Gene Section
Mini Review

STOML2 (stomatin (EPB72)-like 2)

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Identity
Other names: HSPC108, SLP-2
HGNC (Hugo): STOML2
Location: 9p13.3

DNA/RNA
Description
The gene encoding SLP-2 was 3250 bp long and consisted of ten exons interrupted by nine introns.

Transcription
There are 5 transcripts in this gene. However, a single 1.3 kb mRNA transcript encoding SLP-2 was ubiquitously expressed, and the translation length is 356 residues (Owczarek et al., 2001).

Pseudogene
No known pseudogenes.

Protein
Description
NP_038470; 356 aa.
Human SLP-2 is presented on chromosome 9p13. The sequence at the 5'-end of the mRNA is interesting for the presence of three potential ATG initiator sites, all sharing the same open reading frame however, commonly forms a 356 amino acid residue polypeptide with a predicted molecular weight of 38.5 kDa. Similar to other family members, SLP-2 as well as the stomatin from other species shares a characteristic NH2-terminal hydrophobic domain as well as a consensus cognate stomatin signature sequence that defines the stomatin gene family; however, it lacks the NH2-terminal hydrophobic domain (Wang et al., 2000). The SLP-2 protein contains an alanine-rich domain and a number of potential protein kinase C phosphorylation sites, cAMP-and-cGMP-dependent protein kinase phosphorylation sites and casein kinase II phosphorylation sites.

Expression
SLP-2 is widely expressed in many tissues and thought as a new component of the peripheral membrane skeleton. Especially, in the erythrocyte membrane, it also appears to exist at least partially as an oligomeric protein complex. The overexpression of SLP-2 can be found in many kinds of human tumors, such as esophagael squamous cell carcinoma, laryngeal squamous cell carcinoma, endometrial adenocarcinoma, and lung cancer.

Localisation
Predominantly on plasma membrane and in the cytoplasm.
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Function
Human SLP-2 protein with unknown function, we hypothesize that SLP-2 may link stomatin or other integral membrane proteins to the peripheral cytoskeleton and thereby play a role in regulating ion channel conductances or the organization of sphingolipid and cholesterol-rich lipid rafts. Some recent results indicated that SLP-2 protein can significantly influence on multi-tumor progression, which allowed us to identify this unwell-known gene that maybe modulate invasion and metastasis of different cancers.

Homology
SLP-2 is one of the members of the Stomatin superfamily, among which identified vertebrate homologues are SLP-1, SLP-2, and SLP-3. SLP-1 is most abundant in brain and shares many similarities with UNC-24 (STOML1). SLP-3 is specifically expressed in olfactory sensory neurons (Seidel et al., 1998; Goldstein et al., 2003).

Mutations
No mutations have been reported for SLP-2. Mutation detection of SLP-2 exons was done using PCR and automated sequencing with 30 patient-matched human esophageal cancer tissues. No mutation was found within the open-reading frame of SLP-2 after sequencing results were aligned by the procedure SeqMan of DNASTar software (Zhang et al., 2006).

Implicated in
Various cancers
Note
SLP-2 has been shown to be over-expressed in a number of different cancers, including esophageal squamous cell carcinoma (ESCC), laryngeal squamous cell carcinoma (LSCC), endometrial adenocarcinoma (EAC), lung cancer (LC) and breast cancer (see below).

Esophageal squamous cell carcinoma (ESCC)
Prognosis
As shown in human ESCC, a significant correlation exists between SLP-2 protein high expression and the depth of ESCC invasion (P=0.033) (Wang et al., 2009). Also, decreased cell growth and tumorigenesis in the antisense transfectants revealed that SLP-2 may be important in ESCC tumorigenesis (Zhang et al., 2006).

Laryngeal squamous cell carcinoma (LSCC)
Prognosis
In addition, SLP-2 takes part in human LSCC malignant phenotype formation and development. High-level expression of SLP-2 protein could contribute to the prognostic characteristics of lymph node metastasis in human LSCC (Cao et al., 2007).

Breast cancer
Prognosis
High-level expression of SLP-2 protein shows a worse prognosis, including increase in tumor size, progress in clinical stage, and appearance of lymph node and/or distant metastasis and is associated with decreased overall survival (P=0.011). Moreover, SLP-2 can be strongly associated with another important prognostic factor, HER-2/neu protein expression, which shows that they may act as dependent prognostic factors to indicate poor prognosis (Cao et al., 2007).
**Endometrial adenocarcinoma**

**Prognosis**

Similarly, SLP-2 is also overexpressed in human endometrial adenocarcinoma (EAC) at both mRNA and protein level. Sense transfection of SLP-2 in EAC cell line accelerated cell growth whereas the antisense transfection reduced cell growth in vitro (Cui et al., 2007).

**Lung cancer**

**Prognosis**

At last, SLP-2 was overexpressed in human lung cancer (Zhang et al., 2006). High-level SLP-2 expression was significantly correlated with distant metastasis, decreased overall survival and disease-free survival. SLP-2 overexpression was an independent prognostic factor in multivariate analysis using the Cox regression model (p<0.05) (Chang et al., 2009).

**Mitochondrial component**

**Note**

SLP-2 localizes in mitochondria, affects mitochondrial membrane potential (MMP) and ATP production. Hence, SLP-2 is a mitochondrial protein and therefore, functions in energy process by MMP maintenance, and subsequently affecting cell motility, proliferation and chemosensitivity (Wang et al., 2009).

**References**


This article should be referenced as such: