

ARTICLE



Cellular and Molecular Biology

Mutation of the proline P81 into a serine modifies the tumour suppressor function of the von Hippel–Lindau gene in the ccRCC

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BACKGROUND: The von Hippel–Lindau disease is an autosomal dominant syndrome associated with tumour formation in various tissues, such as retina, central nervous system, kidney, and adrenal glands. VHL gene deletion or mutations support the development of various cancers. Unclassified VHL variants also referred as “of unknown significance” result from gene mutations that have an unknown or unclear effect on protein functions. The P81S mutation has been linked to low penetrance Type 1 disease but its pathogenic function was not clearly determined.

METHODS: We established a stable cell line expressing the pVHL₂₁₃ (c.241C>T, P81S) mutant. Using biochemical and physiological approaches, we herein analysed pVHL folding, stability and function in the context of this VHL single missense mutation.

RESULTS: The P81S mutation mostly affects the non-canonical function of the pVHL protein. The cells expressing the pVHL₂₁₃P81S acquire invasive properties in relation with modified architecture network.

CONCLUSION: We demonstrated the pathogenic role of this mutation in tumour development in *vhl* patients and confirm a medical follow up of family carrying the c.241C>T, P81S.

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INTRODUCTION

The von Hippel–Lindau (VHL) gene is a tumour suppressor gene deletion or inactivation of which by mutations induce multiple tumours, including renal and central nervous system (CNS) haemangioblastoma, clear cell renal cell carcinoma (ccRCC) and pheochromocytoma. The most studied well-known function of pVHL is to be a substrate recognition component of an E3 ubiquitin ligase complex comprising Elongin B/Elongin C, Cullin 2 and Rbx1 [1] to regulate the hypoxia-inducible factor- α (HIF- α) transcription factors. The association of pVHL to HIF-1 α and HIF-2 α is oxygen-dependent and triggered through hydroxylation of HIF [2]; it results in ubiquitination and proteasome-dependent degradation of HIF- α .

Based on the pathologies, VHL disease is classified into two distinct types, Type 1 and Type 2, depending on the development of pheochromocytoma (Type 2) or not (Type1). Type 1 subtype describes typical phenotype VHL manifestation as haemangioblastoma and RCC. Type 2 is subdivided into three subtypes: patients with Type 2A and B develop pheochromocytomas and other VHL manifestations, with a low risk (Type 2A) or high risk (Type 2B) of RCC, patients with Type 2C develop only

pheochromocytomas. Patients with ccRCC (kidney tumour of epithelial origin) are therefore mostly classified into Type 1 and 2B [3]. Finally, a third class of patients (Type 3) is characterised by the development of erythrocytosis, the most described being the Chuvash polycythemia associated with the homozygous *VHL*-R200W mutation [4, 5]. At the molecular level, Type 1 families are characterised with various mutations (missense, frameshift, nonsense, splice) as well as in-frame deletion/insertions or partial/complete deletions of *VHL* gene, leading to a loss of pVHL function and the development of a large spectrum of cancerous tumours [3]. On the other hand, VHL Type 2 families were mainly characterised by missense mutations (83.5%), with a low percentage of nonsense, frameshift, splice, in-frame deletion/insertions or partial deletions.

With the exception of deletions that account for 30–40% of cases, most mutations cluster within two regions of high functional importance in pVHL protein, the Elongin C (amino acid (a.a.) residues 157–171) and HIF- α (a.a. residues 91–113) binding domains that are highly evolutionarily conserved sequences [6]. Missense mutations could be deleterious for the protein leading to its functional inactivation and resulting in HIF- α

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accumulation and the expression of HIF target genes involved in signal transduction pathways responsible for hyperproliferation and/or tumourisation.

Structurally, the pVHL protein consists of two functional protein-binding domains, the β -domain (comprised of residues 63–155 and 193–204) and the α -domain (residues 155–193). When analysing the 3D structure of pVHL, three distinct pVHL interaction interfaces have been described engaging in exclusive interactions [7]. The α domain binds elongins and Cullin2 while the β sheet domain of pVHL extending from residues 63 to 157 binds and participates to the polyubiquitination and ultimately targets HIF- α for proteasomal degradation [8].

Among the 1230 mutations listed in the VHL database (<http://umd.be/VHL>), some mutants still remain biochemically uncharacterised [3]. Referred families diagnosed with P81S mutation linked to low penetrance Type 1 VHL disease and a mild phenotype [9, 10]. A previous study investigating defects of Type 2C-associated mutant protein demonstrated at the molecular level the deleterious role involvement of pVHL^{L188V}, pVHL^{P81S/L188V} and pVHL^{V84L} [11].

In this study, we were interested in a family with two members who showed clinical symptoms of VHL disease. One member (III.2) developed a ccRCC at the age of 37 years. The genetic analysis has revealed the presence of c.241C>T (P81S) germline mutation. The genetic study of the progeny evidenced the presence of this same mutation in children (IV.4,5).

The use of *in silico* algorithms (HOPE, Symphony) indicated a possible pathogenicity of P81S mutation but not the GVGDT that assigned a low genetic risk [10]. Most of the analysis of the effect of the P81S mutations were performed in relation with an additional mutation in the gene or exposure to trichlorethylene [12]. Most carriers with the only P81S mutation have no VHL-related manifestations [13]. The clinical observations made for the above family raised the need to understand the involvement of the mutation P81S in the development of VHL pathologies. We have undertaken a structural, biochemical and cellular study to characterise the pathogenicity of this mutation and to conduct a medical follow-up for practitioners.

MATERIALS AND METHODS

Site-directed mutagenesis and plasmid construction

The plasmids pcDNA3.1-*P*_{PGK}-FlagHA-VHL₂₁₃ and -VHL₂₁₃ P81S were generated as follows: The open-reading frame of VHL variant 1 (excised from pCMV2c-VHL₂₁₃, a generous gift from Dr A. Buchberger, Würzburg, Germany) was subcloned in pcDNA3.1-FlagHA (a kind gift from Dr S. Rouquier, Toulouse, France) with murine phosphoglycerate kinase (PGK) promoter [14]. P81S point mutation was introduced into the VHL cDNA inserted into pcDNA3.1-*P*_{PGK}-FlagHA-VHL₂₁₃ using a sequential two-step polymerase chain reaction (PCR) approach with the high-fidelity PCR master polymerase (Sigma Aldrich, St Quentin-Fallavier, France). The oligonucleotides used to carry out the site-directed mutagenesis were as follows: P81Sfor, 5'-TGC AAT CGC AGT TCG CGC GTC-3'; P81Srev, 5'-GAC GCG CGA ACT GCG ATT GCA-3'. The resulting final amplicon was cut with BamHI and XhoI (Promega, Charbonnière les bains, France) and inserted into empty pcDNA3.1-*P*_{PGK}-FlagHA (first linearised with the same restriction enzymes) with T4 DNA ligase (Promega).

