

IDENTIFICATION OF POLYMORPHISM XRCC3 (THR241MET 316 A> G) AND ERCC2 (Lys751Gln SNP 2251A> C) GENES AMPLI-set-XRCC3-ERCC2 Cat. n.2.023RT

The gene encoding XRCC3 a family member protein RecA / Rad51 participating in homologous recombination to maintain chromosome stability and repair DNA damage. This gene is located on chromosome 14q32, functionally complementary to irs1SF Chinese hamster, a mutant deficient shelter exhibiting unusual in a number of different DNA damaging agents (alkylating agents) and chromosomally unstable. A rare microsatellite polymorphism in this gene is associated with cancer in patients with different radiosensitivity. Recently, XRCC2 (Excision Repair Cross-complementary group 2) (aka XPD) is located on chromosome 19q13.3. The protein encoded by this gene (transcription by 24 exons) is involved in transcription and nucleotide excision repair is an integral member of the basal transcription factor complex / TFIIF BTF2. The gene product has ATP-dependent DNA helicase activity and belongs to the subfamily RAD3 / XPD helicase of It was assigned to play an important role in the effectiveness of alkylating agents platinum derivatives (2). In particular XRCC3 Thr241Met 316 A> G (rs1799794) was associated with an increased risk of severe neutropenia and hematology toxicity in patients treated with FOLFOX4 (p = 0.0008) in Caucasian patients (2). Were also reported in a meta-analysis of XRCC3 Thr241Met polymorphism is associated with response to platinum-based chemotherapy and there was a prognostic value of polymorphism of Thr241Met XRCC3 in patients with advanced NSCLC. In particular, a total of 14 Eligible studies with 2828 patients treated agents platinanti showed that carriers of the '241 variant allele were significantly associated with a good REPLIE, compared with those carrying the wild type allele Thr 241 (Thr Met vs., OR = 1.453, 95% CI 1.116- 1.892, P = 0.968 and ThrMet + MetMet vs. ThrThr, OR = 1.476, 95% CI :. 1087-2004, P = 0,696). This significant association was observed in Caucasian populations but not in Asia. Besides, there was no significant association of the polymorphism of Thr 241Met XRCC3con survival (ThrMet + MetMet vs. ThrThr, HR = 1.082, 95% CI: 0929-1261, P = 0.564), and there was no difference between the population Asian and Caucasian (3).

Principle of assay: A) extraction of genomic DNA;
B) amplification and detection using real-time PCR equipment;

Applicability: of genomic DNA extracted and purified from whole blood samples and tissue samples from fresh and paraffin.

Numero di Test: 25x2.

KIT CONTAINS AND STORAGE

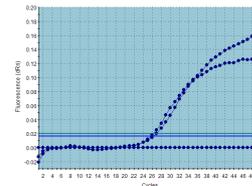
AMPLIFICATION	
PCR mix	+4°C
H ₂ O sterile	-20°C
Primer-probe mix 20 XRCC3	-20°C
Primer-probe mix 20 ERCC2	-20°C
Eterozigous Control	-20°C

Stability: more than 18 months if properly stored.

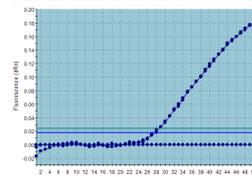
ANALYSIS OF RESULTS

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

AMPLIFICATION PLOTS XRCC3 ETEROZIGOUS



AMPLIFICATION PLOTS ERCC2 ETEROZIGOUS



Referenze:

Zou Y et al. *Jpn J Clin Oncol*, 44, 3, 241-248 (2014)
Cecchin E et al. *Pharmacogenomics J*, 13, 5, 403-409 (2013)
Qiu M et al. *PLoS One*, 8, 10, e77005 (2013)
Di Francia R et al. *Anticancer Drugs*, 24, 10, 1069-1078 (2013)