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## From protein uptake to Dent disease: An overview of the *CLCN5* gene

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### Abstract

Proteinuria is a well-known risk factor, not only for renal disorders, but also for several other problems such as cardiovascular diseases and overall mortality. In the kidney, the chloride channel  $\text{Cl}^-/\text{H}^+$  exchanger C1C-5 encoded by the *CLCN5* gene is actively involved in preventing protein loss. This action becomes evident in patients suffering from the rare proximal tubulopathy Dent disease because they carry a defective C1C-5 due to *CLCN5* mutations. In fact, proteinuria is the distinctive clinical sign of Dent disease, and mainly involves the loss of low-molecular-weight proteins. The identification of *CLCN5* disease-causing mutations has greatly improved our understanding of C1C-5 function and of the C1C-5-related physiological processes in the kidney.

This review outlines current knowledge regarding the *CLCN5* gene and its protein product, providing an update on C1C-5 function in tubular and glomerular cells, and focusing on its relationship with proteinuria and Dent disease.

### Keywords

C1C-5; C1C-5 mutant proteins; Kidney; Proximal tubular cells; Podocytes; Endocytosis

## 1. Introduction

Excess protein in the urine (proteinuria) is a well-known risk factor not only for renal disorders (Tsai et al., 2016), but also for several other problems, such as cardiovascular diseases (Schmieder et al., 2011; Lim et al., 2017; Wang, 2018), bone disorders (Tung et al., 2018); diabetes (Klein et al., 1993); and overall mortality (Grimm et al., 1997).

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.gene.2020.144662>.

Nowadays, we know that maintaining the right level of protein in the urine demands a coordinated effort in the kidney on the part of two main actors the glomerular filtration barrier (GFB) —a zip-structure built by podocytes, fenestrated endothelial cells, and the glomerular basement membrane (GBM), which prevent protein loss by acting as a size- and charge-exclusion filter (Kriz and Lemley, 2017) — and the proximal tubular cells (PTCs), which are implicated in protein re-uptake (Maunsbach, 1966).

In the past, proteinuria was considered a consequence of glomerular rather than tubular damage because it was believed that the GFB was impossible for proteins to cross. Micropuncture experiments in mice (Oken and Flamenbaum, 1971; Stolte et al., 1979; Tojo and Endou, 1992; Remuzzi et al., 2007) have demonstrated, however, that proteins can easily pass through the GFB, and that PTCs, which reabsorb more than 99% of them, have a more important role (Castrop and Schiebl, 2017).

The main player in albumin and low-molecular-weight (LMW) protein reuptake by PTCs is the endocytic complex. It comprises two multiligand receptors, megalin (encoded by the *LRP2* gene) and the cubilin-amnionless complex (protein products of the *CUBN* and *AMN* genes, respectively), which are well-known partners of the chloride channel  $\text{Cl}^-/\text{H}^+$  exchanger *CIC-5* encoded by the *CLCN5* gene (Gianesello et al., 2016). Disruption of this macromolecular complex clearly plays a part in the onset of the proteinuria that points to the clinical diagnosis of a rare renal proximal tubulopathy known as Dent disease (Wrong et al., 1994).

In this review we discuss the *CLCN5* gene and its gene product *CIC-5*, whose mutations have been found responsible for Dent disease type 1. We also report on recent findings concerning the role of *CIC-5* in renal glomerular cells.

## 2. The *CLCN5* gene

The human *CLCN5* gene (MIM#300008, reference sequence NG\_007159.2) was identified 25 years ago (Scheinman et al., 1993; Fisher, 1994). It is located in the pericentromeric region on chromosome Xp11.23. Spanning about 170 Kb of genomic DNA, it has a coding region of 2,238 bp, and consists of 17 exons, including 11 coding exons (from 2 to 12) (Scheinman et al., 1993; Fisher, 1994; Fisher et al., 1995; Scheel et al., 2005). The *CLCN5* gene has 201 orthologues among jawed vertebrates (Gnathostomata), and 8 paralogues (*CLCN1*, *CLCN2*, *CLCN3*, *CLCN4*, *CLCN6*, *CLCN7*, *CLCNKA*, *CLCNKB*).