All constructs were confirmed by Sanger sequencing, amplified in NEB5alpha bacteria (New England Biolabs, Evry, France) and purified using the Nucleobond Endofree plasmid purification kit (Macherey Nagel, Hoerd, France) before transfection in mammalian cells.

Cell culture and transfections

The 786-O kidney cancer cell line, from the ATCC (LGC Standards), was cultured in RPMI-1640 (Life Technologies, Courtaboeuf, France) supplemented with 10% foetal calf serum and 1% penicillin/streptomycin at 37 °C with 5% CO₂. Stable cell lines were generated by transfecting 786-O cells with pcDNA3.1-*P*_{PGK}-Flag-HA-VHL₂₁₃P81S using Avalanche-Omni (EZ-Bio-systems, College Park, USA) and selected with 500 µg/ml G418 (Life Technologies). The 786-O cells with pcDNA3.1-*P*_{PGK}-Flag-HA-VHL₂₁₃wt have been previously generated in the laboratory [14].

Protein extraction and immunoblotting

Cells were lysed in RIPA extraction buffer, or directly in Laemmli loading buffer. Equal amounts of proteins were separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis and transferred to nitrocellulose. Membranes were probed with antibodies against VHL (1:1000; clone JD1956 [15]), HA (1:4000; Roche), Flag (1:2000; Sigma-Aldrich), β -tubulin (1:2000; Sigma-Aldrich), cyclin D1 (1:500; Cell Signaling Technology), cullin-2 (1:450; Life Technologies), Elongin-C (1:1000; Bio Legend), HIF2- α (1:500; Novus Biologicals). Immune complexes were detected as previously described [15].

Reporter assays

The parental 786-O or the stable 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S cell lines were transfected with plasmids encoding Firefly-luciferase under the control of Hypoxia-Response-Elements (HRE-luciferase), and Renilla-luciferase for normalisation. After a 24-h culture, luciferase activity was measured using a Dual-Luciferase® Reporter Assay System (Promega).

Wound healing assay

Cells were cultured at 37 °C in a humidified atmosphere containing 5% CO₂ until confluence in culture inserts 2 wells (Ibidi-Cell in focus; Clinisciences, Nanterre, France). Cells were treated or not with 10 µg/ml mitomycin C (Sigma-Aldrich). Cell migration was then recorded every 15 min for 24 h using an Axiovert 200M microscope equipped with a LD Plan-Neofluar x20/0.4 Ph2 lens and an AxioCam MRm camera under the control of the ZEN 2012 software (Zeiss). The wound area was measured using the Simple PCI6 software (Hamamatsu Photonics, Massy, France). The analysis of cell migration during the assay was performed with the MRI Wound Healing Tool (http://dev.mri.cnrs.fr/projects/imagej-macros/wiki/Wound_Healing_Tool) using the Image J software.

Spheroid formation

Five thousand cells were plated in medium per well of a 96-well plate with round bottom previously coated with Poly(2-hydroxyethyl-metacrylate) (Sigma-Aldrich) and incubated for up to 4 days to allow spheroid formation. The spheroids were analysed by microscopy (DMIRB Leica) and the size was calculated using the Image J software.

Invasion tumour assay on Matrigel

The spheroids were embedded in a gel composed of a mixture of Matrigel (2 mg/ml; Corning) in full medium RPMI-1640 supplemented with 10% foetal calf serum and 1% penicillin/streptomycin at 37 °C with 5% CO₂. Cell migration away from the spheroids was recorded under a video microscope (Delta vision-MRIC-SFR-UMS-CNRS 3480-INSERM018) for several hours.

Modelling

The pVHL₂₁₃ model is derived from the protein databank structure PDB ID:1VCB completed by the i-tasser server (<https://zhanglab.ccmb.med.umich.edu/I-TASSER/>).

RESULTS

Clinical evaluation

Family A with members suffering from VHL disease studied in the present study was recruited in the PREDIR centre (France). A ccRCC was diagnosed in the proband (III.2) at the age of 37 years and treated with radical nephrectomy. Genetic analysis revealed the germline missense mutation c.241C>T, p.Pro81Ser (P81S) in the VHL gene (Reference sequence: NM_000551). A retrospective study of the potential presence of mutation in parents and descendants was undertaken. There were originally three patients with the P81S mutation in the VHL gene (II.8). Genetic testing of the descendants identified the P81S mutation in the genome of the two 8- and 13-year-old children. In addition, sequencing of the VHL gene of members of the background family showed the presence of the mutation for the sister of and the father who are, respectively, 65 and 38 years old (Fig. 1; II.1, III.1). Besides the proband's ccRCC, none of the carriers displayed any other signs of VHL-related manifestations including the 65-year-old father. The

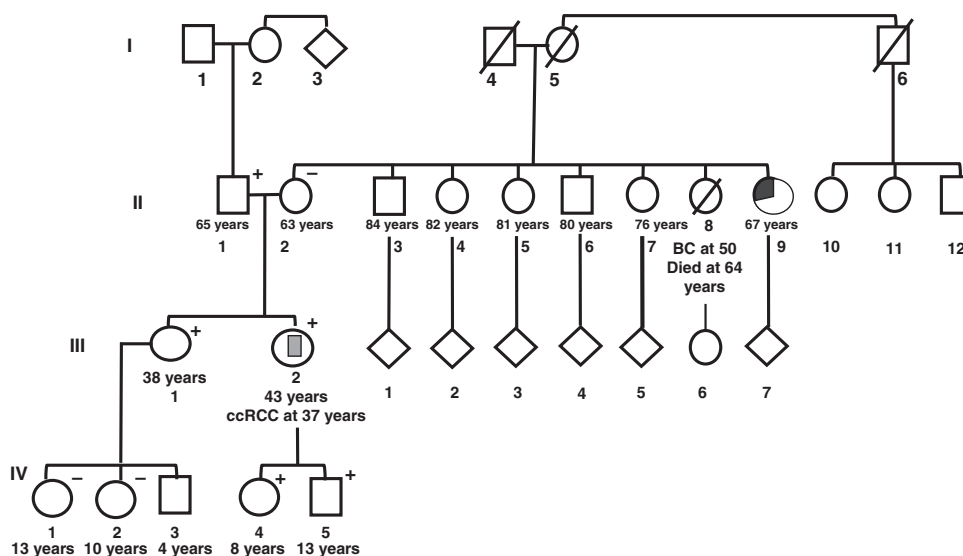


Fig. 1 Description of the pedigree of the family that is affected by the P81S mutation. Pedigree of family A. ccRCC clear cell renal cell carcinoma, BC breast cancer, + carrier of the germline c.241C>T, p.Pro81Ser in the *vhl* gene, – non-carrier of the germline c.241C>T, p.Pro81Ser in the *vhl* gene.

variant was identified in the index case and was declared as pathogenic. The hypothesis is that in the case of a spectrum tumour in a person carrying a VHL variant, the portal of entry here being renal, there is probably a loss of the 3p on the wild-type allele. Tumour material was not available to perform the analysis. Surveillance programme, according to the French VHL guidelines (Centre PREDIR) (including magnetic resonance imaging (MRI) of the CNS, MRI or ultrasound of the abdomen, ophthalmological examination, measurement of urinary metanephrines), was normal for all of the carriers. The single manifestation in the proband and the absence of clinical signs in the other mutation carriers questioned about the penetrance of the P81S germline mutation.

