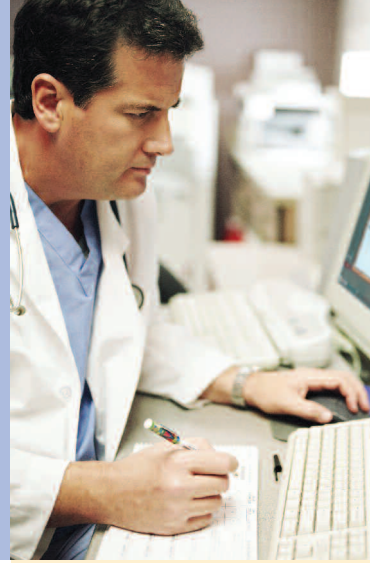


Human Population Genetics

Evolution and Variation

27 seminar style presentations by leading world experts

Series Editors: Prof. Luigi Luca Cavalli-Sforza and Prof. Marcus Feldman – Stanford University, USA



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Topics covered

- Evolutionary history
- Evolutionary forces at play
- Markers
- The human phenotype
- Population structure
- Complex patterns of natural selection
- The Human Genome Project
- HapMap Project
- Historical and geographical genetic variation

Target audience

- Human geneticists
- Population geneticists
- Evolutionary biologists
- Molecular geneticists
- Physiologists
- Biological anthropologists
- Social anthropologists
- All researchers interested in human evolution

The Speakers

Prof. Sir Walter Bodmer
 Prof. Luigi Luca Cavalli-Sforza
 Dr. Nancy Cox
 Prof. Kaare Christensen
 Prof. Andrew Clark
 Dr. Bertrand Desjardins
 Dr. Anna Di Rienzo
 Prof. Marcus Feldman
 Prof. Henry Greely
 Prof. Austin Hughes
 Dr. Toomas Kivisild
 Prof. Richard Klein
 Prof. Gil McVean
 Prof. S. Qasim Mehdi
 Prof. Joanna Mountain
 Prof. Masatoshi Nei
 Dr. Yoshihito Niimura
 Prof. Neil Risch
 Dr. Noah Rosenberg
 Dr. Merritt Ruhlen
 Dr. Theodore Schurr
 Prof. Antonio Torroni
 Prof. Peter Underhill
 Dr. James Weber
 Prof. Kenneth Weiss
 Dr. Piri Welch

"These talks by many of the world's leading authorities are clearly presented, up-to-date and well-illustrated. They provide excellent and wide-ranging reviews of human genetic variation and its implications for recent human evolution, human diversity and health."

Professor Chris Stringer
 Natural History Museum, London, UK

Human Population Genetics

Evolution and Variation

Human Population Genetics: An Overview

1. Modern Human Origins

Prof. Richard Klein – Stanford University, USA

Human evolution – Anatomical differences between Neanderthals and modern humans – African origin of modern human anatomy – Subsequent African origin of modern human behavior, including art and jewellery – Fate of the Neanderthals and other non-modern humans – Possibility that a genetic change prompted the modern human expansion from Africa

2. History and Geography of Human Genetic Diversity I

Prof. Luigi Luca Cavalli-Sforza – Stanford University Medical School, USA

Four major factors of evolution: mutation, natural selection, drift, migration – Role of demography in the quantitative study of evolution – Drift: the Parma Valley study – Equilibrium of migration and drift – Founders' effect – Reconstructing evolutionary history of a population – Evidence of the importance of drift from molecular evolution – Molecular evolution of proteins – Trees with proteins and trees with DNA – Phylogeographic analysis – Microsatellites – Graphic presentation of evolution data by principal components analysis

3. History and Geography of Human Genetic Diversity II

Prof. Luigi Luca Cavalli-Sforza – Stanford University Medical School, USA

Genetic markers inherited from a single parent – Mutational history of the Y chromosome (NRY) – Genealogies of Y chromosome and mitochondria – Of Adam and Eve – Primates and *Homo sapiens* – Neanderthal and the spread of modern humans from East Africa – The spread of modern humans according to Y chromosome – Areas of origin of agriculture and animal breeding – Spread of cultivated wheat to Europe in the Neolithic period – Geographic maps of the first three principal components of Europe – Coevolution and hitchhiking of commensals: *Helicobacter pylori* – Coevolution of humans and cattle

