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# Current and Future Viewpoints on Methylation Biological Markers for Early Cancer Detection and Treatment

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## DESCRIPTION

The increased number of recent scientific studies on cancer biomarkers has resulted in significant new insights into the field. Furthermore, novel technological breakthroughs such as long read sequencing and microarrays have enabled high throughput profiling of many biomarkers, while advances in bioinformatics tools have enabled the development of highly reliable and accurate biomarkers. These developments sparked renewed interest in biomarker research and created enormous opportunities for improving cancer management and early disease detection. Because of their stability, frequency, and accessibility in bodily fluids, DNA methylation alterations are known to accompany and contribute to carcinogenesis, making them promising biomarkers for cancer. The introduction of newer minimally invasive experimental methods, such as liquid biopsies, creates an ideal environment for the development and application of methylation-based biomarkers. Despite their enormous potential, accurate and robust biomarkers for the definitive diagnosis of most cancer types are still not routinely used, implying a strong need for ongoing research in this field. This review provides a brief overview of current methylation biomarkers for cancer diagnosis and early detection, including markers that are already in clinical use as well as several that are on the horizon. It also describes how recent big data and novel technologies will transform the next generation of cancer tests by supplementing or replacing currently available invasive techniques. Cancer, according to the World Health Organization (WHO), is a broad group of diseases marked by uncontrolled cellular proliferation and evasion of host regulatory mechanisms. Cancerous lesions can begin in almost any bodily tissue or organ and spread to other parts *via* metastasis. Cancer is the world's second leading cause of death, accounting for approximately 9.9 million deaths and 19.2 million cases in 2020 alone. These figures are expected to rise further, with 30.2 million new cases and 16.3 million deaths occurring globally by 2040. The most common cancers in men are lung, prostate, colorectal, stomach, and liver cancers, while the most common cancers in women are breast, colorectal, lung, cervical, and thyroid cancer. As a result, cancer is a major public health concern. Unfortunately, cancer is highly variable at the tissue and cellular levels, making accurate diagnosis and treatment difficult. Cancer disrupts cellular relationships, resulting in the impairment of vital genes, which leads to abnormal proliferation, among other things. In general, all cancers share certain distinguishing characteristics, but the driving phenomena and resulting phenotypes of cancerous tissue are highly variable, which contributes significantly to cancer's chaotic nature. While genetic mutations have long been recognised as drivers of carcinogenesis, the role of epigenetic modifications in cancer has recently received widespread attention. DNA methylation is crucial in the regulation of gene expression. It is the (reversible) addition of a methyl group ($CH_3$) to the fifth carbon of cytosine in DNA by DNA methyl transferases to form 5-methyl-cytosine (5mC).

## CONCLUSION

It is most common, but not always, at cytosine-phosphate-guanine (CpG) dinucleotide sites. It also occurs to a lesser extent at non-CpG sites, where the effect on gene structure and function is different. Approximately 80% of CpGs in the human genome can be methylated, with the remainder enriched in CpG islands near gene promoters.

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## CONFLICT OF INTEREST

The author's declared that they have no conflict of interest.

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