical models of adaptive evolution in spatially distributed populations and in large populations. Taken together, the results make clear that the human response to pathogen-induced selection pressures is a complex process. The outcomes depend on an interplay between the spatial and temporal dynamics of the pathogen, the genetic basis of potential resistance phenotypes, and how population structure impacts the adaptive process in humans.

**14.45 Discussion**

**15.00 Tea/coffee**

**15.30 Human skin pigmentation, migration, and disease susceptibility**
Professor Nina Jablonski, The Pennsylvania State University, USA

Variation in human skin pigmentation is the result of adaptive evolution to regulate the penetration of ultraviolet radiation (UVR) into the skin. Skin pigmentation is an evolutionary compromise between the conflicting demands of photoprotection and photosynthesis of vitamin D by UVR. In the history of the genus *Homo* and of *Homo sapiens* in particular, skin pigmentation has been a highly labile trait. Similar skin tones have evolved independently numerous times in response to similar environmental conditions. In the last 500 years, humans have developed abilities to move long distances quickly, resulting in many

people living under solar regimes markedly different from those experienced by their ancestors. This has had profound effects on all aspects of health in which UVR is implicated, especially those mediated by vitamin D. In this presentation, the state of knowledge about the evolution of human skin pigmentation will be reviewed, and the effects of rapid long-distance migrations and other aspects of modern culture on pigmentation-mediated patterns of disease susceptibility will be highlighted.

**16.00 Discussion**

**16.15 Host genetics and population structure effects on parasitic diseases**

Dr Sarah Williams-Blangero, Southwest Foundation for Biomedical Research, USA

Host genetic factors exert significant influences on differential susceptibility to many infectious diseases. In this presentation, the effects of host genetics on risk for parasitic diseases are explored in two populations. First, the genetic influences on variation in worm loads are assessed in a Nepalese population experiencing moderate rates of infection with geohelminths, including hookworm, roundworm, and whipworm. Second, the genetic epidemiology of the cardiac form of Chagas disease is characterized in a rural Brazilian population where over half of the adults in the population are infected with *Trypanosoma cruzi*, the protozoan cause of Chagas disease. Utilizing genome-wide approaches, we demonstrate that individual genes influence risk for parasitic infection and risk for disease outcomes associated with infection in both populations. In addition to host genetic factors, human population structure and genetic variation in the parasites themselves also shape the observed distribution of parasitic diseases.

**17.00 Close**

## Organiser, speaker and chair biographies

**Professor Mark Achtman, University College Cork, Ireland (Speaker)**
Mark Achtman is a Canadian who performed research at Max-Planck Institutes in Berlin, Germany from 1971-2008. He moved to University College Cork, Ireland in 2007 as a Professor in Microbiology and Principle Investigator of the Science Foundation of Ireland. He is an internationally recognized and highly cited expert on population genetics of pathogenic bacteria. Prior work focussed on epidemic waves of cerebrospinal meningitis caused by *Neisseria meningitides.* More recently, he has used the differentiation of the gastric pathogen *Helicobacter pylori* to resolve ancient global patterns of spread of its human host. He has a particular interest in historical evolution of a variety of bacterial pathogens, which has resulted in investigating the correlations between historical accounts of the pandemic spread of plague with microevolution in the causative agent, *Yersinia pestis*. Currently, considerable efforts are being exerted on understanding the population genetic patterns within the gastrointestinal pathogen, *Salmonella enterica.*

**Professor Danny Altmann, Imperial College London, UK (Organiser and Chair)**
Danny Altmann is Professor of Immunology in the Department of Medicine, Imperial College London and, as of 2011, Head of Pathogens, Immunity and Population Health at the Wellcome Trust. He is also Editor in Chief of Immunology. As Head of the Human Disease Immunogenetics Group, his major research interest has been in the immunogenetics of autoimmune diseases and bacterial infections. This has in recent years included a major emphasis on T cell immunity to serious bacterial infections. Prior to joining Imperial College he was a senior scientist in the Medical Research Council Clinical Sciences Centre.