4. History and Geography of Human Genetic Diversity III

Prof. Luigi Luca Cavalli-Sforza – Stanford University Medical School, USA

The human genome diversity project (HGDP) – Method structure – Limitations of HGDP-CEPH – Are the clusters established by structure, "good" races – Correlation between genetic and geographic distance – Decrease of genetic diversity in the human expansion as serial founder effect – Coevolution of genes and languages – Linguistic families: correlation of the genetic and linguistic trees – Darwin's statement – The complete tree of language evolution

5. Cultural Evolution

Prof. Marcus Feldman – Stanford University, USA

Culture definition – Analogies between genes and culture – An example of cultural mutation – Vertical cultural transmission – Case studies – Selection with vertical transmission – The "Kuru" model – Transmission in models with three sexes – Oblique transmission – Horizontal transmission – Rates of change – Cultural niche construction in vertical transmission rates – Constraints on cultural variation – Culture and its effect on genes – Quantification of genetic and cultural spread

6. Linguistic Evolution

Dr. Merritt Ruhlen – Stanford University, USA

Discovery of comparative linguistics – The Indo-Hittite family – Fundamentals of linguistic taxonomy – Alfredo Trombetti – The Eurasiatic language family – African language families – The Dene-Caucasian family – The Amerind language family – Monogenesis – Origin and evolution of word order – Linguistic, genetic and archaeological evidence for human migrations

7. The Human Genomes

Prof. Gil McVean – University of Oxford, UK

The nature of genetic polymorphism – Single nucleotide polymorphisms – Differences between genomic regions – Differences between populations – Inferences about human history from genetic variation – Detecting natural selection

8. Human Microsatellite and Minisatellite DNA Polymorphisms

Dr. James Weber – PreventionGenetics, USA

Microsatellites: nomenclature and definitions – Discovery – Typing methodology – Abundance and types – Applications – Mutation – Biological functions – Evolution – Minisatellites

9. Human Population Structure

Dr. Noah Rosenberg – University of Michigan, Ann Arbor, USA

Geographic distribution of genetic variants – Private alleles – Pairwise differences between individuals – Partition of genetic variation – Population structure and inference of ancestry – Decline of heterozygosity with distance from Africa – Serial sampling model for human evolution – Clines and clusters

10. The Signature of Local Adaptations in Human Polymorphism Data

Dr. Anna Di Rienzo – University of Chicago, USA

Changes in habit and life style during human evolution – Evolutionary dynamics of neutral and advantageous mutations – Signature of natural selection on patterns of variation linked to an advantageous variant – Distinguishing between demography and natural selection – Duffy blood group locus – Lactase persistence – Skin pigmentation – Salt sensitivity variants and hypertension

The Human Genome Project

11. The HapMap Project

Prof. Andrew Clark – Cornell University, USA

The problem in pedigree analysis – A possible solution for the resolution limitations in pedigree analysis – Theory of two loci – Linkage equilibrium and disequilibrium – Recombination events between SNPs – Genealogical interpretation – Statistical significance of LD – The effect of random drift on linkage disequilibrium – Variability of LD among different populations – Heterogeneity of LD across the genome – Hotspots of recombination – Tag SNPs – The HapMap website – Design of GWAS – Wellcome Trust Case Control Consortium – Etiology

12. Major Gene Families in Humans and their Evolutionary History

Dr. Yoshihito Niimura – Tokyo Medical and Dental University, Japan and Prof.

Masatoshi Nei – The Pennsylvania State University, USA

Multigene family – Olfactory Receptors (ORs) – OR genes in humans – Comparison of OR genes between humans and mice – Evolution of OR genes in vertebrates – Other chemosensory receptor genes

13. Natural Selection and Sequence Polymorphism

Prof. Austin Hughes – University of South Carolina, USA

Inferring selection from patterns of nucleotide substitution – The Major Histocompatibility Complex as an example of positive selection – Immunodeficiency virus escapes from immune recognition – Purifying selection on Single Nucleotide Polymorphisms

14. Human Y Chromosome Phylogenetics and Phylogeography

Prof. Peter Underhill – Stanford University Medical School, USA

Framework of human genetic variation – Locus specific forces vs. population level forces – Y chromosome DNA sequence variation – Genetic memory – Phylogenetics, principles and characteristics – Out of Africa – Y chromosome phylogeography – Recovering population histories

