

University of Rome "La Sapienza"
3-5 December 2009

In the past twenty years, molecular anthropology has played an increasingly important role in the wider context of physical anthropology, becoming one of its most promising and rapidly growing sectors. Several aspects of human evolution have, in fact, been elucidated thanks to a molecular approach, leading to substantial advances in different fields (such as primate phylogeny, population history, and adaptation). One of the key examples concerns the insights gained into the origin and diffusion of *Homo sapiens* through the study of mitochondrial DNA, which has given important support to the "Out of Africa" model since the late 80s, and has led to the spread of the popular concept of "mitochondrial Eve". Since then, much attention has been paid to the analysis of uniparental transmitted polymorphisms of mitochondrial DNA and Y-chromosome. Studies have covered different geographic scales, from regional to worldwide distributed populations, while focusing on global variation or specific lineages.

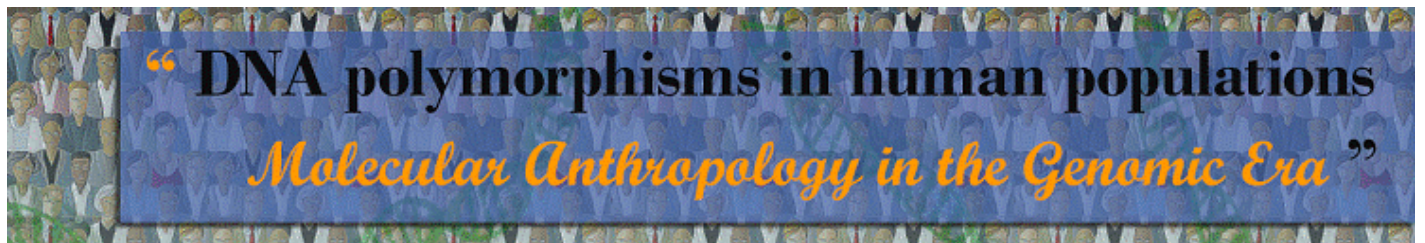
Molecular anthropology has also moved beyond its traditional disciplinary boundaries, such as the genetics of complex diseases. Fortunately, many researchers outside our discipline have understood the importance of studying the genetic structure and demographic history of populations, two aspects which are now routinely taken into account when choosing samples for association studies, or when identifying potential confounding factors.

At present, molecular anthropologists have two challenges. In fact, they need to develop strategies to optimize their interaction with researchers from different disciplines (not only genetic epidemiology, but also molecular archaeology and primatology). At the same time, the constantly increasing number of informative polymorphisms, discovered thanks to important projects on the human genome (such as the Human Genome Project, Human Genome Diversity Project and HapMap), requires constant methodological and theoretical updates.

"DNA Polymorphisms in Human Populations: **Molecular Anthropology in the Genomic Era**" is part of a biennial series of meetings organized by Franz Manni (Musée de l'Homme, Paris, France). Rome was chosen as the location to host the 2009 meeting to enhance the collaboration between the Musée de l'Homme and the Istituto Italiano di Antropologia, two institutions which share the same strong commitment towards an interdisciplinary perspective concerning human evolution.

The aim of this meeting is to present the state-of-the-art of human genetic history in continent-specific sessions, and to discuss how our discipline could better interact with other fields of research. Particular attention will be given to the impact of new analytical methods developed by the scientific community in the last few years. Topics to be discussed will include both theoretical aspects of these new developments, and new data, as well as an account of the evidence we are obtaining through the analysis of new and next-generation DNA sequencing methods and bioinformatic tools. The final session will be dedicated to the discussion of theoretical and practical aspects of interdisciplinary interactions in human evolutionary research, putting molecular anthropologists face-to-face with researchers from Paleoanthropology, Archeology, Linguistics and Medicine.

Visit http://www.mnhn.fr/mnhn/ecoanthropologie/Rome2009/Rome_index.html for further information.



December 3, 2009

15.00 - 18.30 Registration and poster posting (Anthropology Building, Aula 1)

Opening Session (Statistics Building, Aula Gini)

16.30 - 16.45 Giovanni DESTRO-BISOL (Italy); Franz MANNI (France)
Welcome message

Opening lecture

16.45 - 17.45 **Mark JOBLING (UK)**
Molecular anthropology in the genomic era

17.45 - 18.30 Cocktail (Anthropology Building, Aula 1)

December 4, 2009

8.00 - 10.00 Registration (Anthropology Building, Aula 1)

Session 1 – Africa (Statistics Building, Aula Gini)

Keynote lecture

9.00 - 9.45 **Jorge ROCHA (Portugal)**
The peopling of Africa

9.45 - 10.05 **Jeroen PIJPE (The Netherlands)**
Skewed male population substructure among an agriculturalist Ghanaian tribe

