



—THE— GENOGRAPHIC PROJECT —

WWW.NATIONALGEOGRAPHIC.COM/GENOGRAPHIC

Lucie McNeil
National Geographic/Genographic Project
(202) 857-5841
lmcneil@ngs.org

Michael Loughran
IBM/Genographic Project
(914) 499-6446
mloughra@us.ibm.com

The Genographic Project: Principal Scientific Investigators

EMBARGOED: For release 12:01 a.m. (ET, U.S.) Wednesday, April 13, 2005

The international team of principal scientists and researchers assembled to oversee and conduct field study for the Genographic Project is a distinguished panel of many of the world's leaders in their respective disciplines. Each principal investigator has broad knowledge of genetic research and related fields. The research centers are located in key regions of the world that are well-situated for collaborating with indigenous populations and their representatives.

The Genographic Project is a landmark, five-year research partnership of National Geographic and IBM, which is providing sophisticated laboratory and computer analysis of DNA contributed by hundreds of thousands of indigenous and traditional peoples as well as the general public. The field research, at the core of the Genographic Project, is funded by the Waitt Family Foundation.

Australia/Pacific

Principal Investigator: Robert John Mitchell, Ph.D.
Institution: Department of Genetics
LaTrobe University
Melbourne, Australia

Robert (John) Mitchell is a reader and associate professor in the Department of Genetics at LaTrobe University in Melbourne, Australia. He has conducted research on many aspects of human genetic variation for more than 30 years. His initial training was in biological anthropology and, coupled with an intense interest in how humans have traveled and inhabited the planet, led to his research career in human genetic variation.

Dr. Mitchell's region for the Genographic Project will cover the areas of Oceania and the Pacific, which, outside of Africa, contain some of the oldest populations in the world — those of Papua New Guinea and Australia — as well as some of the youngest, such as the Maori of New Zealand, who colonized there approximately 1,200 years ago. Such wide-ranging time-depths for various populations in the region pose a great number of questions that scientists hope will be answered by the Genographic study.

Dr. Mitchell states, "Conducting such DNA research gives us the power to delve into our history — at a local population level, and even at the whole species level. Before the detection of variability at the DNA level, such investigations were impossible." Dr. Mitchell will be sampling and studying primarily aboriginal peoples in Australia. This work will require travel to remote areas and addressing issues particular to the region.

(OVER)



Global field science supported by the Waitt Family Foundation



A research partnership of National Geographic and IBM

PRINCIPAL INVESTIGATORS (PAGE 2)

East/Southeast Asia

Principal Investigator: Li Jin, Ph.D.
Institution: Center for Anthropological Studies
School of Life Sciences
Fudan University
Shanghai, China

Dr. Li Jin is the Cheung Kong Lecture Professor at Fudan University and a professor and director of Genomics Laboratories of the Center for Genome Information at the University of Cincinnati (Ohio, USA). He received his bachelor's and master's degrees in genetics from Fudan University's Institute of Genetics and his Ph.D. in genetics and biomedical sciences from the Graduate School of Biomedical Sciences at the University of Texas — Health Science Center. Dr. Jin received post-doctoral training in population genetics at Stanford University, in California, USA, under the tutelage of world-renowned geneticist Dr. Luca Cavalli-Sforza, where he first became interested in the origins and migration of human populations. Since that time, Dr. Jin has founded a research group at Fudan University to study the origin and migrations of East Asian populations, and expanded it to become the Center for Anthropological Studies, which has played a central role in revealing the migrations of human populations in East Asia.

A computational and experimental population geneticist by training, Dr. Jin's research includes the genetic etiology of complex diseases and complex traits, genetic variations in human populations, and molecular evolution. He has received numerous awards and recognitions for his research achievements and promotion of international academic exchanges and has authored one book and more than 160 peer-reviewed articles and papers in a wide range of publications. He is currently managing editor of *Human Genomics* and is president-elect of the Association of Chinese Geneticists in America.

For the Genographic Project, Dr. Jin's team will be responsible for collecting DNA samples from and studying the populations of East and Southeast Asia. Specifically, the team will investigate the major migrations that led to the initial settlement of East and Southeast Asia and to the differentiation of major ethnic and linguistic groups and gene flow among human populations in these regions.