15. Evolution of Human Mitochondrial DNA Lineages

Dr. Toomas Kivisild – University of Cambridge, UK

Origins of mitochondria – Maternal pedigrees – Selective constraints – mtDNA population structure – Human origins models – Continental variation of mtDNA lineages – Distribution of synonymous and non-synonymous mutations

16. Ethical Issues in Human Population Genetics

Prof. Henry Greely – Stanford University, USA

General ethical issues in genetics – Special concerns in population genetics research – Importance of broader consent, population control over uses of material, population confidentiality, communication of results and sharing of commercial value – Crucial role of trust

Important Phenotypic Phenomena

17. Evolution: how Genes and their Variation got here

Prof. Kenneth Weiss – The Pennsylvania State University, USA

Evolution by phenotype – Basic factors of evolutionary change – Mutation – Genetic drift – Natural selection – Gene flow – Current human variation – Human global Y chromosome haplotype distribution – Human global mtDNA haplotype distribution – Selection for skin pigmentation and human evolution – Genetic variation and selection for resistance to various forms of malaria – Phenylketonuria (PKU) – Deafness – Breast cancer

18. Human Population Genetics: Lifespan

Prof. Kaare Christensen – University of Southern Denmark, Denmark and Duke University, USA

Human lifespan as a heritable trait – Lifespan phenotypes – Genetic epidemiology of human lifespan – The genetic architecture of human longevity – Genetic study designs in longevity research

19. The Genetic Component to Diabetes

Dr. Nancy Cox – University of Chicago, USA

Diabetes mellitus: definition, classification and its use as a model for genetic studies of complex disorders – Genetic forms of diabetes mellitus: monogenic and polygenic – Identification of diabetes genes – Monogenic forms of diabetes: human HNF-1 α /MODY3 gene – Polygenic forms of diabetes – HLA and ISN in type 1 diabetes – Genes for type 2 diabetes and linkage mapping – TCF7L2 in type 2 diabetes – Genome wide association studies and gene loci implicated in these studies – Allelic variation in human gene expression – Ancestral susceptibility models

20. The Genetics of Breast and Ovarian Cancer

Dr. Piri Welch – University of Washington, USA

General cancer genetics – Tumor suppressor and oncogenes – Knudson's 'two hit' hypothesis – Genetic predisposition to breast and ovarian cancer – How much breast and ovarian cancer is inherited and the causes (genes responsible) – Cancer risk in populations – Factors that affect penetrance – Mutation detection – Risk reduction and prevention strategies

21. Colorectal Cancer and the Rare Variant Hypothesis

Prof. Sir Walter Bodmer – University of Oxford, UK

Cancer: a somatic evolutionary process – Colorectal cancer: a good model to study – Two clear cut familial forms: FAP and HNPCC – Mutation selection balance for dominants and recessives: application to FAP – APC gene found by positional cloning – Loss of heterozygosity proved its role in sporadic cancers – Selection for mutations in the APC "mutation cluster region" – HNPCC mismatch repair genes found by candidate guess – Mutated genes in colorectal cancer include p53 and wnt pathway, occur in adenoma to carcinoma sequence – Arguments for and against need for genomic instability in cancers – Epigenetic changes – Mathematical model of normal and cancerous crypt – Types of familial cancers: mostly rarer than FAP and HNPCC – Approaches to studying multifactorial inherited susceptibility – HLA and disease: the model – Role of linkage disequilibrium – Principles of SNP association analysis – Rare missense variants in the APC gene confer susceptibility – The "rare variant hypothesis" for multifactorial inherited susceptibility: exemplified by study of colorectal adenomas

22. Genetic Diseases in the Jewish Population

Prof. Neil Risch – University of California, San Francisco, USA

Jewish history and genetics – Classification of Jews – Genetic diseases found in Jews, particularly Ashkenazi Jews – Lysosomal storage diseases – Natural

selection (heterozygote advantage) vs. genetic drift – Mutation frequencies, ages and geographic distributions – Bottlenecks in Jewish history

23. The Genetics of French Canadians

Dr. Bernard Brais, Dr. Bertrand Desjardins and Dr. Damian Labuda – Université de Montréal, Dr. Marc St-Hilaire – Université Laval, Prof. Marc Tremblay and Prof. Hélène Vézina – Université du Québec à Chicoutimi, Canada