*CLCN5* has five different transcripts, one of which does not encode for any protein (transcript variant 5, NM\_001272102.2), while two (transcript variants 3 [NM\_000084.5] and 4 [NM\_001282163.1]) encode for the canonical 746 amino acid protein (Table 1), and the other two (transcript variants 1 [NM\_001127899.3] and 2 [NM\_001127898.3]) encode for the  $\text{NH}_2$ -terminal extended 816 amino acid protein (Ludwig et al., 2003).

The 5' untranslated region (5' UTR) of *CLCN5* is complex and has yet to be fully clarified. It was predicted that the *CLCN5* gene would include two strong, and one weak functional promoters (Tosetto et al., 2014; Hayama et al., 2000). Several different 5' alternately-used exons, some remaining untranslated, have been identified (Ludwig et al., 2003; Tosetto et

al., 2014; Hayama et al., 2000; Lloyd, 1996; Forino et al., 2004). In the human kidney, three promoters give rise, with a varying degree of efficiency, to 11 different mRNAs, with transcription initiating from at least three different start sites (Tosetto et al., 2014). When the significance of these different 5'UTR isoforms was recently investigated in control and proteinuric kidney biopsies, a different expression pattern emerged, suggesting a possible involvement for proteinuria in the CIC-5 transcriptional regulation (Ceol et al., 2020).

### 3. The CIC-5 protein

CIC-5 is the protein product of the *CLCN5* gene, and part of the family of CIC channels and ion exchangers (Jentsch et al., 2002). Studies on rat tissues demonstrated that CIC-5 is less widely distributed than CIC-3 or CIC-4, indicating a prominent expression in the epithelia of kidney and intestine in addition to other tissues such as brain and liver (Steinmeyer et al., 1995; Vandewalle, 2001).

#### 3.1. Protein structure

The CIC-5 protein's structure is complex. The canonical isoform consists of 746 amino acids (Table 1), but there is also a second isoform comprising 816 amino acids of unknown biological significance (Ludwig et al., 2003). In 2003, the sequence alignment of the canonical human CIC-5 with its paralogues from *Escherichia coli* and *Salmonella enterica serovar typhimurium* led to the identification of the 18  $\alpha$ -helices (named A to R) that form its secondary structure (Wu, 2003) (Fig. 1). Helices B, H, I, O, P, and Q are the six main helices involved in the dimer interface's formation, and are necessary for proper pore configuration (Wu, 2003; Mansour-Hendili, 2015). In particular, helices B and I are on the side of the subunit, while helices O and P are located more centrally at the dimer's interface (Wu, 2003). The Cl<sup>-</sup> selectivity filter is provided mainly by helices D, F, N, and R, which are brought together near the center of the channel (Wu, 2003; Mansour-Hendili, 2015; Grand et al., 2009; Pusch et al., 1997). The role of the E helix in CIC-5 function is still unclear, but mutations nearby reportedly produce a loss of Cl<sup>-</sup> conductance, or current failures due to endoplasmic reticulum retention (Lloyd; 1996; Wu, 2003; Grand et al., 2009). Molecular modelling studies indicated that many *CLCN5* missense mutations cluster in the helices at the dimer interface of CIC-5, potentially destabilizing its formation and disrupting the pore configuration, with a loss or reduction of channel activity (Wu, 2003; Günther et al., 1998; Lourdel et al., 2012; Pusch and Zifarelli, 2015).

The most important amino acids for proper CIC-5 function are the "proton glutamate" Glu 268 (Zdebik, 2008; Grieschat and Alekov, Mar. 2012) and the "gating glutamate" Glu 211 (Dutzler et al., 2003; Yin et al., 2004). The proton glutamate is crucial to the H<sup>+</sup> transport acting as an H<sup>+</sup> transfer site (Zdebik, 2008; Accardi et al., 2005; Neagoe et al., 2010). Its importance was further highlighted by experiments using *Xenopus* oocytes, in which mutations mapping in the loop between nearby helices H and I were reportedly associated with chloride current abolition (Igarashi, Dec. 1998). The gating glutamate Glu 211 is necessary for both H<sup>+</sup> transport and CIC-5 voltage dependence (Scheel et al., 2005; Friedrich et al., 1999; Picollo and Pusch, 2005). Mutations that affect this amino acid lead to

a mutant protein that conducts both outward and inward  $\text{Cl}^-$  currents and acts as a  $\text{Cl}^-$  channel (Smith and Lippiat, 2010).

