MADS Box Transcription Enhancer Factor 2, Polypeptide A

Alternative Names
MEF2A

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
600660

Mode of Inheritance
N/A

Gene Map Locus
15q26.3

Description
The MEF2A gene encodes a member of the myocyte enhancer factor 2 (MEF2) family of transcription factors, that is conserved from yeast to humans. The encoded protein is required at different stages of the life cycle, and is expressed at high levels in cardiac, skeletal, neuronal cells, smooth muscles, and in the endothelium of coronary arteries. It is necessary for post-natal function, and activates many muscle-specific, growth factor-induced, and stress-induced genes. It also plays important roles in several cellular processes, including cell growth control, neuronal differentiation, apoptosis, and muscle development.

Within the last decade, a 21-bp deletion in exon 11 of this gene was reported as a causative mutation in a single large family with Autosomal Dominant Coronary Artery Disease. Later, more variants in this gene were discovered in families with CAD.

Molecular Genetics
The MEF2A gene, located at chromosome 15q26.3, consists of nine coding exons spanning approximately 115 kb in the genomic DNA. The gene is transcribed in a wide range of cell types, and has alternative mRNA splicing variants that give rise to muscle-specific isoforms. The N termini of MEF2 proteins contain highly conserved MADS and MEF2 domains, which together mediates protein dimerization and binding to AT-rich DNA sequences. The C terminus function as a transcriptional activation domain, has complex patterns of alternative splicing, and also has a role in nuclear localization.

The genomic sequence of MEF2A gene is highly polymorphic, with exon 11 being the most polymorphic. Exon 11 harbours several substitutions as well as indels.

Epidemiology in the Arab World

Saudi Arabia
Elhawari et al., (20102) conducted a study among 1186 coronary artery disease patients, and 885 healthy individuals to evaluate the role of the MEF2A gene variants and their association with CAD in Saudi population. Screening of the MEF2A gene showed several point mutations, and exon 11 was the most polymorphic locus with various substitution and insertion/deletion variants. One of these variants was an 11 CAG trinucleotide chain and a CCGCCGCCA sequence, resulting in frameshift and premature stop codons at nt146637 and nt146647, nt146780, or nt146783. However, these variants were not significantly associated with CAD. Another eight SNPs were identified in exon 11; three of them were coding and synonymous, while four were in the untranslated region (UTR). One of these SNPs (rs1059759 G>C) was associated with CAD, while another (rs34851361) exhibited a weaker relationship. In addition, one haplotype (1A-2G-3G-4A-5G-6A-7G-8A) with a frequency of 44.2% was associated with increased risk for CAD. These results conferred that MEF2A gene is a susceptibility gene for CAD.

References
Elhawari S, Al-Boudari O, Muiya P, Khalak H, Andres E, Al-Shahid M, Al-Dosari M, Meyer BF,

Al-Mohanna F, Dzimiri N. A study of the role of the Myocyte-specific Enhancer Factor-2A gene in coronary artery disease. Atherosclerosis. 2010; 209(1):152-4. PMID: 19782985

Related CTGA Records

Coronary Artery Disease, Autosomal Dominant, 1

External Links

https://ghr.nlm.nih.gov/gene/MEF2A
http://www.genecards.org/cgi-bin/carddisp.pl?gene=MEF2A

Contributors

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