**Dr Kristian Andersen, Harvard University, USA (Speaker)**
Kristian Andersen is a researcher at FAS Center for Systems Biology and Department of Organismic and Evolutionary Biology at Harvard University and the Broad Institute. Originally from Denmark, he received his PhD from the University of Cambridge and MRC Laboratory of Molecular Biology in 2009. Here, he worked on mechanisms of immunological tolerance and the evolution of the adaptive immune system. Since moving to Harvard he has been investigating the complex relationship between host and pathogen. Using a combination of experimental and computational techniques he is investigating how the human immune system impacts the evolution of viral pathogens such as Lassa and Ebola. Given the strong selection pressures caused by these microorganisms, he is also investigating signals of natural selection in the human genome in response to infectious agents.

**Dr Francois Balloux, Imperial College London, UK and Switzerland (Organiser and Chair)**
Francois Balloux is a Reader in the Department of Infectious Disease Epidemiology at Imperial College. He was trained as a population geneticist and obtained his PhD in 2000 from the University of Lausanne (Switzerland). After a postdoc at the University of Edinburgh, he was offered a faculty position in the Department of Genetics in Cambridge in 2002. There, he led a group working on human evolutionary genetics for five years but became increasingly interested in the evolution of human pathogens and the interplay with their host. In 2007, he joined the Department of Infectious Disease Epidemiology at Imperial College and the newly founded MRC Outbreaks Centre.

**Dr Rosemary Boyton, Imperial College London, UK (Organiser)**
Rosemary Boyton is Head of the Lung Immunology Group in Imperial College London Department of Medicine and a Consultant in Respiratory Medicine at the Royal Brompton Hospital. Her research group work on fundamental aspects of T lymphocyte polarisation and on models of immune control and inflammation in the lung. She has had a particular interest in the immunogenetics of chronic lung infection.

**Professor Marc Feldmann FRS, Imperial College London, UK (Chair)**
Professor Marc Feldmann trained in medicine at Melbourne University, then did a PhD in Immunology at the Walter & Eliza Hall Institute. His research interests are immune regulation and autoimmune diseases, especially the role of cytokines. His major discovery has been uncovering the importance of TNF in rheumatoid arthritis and consequently developing anti TNF therapy. This has led to his election to the Royal Society, the National Academy of Sciences USA and the Australian Academy of Science and the award of prizes such as the Crafoord Prize of the Royal Swedish Academy of Sciences and Lasker Award together with his colleague, Sir Ravinder Maini. His current interest is the role of cytokines in multiple diseases.

**Professor Marcelo Fernández-Viña, The University of Texas, USA (Speaker)**
He is a Professor in the Department of Laboratory Medicine at The University of Texas MD Anderson Cancer Center, in Houston, and he is the Co-Chair of the Immunobiology Committee of the CIBMTR. His involvement in Histocompatibility and Immunogenetics started 1982. He is Past President of the American Society for Histocompatibility and Immunogenetics. He has over 120 peer reviewed publications, many of them focusing on HLA variation in multiple world populations, identifying susceptibility and resistance factors for diseases and in the impact of HLA mismatches in allogeneic transplantation; and more than 10 book chapters. He is Councilor of the International Histocompatibility Workshop and a member of the WHO Nomenclature Committee for Factors of the HLA System. He is Section Editor of *Human Immunology*. He serves as a HLA Expert Consultant for the National Marrow Donor Program (U.S.A.). He is a member of the Board of Directors and the Executive Committee for the United Network for Organ Sharing (U.S.A.).

**Dr Sebastien Gagneux, Swiss Tropical and Public Health Institute, Switzerland (Speaker)**
Sébastien Gagneux holds a joint Group Leader appointment at the Swiss Tropical and Public Health Institute in Basel, Switzerland and at the MRC National Institute for Medical Research in London, UK. Dr. Gagneux received his PhD from the Swiss Tropical Institute/University of Basel, Switzerland in 2001, and then spent four years as a postdoctoral fellow at Stanford University in the laboratory of Dr. Peter Small. Between 2005 and 2007 he worked at the Institute for Systems Biology in Seattle.