Founder effect – Population history and the French Canadian founder effect – The contemporary population in relation to its founders – Regional gene pools: the examples of the Saguenay and the Gaspésie regions – Regional distribution of disease mutations

Historical and Geographical Genetic Variation

24. Human Genetic Variation of Africa

Prof. Joanna Mountain – 23andMe, Inc. and Stanford University, USA

Neutral genetic variation and African prehistory – Non-neutral genetic variation of Africa and natural selection – Social and medical implications of genetic variation in Africa – Resources

25. The Peopling of the Americas: New Insights from Genetic Studies

Dr. Theodore Schurr – University of Pennsylvania, USA

The prehistory of the Americas is a fundamental problem in American anthropology – Archeological, ethnographic, linguistic and biological perspectives – New data from each field is changing our view of the timing and process by which the first Americans entered the New World – mtDNA and Y-chromosome data – Coastal route would have had to be taken to account for diversity of genes, languages and cultures present in the American continents – Genetic data

26. Genetics of Pakistani Populations in an Asian and Global Context

Prof. S. Qasim Mehdi – University of Karachi, Pakistan

Population genetics – Pakistan and Southwest Asia – Human migrations – DNA markers – Alu repeats, SNPs and STRs – Y chromosome, mitochondrial DNA and HLA markers unravel genetic relationships among populations in Asia and Pakistan

27. Historical and Geographical Genetic Variation: Europe

Prof. Antonio Torroni – University of Pavia, Italy

Origin of modern Europeans – Genetic tools – Neanderthal vs. modern humans – Complete mitochondrial DNA sequences: new data on the early events after the Out of Africa exit – Paleolithic vs. Neolithic origin of the European gene pool – Expansions from glacial refugia after the Last Glacial Maximum – Unexpected genetic links between modern populations: the case of the Saami and Berbers – Population studies at the microgeographic level: the paradigmatic case of the Etruscans



Speaker Biographies

Prof. Sir Walter Bodmer – University of Oxford, UK

Walter Bodmer is Head of the CRUK Cancer and Immunogenetics Laboratory at the Weatherall Institute of Molecular Medicine, University of Oxford. He studied mathematics in Cambridge and then did his PhD there under the renowned statistician and population geneticist R. A. Fisher. His research interests have ranged from population genetics, especially of humans, through bacterial genetics, somatic cell genetics, pioneering studies with Julia Bodmer on the HLA system and its association with disease and more recently on colorectal cancer genetics and biology. He was a prime mover in promoting the Human Genome Project and the second President of the Human Genome Organisation, HUGO. His book with Luca Cavalli-Sforza, on Human Population Genetics, first published in 1971, is now considered a classic.

Dr. Bernard Brais – Université de Montréal, Canada

Bernard Brais was trained in neurology, genetics and history. He is currently Assistant Professor of Neurology at the Université de Montréal and Director of the Laboratory of Neurogenetics of Motion. His major interests are in the fields of neurogenetics and of the genetic epidemiology of hereditary diseases with founder effects in the French-Canadian population. Bernard is presently working on the genetics and molecular biology of eleven disorders with founder effects in Quebec.

Prof. Luigi Luca Cavalli-Sforza – Stanford University School of Medicine, USA

Luigi Luca Cavalli-Sforza is an Emeritus Professor at Stanford University, where he has been since 1970. He is one of the most distinguished geneticists of the twentieth century and has dedicated his research to the study of the origin of modern humans and their evolutionary history by using genetic markers. His work has always taken a multi-disciplinary approach including demography, archaeology, linguistics, anthropology, surnames and to the interactions of genetic and cultural evolution.

Dr. Nancy Cox – University of Chicago, USA

Nancy Cox is an Associate Professor in the Department of Human Genetics at the University of Chicago, USA. Her research focuses on the identification and characterization of genetic variation influencing susceptibility to complex disorders. She received her BS in biology from the University of Notre Dame in 1978 and her PhD in human genetics from Yale University in 1982.

Prof. Kaare Christensen – University of Southern Denmark, Denmark and Duke University, USA
Kaare Christensen is a Professor of Epidemiology, Director of the Danish Twin Registry and Senior Research Scientist at the Terry Sanford Institute, Duke University. He has conducted a long series of twin studies among the elderly in order to shed light on the relative contribution of genes and environment in ageing and longevity.