Structural evaluation of the P81S mutation

The *VHL* tumour suppressor gene encodes a protein that contains two main structural domains: (β domain a.a. 65–154 and α domain a.a. 157–193) held together by two linkers and a polar interface. (Fig. 2a). Previous studies combining structural information and computational analysis have distinguished three distinct interfaces [6], each interface-refined motifs involved in specific protein–protein interactions. Moreover, five distinct pVHL interaction interfaces (A, B, C, D and E, Fig. 2a) are engaged in exclusive interactions with different interactors and may partially explain the pVHL binding plasticity. Interface A (a.a. 154–189) is important for VCB complex formation and interface B (a.a. 60–103) forms the HIF-1 α binding site while interface C (a.a. 157–190) participates in the Cullin2 interaction.

The proline 81 is located in the β domain and included in a turn in the molecular structure (between the β strands #1 and #2, Fig. 2b, c). As many other proline residues of pVHL, Pro81 defines boundaries of secondary structure elements such as the β strands and could be essential for ternary structure formation (Fig. 2b).

Due to its localisation, the P81S substitution might cause significant structural perturbations in the β domain organisation [7]. Nevertheless, the reported link of the P81S substitution to Type 1 VHL disease remains enigmatic, given the lack of significant functional defects of the pVHL-P81S mutant protein in vivo [13]. Such altered pVHL may still be able to exert some of its functions and/or may gain novel ones. Structural analyses suggest a modification of the β domain, but biochemical studies are required to clarify the alterations in biological functions.

Biochemical impact of P81S mutation on pVHL₂₁₃ function(s)

To analyse the potential effect(s) of the mutation P81S on the function of pVHL, the proline in position 81 was mutated into the polar uncharged a.a., serine. We stably transfected the renal carcinoma cell line 786-O (*VHL*–/–), which does not express wild-type *VHL* with the plasmid pcDNA3.1-*P*_{PGK}-Flag-HA-VHL₂₁₃P81S to moderately express the pVHL protein with the mutation of interest. Three positive clones (namely E1, E6 and C7) were obtained and controlled for mutation by sequencing. The expression level of the protein pVHL was then analysed in different cell lines: parental 786-O, 786-O-pVHL₂₁₃ (wild type), and the three clones corresponding to 786-O-pVHL₂₁₃-P81S. The immune detection revealed a positive expression of the VHL protein in the three clones (Fig. 3a).

Loss of pVHL activity might be the result of pVHL functional inactivation or degradation that is often observed in Type 1 pVHL mutants. We thus addressed the question whether the prediction of the stability of pVHL mutants may influence its functionality. As all clones obtained after selection expressed identical levels of the protein (Fig. 3a), we selected one of the three clones (E6). Tubulin visualisation showed that no obvious architectural differences were discriminant for the three cell lines (Supplementary Fig. 1). In order to control the stability of the mutant pVHL₂₁₃-P81S protein, the different stable cell lines were treated with the protein synthesis inhibitor cycloheximide (CHX) for 3 and 7 h. CyclinD1 expression confirmed the CHX treatment efficiency. Expression levels of pVHL in the 786-O-pVHL₂₁₃-P81S stable cell line compared to that of wild-type pVHL in the 786-O-pVHL₂₁₃ were measured by immunoblotting (Fig. 3b, c). The stability of the pVHL₂₁₃-P81S was not significantly changed. Indeed, evaluation of the amount of the pVHL₂₁₃-P81S and pVHL₂₁₃ showed that in both cases the remaining amounts of proteins after a 7-h treatment with CHX consist of, respectively, 56 and 66% of the initial amount of endogenous protein (Fig. 3c, $p = 0.396$).

The pVHL tumour suppressor functions as a redox sensor, which controls stability of the hypoxia-inducible transcription factor family (HIFs) among other proteins.

The VHL gene product is the substrate recognition subunit of a multiprotein E3 ubiquitin ligase complex, in association with the scaffold protein Cul2, the ring box protein Rbx1 and the adaptor proteins, Elongins B and C. As most VHL mutations affect the oxygen-dependent regulation of HIF2- α cellular levels, we tested

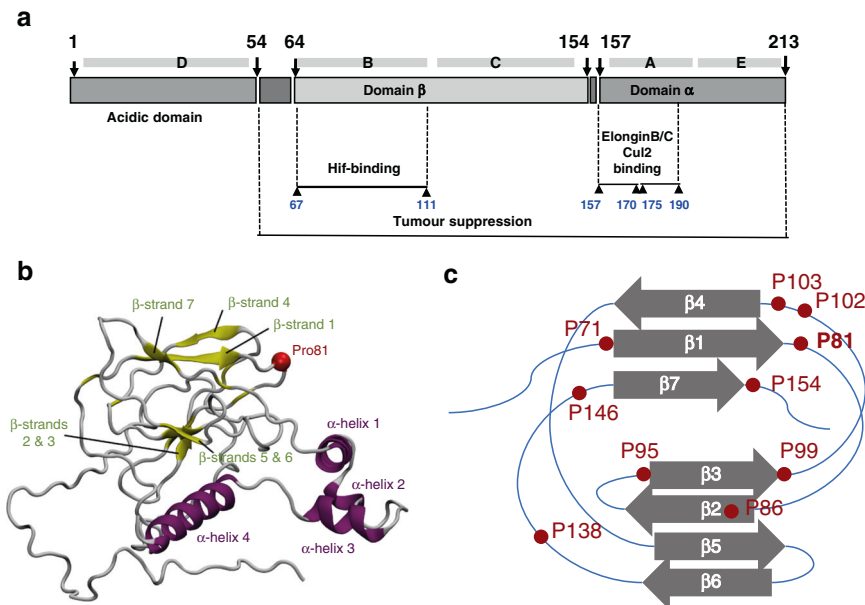


Fig. 2 Representation of the pVHL₂₁₃ protein structure. **a** Organisation of the functional domains and amino acid sequence alignment of pVHL₂₁₃. **b** Structural organisation of the different domains and amino acid sequence alignment of the pVHL₂₁₃ isoforms. **c** Pro81 is defining the boundary of secondary structure elements between the beta strands β 1 and β 2 composing the core of the protein. Several other proline residues are localised in the extremities of a strand: Pro71 and Pro81 (start and end of beta 1), Pro95 and Pro99 (start and end of beta 3), the pair Pro102 and Pro103 (start of beta 4), and Pro146 and Pro154 (start and end of beta 7).

