

Translational epigenetic research: Cancer - an epigenetic disease? Identification of biomarkers and elucidation of the causes and consequences of epigenetic modification in cancer

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Epigenetic alterations occur during various biological processes such as differentiation, development, senescence, stress response and transformation. De-regulations of these processes are closely associated with monogenic and complex diseases. Cancer for example is no longer solely seen as a genetic disease where genetic defects such as mutations and copy number variations affect gene regulation and eventually lead to aberrant cellular functions. Rather, it has become obvious that epigenetic alterations represent another early layer of (de-)regulation of gene activity. Currently, DNA methylation is probably the best characterized epigenetic modification and is required to ensure genome stability and proper lineage specification. Cancer epigenomes differ on more than 150,000 positions genome-wide in their methylation pattern from normal tissues. On one side these large differences provide the basis for the identification of candidate biomarkers, on the other side it poses the questions how these alterations are initiated and what consequences they have on cancer surveillance. The concept of the professorship is to further investigate the causes and consequences of cancer-specific epigenetic alterations and explore their utility as biomarkers and therapeutic targets. In this direction, recent large-scale sequencing studies have revealed that epigenetic modifiers are among the most frequently mutated proteins in cancer. It will be investigated if and how these mutations interfere with the epigenome and how they regulate cancer-specific transcriptional processes. Additionally, it will be dissected what other factors than mutations, for example noncoding RNAs can turn an epigenome into a cancer epigenome with the intention to understand basic oncogenic processes.

Projektbeteiligte

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