

Gene Section

Review

VHL (von Hippel-Lindau tumor suppressor)

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Identity

HGNC (Hugo): VHL

Location: 3p25-26

Note

Tumour suppressor.

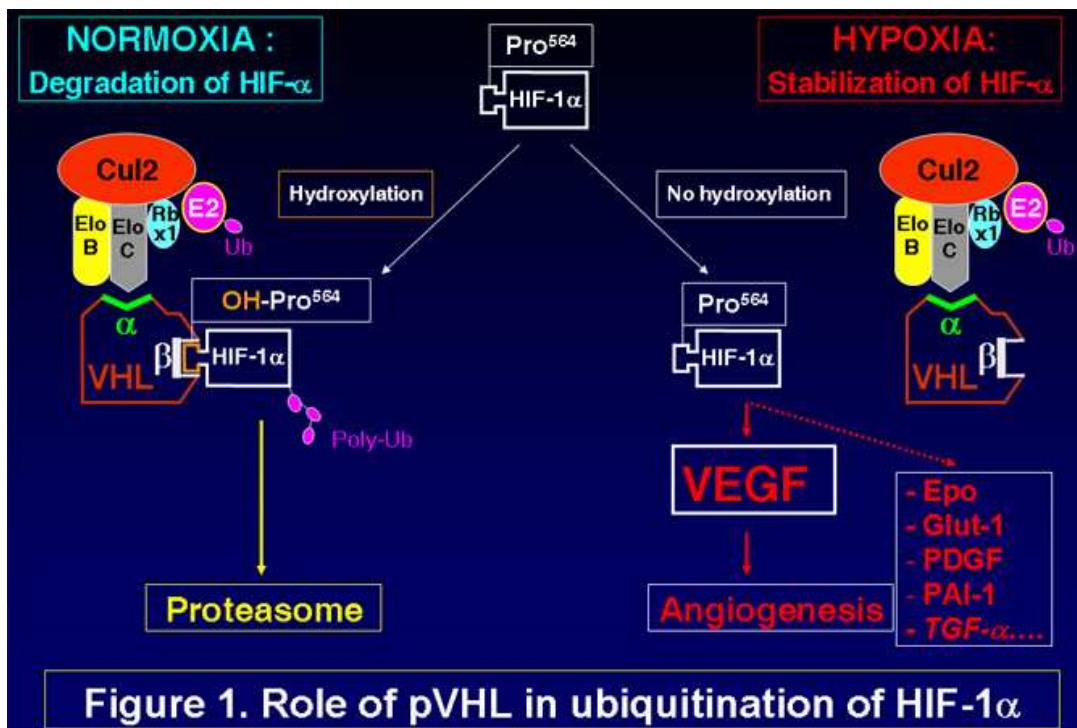
DNA/RNA

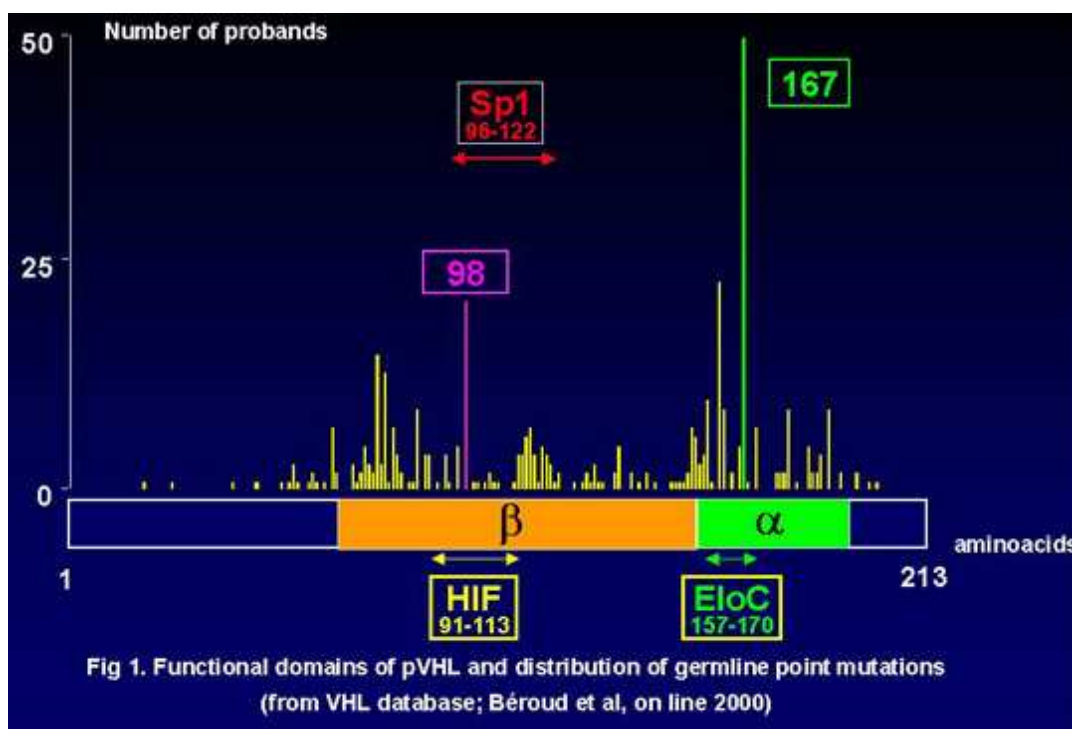
Description

The VHL gene spans 10 kb and is composed of three exons.