(MORE)



—THE— GENOGRAPHIC PROJECT—

WWW.NATIONALGEOGRAPHIC.COM/GENOGRAPHIC

PRINCIPAL INVESTIGATORS (PAGE 3)

North Eurasia

Principal Investigator: Elena Balanovska, Ph.D.
Institution: Laboratory of Human Population Genetics
Research Centre for Medical Genetics
Moscow, Russia

One of the most recognized human population geneticists in Russia, Elena Balanovska also brings computer-aided DNA mapping expertise to this project, having already analyzed and mapped a database of 40,000 individuals studied by mitochondrial DNA polymorphisms (mtDNA). This database, and its special cartographic gene pool-mapping programs, will contribute to the Genographic database. Dr. Balanovska, who worked at Moscow State University's Department of Anthropology, began her career in population genetics — the study of diversity of “classical genetic markers.” Her first Ph.D. thesis was dedicated to the analysis of the gene pools of indigenous populations in America, Siberia, Western Europe and the correlations between patterns of linguistic, cultural and biological diversity. Her second thesis included the genetic analysis and effects of selection on the gene pool of indigenous populations of all regions of the world except the Mediterranean. Now she heads the Laboratory of Human Population Genetics and is carrying out investigations of mtDNA and Y-chromosome diversity in collaboration with the Estonian Biocenter and its director Richard Villems. Her laboratory also studies variation of different genes, as well as the geography of Russian surnames based on a database with millions of records.

Dr. Balanovska has extensive field study experience, having participated in numerous genetic expeditions to all parts of North Eurasia: Russian Far East, Middle Siberia, Kazakhstan, the Caucasus, and Eastern Europe. She has also conducted investigative field studies of Paleolithic sites/caves in Siberia, Ural and Transcaucasia, working with archeologists and speleologists.

North Eurasia — a region Spencer Wells calls “crucial” to the Genographic Project — will encompass the territory where Dr. Balanovska and her team will conduct their field studies. She will be accompanied by her son, Oleg Balanovsky, himself a Ph.D. in molecular genetics. This area is homeland to many indigenous peoples of Eastern Europe, Caucasus, Central Asia and Siberia — as well as aboriginal Americans. The research, among other things, will hope to identify the genetic history of Siberians and Americans that link these two populations.

Dr. Balanovska says, “Through this study, restoring a genetic chronicle during the last 30,000 years will permit us to understand the common genetic processes in the populations. It helps us see the distant past — not to find a single thread connecting it with the present as much as to see the design of the overall gene pool.”

(OVER)



Global field science supported by the Waitt Family Foundation



A research partnership of National Geographic and IBM

PRINCIPAL INVESTIGATORS (PAGE 4)

India

Principal Investigator: Ramasamy Pitchappan, PhD
Institution: Center for Excellence in Genomic Sciences
Madurai Kamaraj University
Tamil Nadu, India

Ramasamy Pitchappan, a biologist, studied zoology at the undergraduate and graduate levels at Madurai Kamaraj University in India. Following his master's degree, he began research on immunology at the University's School of Biological Sciences and completed his Ph.D. there. Dr. Pitchappan then became a lecturer, reader, professor and the Head of Immunology at his alma mater. He has also served as director of the Science Education Centre and the Education Media Research Centre at Madurai Kamaraj University.

Dr. Pitchappan turned his attention to human immunogenetics in 1981, and shortly thereafter developed a computer software program and database for human immunogenetics. He then established an immunogenetics laboratory in southern India and has, among other achievements, identified many new alleles (mutational signatures) unique to southern India and helped develop India's first HLA tissue-matching service from a university set up for organ transplantation. He is also credited with creating a pioneering, low-cost method of preparing laboratory smears. In 2001, Dr. Pitchappan collaborated with Spencer Wells to complete the study of Indian DNA samples for National Geographic's "The Journey of Man." This work provided the crucial evidence needed to substantiate the theory that modern humans migrated from Africa to Australia 50,000 years ago via the coastline of India.

