

COST ACTION BM083

“A European Network of the HLA Diversity for Histocompatibility, Clinical Transplantation, Epidemiology and Population Genetics (HLA-NET)”

Meeting title: Genetic Diversity and Origins of Europeans
Reference: ECOST-MEETING-BM0803-170113-020425
Meeting dates: from 15 to 16 January 2013
Organisation: Prof. Alicia Sanchez-Mazas
Location: University of Geneva, Switzerland

SCIENTIFIC REPORT

A scientific conference was organized in Geneva on 15-16 January 2013 by the Laboratory of anthropology, genetics and peopling history on the theme *Genetic diversity and origins of Europeans*. The main objective of this conference was to round up our knowledge on this subject by addressing several issues either not yet resolved or not formerly taken into account since the first demic diffusion model of Neolithic farmers proposed in the 1970's by Amermann and Cavalli-Sforza. Prominent population geneticists but also renowned researchers in archaeology and linguistics were thus invited to present a talk. A second aim of this meeting was to relate our comprehension on the genetic diversity of Europeans to critical problems in public health, and more specifically organ and haematopoietic stem cell transplantation.

The first session on Tuesday 15 morning was dedicated to make a state-of-the art of the non-genetic information related to the peopling history of Europe. The speakers presented their current views according to archaeology (Dr Ron Pinhasi, University College Dublin, Ireland), archaeozoology (Prof. Jean-Denis Vigne, National Museum of Natural History of Paris, France) and linguistics (Prof. Russell Gray, University of Auckland, New Zealand). The two following sessions were devoted to the genetic diversity of Europeans. On Tuesday 15 afternoon, the talks presented the point of view of ancient DNA (Dr Marie-France Deguilloux, CNRS, Bordeaux, France) and two

case studies on the European Romani (Prof. David Comas, Universitat Pompei Fabra, Barcelona), on one side, and the Icelanders (Prof. Agnar Helgason, DeCode Genetics, Reykjavik, Island), on the other side. In the session held on Wednesday 16 morning, current hypotheses on the peopling history of Europe were presented from the viewpoint of prehistoric demographic changes (Prof. Guido Barbujani, Università di Ferrara, Italy), of computer simulation results (Dr Mathias Currat, University of Geneva, Switzerland) and of HLA molecular variability (Prof. Alicia Sanchez-Mazas, University of Geneva, Switzerland). In the afternoon, the topics focused on the implications of HLA variation in Europe for both organ (Prof. Frans Claas, Leids Universitair Medisch Centrum, Leiden, Netherlands) and haematopoietic stem cell (Dr Jean-Marie Tiercy, Laboratory of Transplantation Immunology, University Hospital of Geneva, Switzerland) transplantation.

Apart from a robust model proposed for the differentiations of Indo-European languages from Anatolia about 10,500 years Before Present, the discussions showed that no simple scenario for the peopling history of Europe has yet emerged, as the present European genetic diversity may be explained by genetic contributions at different periods of time (Palaeolithic, Neolithic,..) and according to complex demographic models. However, the talks emphasized the close relationships between genetic and geographic variation for both HLA and other genetic markers and the usefulness to develop sophisticated computer tools to decipher intricate signatures of human peopling history. The presentations focusing on tissue transplantation showed how current European programs (like Eurotransplant) are progressing towards a better understanding of the factors involved in graft rejection and how the maintenance of local European donor centres (e.g. in Switzerland) are crucial to represent rare HLA types and hence to optimise compatible donor search.