Epigenetics and Human Health

Journal für Ernährungsmedizin 2010; 12 (1), 26-27

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Mehr als nur eine Dekoration:

- Sie wollen das Besondere?
- Sie möchten Ihre eigenen Salate, Kräuter und auch Ihr Gemüse ernten?
- Frisch, reif, ungespritzt und voller Geschmack?
- Ohne Vorkenntnisse und ganz ohne grünen Daumen?

 Dann sind Sie hier richtig
The term epigenetics describes mechanisms inducing changes in gene expression or phenotype not caused by alterations in the underlying DNA sequence. Compared to the genome, which is almost identical in different cell types and conserved throughout life, the epigenome is varying between different cell types as well as over the course of a lifetime (1). Two studies demonstrated, that identical twins, being epigenetically indistinguishable at early life exhibit strong DNA methylation differences over time they accumulated significant differences in global levels of epigenetic marks (2).

It is becoming increasingly evident that disturbances in various epigenetic marks disturbs the DNA configuration at critical ontogenetic stages as well as that these alterations are heritable. Occurring in the gametes these changes may be heritable and they are affected from the moment testes and ovaries develop during fetal growth (3-5). A well-known famous study of how maternal nutrition affects the epigenetic state of the unborn addressed the Dutch hunger winter 1944-45. The methylation of the IGF2, which plays a crucial role in growth and development, was investigated in individuals being epigenetically indistinguishable at early life exhibiting strong DNA methylation differences over time they accumulated significant differences in global levels of epigenetic marks (2).

The first articles in the book emphasize on the interactions between concepts of genetic diversity, epigenetics, environmental health, molecular epidemiology, nutrition and evolution theory. Paola Vinnes describes epigenetics as a new paradigm for research: “it refers not to structural but to functional changes in DNA (gene regulation). We are observing continuous quantitative changes, i.e. nature turns to work in degrees, not according to leaps like mutations: the ratio between hypo- and hyper-methylation, for example, is very relevant to cancer. Epigenetic changes are reversible: animal experiments have been conducted with dietary supplements that were able to reverse methylation patterns. Epigenetic patterns seem to be heritable (though this may be the weakest part, since the evidence is not entirely persuasive). Epigenetic changes fill the gap between genes and the environment: the mysterious connections between spontaneous heritable mutations and selection in neo-Darwinian theory may be overcome by a more sophisticated paradigm that resembles Lembark’s research program “.

Imbibl Eimalda focuses the role of nutrition on gene regulation and its correlati on with carcinogenesis, the prevalence of overweight and related metabolic disease. Friz Scharni, coming from ecology, identifies epigenetics as a main research area to study ecological factors affecting the interactions between human societies and their environment. The working group of Alexander Haslerberger focused on the interaction of hereditary and epigenetic mechanisms in the regulation of gene expression on the molecular level.

They explain epigenetic mechanisms and what consequences environmen tal influences like diet and toxins can have on the immune system and aging. Part II emphasizes on hereditary aspects: Stefania Biocca discusses key concepts of genetic association studies with the core area of meta-analysis. She reports on the scientific review of the published meta-analyses of the effect of methylene tetrahydrofolate reductase gene polymorphism on cancer risk. The group of Kurt Zatloukal discusses the challenges faced by biobanks and for investigation of gene-environment interactions with the example of non-alcoholic fatty liver disease. Gunnar Kaati summarizes case studies on epigenetic inheritance and asks for translational effects because of nutritional constraints during key fetal organ development and other critical phases of the life cycle.

Chemical compounds can modify the rate of carcinogenesis by affecting mutational frequency, growth rate, or expression of phenotypic deviations. Wilfried Bursch highlights the importance of chemicals to induce epigenetic effects in safely evaluating the example with the compound hepatocarcinogenesis. The group of Sigfried Knasmuller summarizes groups of food carcinogens as a basis for epigenetic evaluation. They discuss occurrence, modes of action and modulation of histone and epigenetic factors and dietary constituents.

Part IV extends on nutritional aspects. Guy Vergères describes technologies used in nutrigenomics, nutrigenetics and nutrigenetics. He focuses on the nutritional aspects of nutrition in the expanding areas of epigenetics. Carloiner Alexander and Müller Sabine (Hrsg.) Wiley-VCH, 2009

Food components, participating in the one-carbon metabolism, including vitamin B12, vitamin B6, folic acid and methionine provide methyl groups for the biochemical pathway of methylation processes. Epidemiological data reveal diminished dietary folate induced inhibition of DNA methylation to be associated with increased cancer susceptibility and low folate status is linked to risk in developing colorectal cancer (10, 11). Several more bioactive food components have also been suggested to alter cancer susceptibility. Genistein, e.g. was associated with cancer chemoprevention and decreased DNA methyltransferases expression (12). Interestingly most dietary HDAC inhibitors identified to far have shown weakly linked to cancer chemoprevention. There is also evidence that oxidative stress can inhibit HDAC activity and enhance inflammatory gene expression, leading to a chronic inflammatory response (13). Furthermore, the histone deacetylase inhibitors are linked to dietary restriction. Resveratrol, a dietary polyphenol, appears to be a dietary modifier of effects of dietary restriction by activating SIRT1 (14). Due to the central role epigenetics plays in mediating environmental and nutritional effects on hereditary disposed genes as well as translational and evolutionary aspects, the book assembles works from these different areas.


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health policy makers have to face with the emerging fields in genomic research. They introduce the field of Public Health Genomics as a translational research and the Public Health Genomics European Network (PHGEN) as a successful platform for researchers, policy makers and their institutions in organizing this process. Astrid Gersch provides a comprehensive overview of the new understanding into public health from which to deal with emerging ethical and social issues in the expanding areas of epigenetics.

Buchtipp

Haslerberger, Alexander / Greiller, Sabine (Hrsg.) Wiley-VCH, 2009

**REFERENCES**