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Epigenetics 2018: Epigenetics for precision health & performance- Mickra Hamilton- Apeiron Center for Human Potential, USA

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Introcduction & Aim: A precision, whole systems genomics approach to thriving health and wellbeing has enormous clinical applications in the emerging field of environmental epigenetics research. We can now look at all aspects of an individual's life, their medical and family history, occupation, their lifestyle, the environments they function in, individual systems diagnostics and genetics along with real time markers from sensor and mobile data to provide precise lifestyle interventions to optimize and enhance gene expression.

Findings: This new precision offers high specificity on health, tracks how individual choices affect health now and how that translates to the future. It also provides new insights about how we are interacting with our environment, in real time and in detail. The interplay of our genes and our experiences, of nature and how it interacts with nurture, has now moved from the mysterious to the knowable. The Science of Epigenetics assists us to create precise optimization strategies by taking the reigns of gene expression to adapt and thrive under modern environmental pressures. Every decision we make contributes to this process in some way. The food we eat, the quality of sleep we experience, the cars we drive, the products we clean with and put on our skin, the thoughts we think, the levels of stress we carry and the chemicals and medications we dump into our water supply, all have an effect. This discussion will detail the evidence-based use of precision epigenetics and genomics as strategies to mitigate the effects of environmental toxins in the human system. Additionally, we will discuss actionable lifestyle modifications and system support processes to fine tune and enhance our human experience as we interact with our environment. Precision medicine promises to greatly improve individualized medical care, and this promise hinges not only on genetic tests and therapies, but also epigenetic insights. Although the massive power of DNA sequencing has largely been applied to genome and exome sequencing as a means to trace sequence variants in myriad diseases, such applications do not capture the tissue, context, or temporal dynamism to the epigenome that defines cell state and drives phenotypes9. Take the case of a woman who brings her young son to the pediatrician, explaining a set of symptoms. After some testing, the doctor confirms that the child has a fairly common autoimmune disease. The doctor is intrigued, however, when the woman explains that her son's identical twin does not show any symptoms. He suggests that although the two boys share the same genetic information, their discordance for the disease could perhaps be explained by differences in epigenomic states, leading to changes in gene expression. The woman consents to giving blood samples from her children for a research study, which finds a handful of changes in DNA methylation and chromatin accessibility in the blood of the two boys that could be related to the disease. This study is powerful in its ability to ascertain how epigenomic changes lead to disease or other phenotypes because of the controlled genetic makeup of the twins.

Note : This work was partially published at Annual Epigenetics Conference scheduled during November 28-29, 2018 in Tokyo, Japan

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