

## 综述

### 肥胖的全基因组关联研究

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摘要:

肥胖是2型糖尿病和某些癌症的重要危险因素,同时也是影响世界范围内公众健康的重要负担。作为一种传统的复杂疾病,肥胖症被认为是基因与环境交互作用的产物。然而上述两个因素中哪一个对肥胖的产生发挥更大的作用尚存争议。近年来,通过全基因组关联分析(GWAS)发现了一些影响肥胖进展的基因位点。GWAS研究对探寻基因变异在复杂疾病中的潜在作用发挥日益重要的作用。为进一步了解遗传因素导致肥胖的风险,笔者回顾并收集Pubmed上近期有关GWAS研究报道的基因,总结已发表的关于GWAS的研究论文,共找出与人类肥胖患病风险强相关的49个候选基因。尽管该发现与当前的研究存在相似性,但这一研究领域的许多单核苷酸多态性(SNPs)的详细信息和潜在机制尚未阐明。因此,有必要对人类肥胖症患病风险进行更为深入的研究。

关键词: 肥胖 全基因组关联分析 基因

### Genome wide association study of obesity

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Abstract:

Obesity is a great risk factor for type 2 diabetes and certain types of cancer, which become a major burden for public health worldwide. As a classic complex disease, obesity is regarded as the interaction of genetic and environmental factors. However, it is controversial which of these two factors have greater effect on obesity. Several genetic loci have recently been reported to contribute to the development of obesity reported in genome-wide association study (GWAS) these years. GWAS play an important role in complex disease research and explore the potential effect of genetic variance. To further understand the genetic influence on obesity risk, we reviewed and collected articles on Pubmed for genes that reported in recent GWAS. We summarized the publications in GWAS and found 49 candidate genes, which were strongly suggested to relate to obesity risk in human. Despite the findings of this and other similar, contemporary research projects, much of the single nucleotide polymorphism details and underlying mechanism in this field of study remains, to a great extent, unknown. As a result, future studies are needed for obesity risk in human beings.

Keywords: obesity genome wide association study (GWAS) genes

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