10.05- 10.25 **Sergio TOFANELLI (Italy)**
Malagasy admixture: the tale of a recent encounter between deep-rooted lineages and beyond

10.25 - 10.45 **Fulvio CRUCIANI (Italy)**
Human Y-chromosome haplogroup R1b1a (R-V88): A paternal genetic record of early-mid Holocene trans-Saharan connections

10.45 - 11.05 **A. RANCIARO (USA)**
The Genetic Basis of Lactase Persistence in Africa

11.05 - 11.20 Africa: **Poster presentations** (5 minutes each)

Sara PIACENTINI (Italy)
GSTM1 and GSTT1 gene polymorphisms in European and African populations

Sarah MARKS (UK)
Molecular characterization of low recombination genomic regions for bio-anthropological studies: The peopling of Southern Africa

Valeria MONTANO (Spain)
A genetic perspective on the spread of Bantu communities

11.20 - 11.50 Coffee Break

Session 2 – Europe (Statistics Building, Aula Gini)

Keynote lecture

11.50 - 12.35 **John NOVEMBRE (USA)**

The genetic variability of the European continent

12.35 - 13.35 Europe: **Poster presentations** (5 minutes each)

Alessio BOATTINI (Italy)

The Genographic Project in Italy: Y-chromosome preliminary results and perspectives

Carla CALO' (Italy)

Analysis of Y-chromosome polymorphisms in the linguistic isolate of Carloforte (Sardinia)

R. LELLI (Italy)

The peopling of Southern Italy: A maternal view

Valentina COIA (Italy)

Italian oriental Alps: mtDNA variation in geographically and linguistically isolated populations

Maria LOPEZ-VALENZUELA (Spain)

Analysis of Y-chromosome variation in Gypsies

Roberto RODRIGUEZ-DIAZ (Spain)

Distribution of Surnames and Genetic Flow in a Rural Spanish Region: Genetic Structure

Ashot HARUTYUNYAN

When genetics and history clash: The origins of Hamshen Armenians

Renato POLIMANTI (Italy)

GST polymorphism in the Italian population: Anthropogenetic marker or marker of susceptibility?

Andrea NOVELLETTO (Italy)

Diet-driven dynamics of NAT2 variants in dispersed human populations

Elena GIGLI (Italy)

An improved PCR method for endogenous DNA retrieval in contaminated Neanderthal samples based on the use of blocking primers

A. ZAULI (Italy)

HaPlone: A user-friendly web-based application for the management of molecular anthropology data

13.35 - 14.45 Free lunch offered to all registered participants (Anthropology Building, Aula 1)

14.45 - 15.05 **Avshalom ZOOSMANN-DISKIN (Israel)**

The origin of Eastern European Jews revealed by autosomal and sex chromosomal polymorphisms

15.05 - 15.25 **Luca PAGANI (UK)**

Characterization, through re-sequencing, of genetic variants associated with high altitude adaptation in North Caucasian ethnic groups

15.25 - 15.45 **Turi KING (UK)**

Genome-wide analysis of coancestry among men sharing British surnames

Session 3 – Beyond geography (Statistics Building, Aula Gini)

*The Falush Corner*15.45 - 16.15 **Daniel FALUSH (UK)***A new statistical method to infer population admixture events using genetic variation data*16.15 - 16.45 *Coffee Break*16.45 - 17.05 **Marco SAZZINI (Italy)***Is Molecular Anthropology ready for the Next-Generation Sequencing Technologies revolution? A whole transcriptome sequencing case study*17.05 - 17.25 **Roscoe STANYON (Italy)***Evolutionary Molecular Cytogenetics provides a Pictorial Legacy of Human Origins and an Explicative Foundation for Contemporary Genomics*17.25 - 17.45 **Vincenza COLONNA (Italy)***Detection of genetic structure in isolated populations: effects of consanguinity, divergence time and effective population size*17.45 - 18.05 **Francesc CALAFELL (Spain)***Recombination-based human population genomics*18.05 - 18.45 *Poster viewing (Anthropology Building, Aula 1)*21.00 - *Conference Dinner*

