

Gene Section

Mini Review

SEL1L (sel-1 suppressor of lin-12-like (C. elegans))

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Published in Atlas Database: October 2005

Online updated version: <http://AtlasGeneticsOncology.org/Genes/SEL1LID42246ch14q24.html>
DOI: 10.4267/2042/38293

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Identity

Hugo: SEL1L

Other names: IBD2; SEL1-like

Location: 14q24.3-q31

Local order: SEL1L is located within a 'Gene Desert area' or 'Genome Deserts'; centromeric to FLRT2 (fibronectin leucine rich transmembrane protein 2) and telomeric to GTF2A1 (general transcription factor IIA) and TSHRq31 (thyroid stimulating hormone receptor).

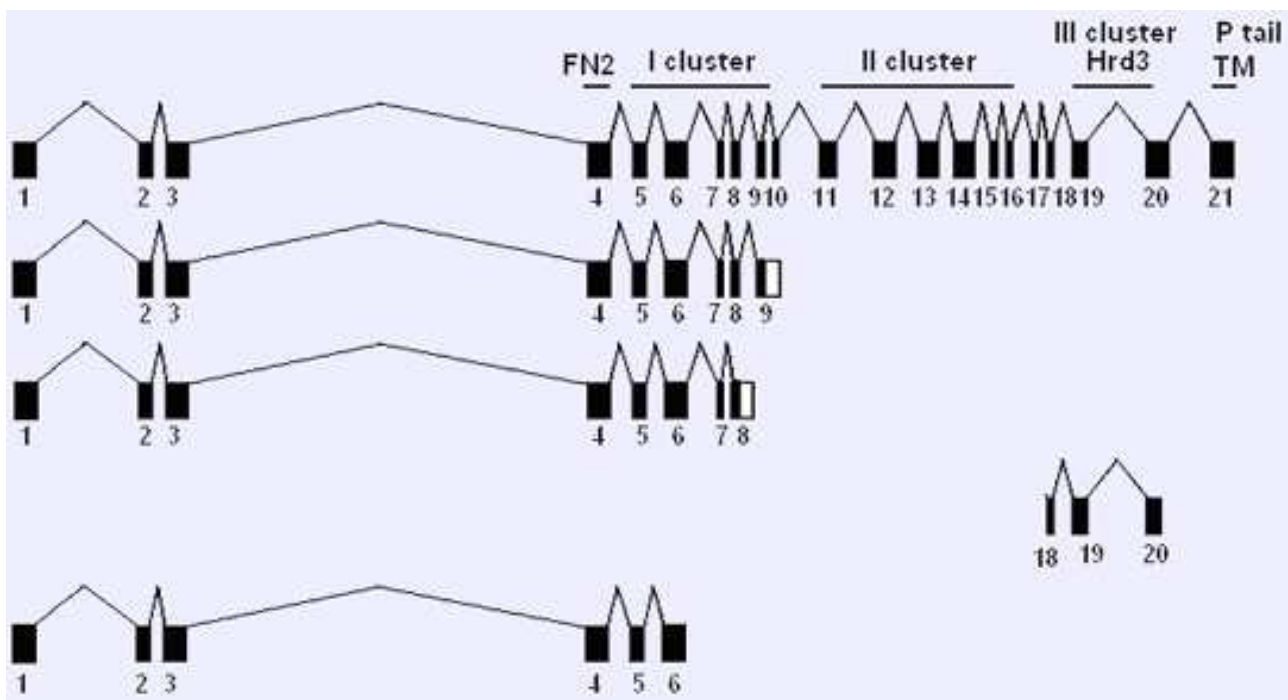
Note: SEL1L is the human ortholog of the C.Elegans

sel-1 (suppressor enhancer of lin-12) gene. It shows a high degree of cross-species conservation in its nucleotide and protein sequence.

DNA/RNA

Description

SEL1L genomic size is of 62,24 Kb localized from 81069886 to 81007646. 3' the first exon lies the basal core of the promoter, a TATA-less promoter containing four SP1 binding sites and a CAAT box. A CpG island



A graphical representation of SEL1L isoforms. The black numbered rectangles correspond to the exons, while the white rectangles correspond to the intronic sequence which is retained in the alternative isoforms. The SEL1L domains are indicated on the top of the isoforms. (FN2=fibronectin type II domain; I, II and III clusters of SEL-1 like repeats; Hrd3; TM=transmembrane; P= proline rich domain).

is located between -550bp and the start codon. SEL1L embryonic kidney cells. The C-terminal tail consists of over 5,0Kb untranslated sequences likely containing key regulatory elements.

Transcription

The sequence is composed of 21 exons and produces at least five different alternative transcripts (A-E) which originate from alternative splicing and putative promoter usage. Exons 1-6 are common to forms A-B-C-E.

Pseudogene

No known pseudogenes

Protein

Note: SEL1L is a multimodular protein consisting of several domains and signal sequences that confer the multifaceted specificities to the molecule.

Description

SEL1L is not a member of a vast family of proteins but the several described isoforms (over 4) give the appearance of belonging to a multifamily of molecules having perhaps redundant functions.

Expression

Ubiquitously expressed only in fetal and neoplastic tissues. In normal adult tissues is highly expressed in the acini and in the alpha cells of the pancreas; in general is highly represented in secretory cells such as plasma cells.

Localisation

SEL1L protein can have a nuclear, cytoplasmic and nuclear-cytoplasmic location.

