

“Genome Wide Association Studies: the last mile problem”

Room Linz
Hilton Vienna Danube
Vienna, Austria

23rd May 2009

7.30 – 8.30	Speakers arrive and hand in presentations (or have emailed them) Registration
8.30 – 8.35	President’s Welcome Graham R. Taylor
Session 1	Chair: Graham R. Taylor
8.35 – 9.05	INVITED SPEAKER Steven McCaroll CNVs, GWAS signals, and the "last mile" problem
9.05 – 9.25	A. Darvasi Using the Hebrew University Genetic Resource (HUGR) for genome wide association studies (GWAS) and replication studies
9.25 – 9.45	A. Zhernakova Identification of the shared genetics of immune-related diseases
9.45 – 10.15	COMPANY LECTURE Illumina Inc. Carsten Rosenow Microarrays and Next Generation Sequencing: Leading The Way For Genomic Research
10.15 – 10.45	<i>Coffee Break</i>
Session 2	Chair: Alastair F. Brown
10.45 – 11.05	F. Kronenberg A Genome-Wide Association Analysis of HDL-Cholesterol in the Population-Bases KORA Study Sheds New Light on Intergenic Regions

11.05 – 11.25	Jacques S. Beckmann Eight blood pressure loci identified by genome wide association study
11.25 – 11.45	Peter Antal Adaptive Sequential Partial Genome Screening Studies: a Case Study in Asthma
11.45 – 12.05	F. Rigo High-throughput analysis of <i>SCN1A</i> tagSNPs: development of a protocol on a microarray platform for a candidate-association study in Italian patients with migraine
12.05 – 12.25	S. Nejentsev High-throughput sequencing identifies multiple rare variants in the virus receptor gene IFIH1 that protect from type 1 diabetes
12.25 – 12.45	Anthony Brookes HGVbaseG2P: Visual Integration of Association Study Results
12.45 – 13.45	<i>Lunch</i>
Session 3	Chair: Jacques Beckmann
13.45 – 14.15	INVITED SPEAKER Ian Tomlinson Genome-wide association studies: (not) the final mile
14.15 – 14.35	Johan T. den Dunnen Collecting gene sequence variants and their phenotypic consequences in web-based LSDBs
14.35 – 14.55	Bruce Gottlieb How New “Over-Sequencing” Techniques Can Lead to Revealing Subtle Intercellular Differences Within An Individual’s Genome and Their Possible Affects on Genome Wide Association Studies
14.55 – 15.00	Concluding remarks <i>Meeting Ends so delegates may attend ESHG Plenary Session</i>

Poster Presentations

Johan T. den Dunnen

Describing complex sequence variants by extending HGVS sequence variation nomenclature

Mauno Vihinen

Variation Ontology – VariO