

COROGENE Study

Information for researchers interested in using stored samples and data

1. Introduction

The Corogene study (Genetic Predisposition of Coronary Heart Disease in Patients Verified with Coronary Angiogram) was designed as a large cohort to study pathophysiology, genetics and epidemiology of coronary artery disease and its risk factors. Focus was to identify genetic loci or gene variations contributing to the development of coronary heart disease and other related heart diseases such as heart failure and aortic valve disease. Research is conducted by Helsinki University Hospital (HUS) in collaboration with University of Helsinki and National Institute for Health and Welfare (THL).

The research started in 2006. Patient information and blood samples were collected from patients assigned to coronary angiogram in the Division of Cardiology in Meilahti Hospital (Helsinki) between 2006 and 2008. Both male and female patients over 18 years-old were recruited and the average age of the study subjects were 65 (65.6 ±11.1) years at the time of the collection. Patients of non-Finnish origin, previous heart transplantation, low haemoglobin or previous blood transfusion during the same hospitalization were excluded from the study. Written informed consent was obtained from every patient who participated in the study. The matching healthy controls are defined for the Corogene participants from the population cohort FINRISK, also available from THL Biobank.

2. Ethical considerations

Corogene sample collection has been transferred to THL Biobank in October, 2018, following a public notification process allowed by the Finnish Biobank act. The transfer of the Corogene study to the biobank has been approved by the Coordinating Ethics Committee of Helsinki University Hospital on 12 December 2017 and public notification was approved by the Ministry of Social Affairs and Health on 21 May 2018.



3. Corogene study samples available for biobank research

DNA samples are available from nearly 5 300 sample donors. Approximately 2 500 of donors have been diagnosed with infarct.

4. Corogene study phenotype and omics data available for biobank research

The updated list of data variables can be uploaded from the **variable descriptions -file** found on the right panel of the <u>Corogene Research collection page</u>

For availability of genome-wide genotypes and sequencing data, see more information in the <u>'THL</u> Biobank Omics data availability table' at the THL Biobank sample collection page.

5. Registry data

Information from the Finnish national health registries, such as Care Register for Health Care (HILMO), Cancer Register, Cause-of-Death Register and Drug Imbursement Registers etc., can be linked to sample donors by the separate application process and project-specific data permit from <u>Findata</u>.

6. Research group

Principal Investigator:

Juha Sinisalo, University of Helsinki and Helsinki University Hospital

7. Key references

Laaksonen R, Ekroos K, Sysi-Aho M, Hilvo M, Vihervaara T, Kauhanen D, Suoniemi M, Hurme R, März W, Scharnagl H, Stojakovic T, Vlachopoulou E, Lokki ML, Nieminen MS, Klingenberg R, Matter CM, Hornemann T, Jüni P, Rodondi N, Räber L, Windecker S, Gencer B, Pedersen ER, Tell GS, Nygård O, Mach F, Sinisalo J, Lüscher TF. Plasma ceramides predict cardiovascular death in patients with stable coronary artery disease and acute coronary syndromes beyond LDLcholesterol. European Heart Journal. 2016;37(25):1967-1976.

Vaara S, Tikkanen E, Parkkonen O, Lokki ML, Ripatti S, Perola M, Nieminen MS, Sinisalo J. Genetic Risk Scores Predict Recurrence of Acute Coronary Syndrome. Circ Cardiovasc Genet. 2016 Apr;9(2):172-8.

Vaara S, Nieminen MS, Lokki ML, Perola M, Pussinen PJ, Allonen J, Parkkonen O, Sinisalo J. Cohort Profile: The Corogene study. Int J Epidemiol. 2012 Oct;41(5):1265-71.



Ripatti S, Tikkanen E, Orho-Melander M, Havulinna AS, Silander K, Sharma A, Guiducci C, Perola M, Jula A, Sinisalo J, Lokki ML, Nieminen MS, Melander O, Salomaa V, Peltonen L, Kathiresan S. A multilocus genetic risk score for coronary heart disease: case-control and prospective cohort analyses. Lancet. 2010;376(9750):1393-1400.

Soranzo N, Spector TD, Mangino M, Kühnel B, Rendon A, Teumer A, Willenborg C, Wright B, Chen L, Li M, Salo P, Voight BF, Burns P, Laskowski RA, Xue Y, Menzel S, Altshuler D, Bradley JR, Bumpstead S, Burnett MS, Devaney J, Döring A, Elosua R, Epstein SE, Erber W, Falchi M, Garner SF, Ghori MJ, Goodall AH, Gwilliam R, Hakonarson HH, Hall AS, Hammond N, Hengstenberg C, Illig T, König IR, Knouff CW, McPherson R, Melander O, Mooser V, Nauck M, Nieminen MS, O'Donnell CJ, Peltonen L, Potter SC, Prokisch H, Rader DJ, Rice CM, Roberts R, Salomaa V, Sambrook J, Schreiber S, Schunkert H, Schwartz SM, Serbanovic-Canic J, Sinisalo J, Siscovick DS, Stark K, Surakka I, Stephens J, Thompson JR, Völker U, Völzke H, Watkins NA, Wells GA, Wichmann HE, Van Heel DA, Tyler-Smith C, Thein SL, Kathiresan S, Perola M, Reilly MP, Stewart AF, Erdmann J, Samani NJ, Meisinger C, Greinacher A, Deloukas P, Ouwehand WH, Gieger C. A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. Nat Genet. 2009 Nov;41(11):1182-90.