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GENETIC EPIDEMIOLOGY IN HOMOGENEOUS POPULATION **SYMPOSIUM**

2015



Nantes, France Friday June 12th, 2015







Registrations and abstract submissions are open!

www.gehops2015.univ-nantes.fr















Exploring the genetic architecture of complex traits requires identification of low frequency variants with large effect size.

Founder and isolated populations provide a unique and powerful resource for the identification of such causal genetic variants.

Recent studies highlight that open population may also display genetic structure related to demographical history (Western France, The Netherlands).

This Symposium will cover methodology and examples of gene identification in all homogeneous populations

SPEAKERS

Paul de Bakker - Marina Ciullo - Christian Dina - Emmanuelle Génin

Daníel Guðbjartsson - Ida Moltke - Aarno Palotie - Itsik Pe'er -

Richard Redon - Serena Sanna - Eleftheria Zeggini