Atlas of Genetics and Cytogenetics in Oncology and Haematology

OPEN ACCESS JOURNAL

INIST-CNRS

Gene Section
Short Communication

FAM107B (family with sequence similarity 107, member B)

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Published in Atlas Database: January 2015
Online updated version : http://AtlasGeneticsOncology.org/Genes/FAM107BID53778ch10p13.html
Printable original version : http://documents.irevues.inist.fr/bitstream/handle/2042/62513/01-2015-FAM107BID53778ch10p13.pdf
DOI: 10.4267/2042/62513

Abstract

FAM107 members contain an N-terminal domain of unknown function (DUF1151) that is conserved across species. Mammals have two genes, FAM107A and FAM107B, which expressions are strong in neural cells, whereas their expressions are mostly down-regulated in cancer cells. Both proteins appear to alter cytoskeleton rearrangements and are involved in cell migration and invasion. The molecular mechanisms underlying the diverse biological functions of FAM107 remain unclear, while it shows functional similarity with heat-shock proteins (HSPs) as well as reactions to cellular stress.

Keywords
tumor suppressor gene, heat-shock protein, neuron

Identity

Other names: HITS, C10orf45

HGNC (Hugo): FAM107B

Location: 10p13

Note
The FAM107B protein is encoded by FAM107B gene.

DNA/RNA

Description

FAM107B gene is located on the minus strand of chromosome 10, p13, which is on the short arm of the chromosome.

Transcription

FAM107B has ten transcript variants. Variant 1 and 3 through 10 encode the same isoform (a: 131 aa) with coding DNA sequence consisting of 396 bps on three exons. Variant 2 lacks an exon and initiates translation at an alternate start codon, which encodes longer isoform (b: 306 aa) with a distinct N-terminus.

Protein

Note
FAM107 members contain an N-terminal domain of unknown function (DUF1151) that is conserved across species, including mammalian, xenopus, fish, and drosophila, and show no homologous matches to other functionally conserved domains. Mammals have two genes, FAM107A and FAM107B, which encode for proteins of 144 amino acids (aa) and 131 aa, respectively.

Description

131 amino acids, 15.6 kDa. FAM107B protein includes an N-terminal (aa 1-66) conserved domain DUF1151, a nuclear localization signal (NLS) and a C-terminal (aa 61-112) variable coiled-coil domain (Nakajima et al., 2010; Nakajima et al., 2014).

Expression

FAM107B is expressed in most tissues and found in all stages of human development. FAM107B gene has a promoter region with heat-shock transcription factor 1 (HSF1) binding sites, and FAM107B expression is increased after heat-shock or hyperthermia treatment (Nakajima et al., 2010).

Localisation

Nucleus (Nakajima et al., 2010)

Function

FAM107B is regarded as a candidate tumor suppressor gene because a loss of FAM107B expression was observed to be a common phenomenon in cancers of various organs, resulting in tumor development and proliferation. Forced expression of FAM107B inhibited cancer cell proliferation in response to growth factors in vitro and tumor xenograft growth in vivo (Nakajima et al., 2010; Nakajima et al., 2012).

Homology

FAM107B protein sequence is nearly 98% identical with mouse and rat homologues. FAM107A and FAM107B proteins have 65% sequence similarity in their DUF1151 regions (Nakajima et al., 2010; Nakajima et al., 2014).

Mutations

A point mutation in the C-terminal region (chromosome 10:14603968 CïG?TïA transition) is frequently observed in basal-like breast cancer (Ding et al., 2010).

Implicated in

Breast cancer

A point mutation in the C-terminal region was frequently observed in basal-like breast cancer (Ding et al., 2010), and mutated amino acid sequence of FAM107B in breast cancer was identified as a unique tumor antigen predicted to bind to HLA-A2 (Li et al., 2011). Copy number aberrations (CNA) of FAM107B are found specifically in basal-like breast cancer (Weigman et al., 2012). In addition, genome-wide DNA methylation study was performed to identify differentially methylated sites between monozygotic twins discordant for breast cancer. FAM107B was identified as a hypermethylated region in breast cancer blood samples (Heyn et al., 2013). In analysis for FAM107B expression and the clinico-pathological parameters, FAM107B expression intensity was positively correlated with the expressions of HER2 and Ki-67, but it was inversely correlated with PR expression. Accordingly, FAM107B expression was mostly lost in HER2 negative, Ki-67 negative, PR positive, and desmoplastic reaction-negative type breast cancer, which is believed to be a non-aggressive or indolent phenotype (Nakajima et al., 2012).

Stomach Cancer

FAM107B expression is decreased in intestinal-type gastric adenocarcinomas but not in diffuse type or mucinous adenocarcinomas (Nakajima et al., 2010).

Colon Cancer

FAM107B expression is decreased during the processes in the colorectal adenoma-to-carcinoma transition (Nakajima et al., 2010).

Uterine Cervical Cancer

In uterine cervical diseases, FAM107B expression is lost in invasive squamous cell carcinoma but not in cervical intraepithelial neoplasia (CIN) (Nakajima et al., 2012).

Autism Spectrum Disorder

Six genome-wide association studies (GWASs) were integrated to figures out genetic networks of candidate genes associated with autism spectrum disorders (ASD). SNP close to FAM107B is mentioned as one of the ASD associated candidates (Poelmans et al., 2013).

Major Depression

Genome-wide DNA methylation study using post mortem frontal cortex of healthy and major depression subjects figured out FAM107B region is differentially methylated in neural cells of major depression (Guintivano et al., 2013).

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This article should be referenced as such:

Nakajima H, Koizumi K. FAM107B (family with sequence similarity 107, member B). Atlas Genet Cytogenet Oncol Haematol. 2016; 20(2):71-73.