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[Medicine] Taiwan Scientists Identify Two Genes Associated with Increased Susceptibility to Type 2 Diabetes in Han Chinese

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Academia Sinica Newsletter (2010/02/23) A group of Taiwan scientists recently successfully identified two genes associated with type 2 diabetes in Han Chinese. Their research was published in the February 19 issue of the international scientific journal PLoS Genetics.

Type 2 diabetes is a chronic metabolic disorder caused by inadequate response to insulin by the body. Both environmental factors, such as diet and exercise, and genetic factors affect the age of disease onset and symptom progress. Type 2 diabetes currently affects approximately 360 million people or about 6% of the world population; by 2025 this figure is expected to rise to around 25%.

For this study researchers analyzed the genes of 2798 patients with type 2 diabetes using high density genotyping technology. They identified two genes named protein tyrosin phosphatase receptor (PTPRD) and serine racemase (SRR) that were associated with type 2 diabetes in ethnic Chinese. Variation in PTPRD may affect the body's resistance to insulin and, therefore, influence the body's blood glucose metabolism. SRR gene variation may alter glutamate signaling in the pancreas, thus regulating insulin and/or glucagon secretion. The study also confirmed that the KCNQ1 gene, which was previously identified in a study of type 2 diabetes in Japanese, also plays an important role in the pathogenesis of type 2 diabetes in Han Chinese.

Dr. Fuu-Jen TSAI of China Medical University who lead the research said that this study marks important progress in the identification of disease genes for type 2 diabetes in Han Chinese. Many severe complications are caused by type 2 diabetes including cataract, glaucoma, kidney failure, coronary heart disease, retina damage, neuropathy, stoke, peripheral arterial disease and gangrene. Dr. TSAI said that, with the combined the effort of public health and medical centers, he hopes that in the future genetic factors associated with these complications can also been identified, leading to advances in medical care, therapy and prevention.

The full article entitled "A Genome-Wide Association Study Identifies Susceptibility Variants for Type 2 Diabetes in Han Chinese" is available at the PLoS journal website at: http://www.plosgenetics.org/home.action

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