



ampli set LUNG 24 tests (144 reactions)

cat 1411

detection of methylation of promoter of genes involved in lung cancer

The methylation of the residues of cytosine in the "CpG islands" is very important for the regulation of the genic expression. The hyper-methylation of the "CpG islands" in the promoter region of a gene suppress the transcription of the same gene. In many tumors the hyper-methylation of the promoter of the suppressor genes, as p16, p15, E-cadherine and other genes as "DAP-kinase", inhibitor gene of the metastatic progression, O6-metilguanina DNA metiltransferase (MGMT), gene involved in the repair of DNA, Glutathione-S-transferasi (GSPT1) involved in the prevention of the oxidative damage of DNA etc.

Plasma and serum of patients carrier of malignant neoplasia contains much genomic DNA than the control subjects.

The principle of the assay is the extraction of genomic DNA from plasma or serum, the treatment with bisulfite sodium in order to convert the unmethylated residue of cytosine in uracil, the PCR amplification with specific oligonucleotides for the methylated sequences and unmethylated (MSP: methylation specific PCR) followed by the detection by electrophoresis on agarose gel. The assessment of the state of hypermethylation of a gene is an appreciable molecular marker of the risk, and allows a precocious diagnosis and a prognosis of a neoplastic diseases. The kit allows the detection of the methylation of the promoter of the tumor suppressor gene p16, of the DAP-kinase gene and of the O6-methylguanina DNA methyltransferase (MGMT). In the carcinoma of the lung 68% of the patients show at least one of these genes hyper-methylated.

Principle of assay

Extraction from :serum, tissue, sputum.

Conversion :treatment with sodium bisulfite.

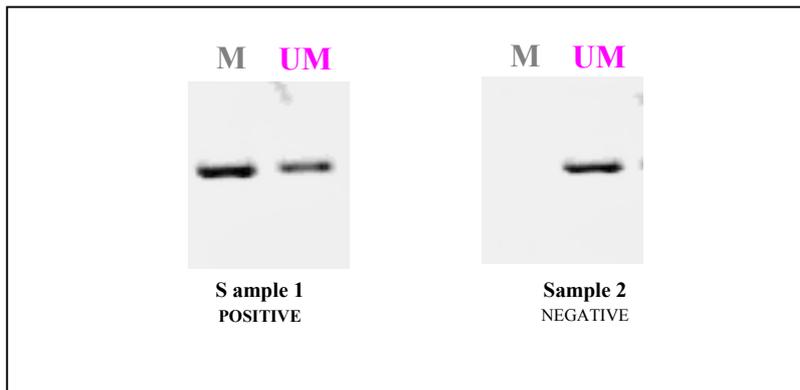
Amplification with specific primers for methylated and unmethylated sequences of the promoter of the genes:

p16 - DAP-Kinase - MGMT

Detection on agarose gel

Applicability

Serum, tissue, sputum, bronchial washing



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