Epigenetic biomarkers in precision treatment of obesity: differential methylation levels between responders and non-responders to weight loss diets

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Epigenetic marks, particularly DNA methylation levels in CpG sites, may be useful in the personalized treatment of obesity, helping to predict a better response to specific weight loss diets.
The purpose of the present research was to examine whether DNA methylation levels could be associated with the metabolic response to weight loss diets. For this purpose, DNA methylation was analyzed in responders and non-responders to two different hypocaloric diets (30% energy restriction), at the beginning of the dietary intervention.
DNA from white cells of 100 volunteers who participated in the Obekit dietary intervention program for 6 months was used. Volunteers were randomized in two different diets: moderately high-protein (30% protein, 30% lipids and 40% carbohydrates) and hypolipidic (18% protein, 22% lipids and 60% carbohydrates). To analyze the CpGs whose methylation was associated with better response to each intervention, the population of each diet was divided into quartiles according to their weight loss response, and the methylation levels of quartiles 1 and 4 were compared for each diet. DNA methylation levels were quantified using Infinium Methylation EPIC Bead Chip kits (Illumina).
This study identified 14 CpG sites with DNA methylation differences greater than 5% between responders and non-responders to hypocaloric diets. Seven genes were associated with a better response to the high-protein diet and five genes with better response to the hypolipidic diet ($p < 0.05$).
In summary, epigenetic biomarkers could help to predict the response to a weight loss diet and be used in the personalization of obesity treatment.