December 5, 2009**Session 4 - Asia and the Americas (Anthropology Building, Aula Sergi)***Keynote lecture*9.30 - 10.15 **Martin RICHARDS (UK)***Archaeogenetics and the peopling of Asia*10.15 - 10.35 **Laure SEGUREL (France)***Looking for genetic adaptations to diet from a comparative study of herders and agriculturalists in Central Asia*10.35 - 10.55 **Frederick DELFIN***Y-chromosome genetic diversity of Filipino Negrito and non-Negrito groups*10.55 - 11.15 **Ellen Droefn GUNNARSDOTTIR (Germany)***High-throughput sequencing of complete mtDNA genomes in three groups from the Philippines*11.15 - 11.45 *Coffee Break and poster viewing*11.45 - 12.05 **Irina PUGACH (Germany)***A genetic record of Australian aborigines based on large-scale genotyping data*12.05 - 12.25 **Mannis VAN OVEN (The Netherlands)***Unexpected island effects at an extreme: human genetic diversity in Nias**Keynote lecture*12.25 - 13.10 **Connie MULLIGAN (USA)***A genetic perspective on peopling of the Americas*13.10 - 14.30 *Free lunch offered to all registred participants (Anthropology Building, Aula 1)*14.30 - 14.50 **Rebecca JUST (USA)***Characterization of a Native American mtDNA haplogroup C lineare*

14.50 - 15.10 **Jodi IRWIN (USA)**

Geographic substructure in the mitochondrial DNA distribution of U.S. "Hispanic" populations

15.10 - 15.20 *Poster presentations (5 minutes each)*

Mark WHITTEN (Germany)

Investigating potential ascertainment bias in sample selection using complete mitochondrial DNA genome sequences of Siberian populations

L. ROEWER (Germany)

Local evolution in the Amazon basin: Studies of Y-chromosome markers

15.20 - 15.50 *Coffee Break and poster viewing*

Session 5 - Anthropology in the Genomic Era (Anthropology Building, Aula Sergi)

Invited lectures

15.50 - 16.15 **David COMAS (Spain)**

Overview of the Genographic project: preliminary results

16.15 - 16.40 **Guido BARBUJANI (Italy)**

Inference of demographic processes from comparisons of ancient and modern DNAs

16.40 - 17.05 **Claudio FRANCESCHI (Italy)**

Medical Anthropology

17.15 - 17.40 **Mark COLLARD (Canada)**

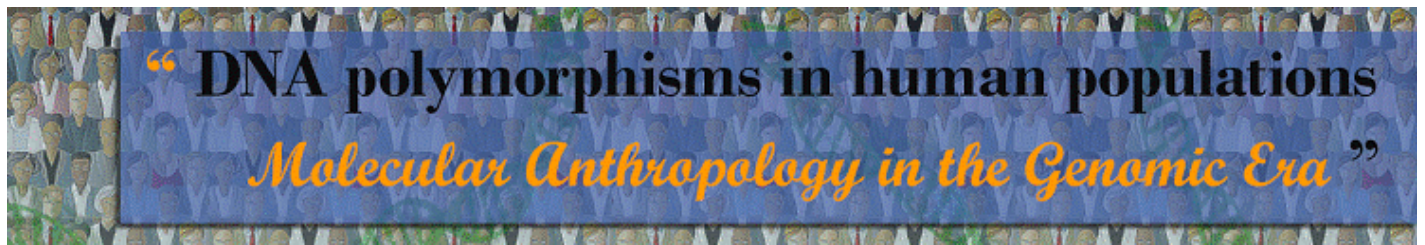
Anthropology and Archaeology

17.40 - 18.05 **Quentin ATKINSON (UK)**

The prospects for tracing deep language ancestry

18.05 - 18.30 **General discussion**

18.30 - 18.45 **Final remarks and poster Prize**



Leading organizers

Franz Manni, Musée de l'Homme, Paris

Giovanni Destro Bisol, Istituto Italiano di Antropologia and University of Rome "La Sapienza"

Invited speakers

Quentin Atkinson, University of Oxford, UK

Guido Barbujani, Università di Ferrara, Italy

David Comas, Barcelona, Universitat Pompeu Fabra, Spain

Claudio Franceschi, Università di Bologna, Italy

Mark Jobling, University of Leicester, UK

Connie Mulligan, University of Florida, USA

John Novembre, University of California, USA

Martin Richards, University of Leeds, UK

Jorge Rocha, Ipatimup, Porto, Portugal

Scientific committee

Chiara Batini, University of Rome "La Sapienza", Italy

Cristian Capelli, University of Oxford, UK

Oscar Lao Grueso, Erasmus University, Rotterdam, The Netherlands

Andres Moreno-Estrada, Cornell University, Ithaca, NY, US

Paul Verdu, University of Michigan, Ann Arbor Michigan, USA

Executive committee

Vera Damiani, University of Rome "La Sapienza", Italy

Veronica Marcari, University of Rome "La Sapienza", Italy

Francesco Montanaro, University of Rome "La Sapienza", Italy

“DNA polymorphisms in human populations *Molecular Anthropology in the Genomic Era*”

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The congress “DNA Polymorphisms in Human Populations: **Molecular Anthropology in the Genomic Era**”

has been jointly organized by



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