

## Abstract/Session Information for Program Number 259

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### Session Information

**Session Title:** Diabetes and Growth **Session Type:** Platform

**Session Location:** Room 28 **Session Time:** Sat Oct 27, 2007 08:00AM-10:30AM

### Abstract Information

**Program Number:** 259 **Presentation Time:** 08:30AM-08:45AM

**Keywords:** Mapping, Linkage and Linkage Disequilibrium, KW065 - GENOME-WIDE ASSOCIATION, KW060 - GENETIC EPIDEMIOLOGY, KW084 - MAPPING COMPLEX TRAITS, KW013 - CARDIOVASCULAR SYSTEM, KW033 - DIABETES

### Abstract Content

**Genome-wide association scans in cohorts from Sardinia and Finland identify a locus for fasting glucose levels.** *W.M. Chen<sup>1</sup>, A.U. Jackson<sup>1</sup>, A. Scuteri<sup>2,6</sup>, M.R. Erdos<sup>3</sup>, M. Uda<sup>4</sup>, W.L. Duren<sup>1</sup>, S. Sanna<sup>1,4</sup>, H.M. Stringham<sup>1</sup>, A. Mulas<sup>4</sup>, H. Shen<sup>5</sup>, L.J. Scott<sup>1</sup>, S. Najjar<sup>6</sup>, A.R. Shuldiner<sup>5</sup>, J. Tuomilehto<sup>7</sup>, E. Lakatta<sup>6</sup>, R.N. Bergman<sup>8</sup>, D. Schlessinger<sup>6</sup>, M. Boehnke<sup>1</sup>, G.R. Abecasis<sup>1</sup>, R.M. Watanabe<sup>8</sup>* 1) Biostats, U of Michigan, Ann Arbor, MI; 2) Operativa Geriatria, INRCA, Rome, Italy; 3) National Human Genome Research Institute, Bethesda, MD; 4) Istituto di neurogenetica e neurofarmacologia, CNR, Cagliari, Italy; 5) U of Maryland, Baltimore, MD; 6) National Institute on Aging, Baltimore, MD; 7) Public Health Institute of Finland, Finland; 8) School of Medicine of USC, LA, CA.

Fasting glucose levels are a function of glucose production and utilization. Glucose is tightly regulated within a narrow range and dysfunction of this regulation can lead to type 2 diabetes. We carried out two independent genome-wide association (GWA) scans for fasting glucose levels: a scan of 4,305 Sardinians in large pedigrees from the ProgeNIA study genotyped using the Affymetrix 500K chip set and a scan of 1,256 mostly unrelated nondiabetic Finnish individuals from the FUSION study genotyped on the Illumina HumanHap300 chip. In both GWA scans, an additive genetic model was used to test for association between fasting glucose levels and SNPs, adjusting for familiarity and covariates including sex, age, and age<sup>2</sup>. To minimize the impact of outliers and skewed distribution on the association testing, quantile normalization was applied to each trait prior to GWA scans. Analysis of our two GWA scans identified a SNP that is strongly associated in both the ProgeNIA ( $p = 4.0 \times 10^{-7}$ ) and FUSION ( $p = 1.9 \times 10^{-3}$ ) studies, and achieves clear genome-wide significance in our two-study meta-analysis ( $p = 2.8 \times 10^{-9}$ ). This SNP is located within 10kb of a gene that encodes an enzyme involved in the release of glucose into bloodstream. To confirm and follow-up the signal, we currently are genotyping additional SNPs in the region and following up in additional samples. Preliminary replication analysis on 973 Finish individuals and 451 Amish individuals are promising, showing a significant result in the same direction ( $p = 6.5 \times 10^{-5}$  for replication data only and  $1.1 \times 10^{-12}$  for combined data).

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