Dr. Gagneux studies the cause and consequence of genetic diversity in *Mycobacterium tuberculosis* from a micro- and macroevolutionary perspective. The micro-evolutionary perspective comprises evaluating the effect of bacterial genetics and compensatory evolution on the reproductive fitness and transmission dynamics of drug-resistant *M. tuberculosis*. The macro-evolutionary arm of his research focuses on the global biogeography and population genomics of *M. tuberculosis*, and on the effect of mycobacterial variation on host-pathogen interaction.

**Professor Adrian Hill, University of Oxford, UK (Speaker)**
Adrian Hill trained at Trinity College Dublin and Oxford and is now Professor of Human Genetics and Director of the Jenner Institute at Oxford University. He leads research programmes in genetic susceptibility to tropical infectious diseases and in vaccine design and development.

As a founder member of the Wellcome Trust Centre for Human Genetics since 1994 his research group has studied multiple genetic factors associated with or genetically linked to resistance to malaria, tuberculosis, bacterial pneumonia, and viral infections such as hepatitis B and C and HIV. His group has pioneered genome-wide linkage and association analyses of genetic susceptibility to common human infectious diseases, particularly tuberculosis, more recently as part of the Wellcome Trust case control consortium. Data on immunogenetic susceptibility factors have provided new insights into the impact of infections on human genomic diversity.

He has published over 350 research papers, is a Fellow of the UK Academy of Medical Sciences and the Royal College of Physicians, and a NIHR Senior Investigator.

**Professor Nina Jablonski, The Pennsylvania State University, USA (Speaker)**
Nina G Jablonski is Professor and Head of Anthropology at The Pennsylvania State University. A biological anthropologist and paleobiologist, she studies the evolution of adaptations to the environment in Old World primates including humans. Her research extends into problems that do not have immediate answers in the fossil record, but require synthesis of comparative anatomical and physiological information with that on the physical and environmental characteristics of ancient ecosystems. In the last 20 years, her pursuit of 'unseen' aspects of human evolution has been focused on the evolution of human skin and skin pigmentation. She is a Fellow of the American Association for the Advancement of Science and the California Academy of Sciences, a member of the Advisory Council for the Social, Behavioral, and Economic Sciences of the National Science Foundation, and a member of the Board on Behavioral, Cognitive, and Sensory Sciences of the National Research Council. She received one of the first Alphonse Fletcher, Sr. Fellowships in 2005 and the W.W. Howells Book Award of the American Anthropological Association for 2007 for her book, *Skin: A Natural History* (University of California Press, 2006). In 2009, she was elected to membership of the American Philosophical Society.

**Professor Mark Jobling, University of Leicester, UK (Speaker)**
Mark Jobling is a Wellcome Trust Senior Research Fellow at the University of Leicester. His group uses human Y chromosome diversity to investigate processes of colonisation, migration and admixture, and to study haploid mutation including ectopic recombination and gene conversion, and natural selection through Y-chromosomal genes. He also applies Y markers to forensics, and to understanding the relationships between Y types and patrilineal surnames. Current projects include next-generation sequencing approaches to understanding sex-chromosomal evolution, and the use of Y-, X- and autosomal haplotypes to investigate the impact and timing of migrations, including those of the Vikings.

**Professor John Novembre, University of California, Los Angeles, USA (Speaker)**
John Novembre is an Assistant Professor in the Department of Ecology and Evolutionary Biology and the Interdepartmental Bioinformatics Program at the University of California – Los Angeles. Dr. Novembre earned his PhD in 2006 under Dr. Montgomery Slatkin at the University of California-Berkeley, before taking an NSF Bioinformatics Fellowship at the University of Chicago under Dr. Matthew Stephens, and ultimately his post at UCLA in 2008. His research focuses on developing theory and statistical methods for genomic-scale population genetic data, such as high-throughput single nucleotide polymorphism data and next-generation sequencing data. His work investigates questions in population genetics, focusing on human ancestry, the evolution of domestic dogs and their wild relatives, the mapping of disease traits, and spatial population structure.

