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COST ACTION BM083

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

Meeting title:	Next Generation Sequencing course
Reference:	ECOST-MEETING-BM0803-131212-024929
Meeting dates:	13-14 December 2012
Organisation:	Professor Gottfried Fischer
Location:	Institute of Blood Group Serology and Transfusion Medicine, General Hospital, Vienna, Austria

SCIENTIFIC REPORT

A two-day course on *Next Generation Sequencing (NGS)* was organized in Vienna on 13-14 December 2012 with the aim to learn about and discuss on different NGS technologies and their possible application to HLA in routine practice. Indeed, while NGS is replacing classical molecular typing methodologies in most genetic and genomic studies, it is still not yet fully successful to type HLA genes due in great part to DNA sequence-length limitations to a few hundred base pairs, thus not covering all HLA exons relevant for transplantation, disease-association or population genetics studies. Another important issue is the bioinformatic processing of the generated data, as NGS techniques may still produce large amounts of ambiguous typings instead of unique genotypes despite the use of DNA cloning.

To understand better how each NGS technology works and which are the possible problems which may occur at the different steps of the DNA typing and sequence analysis, both private company representatives and HLA-typing experts were invited to present their NGS methods and share their practical experience in this domain. About 15 researchers interested by this topic were accepted to participate to this course.

The first day started, in the morning, with several presentations. Professor Gottfried Fischer, the organizer of this course, first made a review of the literature on the subject, and also explained his own attempts to get unambiguous HLA genotypes by NGS and the main problems that could arise in this specific case. Then Sabine Wenda from the Medical University of Vienna (MUW), Johannes Pröll from the Red Cross Upper Austria and Ingrid Faé

(MUW) presented the technologies to prepare the libraries which are the sequence templates for devices developed by either IonTorrent or Roche 454. The advantages and disadvantages of each technology were then discussed among all participants. In the afternoon, the attendees were invited to follow the main steps of the IonTorrent procedure at the bench thanks to thoroughly prepared demonstrations by Ingrid Faé and Sabine Wenda and to visit the Genomics Centre of the Medical University of Vienna, where the Illumina Devices were presented by Prof. Christoph Bock (MUW).

On the second day, bioinformatic softwares developed by different companies or open source to process NGS data were presented by several speakers after a general introduction by Christoph Bock: Stephane Elmer for Smartgene, Atilla Berces for Omixon, Wietse Mulder and Eric Rozemuller for Genome Diagnostics, and David Sayer for Conexio. Again the advantages and disadvantages of the different programs were discussed among all participants. This was followed by a more general debate on NGS, which addressed some crucial questions like “is there a need for NGS in HLA?”,”Is there a need for new Quality Criteria?”, as well as economical aspects, etc.

This course was extremely useful to the attending HLA researchers as they provided them with clearer ideas on how NGS typing works and which are the main critical steps to get reliable genotypes both during the laboratory work and the sequence data analysis. Also, it was fully appreciated by the invited representatives of the different private companies as they could better understand the needs of the researchers and the specific problems raised by HLA sequencing.