DNA Methylation: The Rising Potential of Blood-Based Multi-Cancer Early Detection Tests

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DNA methylation, the most well-studied epigenetic mechanism, involves the addition of a methyl group to the 5-carbon of cytosines within CpG dinucleotides. While most CpG dinucleotides are scattered across gene coding regions and repetitive sequences, clusters of CpGs, known as CpG islands, are primarily found in gene promoters and first exons. In normal cells, CpG islands tend to be unmethylated, whereas coding and repetitive sequences are typically methylated. However, this methylation pattern is reversed in cancer cells: promoters become hypermethylated, leading to the silencing of tumor suppressor genes, and there is global hypomethylation, which results in genomic instability. This aberrant methylation often occurs very early in the carcinogenic process, making DNA methylation an attractive biomarker for early cancer detection. In the ongoing battle against cancer, one of society's foremost goals is to detect cancer at its earliest stages significantly increasing the prospects of successful treatment and reducing the need for subsequent therapies that often come with severe side effects and additional health complications. Moreover, the pursuit of biomarkers amenable to simultaneously detect the most common cancers has lately gained the attention of several researchers worldwide.

In my talk, I will focus on the major recent findings of my research team in our quest to develop a cell-free DNA (cfDNA) methylation-based test to simultaneously detect the four major cancers: breast (BrC), lung (LC), colorectal (CRC), and prostate (PCa). I will also discuss the current challenges associated with implementing this test in clinical settings.

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