

Early and lifelong remodelling of our epigenomes by nutrition

La nutri-épigénomique : Comment l'environnement précoce, la nutrition, remodelent nos épigénomes

Claudine Junien –

The phenotype of an individual is the result of complex interactions between genome, epigenome and current, past and ancestral environment leading to a lifelong remodelling of our epigenomes. The genetic information expression contained in the genome is controlled by labile chromatin-associated epigenetic marks. The epigenetic code comprises several levels of interconnected and interdependent codes - the DNA methylation code, the histone code (histone methylation, acetylation and phosphorylation) and the coregulator code - that "orchestrate" the activity of the genome, together with RNA interference. The epigenome serves as an interface between the environment and the genome. Depending on the nature and intensity of the environmental insult, the critical spatiotemporal windows and developmental or lifelong processes involved, epigenetic alterations can lead to permanent changes in tissue and organ structure and function, or, to phenotypic changes that can be reversed using appropriate epigenetic tools. Epigenetic misprogramming during development is widely thought to have a persistent effect on the health of the offspring and may even be transmitted to the next generation. Moreover, the flexibility of epigenetic marks may make it possible for environmental, nutritional and hormonal factors, or endocrine disruptors to alter — during a particular spatiotemporal window in a sex-specific manner — the sex-specific methylation or demethylation of specific CpGs and/or histone/chromatin modifications underlying sex-specific expression of a substantial proportion of genes. Links have also been found between circadian rhythms, epigenetic alterations and major components of energy homeostasis, thermogenesis and hunger-satiety, rest-activity rhythms, and the sleep-wake cycle. Moreover, genetic factors, the environment and stochastic events change the epigenetic landscape during the lifetime of an individual. Epigenetic alterations leading to gene expression dysregulation accumulate during ageing and are important in tumorigenesis and age-related diseases. Interestingly the genome-wide decline in DNA methylation occurs in the brain and coincides with a functional decline in learning and memory. Dietary factors - including folate involved in the one-carbon metabolism - and other social and lifestyle exposures have a profound effect on many aspects of health including ageing and do so, at least partly, through interactions with the genome which result in altered gene expression with consequences for cell function and health throughout the life course.