

Method for determining susceptibility to obesity

PATENT

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BACKGROUND

At this moment, pending tasks are the development of robust epigenetic biomarkers participating in weight regulation, the research of epigenetic marks modifiable by dietary or pharmacological exposures, the recognition of active molecules/substances that influence the epigenome or the appraisal of the role of obesity-related factors on epigenetic regulation in order to improve the personalized management of this disease.

ACHIEVEMENTS & RESULTS

Data from our lab pertaining to a testing of 108 DNA paired samples of subcutaneous adipose depots and circulating leukocytes from individuals with a range of BMI were hybridized in the same Illumina Infinium HumanMethylation 450Bead Chip. Our study specifically identified genes that are strongly mirrored between adipocytes and the analyzed circulating blood cells (Figure 1) evidencing a statistical ability to distinguish obese from lean persons (AUC>80; P<0.05) with excellent correlation in methylation patterns and biological expression.

IDENTIFIED PURPOSES & ADVANTAGES

These results raise the possibility to diagnose, treat and predict future outcomes in obese subjects mediated by methylation marks, which are not permanent signatures that can be eventually managed with dietary or medication prescriptions following precision medicine strategies, by using a minimally invasive samples, circulating blood leukocytes.

DEVELOPMENT COLLABORATION OFFER

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