As principal investigator for the India region of the Genographic Project, Dr. Pitchappan and his team hope to identify the genomic diversity of various castes throughout the continent, specifically, their origin, migration pattern, selection, cultural and linguistic diversity.

Of India's remarkable, multi-faceted diversity, Dr. Pitchappan states, "India is a paradise for genetics studies. As famed geneticist and evolutionist Theodosius Dobzhansky observed in 1973, 'The caste system in India was the grandest genetic experimentation ever done on *Homo sapiens*.' We will have plenty to study...and learn."

(MORE)



Global field science supported by the Waitt Family Foundation



A research partnership of National Geographic and IBM

PRINCIPAL INVESTIGATORS (PAGE 5)

Middle East/North Africa

Principal Investigator: Pierre Zalloua, Ph.D.
Institution: Department of Internal Medicine & Ob/Gyn
American University of Beirut
Beirut, Lebanon

Accomplished geneticist, writer and lecturer Pierre Zalloua, an assistant professor at the American University of Beirut Medical Center, is a leading authority on genetic mutations and the genetic pathology of diseases found in and among Lebanese populations. Much of his recent investigative studies have addressed molecular anomalies observed in people with Type-1 diabetes and prenatal conditions. Dr. Zalloua has also conducted extensive research on the genetic links between various Middle Eastern and Mediterranean populations.

After receiving his bachelor's and master's degrees in biological sciences, the first from the University of Beirut in Lebanon and the latter from San Jose State University, in California, USA, Dr. Zalloua obtained his doctoral degree in genetics from the University of California at Davis. After conducting post-doctoral research in the Biotechnology Program at University of California, Davis and Berkeley, he became a research associate and visiting scholar at the Harvard School of Public Health, in Boston, Mass., USA. He is currently an assistant professor in the departments of Internal Medicine, Obstetrics & Gynecology and Pediatrics at the American University of Beirut and is a visiting scientist at the Harvard School of Public Health.

Dr. Zalloua first began collaborating with Spencer Wells in 2000 when both were at Harvard. A study they began in 2003 with Y-chromosome sampling has revealed significant genetic links among populations in the Mediterranean and, of particular importance to Dr. Zalloua, a shared genetic lineage between modern-day Lebanese and the ancient Phoenicians, substantiating his theory that warring Christian and Muslim Lebanese factions have, in fact, descended from a common ancestor.

For the Genographic Project, Dr. Zalloua will lead an investigative team that will obtain DNA samples from indigenous populations in the Middle East and North Africa.

(OVER)



Global field science supported by the Waitt Family Foundation



A research partnership of National Geographic and IBM

PRINCIPAL INVESTIGATORS (PAGE 6)

North America

Principal Investigator: Theodore Schurr, Ph.D.
Institution: Laboratory of Molecular Anthropology
University of Pennsylvania
Philadelphia, Pennsylvania, USA

An authority on genetic variation in Native American and Siberian populations, Dr. Theodore (Tad) Schurr is an assistant professor in the Anthropology Department at the University of Pennsylvania and a consulting curator in the American Section of the University of Pennsylvania Museum of Archeology and Anthropology. Dr. Schurr studied zoology and molecular genetics, first in plants and then in humans, as an undergraduate at the University of Georgia, and continued his studies in the Department of Biochemistry at Emory University under Doug Wallace (a protégé of Dr. Cavalli-Sforza's at Stanford). It focused on mitochondrial DNA (mtDNA) variations in human populations along with biomedical studies of mtDNA disease and bioenergetics.

Over the past 16 years, Dr. Schurr has investigated the prehistory of Asia and the Americas through laboratory studies of mtDNA and Y-chromosome variation in Asian Siberian and Native American populations. His work has helped to define the nature and extent of mtDNA and Y-chromosome variation in indigenous Siberians and Native Americans. He has also conducted studies of genetic diversity in various other world populations, including those that reflect the ancient migrations into the Himalayan region, East and Southeast Asia, Melanesia, and Australia, as well as those focusing on the population histories of South Africa and Pakistan. Investigative fieldwork has also included indigenous populations from different regions of Siberia.

