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JOURNÉES SCIENTIFIQUES DE L'UNIVERSITÉ DE NANTES

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COLLOQUE 4 GENETIC EPIDEMIOLOGY IN HOMOGENEOUS POPULATIONS SYMPOSIUM

AVEC LE SOUTIEN DE :



VACARME
Vaincre les maladies Cardiovasculaires,
Respiratoires et Métaboliques



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LA CITÉ, LE CENTRE DES CONGRÈS DE NANTES - 5 RUE DE VALMY, NANTES (FRANCE)
BUSWAY, LIGNE N°4, ARRÊT « CITÉ INTERNATIONALE DES CONGRÈS »

VENDREDI 12 JUIN 2015

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GENETIC EPIDEMIOLOGY IN HOMOGENEOUS POPULATIONS SYMPOSIUM

The genetic architecture of complex traits may involve low frequency variants with moderate to large effect size. Founder and isolated populations provide a unique and powerful resource for the identification of such causal variants. Recent studies highlight that open populations may also display genetic structure related to demographic history.

This Symposium will cover methodology and examples of complex trait locus identification in homogeneous populations.

This meeting is a great opportunity to bring together researchers involved in the area of demography and population genetics to identify the genetic architecture of human diseases. It is our ambition to initiate a network that would maintain synergy in genetic of homogeneous populations at the European level. This network would aim at promoting research in this field and raising national and European funding. It would increase significantly our ability to achieve our goals in medical and population genetics research.

09:00 | 09:15

Welcoming words

09:15 | 10:20

Methods Part 1

VaCaRMe project

Christian Dina et Richard Redon, l'institut du thorax, INSERM UMR1087 / CNRS UMR6291, Nantes, France

The French Exome Project and inbreeding in open population

Emmanuelle Génin, Genetics, Genomics and Biotechnologies, INSERM UMR1078, Brest, France

Cost effective designs with population specific imputation panels in isolates

Serena Sanna, The Institute of Genetic and Biomedical Research, CNR, Monserrato, Italy

10:20 | 11:05

Poster – Coffee break

11:05 | 12:00

Methods Part 2

Ashkenazi population and Identity By Descent inference

Itzik Pe'er, Department of Computer Science and Center for Computational Biology and Bioinformatics, Columbia University, New York, USA

Taking recent evolutionary and demographic history into account in gene mapping

Ida Moltke, The Bioinformatics Centre, Department of Biology, University of Copenhagen, Denmark

12:00 | 13:30

Lunch

13:30 | 14:45

Open and isolated populations Part 1

Next generation association studies in isolated populations

Eleftheria Zeggini, Department of Human Genetics, Wellcome Trust Sanger Institute, Hinxton, UK

Genetics of complex traits in Italian isolates: the Cilento study

Marina Ciullo, Institute of Genetics and Biophysics "A. Buzzati-Traverso", Naples, Italy

Sequencing Initiative Suomi in Finnish population

Aarno Palotie, Institute for Molecular Medicine Finland, University of Helsinki, Helsinki, Finland

Massachusetts General Hospital and Harvard Medical School, Boston, Massachusetts, USA

Broad Institute of Harvard and MIT, Cambridge, Massachusetts, USA

14:45 | 15:30

Poster – Coffee break

15:30 | 16:20

Open and isolated populations Part 2

Exploring de novo variation in human genomes - the GoNL project

Paul de Bakker, Department of Medical Genetics and Department of Epidemiology, Utrecht, The Netherlands

Whole Genome Sequencing in Icelandic population

Daniel Guðbjartsson, Population Genomics, deCODE Genetics, Reykjavik, Iceland.

16:20 | 17:00

Discussion – Networking

Scientific Committee

Christian Dina, GEHOPS Chairman, l'institut du thorax, INSERM UMR 1087 / CNRS 6291, Nantes, France

Richard Redon, l'institut du thorax, INSERM UMR 1087 / CNRS 6291, Nantes, France

Emmanuelle Genin, Genetics, Genomics and Biotechnologies, INSERM UMR 1078, Brest, France

Anne-Louise Leutenegger, Genetic variability and human diseases, INSERM UMR 946, Paris, France

Serena Sanna, The Institute of Genetic and Biomedical Research, CNR, Monserrato, Italy

Eleftheria Zeggini, Department of Human Genetics, Wellcome Trust Sanger Institute, Hinxton, UK

Local Organisation Committee

l'institut du thorax

Stéphanie Chatel, Ophélie Tindilière, Séverine Abramatic, Richard Redon, Christian Dina