whether the mutant pVHL₂₁₃-P81S participated to the E3 ligase complex to ubiquitinate and ultimately lead to HIF2- α degradation. In order to prevent HIF2- α proteasomal degradation that rapidly occurs upon polyubiquitination by pVHL and therefore allow its co-immunoprecipitation, the cells were first treated with the proteasome inhibitor (MG132) up to 5 h before harvest and the proteasome inhibitor efficacy in preventing HIF2- α degradation was verified by western blotting (Fig. 4a). Immunoprecipitation of flagged proteins expressed in 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S was then performed. As observed on Fig. 4b, Cullin 2 was similarly co-precipitated by both pVHL₂₁₃ and pVHL₂₁₃-P81S proteins. Likewise, HIF2- α that associated with the pVHL₂₁₃ was also detected with the immunoprecipitated pVHL₂₁₃-P81S (Fig. 4b). The ratio HIF2- α /pVHL and Cul2/VHL evaluated on three distinct experiments revealed that HIF2- α /pVHL ratio appears stronger in the 786-O-pVHL₂₁₃-P81S than in the 786-O-pVHL₂₁₃ cells but only after 2 h (Fig. 4c $p=0.0313$) and 5 h (Fig. 4c $p=0.0041$) of treatment with MG132 ($n=5$ —Fig. 4c). This ratio is not significantly different in non-treated cells (Fig. 4c). The amount of Cul2 immunoprecipitated with the 786-O-pVHL₂₁₃-P81S did not change notably from the amount of Cul2 detected in the 786-O-pVHL₂₁₃. These first results show that the P81S mutation neither diminished recruitment of E3-ligase subunit such as Cullin2 nor the binding of the major substrate HIF-2 α .

We then evaluated the amount of HIF2- α in the different cell lines incubated in the presence of protein synthesis inhibitor (CHX) (Fig. 3b). In the absence of CHX treatment ($t=0$), the amount of HIF2- α was significantly diminished in the 786-O-pVHL₂₁₃ cells as well as in 786-O-pVHL₂₁₃-P81S cells, compared to the level detected in 786-O cell lines (p value = 0.00173 and 0.04156, respectively) (Fig. 3d). No difference in HIF2- α level was observed between 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S cells (p value: 0.685) (Fig. 3b, d). After treatment with CHX, the quantity of HIF2- α remaining in the pVHL₂₁₃ and pVHL₂₁₃-P81S cells represented 39% of the initial amount of the HIF2- α evaluated in the 786-O cells (Fig. 3d). The level of immunodetected HIF2- α associated to pVHL did not seem to change in 786-O pVHL₂₁₃-P81S cells as well as in 786-O pVHL₂₁₃ (Fig. 3d).

To go further in understanding the role of the mutation towards the canonical function of pVHL, we also compared the amounts of the protein HIF2- α in the 786-O, 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S cell lines under normoxia versus chemical hypoxia condition (19 h of CoCl₂ treatment). Under normoxic conditions, HIF2- α was lower in 786-O-pVHL₂₁₃ cells (t test, $p=0.02616$) as well as in 786-O-pVHL₂₁₃-P81S cells (t test, $p=0.004998$) in comparison to 786-O (Fig. 3e, f). After treatment of the cells with CoCl₂ for 19 h, the quantity of immunodetected HIF2- α increased in both pVHL₂₁₃ cells and pVHL₂₁₃-P81S cell lines. In the presence of CoCl₂, significant modification of HIF2- α amount was observed between 786-O cells and 786-O-pVHL₂₁₃ (t test, $p=0.0365$) and 786-O-pVHL₂₁₃-P81S cells (t test, $p=0.0194$). In contrast, no significant variation of HIF2- α was observed between when 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S after hypoxic treatment (Fig. 3f).

To better understand the effect of the mutation P81S on the regulation of HIF, a functional study was performed using a hypoxia response element (HRE)-dependent reporter assay [5] (Fig. 4d). The ability of pVHL₂₁₃ and mutant pVHL₂₁₃-P81S to downregulate firefly luciferase activity (reflecting HIF activity) was tested in 786-O cells and the results confirmed that pVHL₂₁₃ as well as pVHL₂₁₃-P81S displayed a similar luciferase activity, largely reduced compared to that in 786-O cells (Fig. 4d).

Altogether, our data show that the formation of the E3 ligase complex is not fundamentally altered when pVHL₂₁₃ is mutated on Pro 81 (to Ser) and the modest variations in HIF2- α (binding and stability) observed in the presence of pVHL₂₁₃-P81S cannot account for the development of the pathology in a member of the family.

The P81S mutation of pVHL₂₁₃ modifies migration properties of renal cells

Dysregulation of the *VHL* gene is closely associated with ccRCC. Other pVHL, HIF-independent, functions have been shown to be required and help to explain why loss of pVHL leads to renal cancer. The way the P81S mutation of pVHL might favour the development of the ccRCC for a 37-year-old patient in a HIF-independent manner was thereafter investigated. As malignant

