

Licensing Opportunity

The PACTT is proposing an exclusive or non-exclusive license for a new method for simultaneous detection of human methylated gene promoters.

Field:

- Epigenetic profiling for cancer diagnosis.

Development Phase

- A pre-commercial kit for membrane detection has to be developed
- Development of the technique for detection in chip.

Patent Status:

- US patent number 61/202,732 filed on the 31st of March 2009 in the name of CHUV naming J. Benhattar and I. Guilleret as inventors.
- PCT/IB2010/051313 filed on the 25th of March 2010.

Innovative aspects:

- Rapid detection method of at least one methylated site on a single strand nucleic acid sequence.
- Possibility to use fixed material

Additional information is available upon request (N Ref. IDF 13/08)

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Methylation Ligation-dependent Macroarray (MLM)

Background

Alteration of DNA methylation is a common change in human cancers. Aberrant methylation of sequences in or near the promoter region of many genes has been associated with transcriptional inactivation of genes involved in tumor suppressor gene, DNA repair and inhibition of metastasis. Therefore, detection of aberrant promoter methylation of cancer related genes may be essential for diagnosis, prognosis and/or detection of metastatic potential of tumors.

Description of the invention

The developed technology concerns a method allowing the detection at a specific time of the presence of at least one human methylated site on a specific location within a promoter gene in a specific single stranded target nucleic acid sequence. For each targeted putatively methylated site, 2 adjacent primers, each with a different tag sequence, and a probe complemented to the junction of the 2 adjacent primers have been designed. The sample used comprises a plurality of different nucleic acid sequences.

The described technology allows the establishment of DNA profiles on many samples (up to 21) on many genes (up to 43) at a time, to subsequently establish DNA methylation signatures in various human samples.

Proof of concept

The analysis of thirteen tumor cell lines and one control cell line in parallel with MS-SSCP and MLM showed an exact correspondence.

Applications and competitive advantages

Criteria	MLM Method	Standard Method
Time needed for 40 genes analysis	2-3 days	2-3 months
Price per sample	~ 20 CHF	~ 1000 CHF
Throughput (data nb/test)	~ 800	1-20
Quantity of DNA	50-100 ng	~ 1000 ng
Fixed material use	Easy	Not possible
Optimization to different genes	Uniform protocol	Mandatory for each gene
Automation	Easy	Poor
Flexibility	High	Medium
Complicate bisulfite step	Not necessary	Mandatory