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TNFR2基因的CA重复多态性在两个独立的白人群体中与肥胖表型的连锁和关联

黄青阳1,4，SHEN Hui4，DENG Hong-Yi4，Theresa Conway4，Leo Elze4，K. Michael Davies4，Robert R. Recker4，邓红文2,3,4
1. 华中师范大学生命科学学院，武汉 430079；
2. 湖南师范大学生命科学学院，长沙 410081；
3. 西安交通大学生命科学与生物技术学院，西安 710049；
4. 美国克瑞屯大学医学中心，内布拉斯加州 68131

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摘要

我们先前通过全基因组扫描发现1p36与体重指数显提示性连锁(LOD=2.09)。肿瘤坏死因子受体2 (TNFR2)定位于1p36，是肥胖的一个极好的图位和功能侯选基因。本研究采用数量传递连锁不平衡检验在两个大的独立的白人样本中进行了TNFR2基因与肥胖表型的连锁与关联检验。第一组受试者由来自79个多代家系的1 836个个体组成；第二组受试者由来自157个核心家庭的636个个体组成。所检测的肥胖表型包括体重指数、脂肪量和脂肪量百分数。在多代家系中我们发现TNFR2基因变异与BMI显著连锁（P=0.0056）。结果表明，TNFR2基因是影响白人BMI变异的一个数量性状位点。

关键词

TNFR2基因；肥胖；传递不平衡检验；连锁；关联

分类号

Linkage and Association Between CA Repeat Polymorphism of the TNFR2 Gene and Obesity Phenotypes in Two Independent Caucasian Populations

HUANG Qing-Yang1,4, SHEN Hui4, DENG Hong-Yi4, Theresa Conway4, Leo Elze4, K. Michael Davies4, Robert R. Recker4, DENG Hong-Wen2,3,4

1. College of Life Sciences, Central China Normal University, Wuhan 430079, China;
2. College of Life Sciences, Hunan Normal University, Changsha 410081, China;
3. School of Life Science and Technology, Xi’an Jiaotong University, Xi’an 710049, China;
4. Medical Center, Creighton University, Omaha NE 68131, USA

Abstract

<P>Previously, our group has reported a suggestive linkage evidence of 1p36 with body mass index (BMI) (LOD = 2.09). The tumor necrosis factor receptor 2 (TNFR2) at 1p36 is an excellent positional and functional candidate gene for obesity. In this study, we have investigated the linkage and association between the TNFR2 gene and obesity phenotypes in two large independent samples, using the quantitative transmission disequilibrium tests (QTDT). The first group was made up of 1 836 individuals from 79 multi-generation pedigrees. The second group was a randomly ascertained set of 636 individuals from 157 US Caucasian nuclear families. Obesity phenotypes tested include BMI, fat mass, and percentage fat mass (PFM). A significant result (P = 0.0056) was observed for linkage with BMI in the sample of the multigenerational pedigrees. Our data support the TNFR2 gene as a quantitative trait locus (QTL) underlying BMI variation in the Caucasian populations.</P>

Key words

TNFR2 gene；obesity；transmission disequilibrium test；linkage；association

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通讯作者 邓红文 deng@creighton.edu