Prof. Andrew Clark – Cornell University, USA

Andrew G. Clark is Professor of Population Genetics in the Department of Molecular Biology and Genetics. He received a BS in biology and applied mathematics at Brown University in 1976 and a PhD in population genetics at Stanford University in 1980. Dr. Clark's research focuses on the genetic basis of adaptive variation in natural populations, with emphasis on quantitative modeling of phenotypes as networks of interacting genes.

Dr. Bertrand Desjardins – Université de Montréal, Canada

Bertrand Desjardins is a Senior Researcher in the Demography Department at the Université de Montréal and he holds a PhD in demography from the University Lumière-Lyon2 and is the author of numerous scientific publications centered on the study of the Canadian and Quebec populations. He has been associated all his professional life with the *Programme de recherche en démographie historique* (Research Program in Historical Demography), a major project at the Université de Montréal aimed at setting up a database of the entire French-Canadian population of Quebec from its beginnings in 1608; this database generates in-depth information allowing studies in the fields of demography, history, anthropology and population genetics.

Dr. Anna Di Rienzo – University of Chicago, USA

Anna Di Rienzo is an Associate Professor in the Department of Human Genetics at the University of Chicago. She received her undergraduate and graduate training at the University of Rome "La Sapienza" (Italy). She has worked on patterns of genetic variation in the mtDNA genome, at microsatellites and nuclear loci. Her current interests are in the evolution of genes influencing the risk to common diseases.

Prof. Marcus Feldman – Stanford University, USA

Marcus Feldman is the Burnet C. and Mildred Finley Wohlford Professor of Biological Sciences and Director of the Morrison Institute for Population and Resource Studies at Stanford University. He received a BSc in mathematics and statistics from the University of Western Australia, an MSc in mathematics from Monash University and a PhD in mathematical biology from Stanford. He has been a member of the Stanford faculty since 1971. His research group uses applied mathematics and computer modeling to simulate and analyze the process of evolution.

Prof. Henry Greely – Stanford Law School, USA

Henry T. Greely is a Professor of Law and Professor, by courtesy, of Genetics at Stanford. He received his undergraduate degree from Stanford and his law degree from Yale. He has been on the Stanford faculty since 1985. He specializes in the legal, ethical and social implications of the biosciences, particularly genetics, stem cell research and neuroscience.

Prof. Austin Hughes – University of South Carolina, USA

Austin Hughes is Professor of Biological Sciences and Director of the Institute for Biological Research and Technology at the University of South Carolina. He received his undergraduate training at Georgetown University and his PhD in zoology from Indiana University, Bloomington. His research focuses on the molecular evolution of the vertebrate immune system, the population genetics of immune system genes and the mechanisms by which parasites evade immune recognition.

Dr. Toomas Kivisild – University of Cambridge, UK

Toomas Kivisild is a Lecturer in human evolutionary genetics, Department of Biological Anthropology, University of Cambridge. He received his PhD at the University of Tartu under the supervision of Professor Richard Villems and did his postdoc with Professor Cavalli-Sforza and Dr. Peter Underhill at Stanford University. His current areas of interest include phylogenetics and human population structure.

Prof. Richard Klein – Stanford University, USA

Richard G. Klein lectures on human evolution at Stanford University. He received his graduate training at the University of Chicago and spent 20 years on the faculty there before moving to Stanford in 1993. His field research is in South Africa, where he has focused particularly on the evolution of fully modern humans.

Dr. Damian Labuda – Université de Montréal, Canada

Damian Labuda is Professor in the Department of Pediatrics at the Université de Montréal and in the Sainte-Justine Hospital Research Center in Montreal. Currently, his research focuses on the genetic history of human species and the underlying mechanisms of genomic evolution, including signatures of selection and recombination, and on the application of this information in genetic epidemiology towards an understanding of simple Mendelian and complex disorders.

Prof. Gil McVean – University of Oxford, UK

Gil McVean is Professor of Statistical Genetics at Oxford University. He runs a research group focusing on the development of new methodologies for making inferences about recombination, natural selection and demographic history from genome-wide patterns of genetic variation. He has co-led the International HapMap Project and is involved in projects to map genetic diversity in major human pathogens.