Due to his extensive knowledge of genetic markers found in indigenous North American populations, Dr. Schurr will head up the Genographic team conducting field study in North America including Canada and Central America. Specific issues that will be addressed include: the timing of the initial colonization and migratory patterns throughout the Americas; regional diversity of Native American populations; effects of selection on mtDNA and Y-chromosome diversity in indigenous New World populations; genetic continuity/discontinuity between ancient and modern Native American populations; and the correlations between patterns of linguistic, cultural and biological diversity in Native American tribes.

Dr. Schurr said, "By relating genetic information to other anthropological evidence, we can better understand aspects of human evolution, migration patterns, behavior, functional morphology and more. While all aspects of human nature cannot be elucidated through genetic studies, a great many of them can be addressed with this approach, which often yields exciting and sometimes surprising insights about our species."

(MORE)



Global field science supported by the Waitt Family Foundation



A research partnership of National Geographic and IBM

PRINCIPAL INVESTIGATORS (PAGE 7)

South America

Principal Investigator: Fabricio R. Santos, Ph.D.
Institution: Institute of Biological Sciences
Universidade Federal de Minas Gerais
Minas Gerais, Brazil

Fabricio Santos, an associate professor of genetics and evolution at the Universidade de Minas Gerais in Brazil, has been conducting pioneering research on the human Y chromosome since 1992. His interest in genetics took hold as an undergraduate student in biology, and since then he has focused his studies on the diversity and evolution of life, especially the evolutionary genetics of human history. His Ph.D. thesis investigated human Y-chromosome polymorphisms and their applications in identity tests and human evolution, considered revolutionary work.

In 1995 Dr. Santos was part of a group that first suggested the presence of a critical genetic lineage among Native American populations, and he was able to substantiate the postulate that indigenous populations in Siberia share a recent common ancestry with most Native American populations and that a likely migration from Central Eurasia could be traced to the Americas. He also performed post-doctoral work with another Genographic principal investigator, Chris Tyler-Smith, during which the team conducted research on Y-chromosome variation and analysis and developed new genetic markers. Dr. Santos has had his own laboratory since 1997, actively participates in field research and has authored numerous articles concerning the human Y chromosome and its importance as an evolutionary marker.

For the Genographic Project, Dr. Santos will serve as the principal investigator for South America. His team's field study will attempt to address questions concerning the pre-Columbian peopling of the Americas — the migratory patterns and their timing, and their ties to Siberian ancestors; the internal migrations leading present-day locations of indigenous tribes; the correlation with languages, culture and trade that can be detected in the Americas, especially in South and Central America; and the presence of Native American lineages in urban Brazilian and other South American populations.

(OVER)



Global field science supported by the Waitt Family Foundation



A research partnership of National Geographic and IBM

PRINCIPAL INVESTIGATORS (PAGE 8)

Sub-Saharan Africa

Principal Investigator: Himla Soodyall, Ph.D.
Institution: Human Genomic Diversity/Disease Research Unit
National Health Laboratory Service
University of the Witwatersrand
Johannesburg, South Africa

Himla Soodyall, director of the Human Genomic Diversity and Disease Research Unit at the University of Witwatersrand, has been conducting research in the field of human genomic diversity since 1987. After receiving her master's degree in biotechnology from the University of Witwatersrand, Dr. Soodyall obtained her Ph.D. and worked as a medical scientist at the South African Institute for Medical Research (SAIMR), now the National Health Laboratory Service. She then spent three years working at Pennsylvania State University, USA, in post-doctoral research with Mark Stoneking, one of the first researchers to advance the "Out of Africa" theory of human evolution.

Since then, Dr. Soodyall has led groundbreaking research into accurately placing the geographic origins of humans' mtDNA ancestor. The recipient of numerous industry and national recognitions, her work currently focuses on attempting to reconstruct, through genetic analysis and mapping, the pre-history of the Sub-Saharan African and Malagasy populations as well as using population genetic variation to study population susceptibility to disease.

Dr. Soodyall will serve as the principal investigator of the Genographic Project for the Sub-Saharan Africa region. Through field study and analysis, her research group will illuminate the demographic and evolutionary processes that have produced the complex patterns of genetic variation in the sub-Saharan African and Malagasy populations.