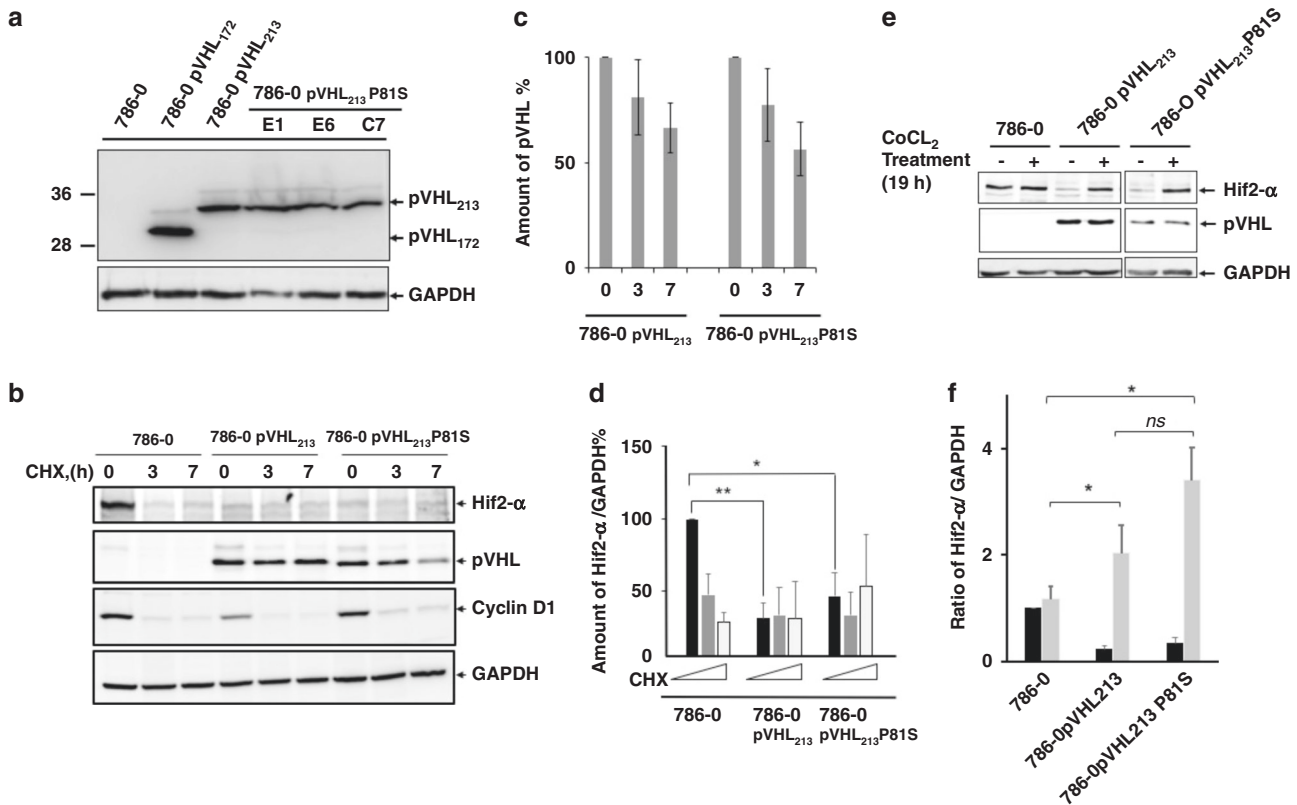


Fig. 3 Characterisation of the stable cell lines expressing the pVHL₂₁₃-P81S. **a** pVHL expression in 786-O, 786-O-pVHL₁₇₂ and 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃ P81S cells (different clones: E1, E6 and C7) assessed by immunoblotting with the indicated antibodies VHL (JD-1956-[15]) and GAPDH. **b** Stability of pVHL was assessed in the different 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃ P81S cell lines after treatment with cycloheximide for 3 and 7 h. HIF-2 α protein expression level was also evaluated by immunoblotting in the three cell lines 786-O, 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃ P81S. Immunodetection of Cyclin D1 was performed as a control of the efficiency of treatment with CHX. GAPDH was used as a loading control. **c** The histogram shows the quantification of the amount of pVHL (mean \pm SEM; $n = 3$) in 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃ P81S. **d** The histogram illustrates the amount of HIF2- α detected in the three 786-O, 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃ P81S cell line before (0) or after treatment with CHX for 4 or 7 h. The results are expressed as the mean \pm SEM of three independent experiments (** p value: 0.00173) and (* $p = 0.04156$). **e** Effect of hypoxia induced by incubation of the cells with CoCl₂ during 19 h on the amount of HIF2- α in the absence (or presence of pVHL₂₁₃ or pVHL₂₁₃ P81S. HIF2- α , VHL (and GAPDH as a loading control) were detected by western blot. **f** Quantification of the immunodetected amount of HIF2- α from five independent experiments (** t test, $p = 0.02616$; * t test, $p = 0.004998$; ns non-significant).

cancer cells exploit their intrinsic migratory ability to invade adjacent tissues and the vasculature, we have studied cell morphology and dynamics. Transformed cells often exhibit different growth characteristics than non-transformed cells. Therefore, in a first round of experiments, we investigated the migration/invasion properties of these different cell lines. First, we set up a standard scratch wound healing assay (Fig. 5a). The migration of cells in the specific wound area was recorded every 15 min during 16 h (=1000 min), i.e. until the scratch area was fully repopulated by all of the tested cell lines (Fig. 5a). The images from the beginning to the end of a 16 h incubation period were captured. The end of recording time was determined at 16 h when the slowest moving cells (786-O-pVHL₂₁₃ cells—dark line) were just about to fully fill in the scratch (Fig. 5b). The 786-O cells, which do not express wild-type pVHL, covered the wound caesura after 7.5 h (Fig. 5b, grey line), whereas the 786-O pVHL₂₁₃-P81S stably transfected cells close the caesura in 6 h (Fig. 5b, dotted line). Therefore, comparison of the cells stably transfected with the pcDNA-VHL₂₁₃ and those transfected with the pcDNA-VHL₂₁₃-P81S showed modification of cell migration when VHL is mutated. The time-dependent changes of the open area due to cell migration were scored for each cell type as the time to repopulate 50% of the gap. The parental 786-O cells invaded 50% of the area after 202.9 \pm 13.7 min versus 368 \pm 48 min for 786-O pVHL₂₁₃ (Fig. 5c) The 786-O cells expressing pVHL₂₁₃-P81S covered 50% of the

caesura in 162.4 \pm 11 min. The statistical analysis of the experiments for each cell line revealed a significant difference in time of migration between 786-O and 786-O-pVHL₂₁₃ ($n = 8$ p value 0.0006333 t test) and between 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S ($n = 7$ p value 0.0003016— t test) (Fig. 5c). A slight difference of migration was observed when comparing the migration of between the 786-O and 786-O-pVHL₂₁₃-P81S ($n = 6$ p value: $p = 0.01342$ — t test) (Fig. 5c).

Impact of pVHL₂₁₃-P81S on aggregation properties of the transfected tumoural cells

Multicellular aggregates of cells and tumour organoids have become preclinical model systems of great interest for studying tumour behaviours. Spheroids more faithfully reproduced the tumour macrostructure compared to classical two-dimensional (2D) monolayers. As previously demonstrated, the spheroid formation assay was performed to determine the properties of 786-O cells to aggregate and the impact of wild-type and mutated pVHL on this cell aggregation. The three cell lines 786-O, 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S were tested for spheroid formation (Fig. 6a) and the expression of pVHL was controlled in the cell lines (Fig. 6b). As previously shown, the 786-O cell line formed multicellular spheroids with highly uniformity in size and cell density [14]. Interestingly the 786-O-pVHL₂₁₃-P81S cells formed a cluster of cells structure of which differed from the

