Macrophage Migration Inhibitory Factor

Alternative Names
MIF
MMIF

Record Category
Gene locus

WHO-ICD
N.B.:Classification not applicable to gene loci.

Incidence per 100,000 Live Births
N/A to gene loci

OMIM Number
153620

Mode of Inheritance

Gene Map Locus
22q11.23

Description
The Macrophage Migration Inhibitory Factor (MIF) gene encodes a lymphokine involved in numerous cellular process such as cell-mediated immunity, immunoregulation, and inflammation. It regulates the function of macrophages in host defense through the suppression of anti-inflammatory effects of glucocorticoids. This lymphokine forms a complex with the JAB1 protein, which may play a role in integrin signaling pathways. Recent studies have also pointed out to a role of this gene in processes beyond immune regulation, including cell proliferation and differentiation, and tumorigenesis.

Studies have supported the notion that MIF-directed therapies might offer new treatment opportunities for human diseases in the future.

Molecular Genetics
MIF gene is located on the long arm of chromosome 22. It is a small gene consisting of three exons separated by introns of only 189 and 95 bp, and it covers less than 1 kb. The encoded protein called macrophage migration inhibitory factor is made up of 115 amino acids with a molecular mass of 12476 Da. The MIF protein contains two catalytic motifs. The 27-amino-acid motif, located at the N-terminus, functions as a phenylpyruvate tautomerase that can catalyze the conversion of 2-carboxy-2,3-dihydroindole-5,6-quinone (dopachrome) into 5,6-dihydroxyindole-2-carboxylic acid (DHICA). The second is a Cys-Ala-Leu-Cys catalytic site between residues 57 and 60 that appears to function as a disulfide reductase.

Two polymorphic sites within the promoter region regulate gene expression. These are a CATT repeat sequence at -794, and the SNP -173G/C. The presence of more than 5 repeats of the CATT sequence and the -173C allele have been known to associate with increased susceptibility to various inflammatory and autoimmune diseases, as well as prostrate and gastric cancers.

Epidemiology in the Arab World

Saudi Arabia
Abdallah et al., (2016) enrolled 124 Saudi patients with rheumatic heart disease (RHD) in a pilot study at pediatric cardiology clinics in Al Madina between 2013 and 2014. The control consisted of 202 healthy Saudi participants. All samples were genotyped for *MIF*-173 (rs755622) and *MIF*-794 (rs5844572) polymorphisms. The authors found that the age of onset was significantly greater for *MIF* -173C allele carriers than non-*MIF*-173C allele carriers in the group of RHD patients. The mean ages of onset of carriers of C-allele and non-carriers were 9.2 ± 1.6 and 7.5 ± 2.4, respectively. No significant association between the tetranucleotide variation and disease age of onset was found. The authors surmised that variations in MIF influenced disease severity and progression and recommended further studies to address and analyze the disease stage and patient age.

References
Abdallah AM, Al-Mazroea AH, Al-Harbi WN, Al-Harbi NA, Eldardear AE, Almohammadi Y, Al-Harbi KM. Impact of MIF Gene Promoter Variations on Risk of Rheumatic Heart Disease and Its Age of Onset in Saudi Arabian Patients. Front Immunol. 2016; 7:98. PMID: 27014277

Related CTGA Records
Rheumatic Fever-Related Antigen

External Links

https://www.genecards.org/cgi-bin/carddisp.pl?gene=MIF

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