

CASE STUDY

The role of satiety mechanisms in genetic risk of obesity (follow-up study).

CATEGORISING

Kind

Research project not involving persons

Type

Research project with existing biological material or genetic data

Subtype

Research project with existing encoded biological material or genetic data

BACKGROUND

Obesity is highly heritable, and researchers are identifying the specific genes involved. Discovering the mechanisms through which obesity-related genes influence weight will help pinpoint novel targets for intervention. This study tested the hypothesis that satiety responsiveness is an intermediate behavioural phenotype associated with genetic predisposition to obesity in children.

METHODS

We used genetic data that was collected previously in a population-based twin birth cohort, with twins born in 1996 (National Twins Cohort). In the original cohort study children made up the cohort; one child was randomly selected from each twin pair. Buccal swabs were used to extract DNA. Genome-wide genotyping was done with SNP array, using standard experimental protocols. Children were assigned a unique ID number and the data did not include their names or addresses. We created a polygenic risk score (PRS) comprising 28 common obesity-related single-nucleotide polymorphisms that had been identified in a meta-analysis of obesity-related genome-wide association studies. The primary outcome was the association between the PRS, adiposity, and satiety responsiveness.

SOURCE

<http://www.ncbi.nlm.nih.gov/pubmed/24535189>

QUESTIONS OF THE CATEGORISER

Does the research project come under the scope of application of the Human Research Act?

Yes

BECAUSE

This project was based on a study protocol that defined the exact procedures to be used. It included a relatively large number of persons and was not based on individual cases ("method-driven search for generalizable knowledge", defined as research by HRA). The goal was determining the association between polygenic risk score (PRS), adiposity, and satiety responsiveness ("research concerning the structure and function of the human body"). We analysed genetic data from children ("persons"), which we collected from a population-based twin birth cohort.

Is the research project a project involving living persons?

No

BECAUSE

We analysed existing genetic data from children, which we collected during a population-based twin birth cohort ("genetic data").

Is the research project a project with existing biological material or genetic data?

Yes

BECAUSE

We analysed existing genetic data from children, which we collected during a population-based twin birth cohort ("genetic data").

Is the research project a project with existing encoded biological material or genetic data?

Yes

BECAUSE

We analysed existing genetic data from children, which we collected during a population-based twin birth cohort ("genetic data"). Children were assigned a unique ID number ("existing encoded genetic data") and the data did not include their names or addresses.
