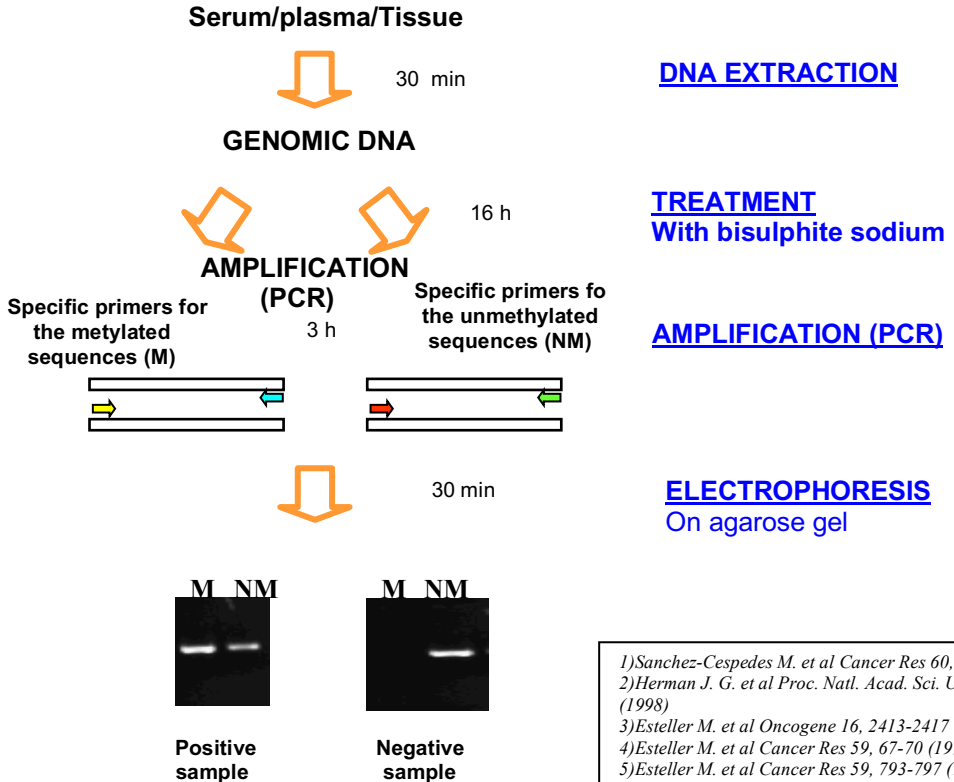
ASESSMENT OF GENE MGMT METHYLATION STATE

AMPLI MGMT Cat. n. 1.419

The methylation of the residues of cytosine in the "CpG islands" is very important for the regulation of the genic expression. The hypermethylation of the "CpG islands" in the promoter region of a gene suppress the transcription of the same gene. In many tumours the hypermethylation of the promoter of the suppressor genes, as p16, p15, E-cadherine and other genes as "DAP-kinase", inhibitor gene of the metastatic progression, O^6–metilguanina DNA metiltransferase (MGMT), gene involved in the repair of DNA, Glutatione-S-transferasi (GSTP1) involved in the prevention of the oxidative damage of DNA, etc has been showed.
The detection of the gene promoter methylation can be performed on genomic DNA. Plasma and serum of patients carrier of malignant neoplasia contains much genomic DNA than the control subjects (up to 4 times as much). The assessment of the state of hyper-methylation of a gene is an appreciable molecular marker of the risk, and allows a precocious diagnosis and a prognosis of neoplastic diseases.
The hyper-methylation state of "CpG island" is a interesting therapeutic target: the recovery of the "silenced" genes caold be carried out by using substances able to reconvert the hyper-methylation state.
The principle of the assay is the extraction of genomic DNA from serum, or plasma or tissue, the treatment with bisulphite sodium in order to convert the unmethylate residue of cytosine in uracil, the PCR amplification with specific oligonucleotides for the methylate sequences and unmethylated sequences using electrophoresis on agarose gel.
The kit allows the detection of the methylation state of the promoter of the MGMT gene.

PRINCIPLE OF METHOD



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