Scientists take early steps toward mapping epigenetic variability

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This is Brock Christensen, a postdoctoral research associate at the department of pathology at Brown University.

Brown University scientists have taken the first steps toward mapping epigenetic variability in cells and tissues. Mapping the human epigenome, similar to the human genome project in the 1990s, could someday allow for quicker and more precise disease diagnoses and more targeted treatments of many chronic ailments.

Details are published online in the latest edition of PLoS Genetics.

Epigenetics, a relatively new endeavor in science, refers to the control of the patterns of gene expression in cells, which gives rise to the necessary

differences responsible for creating the complex and interacting tissues in the body.

Scientists globally have begun working on a Human Epigenome Project in a bid to compile detailed data documenting, within a person, the epigenetic changes in different types of cells and tissues, something that will complement the already-completed Human Genome Project.

The Brown-led effort completes a far-reaching study of more than 200 human tissue samples in a bid to map variations in epigenomic structure. Collaborators from the Harvard School of Public Health and Harvard Medical School, the University of California-San Francisco, University of Minnesota-Minneapolis, Dartmouth Medical School, Women & Infants Hospital in Providence, and Brigham and Women's Hospital in Boston took part in the effort.

Their findings: Human cells display wide epigenetic variation that appears related to aging and smoking, which may increase susceptibility to several diseases such as cancer. While the scientists emphasize that more research is necessary, they say that taking a step to map epigenetic variability will help bring them closer to discovering important epigenetic differences in people, which in turn could help better diagnose disease and create more targeted treatments. Alterations in epigenetic marks in cells have been linked to many diseases and conditions in humans, including cancer.

"Scientists have already found out it is critical to look at genetic variation to diagnose disease," said Brock Christensen, a postdoctoral research associate at Brown University's Department of Pathology and Laboratory Medicine. "What we are trying to do is complement that by looking at what is normal and how much variation in epigenetics exists."

Christensen said that more tissue samples and data are needed to allow

for a thorough mapping of epigenetic variability in cells.

That endeavor is important, as scientists need to gauge normal human epigenomic variability as part of the broader mapping process, said Karl Kelsey, corresponding author and a Brown professor of community health and pathology and laboratory medicine.

"The real importance of the work has to do with beginning to define what is normal in different tissues," Kelsey said. "And then you dig deeper to see what is the same and different about different people."

The study involved analysis of 217 nonpathologic human tissue sampless including blood, lung, head and neck, and brain tissue.

Source: Brown University (news : web)