

Abstract

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DNA methylation and cancer.

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BACKGROUND: DNA methylation is an important regulator of gene transcription, and its role in carcinogenesis has been a topic of considerable interest in the last few years. Alterations in DNA methylation are common in a variety of tumors as well as in development. Of all epigenetic modifications, hypermethylation, which represses transcription of the promoter regions of tumor suppressor genes leading to gene silencing, has been most extensively studied. However, global hypomethylation has also been recognized as a cause of oncogenesis.

FINDINGS: New information concerning the mechanism of methylation and its control has led to the discovery of many regulatory proteins and enzymes. The contribution of dietary folate and methylene tetrahydrofolate reductase polymorphisms to methylation patterns in normal and cancer tissues is under intense investigation.

CONCLUSIONS: As methylation occurs early and can be detected in body fluids, it may be of potential use in early detection of tumors and for determining the prognosis. Because DNA methylation is reversible, drugs like 5'-azacytidine, decitabine, and histone deacetylase inhibitors are being used to treat a variety of tumors. Novel demethylating agents such as antisense DNA methyl transferase and small interference RNA are being developed, making the field of DNA methylation wider and more exciting.

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