Prof. S. Qasim Mehdi – University of Karachi, Pakistan

S. Qasim Mehdi is Distinguished National Professor and Director General of the Biomedical & Genetic Engineering Division, Islamabad and the Institute for Biotechnology & Genetic Engineering, University of Karachi, Pakistan. Prof. Mehdi received his D. Phil. degree from Oxford University, UK in 1969. He is the recipient of numerous National and International scientific awards and the civil awards of Star (1998) and Crescent of Distinction (2003) by the President of Pakistan. His current work is on the clinical and evolutionary genetics of human populations.

Prof. Joanna Mountain – 23andMe, Inc. and Stanford University, USA

Joanna Mountain's expertise is in human evolutionary genetics. She received her undergraduate training in mathematical sciences and her graduate training in genetics at Stanford University. Prior to joining 23andMe, Inc, Dr. Mountain was a Professor in the departments of Anthropological Sciences and Genetics at Stanford University. Her current area of research interest is the genetic diversity of the peoples of Africa.

Prof. Masatoshi Nei – The Pennsylvania State University, USA

Masatoshi Nei is a molecular evolutionary geneticist and has developed many statistical methods that are widely used for evolutionary studies at present. He has also studied human evolution and evolution of multigene families, immune system genes and sensory receptor genes. He has written three major textbooks on molecular evolution. Prof. Nei received a PhD from Kyoto University. He is a member of the National Academy of Sciences, USA, and he has received a number of awards including the International Prize for Biology.

Dr. Yoshihito Niimura – Tokyo Medical and Dental University, Japan

Yoshihito Niimura is an Associate Professor in the Tokyo Medical and Dental University. He received a PhD from the University of Tokyo in physics in 1999. He studies molecular evolution and comparative genomics. His current area of interest is evolution of multigene families, especially olfactory receptor genes.

Prof. Neil Risch – University of California, San Francisco, USA

Neil Risch is the Lamond Family Foundation Distinguished Professor in Human Genetics, Professor and Co-Chair of the Department of Epidemiology and Biostatistics and the Director of the Institute for Human Genetics at the University of California, San Francisco. He received his undergraduate training in mathematics at the California Institute of Technology and his graduate degree in biomathematics from the University of California, Los Angeles. His research focuses on human genetics, genetic epidemiology, population genetics and statistical genetics methodology and application.

Dr. Noah Rosenberg – University of Michigan, Ann Arbor, USA

Noah Rosenberg is an Assistant Professor of Human Genetics at the University of Michigan. He received his BA in mathematics from Rice University and his MS in mathematics and PhD in biology from Stanford University. Prior to joining the University of Michigan in 2005, he was a postdoctoral fellow at the University of Southern California. Noah has a strong interest in genetic approaches to the study of human evolution.

Dr. Merritt Ruhlen – Stanford University, USA

Merritt Ruhlen received his undergraduate training at Rice University and his PhD in linguistics from Stanford University, after study at the University of Paris, the University of Illinois and the University of Bucharest. He has been a lecturer in the Department of Anthropological Sciences at Stanford University since 1994 and co-director of the Evolution of Human Languages program at the Santa Fe Institute since 2001. His main area of interest is the linguistic evidence for the origin and evolution of modern humans, especially the peopling of the Americas.

Dr. Theodore Schurr – University of Pennsylvania, USA

Theodore Schurr has been investigating the genetic prehistory of Asia and the Americas for nearly twenty years. Among his current projects are an analysis of human genetic diversity in the Altai-Sayan region, and a study of ancient DNA diversity in archeological populations from the Lake Baikal region. He is also the Director of the North American Regional Center of the Geographic Project, an international effort to characterize genetic variation in populations from across the world. In addition, he holds the position of Consulting Curator in the Physical Anthropology and American Sections of the University of Pennsylvania Museum of Archeology and Anthropology.

Dr. Marc St-Hilaire – Université Laval, Canada

Marc St-Hilaire teaches human and historical geography at Laval University (Quebec City) and is associated with the Interuniversity Center for Quebec Studies. His research domains encompass Quebec regional geography, landscape history, settlement patterns of the 19th and 20th Centuries, population geography, historical population databases and urbanization.