**Dr Stephen Oppenheimer, University of Oxford, UK (Speaker)**
Dr Oppenheimer qualified in medicine at Oxford in 1971. From 1972-97: a total of 17 years, he was located in the tropics as a paediatrician, with intervening time spent in English universities (London, Oxford, and Liverpool) as bases for overseas secondment. He has published extensively, focussing on the interactions between iron, nutrition, genetics (particularly $^{+}$-thalassaemia) and infections esp. malaria. He was Professor of Paediatrics in Malaysia then HK from 1987-94.

From 1997-present he returned to Oxford for his children's education. He published first book: '*Eden in the East: the drowned continent of Southeast Asia*' in 1998, a multidisciplinary reconstruction of prehistoric migrations in Southeast Asia and the Pacific using climatology, oceanography, archaeology, genetics, linguistics and cultural anthropology; followed by two similar, more genetically focussed books "*Out of Eden: the Peopling of the World*" 2003 and *"The Origins of the British: a genetic detective story"*, 2006.

He has continued collaborative research with numerous peer-reviewed publications supporting the original reconstructions in his three books and also been an adviser and talking head in a number of related TV documentaries

**Professor Peter Parham FRS, Stanford University, USA (Speaker)**
Growing up in London, Peter Parham studied Natural Sciences at Cambridge University and then went as a Kennedy Scholar to Harvard University, where he obtained a PhD for structural studies on HLA class I performed in Jack Strominger's laboratory. As a Junior Fellow of the Harvard Society of Fellows Parham spent a year in Walter Bodmer's group at Oxford University, where with Frances Brodsky he developed monoclonal antibodies against HLA class I and II. Peter Parham joined the faculty at Stanford University in 1980, where he is now Professor of Structural Biology and Microbiology & Immunology. Parham's research concentrates on the genetics and evolution of MHC class I polymorphisms and their functional interactions with rapidly evolving and comparably polymorphic lymphocyte receptors. Peter Parham has received the Rose Payne, Ceppellini and Festenstein Awards for Immunogenetics, and is a Fellow of the Royal Society.

**Dr Alice Roberts, University of Bristol, UK (Chair)**
Alice Roberts studied medicine and anatomy (MB BCh BSc) at Cardiff University, and worked as a junior doctor in South Wales, before moving to Bristol University, where she taught anatomy on the medical course for over ten years. She is interested in physical anthropology, which focusses on what ancient skeletons can tell us about human evolution, the diversity of the human species, and about diseases that have affected us over time. She has a PhD in palaeopathology (the study of disease in ancient human remains). Alice is also interested in science communication, and she has worked as a science presenter on radio and television, as well as writing several popular science books. She is currently the Director of Anatomy for the NHS Severn Deanery School of Surgery, leading the anatomy course for doctors training to be surgeons; a Research Fellow in Hull York Medical School; and an Honorary Fellow in Archaeology and Anthropology at the University of Bristol. She has just finished filming a new series on human evolution for BBC2, and writing a book on the same subject.

**Professor Alicia Sanchez-Mazas, University of Geneva, Switzerland (Speaker)**
Alicia Sanchez-Mazas is Professor of Population Genetics and Head of the Laboratory of Anthropology, Genetics and Peopling history at the University of Geneva (Switzerland) where she conducts research projects related to the genetic history of modern humans. She coordinates laboratory and biostatistical analyses with a special focus on the Major Histocompatibility Complex (MHC) in humans (HLA). Her current investigation is mainly devoted to the human peopling history of East Asia and Africa, the relationships between genetic and linguistic variation, and the impact of both demography and natural selection on the evolution of the HLA polymorphism. She also leads *HLA-NET*, a European network of researchers aiming at improving the number and quality of population data available for donor search in stem cell transplantation and for research studies in immunogenetics, epidemiology and population genetics. She has co-edited two books on the peopling history of East Asia and has published numerous papers.