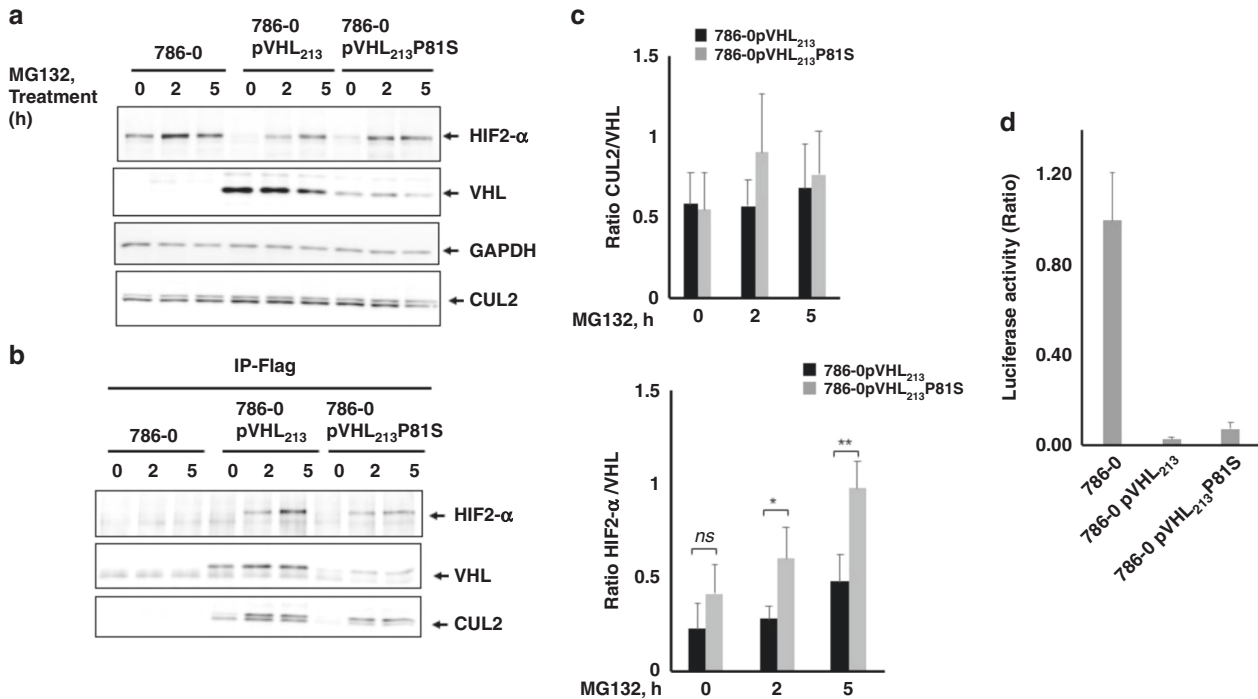


Fig. 4 pVHL₂₁₃-P81S is part of the E3 ligase complex. **a** 786-O, 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S cell lines were cultivated in the presence of MG132 for 2 or 5 h. The amounts of VHL, Cul2 and HIF2- α were estimated following their detection by immunoblotting. GAPDH was used as a loading control to normalise the level of each protein. **b** Flag immunoprecipitation was performed with total protein extracts from the three cell lines and for each time of MG132 incubation. The proteins VHL, HIF2- α and Cul2 were then immunoblotted in the bound fractions. **c** The ratio CUL2/VHL and HIF2- α /VHL was calculated from five independent experiments. The histogram shows the quantification of the amount of CUL2/VHL (mean \pm SEM; $n = 5$) and HIF2- α /VHL in 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S. Quantification of the immunodetected amount of HIF2- α /VHL from five independent experiments (** t test, $p = 0.0041$; * t test, $p = 0.0313$; ns non-significant). **d** Functional HRE-dependent reporter assays were performed in 786-O cells (i.e. VHL negative cells that constitutively accumulate HIF-2 α in normoxia). The results are expressed as relative Firefly luciferase activity with Renilla luciferase as an internal control. One unit denotes the basal activity of endogenous HIF-2 α using the HRE-luciferase reporter plasmid. The abilities of pVHL₂₁₃ and pVHL₂₁₃-P81S to downregulate Firefly luciferase activity (related to HIF activity) were compared.

structures observed with either the 786-O cells or the 786-O-pVHL₂₁₃ cells. The contour of spheroids appeared as an intermediate shape between the one observed when prepared with the 786-O cells and the 786-O-pVHL₂₁₃-P81S with dense cell-cell interactions and borders slightly widespread (Fig. 6a).

The ability of cells to grow in a semi-solid medium was further recorded while testing the characteristics of malignantly transformed cells. The morphology of the spheroids obtained with the 786-O cells was not changed when they were embedded in the Matrigel for 24 h. The appearance of the 786-O-pVHL₂₁₃ aggregates deposited in the Matrigel was transformed and became more compact (Fig. 5c). In contrast, the 786-O-pVHL₂₁₃-P81S spheroids appeared modified, the inner part of the spheroid became dense and compact, whereas the peripheral cells escaped from the spheroids and migrated into the Matrigel (Fig. 6c). These observations strongly suggest that 786-O cells acquire invasive features upon expression of pVHL₂₁₃-P81S. The different 786-O-pVHL₂₁₃-P81S clones obtained in our study showed identical behaviour with respect to spheroid formation and migration into Matrigel (Supplementary Fig. 2).

The actin cytoskeleton undergoes dynamic assembly and disassembly during cell crawling, which regulates protrusion formation, focal adhesion assembly/disassembly, and contractile filament organisation. Assembly of the actin cytoskeleton is essential for invasion and cell migration. Cell migration requires the formation of various structures, such as invadopodia and pseudopodia, which require actin assembly that is regulated by specialised actin nucleation factors. Cell migration is the result of a multistep and complex process initiated by the transformation of the actin cytoskeleton. The length of filaments varies greatly, and

the filaments are cross-linked into imperfect bundles and networks. The disruption of the actin cytoskeleton inhibits cell migration and adhesion [16]. The orientation of F-actin fibres (parallel and random distribution) was analysed in the different cell lines used in this study. The F-actin network was organised as dense and parallel fibres along the long axis of the 786-O pVHL₂₁₃ cells while actin fibres were longer and less dense in 786-O cells (Fig. 6d). In contrast, actin fibres were very short and mostly located near the membrane in cells expressing pVHL with the P81S mutation (Fig. 6d). In conclusion, the architectural network exhibited different organisation in the cells expressing or not pVHL₂₁₃ or pVHL₂₁₃-P81S.