Drawing on the collaborative expertise of the team of geneticists, archaeologists, anthropologists and paleo-anthropologists assembled for the Genographic Project, Dr. Soodyall says, "The fossil record, from which we unravel the most direct account from our past, is fragmentary and many critical gaps remain. The genetic variation found among living peoples offers a fascinating and illuminating way of studying human evolution."

(MORE)



Global field science supported by the Waitt Family Foundation



A research partnership of National Geographic and IBM



PRINCIPAL INVESTIGATORS (PAGE 9)

Western/Central Europe (1)

Principal Investigator, Y Chromosome: Jaume Bertranpetit, Ph.D.

Institution: Pompeu Fabra University
Barcelona, Spain

Jaume Bertranpetit is a Professor of Biology at Pompeu Fabra University and Group leader of the Evolutionary Biology Unit; he has also held the posts of Dean and Vice-Chancellor for Research at the University. His research focuses on the study of human genetic diversity: population genetics, molecular evolution, comparative genomics and the interaction between human evolutionary biology and other fields, including the genetics of complex diseases, statistical genetics and anthropology. Recent publications have focused on linkage disequilibrium and natural selection in the human genome. Dr. Bertranpetit is Director of the Spanish National Genotyping Center (CeGen) funded by Genome Spain. He is a Member of Institut d'Estudis Catalans and a number of international organizations.

Principal Investigator, Y Chromosome: David Comas, Ph.D.
Institution: Pompeu Fabra University
Barcelona, Spain

Dr. Comas is a Research Investigator at Pompeu Fabra University and Laboratory Head of the Evolutionary Biology Unit. He completed his undergraduate studies and Ph.D. in biology at the University of Barcelona, and has conducted research at the Royal Free Hospital in London, the Ludwig-Maximilians Universität in Munich and the University of Helsinki. His research has focused on the analysis of human genome diversity in order to address issues in population genetics, molecular anthropology, genome dynamics and their implications for disease. Dr. Comas' recent publications include genetic studies of population history in Europe, Africa and Asia. He has also developed new technologies for the analysis of mitochondrial DNA and Y chromosome diversity.

Drs. Bertranpetit and Comas will work together on sampling and genotyping the Y-chromosome in Western and Central European populations. Although genome variation in Europe has been relatively well-studied, focused sampling of key populations will allow us to disentangle European microgeographic genetic structure and its historical sources.

(MORE)





—THE— GENOGRAPHIC PROJECT—

WWW.NATIONALGEOGRAPHIC.COM/GENOGRAPHIC

PRINCIPAL INVESTIGATORS (PAGE 10)

Research Associate, Y Chromosome: Chris Tyler-Smith, Ph.D.
Institution: The Wellcome Trust Sanger Institute
Cambridge, England

Chris Tyler-Smith is one of the world's leading authorities on human evolutionary genetics, having helped pioneer the study of DNA variation on the male Y chromosome and its effects on human history. He has developed some of the key genetic markers now widely used in global DNA study as well as pioneered new ways to analyze DNA research results. Currently working under the auspices of The Wellcome Trust Sanger Institute, Cambridge, England, Dr. Tyler-Smith co-authored the first and, to date, only textbook written in the field, *Human Evolutionary Genetics*, which was published in late 2003.

Dr. Tyler-Smith was leader of the team, including Spencer Wells, that in 2003 published the results of a noteworthy study revealing that a staggering 8 percent of modern-day Asian males—representing 16 million men, or one in every 200 males alive today — carry distinct genetic markers in their Y chromosomes that identify them as related to the notorious, and notoriously prolific, 13th-century Mongolian warlord Genghis Khan.

For the Genographic Project, Dr. Tyler-Smith will conduct testing of Y-chromosome variation among modern-day European populations. One issue to be addressed in his field study will be the search for ancient Neanderthal Y chromosomes, which along with Neanderthal mtDNA have never been found in modern populations, even though Neanderthals occupied Europe well before modern humans and were there far longer than modern-day Europeans have been. The Western/Central Europe(1) research team will also attempt to discover the extent to which modern Europeans are the direct descendants of the Paleolithic people who entered Europe some 45,000 years ago, and how much replacement there has been by Neolithic people who entered less than 10,000 years ago — a highly controversial topic among scientists. Finally, how much subsequent change has there been? Have the events in history books also left detectable marks in the genetic patterns?

(MORE)



Global field science supported by the Waitt Family Foundation



A research partnership of National Geographic and IBM



PRINCIPAL INVESTIGATORS (PAGE 11)

Western/Central Europe (2)

Principal Investigator, mtDNA: Lluís Quintana-Murci, Ph. D.
Unit of Molecular Prevention/Therapy of Human Diseases
Institut Pasteur
Paris, France

Lluís Quintana-Murci is a human geneticist, currently based at the Institut Pasteur in Paris, who views genetics research as an invaluable and interesting tool to better understand the broader cultural and social issues of human history and its origins and adaptations. Dr. Quintana-Murci completed his undergraduate studies in biology at the University of Barcelona, Spain. He continued his academic career at the University of Balearic

Islands, in Spain, where he was introduced to the field of human population genetics while conducting research on mtDNA variation in Jewish populations from the Balearic Islands. He carried out his Ph.D. work at the world-renowned Department of Genetics at the University of Pavia, in Italy, under the supervision of Santachiara-Benerecetti, a distinguished geneticist who was among the first scientists to propose a second route of exit from Africa, from Eastern Africa along the coast to South Asia, in man's early migratory history. Dr. Quintana-Murci's doctoral research explored the use of the Y chromosome and mtDNA to retrace parental and maternal ancestries of human populations.

After completing his post-doctoral training at the Institut Pasteur in Paris, Dr. Quintana-Murci began his own independent research in human genetic diversity and evolution. He now heads a research group in human population genetics in the Unit of Molecular Prevention and Therapy of Human Diseases at Institut Pasteur. He has been actively involved in the study of populations located in, among other places, the area between the Middle East and India, and has explored how cultural forces (linguistics and social structure) may influence patterns of genetic variability. Dr. Quintana-Murci has recently concentrated his research on the cultural-biological evolution of traditional societies in central Asia to demonstrate the use of modern genetic markers in allowing scientists to make historical investigations and to practice "ethnogenetics," linking genetic structure and social organizations in societies.

For the Genographic Project, Dr. Quintana-Murci will lead the team that will study mtDNA diversity in European populations and says, "Our past history, in terms of origins, movements and cultural practices, is written in our DNA pool. DNA is an invaluable source to disentangle humankind's past, provided, of course, that its interpretation is accompanied by other disciplines — mainly archeology, paleo-anthropology, and history."

(MORE)



Global field science supported by the Waitt Family Foundation



A research partnership of National Geographic and IBM

PRINCIPAL INVESTIGATORS (PAGE 12)

Ancient DNA

Principal Investigator: Alan Cooper, Ph.D.
Institution (as of April 22): Division of Earth & Environmental Sciences
University of Adelaide
Adelaide, Australia

New Zealand native Alan Cooper brings considerable expertise in ancient DNA and its relation to evolutionary history. Currently an Australian Federation Fellow in the Division of Earth and Environmental Sciences at Australia's University of Adelaide, Dr. Cooper obtained his undergraduate and graduate degrees, all in biochemistry and genetics, from the University of Wellington, in New Zealand. He received post-doctoral training at the Smithsonian Institution's Molecular Genetics Laboratory, in Washington, D.C., and at the Institute of Molecular Medicine and in the Department of Biological Anthropology, both at the University of Oxford, in England.

Since 1999, Dr. Cooper has held several positions and research fellowships at the University of Oxford, most recently as director of the Henry Wellcome Ancient Biomolecules Centre, Professor of Ancient Biomolecules, and the Wellcome Trust University Award Fellow in the University's Department of Zoology. He has also been a research lecturer in the University's Departments of Zoology and Biological Anthropology. Dr. Cooper has received numerous honors and scholarships for his research in the areas of ancient DNA, paleoecology and mammalian/avian molecular evolution, among others, and has authored and co-authored many published works regarding the role of mitochondrial genomes in solving questions about the ancient evolutionary history of humans, mammals and birds.

Dr. Cooper will be extracting and analyzing DNA from ancient species from around the globe, as well as specimens that may be discovered during the course of the project.

###