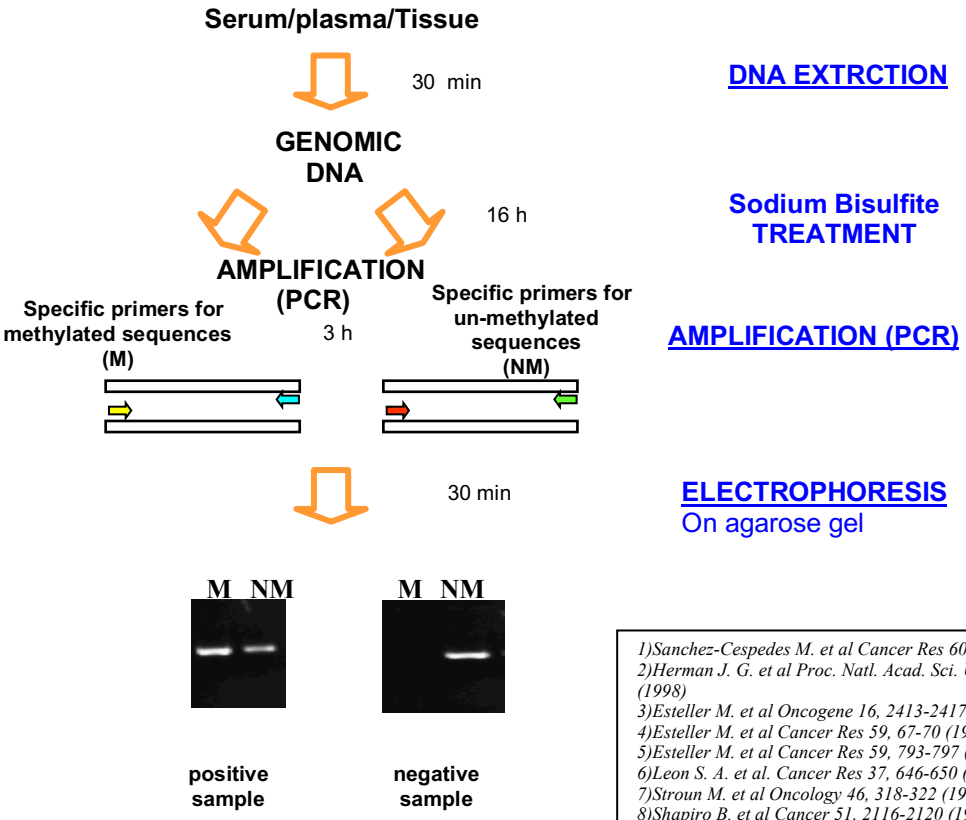
ASSESSMENT OF METHYLATION STATE OF GENE PROMOTER BRCA1 GENE

AMPLI-SET-BRCA1 Cat. n. 1.421

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 suppresses the transcription of the same gene. In many tumors it has been demonstrated 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 , 06-methyilguanine DNA methyltransferase (MGMT), gene involved in the repair of DNA and Glutatione-S-transferasi (GSPT1) etc. 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).Plasma and serum of patients carriers 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 transform the unmethylated residue of cytosine in uracil, the PCR amplification with specific oligonucleotides for the methylated and unmethylated sequences (MSP: methylation specific PCR) followed by detection on agarose gel. The assessment of the state of hypermethylation of a gene is an appreciable 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 of the BRCA1 gene, involved in the repair of DNA

PRINCIPLE OF METHOD



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