**Professor Erik Thorsby, University of Oslo, Norway (Speaker)**
Erik Thorsby is professor emeritus at Institute of Immunology, University of Oslo, Norway. He established the HLA field in Norway and was head of Institute of Transplantation Immunology 1970-1998, and head of Institute of Immunology 1998-2006. His major scientific contributions has been the structure and function of the HLA gene complex, its role as the major histocompatibility complex and the effects of HLA complex genes as strong disease predisposing genes in man. Further he has conducted several investigations on the

use of HLA genetic markers in anthropological studies. He has received multiple scientific awards, and is a member of The Norwegian Academy of Sciences and Commander of the Royal Norwegian St Olav Order.

**Professor Eske Willerslev, Natural History Museum of Denmark, Denmark (Speaker)**
Eske Willerslev (EW) is director for Centre of Excellence in GeoGenetics and the National CryoBank and Sequencing Facility, situated at the National History Museum, University of Copenhagen. His research interests include: human evolution, palaeoecology, palaeontology, domestication, DNA degradation and repair, macroevolution, molecular evolution, barcoding, and genomics. EW did his doctored at University of Copenhagen and a Wellcome Trust Fellowship at Oxford University, UK. EW has also been a visitor at MD Anderson Cancer Research Centre in Texas, US. His group established the fields of sedimentary ancient DNA (Science 2003), and ice core genetics (Science 2007), and were the first to sequence the complete mitochondrial DNA genome (Science 2008) and nuclear genome (Nature 2010) of ancient humans.

**Dr Sarah Williams-Blangero, Southwest Foundation for Biomedical Research, USA (Speaker)**
Sarah Williams-Blangero received her Ph.D. in biological anthropology from Case Western Reserve University in 1987. Since that time, she has worked at the Texas Biomedical Research Institute (formerly the Southwest Foundation for Biomedical Research) in research on infectious disease genetics. Her primary interests are in the genetics of susceptibility to helminthic infections and in the genetic determinants of differential disease outcome in Chagas' disease. Dr. Williams-Blangero directs field studies related to these research projects in Jiri, Nepal and in Posse, Goias, Brazil. She has been the Chair of the Department of Genetics at the Texas Biomedical Research Institute since 1999.

# Upcoming Royal Society Events

## The Summer Science Exhibition 2011

Tuesday 5 – Sunday10 July, Free admission

Explore over 20 fascinating exhibits, Interact with the science that is shaping our world and question UK scientists about their research.

For more information visit **royalsociety.org/sciencelive**

## Is Biodiversity going the way of the Dodo?

Friday 8 July, 6.30pm – 8.00pm

Right now one-fifth of the world's vertebrates are classified as Threatened and every year over 50 mammals, birds, and amphibians species move one stage closer to extinction. Climate change is predicted to become a major threat to biodiversity in the 21st century, but will climate change trigger a mass extinction?

Panel discussion with Professor Jonathan Baillie – Zoological Society of London, Dr William Cheung – University of East Anglia, Professor Adrian Lister – Natural History Museum and chaired by Dr Susan Lieberman – The Pew Environment Group, as part of the Royal Society Summer Science Exhibition.

**Admission is free - but pre booking is essential, to book your free place please visit royalsociety.org/events**

## Talking Primates

Sunday 10 July, 3.00pm – 4.30pm

Dr Simon Fisher and Dr Bridget Waller explain how scientists are starting to identify the genes that help us learn to speak and explore the difference between human language and communication in chimpanzees.

This event is part of the Cafe Scientifique programme at the Royal Society Summer Science Exhibition. Cafes will take place in the Terrace Cafe. They are free and open for all to attend, just grab a drink and get talking! Audience participation is strongly encouraged.

## For more information about these and other Royal Society events, please visit the events diary at royalsociety.org/events

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