Abstract/Session Information for Program Number 1783

Session Information

Session Title: Cardiovascular Genetics **Session Type:** Poster

Session Location: Exhibit Hall E **Session Time:** Wed 4:30PM-6:30PM, Thu 4:30PM-6:30PM, Fri 10:30AM-12:30PM

Abstract Information

Poster Board Number: 1783/T **Presentation Time:** Thu, Oct 25, 2007, 4:30PM-6:30PM

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Abstract Content

Genome-wide association scan for HDL cholesterol, LDL cholesterol and triglyceride levels in 9,000 individuals. *C.J. Willer[1], A. Scuteri[2,3], L.L. Bonnycastle[4], S. Sanna[5], A.U. Jackson[1], A. Maschio[5], W.L. Duren[1], F. Busonero[5], R. Pruim[6], Diabetes Genetics Initiative[7], R.M. Watanabe[8], S.S. Najjar[2], L.J. Scott[1], M. Uda[2], J. Tuomilehto[9], G.R. Abecasis[1], F.S. Collins[4], D. Schlessinger[2], K.L. Mohlke[10], E.G. Lakatta[2]* 1) Dept Biostatistics, Univ Michigan; 2) Gerontology Research Center, National Institute on Aging; 3) Unita Operative Geriatrica INRCA, Rome Italy; 4) Genome Technology Branch, National Human Genome Research Institute; 5) Istituto di Neurogenetica e Neurofarmacologia, CNR, Cagliari, Italy; 6) Dept Mathematics & Statistics, Calvin College; 7) Broad Institute of Harvard & MIT, Lund Univ, & Novartis Institutes of BioMedical Research; 8) Dept of Physiology and Biophysics, Keck School of Medicine, Univ Southern California; 9) Dept Epidemiology & Health Promotion, Dept Biochemistry, National Public Health Institute, Helsinki, Finland; 10) Dept Genetics, Univ North Carolina.

Cardiovascular diseases (CVD) are the leading cause of death in industrialized countries. Low density lipoprotein cholesterol (LDL) is a major risk factor for CVD whereas high density lipoprotein cholesterol (HDL) protects against CVD. Triglyceride levels (TG) may also be associated with risk of coronary artery disease. Heritability of these traits is between 30 and 60%. We have combined genome-wide association data from the ProgeNIA study of 4,301 Sardinian individuals from 450 families, the FUSION study of 2,337 Finnish individuals and 2,659 Caucasian individuals from the Diabetes Genetics Initiative (DGI). To allow for meta-analysis with genotyped SNPs from two platforms (Affymetrix 500k and Illumina 300k), we imputed genotypes for untyped SNPs in the FUSION individuals. Meta-analysis provided clear association with several previously reported loci, including *APOC1* (LDL, $p = 1 \times 10^{-18}$), *GCKR* (TG, $p = 3 \times 10^{-16}$), *CETP* (HDL, 6×10^{-16}), *LPL* (TG, $p = 7 \times 10^{-15}$), *APOB* (TG, 9×10^{-10}), and *LIPC* (HDL, 2×10^{-8}). We detected second independent association signals in 5 of these genes ($p < 5 \times 10^{-6}$). We observed 15 new loci with $p < 5 \times 10^{-6}$ that we are in the process of genotyping in 7,300 individuals. The new loci appear to be involved in pathways such as cell adhesion and lipid metabolism.