Researchers characterize epigenetic fingerprint of 1,628 people

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Until a decade, it was believed that differences between people were due solely to the existence of genetic changes, which are alterations in the sequence of our genes. The discoveries made during these last ten years show that beings with the same genetics like the twins and cloned animals may have different characteristics and disease due to epigenetic changes.

Epigenetics involves chemical signatures that are added to DNA and proteins that package it, to regulate their activity. The more recognized epigenetic brand is DNA methylation, a process based on the addition of a methyl chemical group into a part of our genetic puzzle. Therefore, while the genetic is like the alphabet, epigenetics is like the punctuation marks of a text.

The researcher Manel Esteller, director of the Epigenetics and Cancer Biology Program of the Bellvitge Biomedical Research Institute (IDIBELL), professor at the University of Barcelona and ICREA researcher, has coordinated a work that identifies the "epigenetic fingerprints" of 1,628 people, healthy volunteers and patients suffering from common diseases, such as cancer, and cardiovascular and neurodegenerative diseases. The findings are published this week in the scientific journal *Genome Research*.

'Photo finish'

"The study analyses thousands of sites of DNA methylation in this great set of physiological and pathological tissues, it would be like a photo finish in a race that teaches you the epigenome of the individual at a particular time" says Dr. Esteller.

The results from the research provide understanding of many processes of the human body and how these processes lead to disease. The IDIBELL researcher says that "in the case of cancer, the study shows that all human tumours suffer epigenetic inactivation of cancer-protective genes and also tumour cells lose their epigenetic memory and can not remember what healthy tissue was."

Dr. Esteller explains how these changes related to the cancerous disease are not instantaneous but gradually accumulate with aging of our bodies. The changes are different from those in dementia and other autoimmune diseases with different epigenomes.

A very interesting result for its potential applicability is that we could know the primary tumour of metastases with unknown origin: "If we know the tumour from which emerged these cells, we can provide the most appropriate therapy for a patient and improve his or her survival".

The investigation involves several IDIBELL researchers linked to IDIBELL's scientific partners: the Catalan Institute of Oncology, the University of Barcelona and the Bellvitge University Hospital.

More information: A DNA Methylation Fingerprint of 1,628 Human Samples. *Genome Research.*

Provided by IDIBELL-Bellvitge Biomedical Research Institute