



COMT G742A GENETIC VARIANT

ORDERING INFORMATION

REF: GEN-044-25
Tests: 25 Reactions: 31
Manufacturer: BioMol Laboratories s.r.l.

CONTENTS OF THE KIT

The kit consists of reagents for Real-Time PCR amplification
*Reagents for the extraction of genomic DNA are not supplied in the kit

PRODUCT CHARACTERISTICS

Device belonging to the family of in vitro devices **REAL-TIME QUALITATIVE PCR-GENETIC VARIANTS- RESEARCH USE ONLY**. Detection of the G742A polymorphism of the COMT gene (rs4680), by Real-Time PCR technique. Kit optimized for Real-time PCR instruments Biorad CFX96 Dx, Biorad Opus Dx, Agilent AriaDx, Thermofisher QuantStudio™ 5 Real-Time PCR System.

SCIENTIFIC BACKGROUND

The **COMT gene mutation** plays a significant role in the body's processing of neurotransmitters like dopamine, norepinephrine, and epinephrine. This gene encodes the enzyme Catechol-O-methyltransferase (COMT), which is crucial for regulating mood, stress responses, and cognitive function. It has been proposed as a possible predictor of chronic pain development. It is thought to be involved in central pain processing, mood, and responses to physical and emotional stressors through its direct regulation of dopaminergic pathways, which results in compensatory changes in opioidergic processing in response to pain.

CLINICAL SIGNIFICANCE

The single-nucleotide polymorphism (SNP) rs4680 in the catechol-O-methyltransferase gene (COMT) is a missense variant (G>A, Val158Met) associated with altered activity of the COMT enzyme and suggested as a predictive feature for developing some chronic pain conditions. This polymorphism involves a substitution of the amino acid valine (Val) with methionine (Met) at position 158 of the enzyme. SNP rs4680 determines 3 possible genotypes with different levels of enzymatic activity: homozygous genotype A/A with low activity, heterozygous A/G with intermediate activity, and the homozygous G/G with high activity.

The missense variant Val158Met is most commonly analyzed in the context of pain research and was associated with pain symptoms in FM (Fibromyalgia) patients.

In different studies, the Val/Val genotype was associated with more morphine consumption during the acute postoperative period compared to the other genotypes.

Research suggests that individuals carrying the Met allele may be more susceptible to insomnia symptoms. This could be due to the slower breakdown of neurotransmitters like dopamine, which can lead to increased arousal and difficulty in transitioning to sleep.

§ Pain. 2024 Dec 1;165(12):e184-e189. The polymorphism Val158Met in the COMT gene: disrupted dopamine system in fibromyalgia patients?

§ J Clin Pharmacol. 2024 Mar;64(3):378-381. Genetic Polymorphism as a Possible Cause of Severe Postoperative Pain

§ Meta-Analysis J Geriatr Psychiatry Neurol. 2023 Mar;36(2):98-106. Association of Catechol-O-Methyltransferase Gene rs4680 Polymorphism and Levodopa Induced Dyskinesia in Parkinson's Disease: A Meta-Analysis and Systematic Review

§ PsyChJournal.2022;11:779-791. The effects of catechol-O-methyltransferase single nucleotide Polymorphisms on positive and negative symptoms of schizophrenia: A systematic review and meta-analysis.



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DESCRIPTION	LABEL	VOLUME	STORAGE
		GEN-044-25	
Mix oligonucleotides and probes	Mix COMT G742A 10X	1 x 62 µl	-20°C
Mix buffer and Taq polymerase enzyme	Mix Real-Time PCR 5X	1 x 124 µl	-20°C
Deionized H ₂ O	Deionized H ₂ O	1 x 1 ml	-20°C
Genomic DNA or recombinant DNA	Control 1	1 x 22 µl	-20°C
Genomic DNA or recombinant DNA	Control 2	1 x 22 µl	-20°C
Genomic DNA or recombinant DNA	Control 3	1 x 22 µl	-20°C

TECHNICAL CHARACTERISTICS

COD. GEN-044-25

STABILITY	18 months
REAGENTS STATUS	Ready to use
BIOLOGICAL MATRIX	Genomic DNA extracted from whole blood, tissues, cells
CONTROLS	Recombinant DNA for at least 3 analytical sessions
VALIDATED INSTRUMENTS	Biorad CFX96 Dx, Biorad Opus Dx and Agilent AriaDx, Thermofisher QuantStudio™ 5 Real-Time PCR System.
TECHNOLOGY	Real-time PCR; oligonucleotides and specific probes; 2 FAM/HEX fluorescence channels
RUNNING TIME	85 min
THERMAL CYCLING PROFILE	1 cycle at 95 °C (10 min); 45 cycles at 95 °C (15 sec) + 60 °C (60 sec)
ANALYTICAL SPECIFICITY	Absence of non-specific pairings oligonucleotides and probes; absence of cross-reactivity
LIMIT OF DETECTION (LOD)	≥ 5 ng of genomic DNA
LIMIT OF BLANK (LOB)	>40 Cq
REPRODUCIBILITY	99,9%
SPECIFICITY / SENSITIVITY	99,9%/98%