Prof. Antonio Torroni – University of Pavia, Italy

Antonio Torroni is Professor of Genetics and Director of the PhD program in Life Science at the University of Pavia, Italy. After his undergraduate (1984, Rome University "La Sapienza") and graduate (1988, Pavia University) studies, he was Assistant Professor at Emory University School of Medicine, Atlanta (1990-1994) and Rome University "La Sapienza" (1994-1998) and Associate Professor at the University of Urbino (1998-2000). The focus of his research activity is genetic variation (in particular mitochondrial DNA) in human populations and he is the author of over 120 publications on the topic.

Prof. Marc Tremblay – Université du Québec à Chicoutimi, Canada

Marc Tremblay is a Professor in the Department of Human Sciences at the Université du Québec à Chicoutimi. He holds a PhD in demography from the Université de Montréal. Over the past years, Marc has been conducting research focusing on the genetic structure of Quebec regional populations and on the demographic mechanisms underlying this structure.

Prof. Peter Underhill – Stanford University School of Medicine, USA

Peter Underhill is a Senior Research Scientist in the Department of Genetics at Stanford University School of Medicine where he has worked since 1990. His research involves the molecular analysis of human DNA sequence variation in human populations. He has been doing leading research on human Y chromosome diversification since 1992. In 1995 he co-invented DHPLC technology with Peter J. Oefner, which greatly accelerated the discovery of genetic markers on the human Y chromosome.

Prof. Hélène Vézina – Université du Québec à Chicoutimi, Canada

Hélène Vézina is a Professor in the Department of Human Sciences at the Université du Québec à Chicoutimi. She holds a PhD in demography from the Université de Montréal and received her undergraduate training in anthropology at the University of British Columbia. Over the past years, Hélène has been conducting research focusing on the genetic structure of Quebec regional populations and on the demographic mechanisms underlying this structure.

Dr. James Weber – PreventionGenetics, USA

James Weber is founder and president of PreventionGenetics, a DNA testing and DNA banking company. From 1986-2005, Dr. Weber was a Senior Research Scientist at the Marshfield Clinic Research Foundation. Dr. Weber discovered microsatellite DNA polymorphisms and he is the author or coauthor of over 200 peer-reviewed publications, nearly all in the field of human molecular genetics. Dr. Weber is an ISI Highly Cited Researcher and coauthor of the 2002 Lancet Paper of the Year.

Prof. Kenneth Weiss – The Pennsylvania State University, USA

Kenneth Weiss is Evan Pugh Professor of Anthropology and Genetics, with interests in the nature of the evolutionary processes, their impact on the amount of genetic variation and how that variation is distributed over space and time. His interests and research also include finding and applying the principles that characterize the way genomes are used in development, with particular attention to skeletal and dental mineralization in vertebrate evolution.

Dr. Piri Welsh – University of Washington, USA

Piri Welsh is an Assistant Research Professor in the Department of Medicine, Division of Medical Genetics at the University of Washington. She received her undergraduate training at Marquette University and earned her PhD in molecular biology at The Ohio State University. As a postdoctoral fellow at the University of Texas Southwestern Medical Center in Dallas, she collaborated with Dr. Mary-Claire King on the cloning of BRCA1. She joined Dr. King's lab at the University of Washington in 1996 where she performed studies designed to determine the cellular function of the BRCA1 protein. She continues to collaborate with Dr. King on identifying additional breast cancer predisposing genes. The focus of her independent research is to determine how alterations in the epigenome contribute to breast and ovarian cancer development.

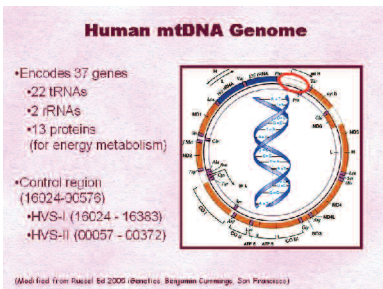
27 seminar style presentations by leading world experts



Henry Stewart Talks in association with Professor Luigi Luca Cavalli-Sforza and Professor Marcus Feldman from Stanford University, USA, has developed a series of 27 seminar style presentations which comprehensively cover the fundamentals and latest developments in the field of human population genetics. This series, presented by leading authorities, will enable everyone accessing the talks to keep up to date with new developments while educating those who are new to the field.

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- Cultural evolution
- Linguistic evolution
- The human genome
- The Human Genome Project
- Ethical issues
- Important phenotypic phenomena: diabetes, aging, cancer
- Population genetics
- Global genetic variation



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