Like all eukaryotic CICs, CIC-5 has a large cytoplasmic C-terminus containing two cystathionine beta-synthase (CBS) domains. Several authors have shown that CBS domains are involved in regulating the activity of CICs, including CIC-5 (Meyer et al., 2007; Wellhauser et al., 2011; Zifarelli and Pusch, 2009) (Fig. 1). Missense mutations affecting these domains are pathogenic (Grand et al., 2009), leading to mutant proteins that target the plasma membrane and early endosomes correctly, but with an altered CIC-5 electrical activity (Lourdel et al., 2012). Studying nonsense mutations at the C-terminus, the Authors found that the resulting truncated proteins targeted the cell surface, but only one of the mutations studied had some residual activity (Grand et al., 2009), and another reportedly resulted in endoplasmic reticulum retention, underscoring the importance of the C-terminus for passing the protein quality control in this organelle (Grand et al., 2009). These findings suggest that truncated CIC-5 proteins at the C-terminus could induce loss of function, also due to a defective protein processing.

Finally, N-glycosylation is known to play a part in protein folding and oligomerization, and proteins that fail to fold or assemble properly undergo endoplasmic reticulum-associated degradation. It has been demonstrated that CIC-5 N-glycosylation site mutants may be poly-ubiquitinated, and conveyed to proteosomal degradation (Schmieder et al., 2007; D'Antonio et al., 2013).

### 3.2. Protein function

CIC-5 has a dual action, as it is involved in the acidification of early endosomes, and it participates in the protein uptake process at the brush border of PTCs (Günther et al., 1998; Devuyst et al., 1999).

CIC-5 was classified as one of the channels working mainly in intracellular membranes (with CIC-3, CIC-4, CIC-6 and CIC-7), rather than among those located largely on the plasma membrane (which include CIC-1, CIC-2, CIC-Ka, and CIC-Kb) (Jentsch et al., 2002).

All CIC channels need to dimerize to create the pore through which the ions pass (Wu, 2003; Mansour-Hendili, 2015; Lourdel et al., 2012), and *CLCN5* mutation studies have confirmed that a proper interaction between the two subunits is crucial to the proper functioning of CIC-5 as a dimer (Wu, 2003). It has also been demonstrated that CIC-5 can form both homo- and hetero-dimers due to its marked sequence homology with CIC-3 and CIC-4 (Jentsch et al., 1995; Okkenhaug et al., 2006; Mohammad-Panah, 2003).

Whether CIC-5 works as a  $\text{Cl}^-$  channel or as a  $\text{Cl}^-/\text{H}^+$  exchanger was a debated question. CIC-0, the founding member of this protein family discovered in the electric organ of *Torpedo marmorata*, is a chloride channel, so all the CLC genes were initially expected to encode for anion channels (Zdebik, 2008). Three independent groups demonstrated, however, that - instead of being a simple  $\text{Cl}^-$  channel - CIC-5 functions as a  $\text{Cl}^-/\text{H}^+$  antiporter when activated by positive voltages (Scheel et al., 2005; Zdebik, 2008; Picollo and

Pusch, 2005). The  $\text{Cl}^-/\text{H}^+$  exchange process wastes more energy than recycling  $\text{H}^+$  between endosomes and cytosol but leads to a more efficient lysosomal acidification (Satoh, 2016).

A small portion of the CIC-5 channel is also located on the cell surface, where it is believed to mediate plasma membrane chloride currents (Günther et al., 1998; Friedrich et al., 1999; Devuyst et al., 1999; Luyckx, 1998), or participate in the macromolecular complexes at plasma membrane level that are responsible for LMW protein and albumin endocytosis (Hryciw et al., 2006).

