MedicalXpress

Researchers identify fundamental differences between human cancers and genetically engineered mouse models of cancer

December 5 2013

Researchers from the Fred Hutchinson Cancer Research Center in Seattle, WA have taken a closer look at existing mouse models of cancer, specifically comparing them to human cancer samples. These genetically engineered mouse models (which usually either overexpress a cancer-causing gene—or "oncogene"—or carry a deletion for a "tumor suppressor" gene) have been extensively used to understand human cancer biology in studies of drug resistance, early detection, metastasis, and cancer prevention, as well as for the preclinical development of novel targeted therapeutics.

Cancer is a multistep process that involves a complex interplay between genetic and epigenetic alterations. Epigenetic modifications mediate changes in gene expression without altering the DNA sequence. One of those modifications, DNA methylation, was found to be significantly different between mouse models of medulloblastoma and primary medulloblastoma human samples.

The findings, published in the December, 2013 Issue of *Epigenetics*, provide an opportunity to both better understand the mechanisms of aberrant DNA methylation in human cancer and construct better mouse models of human cancer for therapy development.

More information: www.landesbioscience.com/journ …

etics/article/26486/