DISCUSSION

In this study, we described the workup of a family carrying a germline missense mutation c.241C>T, p.Pro81Ser (P81S) with carrier members: a 37-year-old adult diagnosed with a ccRCC and some family members carrying the mutations who were asymptomatic. Moreover, the P81S in the VHL gene has been identified in four other French families in the PREDIR molecular genetics laboratories network (<https://predir.org/View/accueil.aspx>). One proband had a ccRCC at a young age (28 years), 3 others had pheochromocytoma or paraganglioma at older ages (68 and 70 years for two of them, age unspecified for the third case). Other proline mutations have been reported in databases as well, including proline in positions 2, 86 and 97 and converted into non-polar residue (Leu, Ala), polar (Ser) or basic a.a. residues (Arg, His). Depending on the a.a., the mutants were classified benign or as variants of uncertain significance (VUS). Patients bearing the

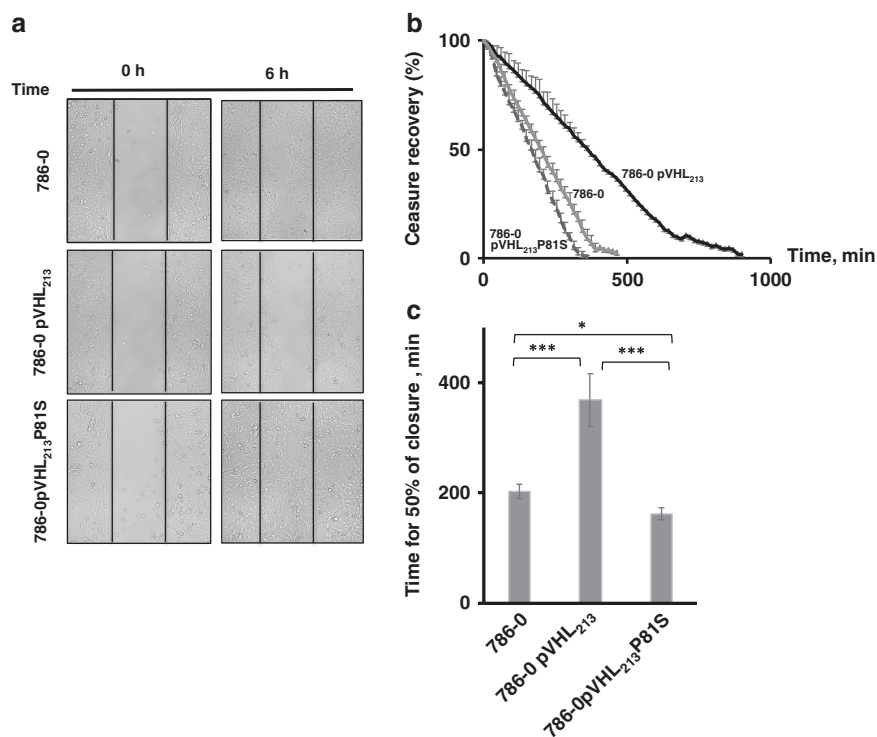


Fig. 5 Expression of pVHL₂₁₃-P81S promotes cell migration. **a** The 786-O, 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S cells were seeded in culture inserts. Analysis of cell migration by wound healing assay was then carried out with images taken every hour for 16 h. **b** Results were expressed as the percentage of wound closure at the indicated time points. The average corresponding to three wells per cell line from six independent experiments is shown. **c** Time needed for 50% closure was estimated for each cell line (mean \pm SEM; 786-O and 786-O-pVHL₂₁₃ (***n* = 7 *p* value 0.0006333—*t* test); 786-O pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S (***n* = 7 *p* value 0.0003016—*t* test) 786-O and 786-O-pVHL₂₁₃-P81S (**n* = 6 *p* value: *p* 0.01342—*t* test).

Pro86Ala/Arg/Ser/His mutations and developing haemangioblastoma and kidney cysts were described as probably pathogenic [3, 17]. The presence of the P81S mutation in various families were associated with low penetrance or mild phenotype together in the German VHL family with one affected member who developed CNS haemangioblastoma and RCC as well as kidney and pancreatic cysts [3]. Moreover, the substitution of the proline 97 by a leucine was described as pathogenic when associated with another mutation Leu166Pro [18]. It was therefore of interest to discriminate the role of the mutant in the P81S VHL pathology. We employed a set of *in silico* predictions and *in cellulo* and *in vitro* methods along with structural analysis to investigate whether the single P81S mutation was involved in disease development or neutral.

Predictions for the impact of the P81S substitution in the *VHL* gene, obtained by *in silico* analysis, showed a discrepancy depending on the prediction tools. The different *in silico* algorithms used to analyse the mutants reported the difficulties to classify the P81S VHL mutation as it could come out as potentially pathogenic or as unclassified variant (www.umd.de). We should have replaced the proline with an alanine, which is also a nonpolar and hydrophobic a.a. This modification brings great complexity to the structural and biochemical structure but it is consistent with the pathology. We are aware that serine not only changes the organisation of the molecule in three dimensions but also induces charge modifications that can generate new bonds. We focussed on the patient's mutation P81S despite the fact that it combines the change in charge and structure.

In particular, replacement of proline by serine at residue 81 might disturb the native pVHL structure by destroying a rigid link known to be associated with proline and to favour the formation of hydrogen bonds with neighbouring polar a.a. However, as many other proline residues of pVHL, proline 81 plays a role in

defining the boundaries of secondary structure elements such as the β -strands composing the core of the protein. Indeed, among the proline residues, several are delimiting the extremities of a β strand: Pro71 and Pro81 (start and end of β 1), Pro95 and Pro99 (start and end of β 3), the Pro102 and Pro103 pair (start of β 4), and Pro146 and Pro154 (start and end of β 7) (Fig. 2c). The distribution of many of these specific a.a. along the pVHL sequence allows the chaining of short β -strands and a succession of turns organising the β domain of the protein. It should nevertheless be emphasised that the *in silico* prediction can only give an approximation for pathogenicity that need to be validated by *in vitro* and *in vivo* experimental validation.

Most frequently reports showed that Type 1-associated pVHL mutant proteins are most frequently reported as failing to assemble the E3-ubiquitin ligase [11]. The risk relevance of this mutation was only identified in TCE-induced ccRCC or in association with other mutations [19, 11]. Moreover, previous studies have speculated that the impact of the P81S mutations might even be stronger in combination with the L188V mutation [13]. Altogether, both mutations likely influence protein–protein interactions. Previous reports on structural studies of the P81S variant mentioned that this proline to serine substitution was not expected to cause significant structural perturbations on its own, but it has been proposed to affect the orientation of the neighbouring residue Arg82, whose side chain forms the centre of a hydrogen bond network stabilising both the α/β domain interface of pVHL-Elongin C [20].