Transcription

The VHL gene encodes a 4.7 kb mRNA which is widely expressed in both foetal and adult tissues. An alternatively spliced VHL transcript has been detected reflecting the absence of exon 2 (isoform II) but no endogenous associated protein has been reported.





Protein

Description

The full-length VHL protein, pVHL, contains 213 amino-acids (28-30 kDa) ("pVHL30"). A second major VHL-gene product arises by internal translation initiation from the codon 54 methionine, producing a 160 amino-acid protein (18-19 kDa) ("pVHL19").

Expression

pVHL is widely expressed in both foetal and adult human tissues.

Localisation

The pVHL is largely a cytoplasmic protein but appears to shuttle between the cytoplasm and nucleus.

Function

pVHL interacts with three other proteins, elongin C and B and Cullin 2 (CUL2), in a complex referred to as VCB-CUL2. pVHL has two main structural domains: an N-terminal domain composed mainly of β -sheets (the β domain) and a smaller C-terminal domain between aminoacids 155-192 composed mainly of a helices (a-domain). The a domain consists of three a helices that combines with a fourth a helice donated by elongin C. The β -domain is on the opposite side of the a domain and is free to contact other protein.

VHL and angiogenesis- A main function of the pVHL is to negatively regulate hypoxia-inducible mRNAs such as the mRNA encoding VEGF, EPO, PDGF and the glucose-transporter GLUT-1. pVHL plays a critical role in targeting the hypoxia-inducible transcription factor HIF-1 α for degradation by the proteasome. HIF-

1 α contributes to form the HIF-1 transcriptional complex responsible for activation of genes involved in metabolism, angiogenesis and apoptosis. The VCB-CUL2 complex has been demonstrated as a ubiquitin-ligase system presenting many similarities with the SCF system ("Skp1-CUL1-Fbox protein"). HIF is normally degraded under normoxic conditions and binding to VHL is dependent on hydroxylation of Pro 564 in HIF-1 α (Figure 1). When the VHL gene is mutated, absence of HIF degradation is responsible for abnormal accumulation of VEGF and other hypoxia-inducible mRNA explaining the angiogenic phenotype of VHL tumours. pVHL may also downregulate VEGF production by direct binding and inhibiting to the transcriptional activator SP1.

In homozygous VHL knock-out mice, embryos will die early because of a major disorder of placental vasculogenesis.

Other functions

pVHL plays a role in:

- ability of cells to exit the cell cycle and enter the quiescent state.

- assembly of extracellular fibronectin matrix.

- degradation of TGF α LYT10, TGF β , and carbonic anhydrases CA9 and CA12.

- regulation of the urokinase-type plasminogen activator system.

- inhibition of the hepatocyte growth factor-induced invasion in renal cell carcinoma.

- a direct interaction with atypical protein kinase C (PKC) ζ and ι has also recently been demonstrated.

Thus, VHL appears as a multifunctional gene and may play a gatekeeper role especially in kidney.

Homology

The primary sequence structure of pVHL shows minimal homology to any known protein but evolutionary conservation of the pVHL is very strong except for the first 53 amino acids.

Mutations

Germinal

Germline mutations cause von Hippel-Lindau disease. VHL mutations are heterogeneous and distributed widely throughout the coding sequence except 5' for the translation initiation site for pVHL19. There is a few recurrent mutations and only one founder effect is known, originating from Germany (T292C resulting in a Tyr98His substitution). Point mutations occur in about 60% of cases (Figure 2) and large deletions in about 40%. VHL 1 (without pheochromocytoma) is mainly produced by mutations responsible for truncated protein (deletions, frameshift mutations and nonsense mutations). VHL type 2 (with high risk of pheochromocytoma) is mainly produced by missense mutations. Type 2B is the potentially "full" form of the disease (frequent mutations: Arg167Gln, Arg167Trp). Type 2A is associated with a very low risk of clear cell renal cell cancer (RCC) (common mutation: Tyr98His). Type 2C is characterized by the occurrence of pheochromocytoma only (example: Leu188Val).

Between 10 and 15% of cryptic VHL cases could be explained by de novo mutations and there are some cases of germline mosaicism.

There is some evidence that genetic modifiers may influence the phenotypic expression of the disease.

Somatic

Mutations are encountered in 60% of sporadic clear cell RCC. In addition, 15% of tumours show evidence of inactivation by methylation. VHL alterations have been associated with occupational exposure to trichlorethylene.

Somatic mutations are also frequent in CNS sporadic hemangioblastoma but rarer in sporadic endolymphatic sac tumours, pancreatic serous cystadenomas and endocrine tumours, epididymal cystadenomas and pheochromocytomas.

Implicated in

von Hippel-Lindau disease

Disease

Von Hippel-Lindau (VHL) disease is a hereditary devastating cancer syndrome, predisposing to the development of various benign and malignant tumours (Central nervous system hemangioblastomas and Retinal hemangioblastomas, endolymphatic sac tumours, clear cell renal cell cancer and/or renal cysts,

pheochromocytoma, pancreatic cysts and neuroendocrine tumours, epididymal and broad ligament cystadenomas). VHL disease is the first cause of hereditary kidney cancer.

Sporadic renal cell carcinomas

Sporadic hemangioblastomas

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