"Engordar o adelgazar, cuestión de genes, dieta y actividad física"

Epigenetics: nutrients and obesity

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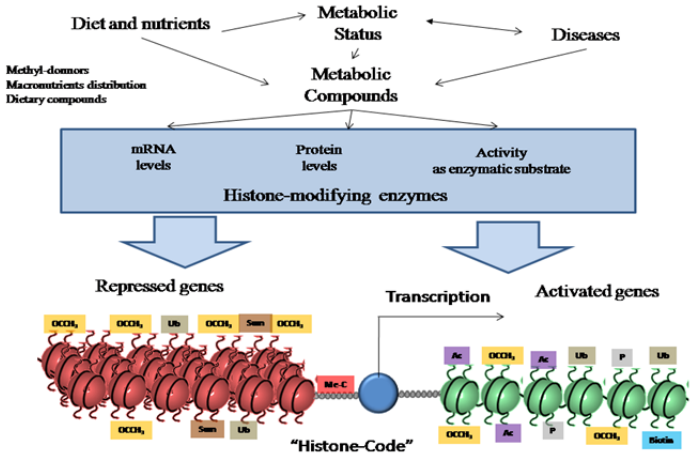
The word *epigenetics* was launched as a conceptual model seeking to explain putative unrevealed interactions between genes and environmental surroundings (diet, excesive, smoking, etc.) to produce a phenotype[1]. Thus, an early definition for epigenetics involved "the study of the mechanisms of temporal and spatial control of gene activity describing pathways different from those directly attributable to the underlying DNA sequence and with an influence on the adaptive response of an organism". Some epigenetic information might be inherited from one generation to the next. Specific epigenetic processes include DNA methylation, histone modifications or chromatin folding (euchromatin vs.herochromatin) and, in general, all those phenomena eventually affecting gene expression patterns[2]. Epigenetics can provide some insights to understand genetic fetal programming, monozygotic twin differences and chronic disease onset in the adult, which interact with dietary intake and nutritional processes. Actually, epigenetic research will contribute to explain the way that cells/organisms carrying identical nucleotide sequences can generate different responses under the same nutrient exposure through mechanisms such as DNA methylation, small and non-coding RNAs and chromatin architecture changes. These mechanisms together with other transcriptional regulatory events ultimately regulate gene activity and expression during development and differentiation or in response to nutritional and environmental stimuli.



In the last years, different examples of dynamical changes in DNA methylation patterns due to the restriction or supplementation with different nutrients have been reported[3]. Furthermore, in the adult state, some examples of diet-induced epigenetic changes have been also reported. In this sense, folic acid has been linked to DNA methylation in a dose-dependent manner. Other dietary factors involved in DNA methylation are alcohol, vitamin B_6, vitamin A and some minerals. Our research group has reported that high fat/sugar intake and situations of excessive body weight in rodents are associated with changes in DNA methylation patterns, affecting the promoter region of different genes involved in energy homeostasis and obesity such as leptin, POMC, FASN, CLOCK, and NDUFB6[4,5]. On the other hand, epigenetic biomarkers are being identified in order to predict body weight maintenance after weight loss in humans, including TNF-alpha, AQP9, ATP10A, CD44[6] as well as some specific miRNAs[7].

In summary, it is becoming evident that interindividual differences concerning the outcomes of nutritionally-related chronic diseases such as diabetes and obesity depend not only on the dietary intake and the subject's DNA sequence, but also on the inherited epigenome and on different nutritional influences (during the intrauterine or the adult periods) that modify the epigenetic marks and are able to affect gene expression, which includes DNA methylation, covalent histone modifications, chromatin folding and, more recently described, the regulatory action of miRNAs[8].

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