Gene Section

Short Communication

RPRM (reprimo, TP53 dependent G2 arrest mediator candidate)

Alejandro H Corvalan, Veronica A Torres

Laboratory of Molecular Pathology and Epidemiology, Department of Hematology - Oncology, School of Medicine - P Universidad Catolica de Chile, 391 Marceola St - Santiago 8330074 Chile (AHC, TorresVAT)

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Identity

Other names: FLJ90327, REPRIMO
HGNC (Hugo): RPRM
Location: 2q23.3

DNA/RNA

Description
Reprimo gene consists of 1 exon. The gene spans 1,47 kb of genomic DNA on the chromosome 2 in the minus strand.

Transcription
The mRNA is 1496 bp in length.

Protein

Description
The open reading frame encodes a 109 amino acid protein with an estimated molecular weight of 11774 Da. Reprimo is a highly glycosylated protein which has two sites in amino acids 7 and 18. The protein has a potential transmembrane site covering amino acids 56 to 76.

Expression
The expression of Reprimo is induced by tumor protein p53 following X-ray irradiation.

Localisation
When Reprimo is ectopically expressed, it is localized in the cytoplasm.

Function

Implicated in

Various cancers

Note
The aberrant methylation of the promoter region of Reprimo is a common event that may contribute to the pathogenesis of some types of human cancer. Promoter methylation of Reprimo was found in pancreatic cancer (91%), gastric cancer (90%), gallbladder cancer (62%), lymphomas (57%), colorectal cancer (56%) and esophageal adenocarcinomas (40%). In breast cancer, leukemias and lung cancer, promoter methylation of Reprimo was found in less than 40% of tested cases.

Gastric cancer

Disease
Aberrant hypermethylation of Reprimo is frequently found in primary gastric cancer as well as in pair plasma samples. In plasma from asymptomatic controls, Reprimo is infrequently methylated. Therefore, plasmatic detection of Reprimo is a putative biomarker for early detection of gastric cancer.
The above histogram represents the percentage of positive cases for Reprimo and other genes (APC, SHP1, CDH-1, ER, SEMA3B and OST2) in 43 prospectively collected gastric cancer cases and 31 asymptomatic age- and gender-matched controls. Only Reprimo shows a significant difference in plasma between gastric cancer and asymptomatic controls (Bernal et al., Clin Cancer Res. 2008;14:6264-9).

Pancreatic cancer

Disease
Aberrant hypermethylation of Reprimo is also common in pancreatic cell lines (91%) and in pancreatic adenocarcinomas (66%). Reprimo methylation is correlated with poor prognosis in a large series of resected pancreatic cancers. This fact raises the possibility that aberrant methylation of Reprimo is an epigenetic event that may have a mechanistic role in pancreatic cancer.

References


This article should be referenced as such: