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The uniform-score gene set analysis of genetic pathways associated with diabetes traits

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Genetic heritability and expression study have shown that different diabetes traits have common genetic components and pathways. The Uniform-Score Gene-Set Analysis (USGSA) is a computationally efficient method for pathway enrichment test that unifies different gene measures by a uniform score for identifying pathways from genome-wide association and expression data and an R package of *snp* Gene Sets is implemented to facilitate the analysis. USGSA was applied to identify common pathways associated with diabetes traits based on public dbGaP GWAS results following a two-stage study strategy: the stage I of 11 Framingham Heart Study (FHS) GWAS and the stage II of 5 independent GWAS. The study identified 7 gene sets that contain binding motifs at promoter region of component genes for 5 Transcription Factors (TFs) of FOXO4, TCF3, NFAT, VSX1 and POU2F1 and microRNA of mir-218. These gene sets include 25 common genes that are among top 5% of the gene associations over genome for all GWAS. To further evaluate the identified diabetes pathways, 30 microarray data of different tissues was retrieved from the Gene Expression Omnibus. The USGSA with meta-analysis showed that 6 gene sets are also enriched for top 5% of the differential gene expressions. The pathway analysis suggested that different diabetes traits share common pathways and diabetes pathogenesis at varied tissues is potentially regulated by common TFs and microRNA.

Biography

Hao Mei has completed his PhD from North Carolina State University with majors in Statistics and Bioinformatics and his Postdoctoral studies from Center for Human Genetics at Duke University. He is currently Associate Professor of University of Mississippi Medical Center and Professor of Shanghai Jiao Tong University. He is an Active Investigator of Jackson Heart Study and Atherosclerosis Risk in Communities Study and he has published more than 20 papers in reputed journals for genetic study of complex disease.

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