SPINK7 (serine peptidase inhibitor, Kazal type 7 (putative))
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Identity

Hugo: SPINK7
Other names: ECRG2; ECG2; MGC133105; MGC133106
Location: 5q33.1
Local order: Telomeric to SPINK5L3 and centromeric to SPINK1.

DNA/RNA

Diagram of ECRG2 gene. Exons are represented by red boxes. Exons 1 to 4 from 5’ to 3’ direction.

Description

The ECRG2 gene contains 4 exons and spans about 3540 bp.

Transcription

The full-length of cDNA of ECRG2 gene was revealed 569 bp, the open reading frame (ORF) is 258 bp. The sequence upstream of the exon-1 upon the NT_2023158.1 genomic sequence revealed a typical TATA box contained promoter at 44 bp from the predicted translation start site. The transcription start site is just 6 bp upstream of the 5’ end sequence.

Pseudogene

None.

Protein

Note: The N-terminal 1-19 is the single peptide of the protein. The C-terminal 30-85 of the protein contains a typical x(8)-C-x(6)-C-x(7)-C-x(6)-Y-x(3)-C-x(2,3)-C-x(17)-C conserved region, coding a Kazal type serine protease inhibitors (Kazal) domain.

Description

The molecular weight of the encoding protein contains 85 amino acids is about 9.23 kDa. ECRG2 gene contains a typical Kazal serine protease inhibitors conserved domain about 56 amino acids at its C-terminal and three kinase phosphorylation site (protein kinase C, Casein kinase II and Tyrosine kinase).

Expression

ECRG2 gene was expressed in normal tissues, such as esophagus, liver, colon and lung. But it was less expressed in the cancerous tissues, especially low frequency of expression of ECRG2 gene in esophageal cancer but was less expressed in the cancerous tissues, especially low frequency of expression of ECRG2 gene in esophageal cancer.

Localisation

The protein was localized on the cell membrane.

Function

The expression of ECRG2 can inhibit the migratory ability of high metastatic tumor cells.
Homology
The sequence of the ECRG2 gene did not reveal remarkable similarity to the known sequence in the homology analysis with the public database of GenBank while the deduced amino acid sequence showed 97% homology to a tumor associated KAZAL-type serine protease inhibitor peptide (US patent 5851987).

Mutations
Note: None

Implicated in
Esophageal cancer
Note: Expression profile of ECRG2 gene in 7 normal esophageal epithelia, 51 esophageal cancers and 33 tumor adjacent tissues were 100%, 21% and 52% respectively. About 79% of ECRG2 gene was no expressed in the esophageal cancer. ECRG2 was highly expressed in the adult normal esophageal tissue, low expressed in the fetal esophageal tissue and completely loss of expression in the esophageal cancer and corresponding adjacent tissues. The results show that the ECRG2 gene may be a specific gene for carcinogenesis of esophagus.

The studies provide more evidences on the role of ECRG2 in the inhibition of tumor cell proliferation, migration and metastasis, and give a straightforward way to block enzymatic activity in extra-cellular matrix to achieve the therapeutic benefit in the tested human cancers.

1. Short tandem repeat polymorphism in a novel esophageal cancer-related gene (ECRG2) implicates susceptibility to esophageal cancer
2. Potential interaction partner for ECRG2 might be involved in regulation of cell proliferation and apoptosis and in various physiological processes.
3. Data suggest that the physical interaction of esophageal cancer related gene 2 (ECRG2) and metallothionein2A (MT2A) may play an important role in the carcinogenesis of esophageal cancer.

References

This article should be referenced as such: