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IDENTIFICATION OF POLIMORFISM Ile105Val del GENE GSTP1

AMPLI-set-Ile105Val GSTP1 RT Cat. n.2.004RT

The family of genes GSTs (glutathione-S-transfere) consists of 16 genes coding for enzymes that have various biological functions, including detoxification of a variety of exogenous and endogenous electrophiles through conjugation with glutathione (GSH).It exert, therefore, a detoxifying role against carcinogens, therapeutic agents, toxins and products of oxidative stress. The platinum compounds are the most common and active used in the treatment of different types of cancer. It is believed that platinum-based substances act through the formation of "DNA adducts" that inhibit DNA synthesis and transcription, causing cell cycle arrest and apoptosis. The major limitation in the treatment with cisplatin is the acquisition of "drug resistance", which can be caused by inactivation of platinum compounds through conjugation with glutathione (GSH). Recently, several polymorphisms have been identified against genes involved in detoxification of drugs that can make the body more or less responsive to therapy as well as more or less susceptible to the toxicity of platinum compounds.
In the gene coding for the enzyme GSTP1 are known two polymorphisms: Ile105Val in exon 5, caused by the transition AG in position 1578 in exon 6 Ala114Val and CT caused by the replacement in position 2293.
The presence of the Val105 was associated with increased responsiveness to therapy, chemotherapy with platinum-containing compounds, increasing the survival of patients entered therapy.
The kit allows the identification of polymorphism Ile105Val, using the technique of Real-time PCR. The research of this polymorphism is performed after amplification with specific primers and hybridization with a probe that recognizes an internal sequence. The kit used for detection of polymorphism Ile105Val, the probe that recognizes the sequence wt (allele A) is conjugated to the FAM reporters, while recognizing the polymorphic sequence (allele G) is conjugated to Joe reporters.

Principle of the method:
A) extraction of genomic DNA
B) amplification and detection using real-time PCR equipment.
Applicability: On genomic DNA extracted and purified from whole blood samples.
Number of Tests: 24.

Kit Contains and storage

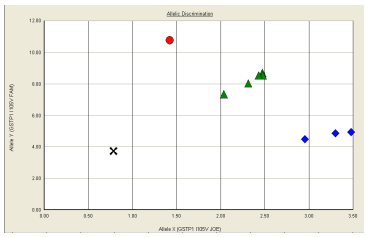
AMPLIFICATION	
PCR mix 2X	+4°C
H_2O sterile	-20°C
Primer-probe mix 20X	-20°C
WILD TYPE CONTROL (AA)	-20°C
Homozigous mutated control (GG)	-20°C
Heterozygous control (AG)	-20°C

Stability: more than 18 months if properly stored.

ANALYSIS OF THE RESULTS

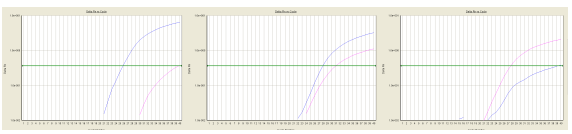
The analysis of the results will be made by the specific program (ALLELIC DISCRIMINATION) Real-time PCR instrument previously set. In any case, however, is also useful to analyze the graphs of Amplification PLOT, to ensure that the reaction has taken place correctly.

Allelic discrimination GSTP-1 Ile105Val



Legend:
Red: Allele WT (A)
Green: AllelesA e G
Blu: Allele MUT (G)

Amplification plots GSTP-1 Ile105Val



Legend: Blu: Allele WT (A) Purple: Allele Mut (G)

References
The Pharmacogenomics Journal (2010) 10, *54-61.*
Gynecologic Oncology (2009) 113, *264-269.*
Cancer Epidemiol Biomarkers Prev (2009) 18 (8), *2176-2181.*
Respiratory Research (2001), 2:*255-260.*