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Team unlocks genetic basis of Type 2 diabetes

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[摘要] February 21, 2007, Researchers from the Broad Institute of MIT and Harvard, Lund University and Novartis have announced the completion of a genome-wide map of genetic differences in humans and their relationship to Type 2 diabetes and other metabolic disorders.

[关键词] diabetes;genome

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Researchers from the Broad Institute of MIT and Harvard, Lund University and Novartis have announced the completion of a genome-

wide map of genetic differences in humans and their relationship to Type 2 diabetes and other metabolic disorders.

All results of the analysis are accessible, free of charge, on the Internet to scientists around the world.

The work is the result of a pioneering public-

private collaboration known as the Diabetes Genetics Initiative (DGI), which was formed in 2004 and is aimed at deciphering the genetic causes of Type 2 diabetes. Although Type 2 diabetes clearly runs in families, suggesting the importance of inherited factors, its genetic origins remain largely unclear.

"The Human Genome Project, HapMap database and new genomic tools have made it possible for the first time to screen the genome for DNA variations that contribute to common diseases," said principal investigator David Altshuler, the director of the Program in Medical and Population Genetics at the Broad Institute and an associate professor at Massachusetts General Hospital and Harvard Medical School. "Since diabetes and cardiovascular risk factors are influenced by many genes, e

As a so-

called "complex" disease, Type 2 diabetes is influenced by several genetic factors that when combined can significantly increase a person's risk of disease, but alone exert only small effects. Initial analyses of the data generated by the DGI reflect this complexity.

Given the subtle nature of each genetic variation and the importance of subsequent scientific validation and replication, the partnership's conclusions have yet to be released, pending peer

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review and publication. However, the public availability of the results enables scientists in academic and industry laboratories worldwide to access the data without delay and to develop and test their own hypotheses about the genes that contribute to Type 2 diabetes.

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