Function

May have a role in the ER-associated protein degradation (ERAD) system (similarity with Hrd3).

Negative regulator of the NOTCH pathway in *C. elegans*.

May play a role in TGF beta signalling.

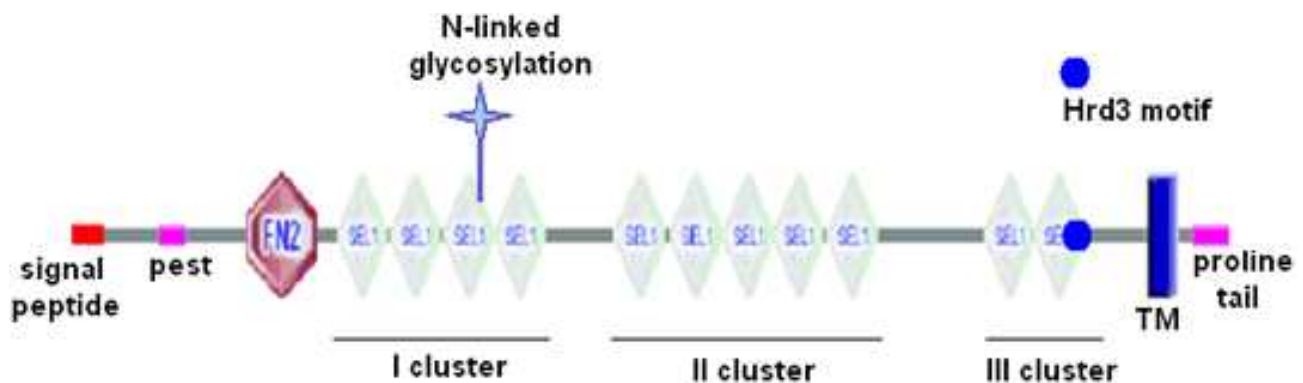
In breast and pancreatic tumor decrease tumor growth and aggressiveness, possibly involving cell-matrix interaction.

Homology

Comparative sequence analysis across different regna, including metazoa, fungi, viridiplantae and bacteria, revealed the remarkable conservation of its primary sequence, although the gene structural complexity increased in evolution. Among mammals, SEL1L shares strict amino acid identity with chimpanzee (99%), dog (97%), hamster (92%), mouse (93%) and rat (92%). It also shows a good similarity with the model organisms such as xenopus (82%), chicken (83%), zebrafish (73%), *Drosophila melanogaster* (51%) and *C. elegans* (46%) (Table 1). *Arabidopsis thaliana* and *Saccharomyces cerevisiae* display lower similarity (34% and 28%, respectively).

Mutations

Note: Neither causative nor functional mutations were found except for the presence of two base substitutions in the minimal promoter region in two well differentiated lung adenocarcinoma that led to a significant increase in the transcription. A polymorphic base substitution was reported in the fibronectin type II domain of the gene in children affected by persistent hyperinsulinemic hypoglycemia (insulinoma) of infancy which induces a major change in the amino acid composition.



SEL1L protein structure: SEL1L is a multimodular protein containing several structural and functional domains as well as signal sequences. The signal peptide (from 1 to 22 amino acid residues) and the Pest sequence (from 80 to 102 amino acid residues) are represented by red and pink rectangles. The fibronectin type II domain (from 120 to 168 residues) is symbolized by the hexagon (FNII), the SEL-1-like repeats are represented by rhombi and are distributed in tandem along the central portion of the protein in three large clusters (I cluster: 183-326; II cluster: 373-554 and III cluster: 664-675 residues). The Hrd3 like motif is located within the last SEL-1-like repeat (664-675 residues) and is represented by an circle. The transmembrane region (TM) (739-761 residues) and the proline-rich tail (770-793 residues) are symbolized by a blue rectangle. The N-linked glycosylation is also underlined.

Implicated in

Considering the overall results published on SEL1L by various investigators working in different organisms, it can, perhaps, safely be deduced that this gene plays a fundamental role in eukaryotic intracellular protein degradation processes. Protein degradation is becoming a central theme in cancer biology and recently therapeutic approaches that use inhibitors of proteins belonging to ubiquitin-proteasoma pathway have been developed in solid tumors and haematological diseases. A survey of the expression of SEL1L mRNA as well as its encoded protein on a series of cancerous and pre-neoplastic lesion, revealed the role of SEL1L in cancer progression. Furthermore, its expression in breast cancer correlated with patient's survival. In vitro studies indicated that SEL1L protein affects those pathways which regulate signalling (cell-cell and or cell-matrix) interactions. Available data derived from several organisms indicate that it may function in the protein degradation processes through ubiquitin-proteasome system and perhaps in regulating important pathways such as Notch and TGF-beta. The fundamental question raised by the observation that SEL1L gets up-modulated during the early steps of tumor transformation is of paramount importance for early diagnosis. Currently it is only possible to hypothesize that the increased SEL1L levels are required in order to meet the advent of genetic and/or genomic structural alterations acquired during cancer initiation or to influence intra-cellular signalling. Its presence may be important in protecting cellular homeostasis from genetic mutations.

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This article should be referenced as such:

Biunno I, Cattaneo M. SEL1L (sel-1 suppressor of lin-12-like (C. elegans)). Atlas Genet Cytogenet Oncol Haematol.2006; 10(2):93-96.
