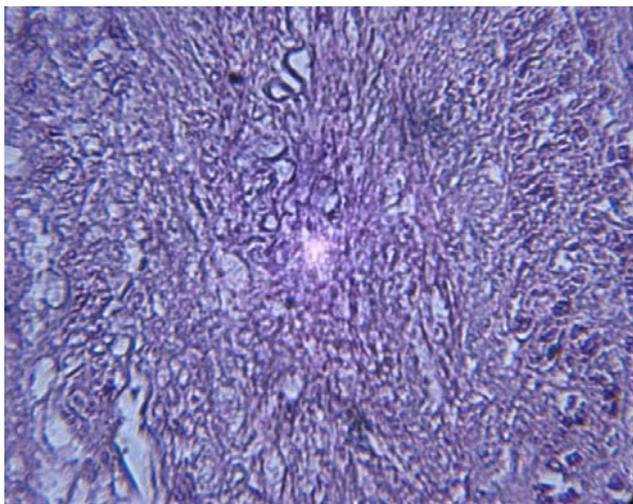


Detection and Classification of Cancer Using DNA Methylation Patterns



DESCRIPTION

CpG islands are short regions of DNA with higher frequency of 5'-CG-3' (CpG) dinucleotides and often harbor the promoters for genes which play an important role in regulation of that gene's expression. Methylation of a subset of CpG islands occurs during tumor development; hence detection of CpG methylation patterns is a very important step for diagnosis, classification and prognosis of many diseases including cancer. There are many approaches used to identify chromosomal regions undergoing methylation changes; however they are very labor-intensive and/or cannot distinguish between different cytosine modifications thus limiting their use. Considering these limitations, there was a need for less labor-intensive approaches with

higher sensitivity and specificity so they could be used in the clinical diagnostic space. It was this need that motivated the generation of a method for detecting methylated CpG islands using easily accessible biological materials. This method is termed methylated-CpG island recovery assay (MIRA) and can be used for cancer diagnosis, prognosis, and stratification of treatment options, for example the choice of 'epigenetic therapy' for tumors with extensive aberrations in methylation patterns.

KEY ASPECTS

- Detection of methylated CpG islands using DNA from any tissue.
- Use of microarrays or next-generation DNA sequencing to determine genome-wide DNA methylation patterns by MIRA
- MIRA is a simple 3 step process:
 1. Incubating genomic DNA fragments with a methylated CpG island binding protein and its binding partner to produce bound DNA containing methylated CpG islands with high sensitivity
 2. Isolating the bound DNA
 3. Detecting CpG island methylation by gene-specific amplification reactions or by whole genome analysis

INTELLECTUAL PROPERTY

Title	US Patent Number	Issued
Method for detecting methylated CpG islands	7,425,415	4/6/06

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