

COST Action no. BM0803

A European network of the HLA diversity for histocompatibility, clinical transplantation, epidemiology and population genetics

HLA-NET

2009 | 2013

Objectives

- HLA-NET aims to offer an innovative framework by which scientists in bone marrow transplantation, epidemiology and population genetics share their expertise in laboratory work, clinical work, ethical issues, population genetics, biostatistics and/or computer science.
- Elaboration of consensual standards and definition of common procedures in immunogenetics to be used in daily practice and fundamental research. Sharing of high quality data and computer tools to analyze the HLA genetic diversity of human populations.

Main Achievements

- **Scientific outputs obtained due to networking:**
- Final HLA-NET population data questionnaire and recommendations for populations' characterization.
- HLA-NET Guidelines for characterizing various levels of HLA molecular typing resolution and for reporting typing ambiguities.
- New algorithms for data and population genetics analyses.
- Common schema for databases.
- Strategies to analyze Bone Marrow Donor (BMD) registries.
- Publication of HLA-NET mid-term report (Sanchez-Mazas et al. 2012, Int J Immunogenet, early view).
- 10 peer-reviewed articles (including HLA-NET mid-term report).
- **Capacity building due to networking:**
- New networks through the European Federation of Immunogenetics (EFI, pan-European) and the International Histocompatibility and Immunogenetics Workshops (IHIW, international).
- Participation of several HLA-NET laboratories in newly funded FP7 project – « EUROSTAM » lead by HLA-NET MC member Prof. Frans Claas (NL)

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Biomedicine and Molecular Biosciences (BMBS)

Participating countries

AL, AT, BE, BG, CH, CY, DE, DK, EE, EL, FI, FR, HR, HU, IT, LV, NL, NO, PL, PT, SI, UK

Contact details

Chair of the Action

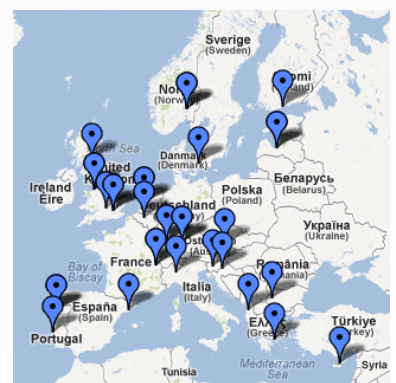
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Map of HLA-NET participating laboratories and universities.



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Working Group activities

Working Group 1

- Works on population definitions and sampling strategies for population genetics analyses.
- Population questionnaire and standard population definitions published in HLA-NET mid-term report.
- Recommendations to be submitted to allelefrequencies.net database.
- Strategies to contact laboratories for providing data, strategies to analyze population and BMD registry data (with WG2).

Working Group 2

- Works on HLA typing standards and on guidelines for acceptable reporting of laboratories results.
- Guidelines published in HLA-NET mid-term report.
- About 200 rare HLA alleles submitted to allelefrequencies.net.
- Analysis of HLA polymorphisms outside the exons coding for the ARS in European populations (HLA-DRB1*14:01:01G, DQB1*03:01:01G and B*44:02:01G ambiguities). Poster with preliminary results to be presented at the 16th IHIW in Liverpool (June 2012).

Working Group 3

- Works on bioinformatic strategies for HLA population data storage and analysis. Manuscript on database schema under preparation.
- Preliminary recommendations for population analyses on complex HLA data published in HLA-NET mid-term report.
- Infrastructure of HLA-NET (website), implementation of other WG recommendations.

Working Group 4

- Works on essential ethical questions to address when carrying out research on population genetic data.
- Important ethical issues related to HLA population studies (e.g. study plan, samples already in collection or to be collected) published in HLA-NET mid-term report.
- Gathering and reviewing of information related to legal and ethical regulations in different countries to obtain a consensus on practice for European countries. Updating of a bibliography.

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European and international participation:

The EFI Society

Website : <http://www.efiweb.eu/>

The IHIW Society

Websites:

<http://www.16ihiw.org/>

<http://ihiwefibshi.org/>



The screenshot shows the Royal Society website with a red header. The main content area features a large article titled "Human evolution, migration and history revealed by genetics, immunity and infection". Below the title, it lists the date (9:30am on 08 June 2011) and the time (5:00pm on 07 June 2011). The location is "The Royal Society, London". The article is organized by Professor Diarmuid Adams, Dr Francisco Balboa and Dr Rosemary Boyton. A registration link is provided: "Registration for this meeting is now full - click here to register for the waiting list". A short description follows: "This meeting offers a journey from individuals to history, bringing together geneticists, immunologists, anthropologists and historians. Infection has been the most potent evolutionary force in human history, driving genes coding for our 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 20,000 years?". A list of speakers and chairs is included, such as Professor Mark Achtman, Professor Diarmuid Adams, Dr Kristian Andersen, Dr Francisco Balboa, Professor Luigi Cavalli-Sforza, Professor Marc Saperstein, Professor Massimo Fernandez-Vava, Dr Sebastian Ogden, Professor Adrian Hill, Professor Nina Jablonka, Professor Mark Jablun, Dr Maria Latorre, Professor John Novembre, Dr Stephen Oppenheimer, Professor Peter Parham, Dr Alisa Roberts, Professor Alicia Sanchez-Mazas, Professor Erik Thorsby, Professor Esteban Willerslev, Dr Sarah Wilton-Bargore.

Royal Society discussion meeting followed by publication: Sanchez-Mazas et al. 2012, Philos Trans Royal Soc B 367(1590):830-9

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Strategies to work with HLA data in human populations for histocompatibility, clinical transplantation, epidemiology and population genetics: HLA-NET methodological recommendations

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