The establishment of the stable cell line became essential to investigate the pathogenicity of pVHL₂₁₃-P81S. As mentioned in previous work, the absence of native conformation could highly lead to a destabilisation of the protein [11, 21]. In addition, the B domain is implicated in substrates' recognition like the hypoxia-induced factors alpha (HIF- α , the A interface is important for the

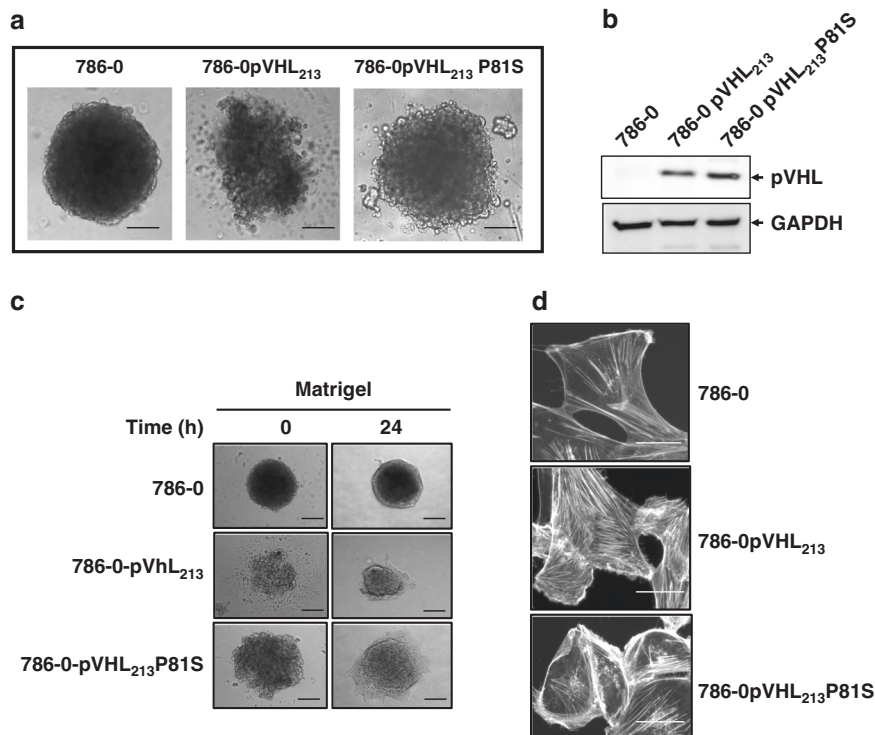


Fig. 6 Tumorigenic effect of pVHL₂₁₃-P81S in 786-O cells. **a** Morphology of 786-O, 786-O-pVHL₂₁₃ and 786-O-pVHL₂₁₃-P81S spheroids. Spheroid aspect was obtained after 48 h of incubation of cells on poly-Hema coated wells. Spheroids were imaged under Leica microscope. Scale bars: 100 μ m. **b** The spheroids were collected 48 h post seeding and pVHL expression was evaluated by western blot. GAPDH was used a loading control. **c** The spheroids corresponding to the three different cell lines were loaded into Matrigel. The spheroid morphology was recorded during 24 h. The picture showed the spheroids after 24 h of incubation. **d** Actin staining, analysed after Rhodamin-phalloidin incubation of 786-O cells (upper panel), 786-O pVHL₂₁₃ (middle panel) and 786-O pVHL₂₁₃-P81S cells (lower panel). (scale bar: 25 μ m).

formation of the VBC complex) [7, 22]. Because of the critical location of P81S within the β -sheet domain of pVHL, we inferred that protein binding, including HIF-2 α , may be impaired. In our hands, the stability of the protein pVHL₂₁₃-P81S amount was not significantly different from that of wild-type pVHL₂₁₃, suggesting that the P81S mutation does not trigger a total protein unfolding as often observed for Type I pVHL mutation. Moreover, the E3 complex was still formed with pVHL₂₁₃-P81S and able to bind HIF2- α . The amount of HIF2- α in cells expressing pVHL₂₁₃-P81S was detected mostly more related to the amount of the protein quantified in the 786-O cells. Therefore, the particular P81S mutation does not seem to abolish (or diminish) HIF binding, as one should expect with a Type I mutation.

The role as hypoxia sensing component was conveniently used to explain some of the main VHL manifestations. However, it fails almost entirely in predicting the pathogenic risk of several mutations not directly connected with HIF-1 α degradation. Defective HIF-1/2- α regulation is believed to be sufficient to induce development of haemangioblastomas and to be a key pathogenic event in the development of RCC, but in the present study, the ability of pVHL₂₁₃ P81S to downregulate HIF, at least in normoxic conditions, suggest that other pVHL-HIF-independent functions may be affected to explain the development of the ccRCC.

Lastly, the experimental results did not explain why in the family described in this study one member developed a ccRCC. These observations reveal a preferentially non-canonical function of pVHL₂₁₃-P81S. pVHL plays many roles, including a very important one in the formation of the extracellular matrix, epithelial differentiation and correct interaction between epithelial cells and the extracellular matrix [23]. Moreover, deletion of the VHL gene can activate β -catenin [an important mediator of EMT] [24]. The inactivation of pVHL in pheochromocytoma has led to

the upregulation of seven genes, such as *CTGF*, *SDCBP*, *CYR61*, *COL3A1*, *COL1A1*, *COL5A2* and *SERPIN1*, which are closely related to cell proliferation, migration and differentiation [25].

This naturally led us to test, in migration 2D and invasion 3D assays, the hypothesis that P81S mutation of pVHL would impact cell migration and/or invasiveness in the 2D or 3D assays. We indeed observed a more migrating potency of the 786-O-pVHL₂₁₃-P81S. The speed of pVHL₂₁₃-P81S cell invasion and the shape and the size of the spheroids, as well as the behaviour of the cells from the spheroids, when included in Matrigel, supported the modified function of pVHL when the P81S mutation is present.

Other prolines (P86 and P97) located in the β domain have been shown pathogenic when mutated, while inducing haemangioblastomas and ccRCC [26]. Also in the B domain, the Ser 72 of pVHL when mutated into proline was described as pathogenic, associated with haemangioblastomas and pancreatic cyst [27, 28]. Functional interaction of pVHL with AURKA was shown to modulate microtubule stability and dynamics. Mutations of the Ser into Pro participate in tumour initiation/progression [29]. In the present situation, the P81S mutation might induce structural transformations that could affect the functions of the surrounding a.a. This would therefore modify the non-canonical functions of the protein. The pVHL₂₁₃-P81S drive morphological cell changes that might be induced by expression of protein involved in cell adhesion and migration expression. Conclusively, our results demonstrate that the P81S mutation changes the cellular tumour suppressor function of pVHL213 and confers to the cells a migratory and invasive behaviour. Moreover, combining MetaDome and Mobidetails [30, 31] web server that help to interpret DNA variants in the context of molecular diagnosis, we observe that the P81S mutant is classified as intolerant and certainly pathogenic (Supplementary Fig. 3). The development of kidney cancer in young subjects in the family studied and the detection

of pheochromocytomas and angioblastomas in patients (<http://www.umd.be/>) strongly suggests a medical follow-up in the members of the impacted families. Further investigations will be necessary to define in more detail the molecular pathway involved in cell transformation with such pVHL mutant.

DATA AVAILABILITY

The data that support the findings of this article are available upon request from the corresponding author.

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AUTHOR CONTRIBUTIONS

Conceived and designed the experiments: FC, YA-B. Performed the experiments: FC, AA, AC, EJ, ML, XLG. Analysed the data: FC, XLG, BG, YA-B. Contributed reagents/materials/analysis data from patients: CA, BG. Wrote the paper: YA-B.

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COMPETING INTERESTS

The authors declare no competing interests.

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

Not applicable.

ADDITIONAL INFORMATION

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