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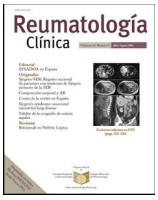

Original Article

Methylation Status of Interleukin-6 Gene Promoter in Patients with Behçet's Disease

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ABSTRACT

Background: IL-6 mRNA expression is significantly high in many autoimmune diseases such as Behçet's disease; this is often related with more aggressive phenotypes. Nevertheless, the essential molecular process for its high expression has not been completely realized. The aim of this study was undertaken to estimate the gene copy number variation and promoter methylation to IL-6's high expression.
Methods: This study was performed on 51 patients and 61 healthy controls. Initially, DNA and RNA were extracted from all specimens. Promoter methylation levels of IL-6 were evaluated by MeDIP-qPCR technique. Also, IL-6 gene expression was measured by Real-time PCR. After that, we evaluated the relationship between gene expression and methylation, as well as their relationship with clinical specification.
Results: As we expected, the expression level of IL-6 gene increased significantly in the patient group compared to the healthy subjects. Also, the relative promoter methylation level of the IL-6 mRNA was significantly lower in patient group compared to healthy group ($p < 0.001$).
Discussion: We disclosed that the promoter hypomethylation may be considered as one of the main defects for IL-6 mRNA high expression in patients with Behçet's disease.

Estatus de la metilación del promotor del gen interleucina-6 en pacientes con síndrome de Behçet

Palabras clave:
Síndrome de Behçet
IL-6
MeDIP-qPCR
Metilación

RESUMEN

Antecedentes: La expresión de ARNm de IL-6 es significativamente elevada en muchas enfermedades autoinmunes, tales como el síndrome de Behçet, y ello se relaciona a menudo con fenotipos más agresivos. Sin embargo, no se ha comprendido plenamente el proceso molecular esencial para esta expresión elevada. El objetivo de este estudio fue la estimación de la variación del número de copias del gen, y la metilación del promotor de la expresión elevada de IL-6.
Métodos: Este estudio se realizó en 51 pacientes y 61 controles sanos. Al inicio, se extrajo ADN y ARN de todas las muestras. Se evaluaron los niveles de metilación del promotor de IL-6 mediante la técnica MeDIP-qPCR. También se midió la expresión del gen IL-6 mediante PCR a tiempo real. Tras ello, evaluamos la relación entre la expresión del gen y la metilación, así como su relación con la especificación clínica.

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