### 3.3. CIC-5 protein partners

Receptor-mediated, clathrin-dependent endocytosis, and the subsequent metabolization of proteins and nutrients are considered as some of the most important functions of renal PTCs. Receptor-mediated endocytosis requires the coordinated functioning of numerous proteins and signal transduction molecules. In particular, megalin and cubilin have a core role in this process (Kerjaschki and Farquhar, 1982; Sahali et al., 1988). These receptors bind a variety of filtered ligands with varying affinities, fulfilling their task via receptor-mediated endocytosis, and mediating the delivery of their ligands to the lysosomes of the proximal tubule (Christensen, 1982; Christensen et al., 2009). The apical expression of both megalin and cubilin in PTCs is finely tuned by a recycling mechanism that involves the endosomal pathway (reviewed in (Christensen and Birn, 2002). Cubilin also depends on the single transmembrane protein amnionless for its proper anchorage to the plasma membrane (Fyfe, 2004). A downregulation of both megalin and cubilin was demonstrated in both murine (Christensen, 2003; Gabriel, 2017) and human PTCs (Santo, 2004; Tanuma et al., 2007; Gianesello, 2020) carrying a defective CIC-5, supporting the importance of CIC-5 in the proper localization and function of these two receptors, and in the LMW protein reuptake process. The Devuyst group reported a rescue in megalin and CIC-5 expression in PTCs of *Cln5* knock-out mice after bone marrow transplantation with wild-type cells, supporting the role of CIC-5 in megalin localization and expression (Gabriel, 2017). The  $\text{Na}^+/\text{H}^+$  exchanger regulatory factor 2 (NHERF2) and the  $\text{Na}^+/\text{H}^+$  exchanger isoform 3 (NHE3) were also shown to take part in albumin endocytosis (Hryciw, 2006; Slattery, 2011). In rat PTCs, CIC-5 was found to interact with megalin via NHERF2 (Hryciw et al., 2012), but whether a direct protein-protein interaction exists between CIC-5 and NHE3 is still not clear, even if NHE3 was found dysregulated in the two CIC-5 knock-out mouse models (Wang, 2000; Piwon et al., 2000; Silva et al., 2003; Günther et al., 2003) (Fig. 2A).

Albumin endocytosis is known to proceed via clathrin-coated vesicles. This process needs a proper cytoskeletal structure, with some remodeling of the actin web to facilitate plasma membrane budding, and this gives rise to empty areas around the clathrin-coated pits (Fujimoto et al., 2000). In eukaryotic cells, the actin-depolymerizing factor/cofilin proteins regulate actin filament turnover and tertiary net formation (as reviewed in (Bamburg, 1999). Two-hybrid system experiments showed that the C-terminal end of CIC-5 can interact with cofilin. This interaction is needed for actin depolymerization and proper albumin endocytosis in two different PTC lines (Opossum -OK- and porcine -LLC-PK1), and it persists throughout the endocytotic cycle (Hryciw et al., 2003) (Fig. 2A).

KIF1B is also thought to facilitate the microtubular transport of endocytic vesicles away from the plasma membrane. It has already been demonstrated that an interaction between KIF1B and CIC-5 is needed for proper CIC-5 expression on the plasma membrane (see below) (Reed et al., 2010). All these data highlight the importance of an intact cytoskeletal structure for proper endocytosis.

An increasing acidification must also take place along the endosomal pathway for endocytosis to proceed (Clague et al., 1994). In PTCs, endosomal acidification is driven by the electrogenic vacuolar H<sup>+</sup>-ATPase (V-ATPase) (Herak-Kramberger et al., 1998). The V-ATPase lacks any coupling to counter-ion transport, and this gives rise to its electrogenic action. In other words, acidification is accompanied by the generation of a positive potential of the inner endosomal membrane (Mellman et al., 1986). This positive potential needs to be counterbalanced by the influx of anions (negative charges) from the extracellular space, or by the efflux of cations (positive charges) from inside the vesicle in order to maintain H<sup>+</sup> translocation into the vesicle lumen (Mellman et al., 1986). Whether the endosomal acidification needs the collaboration between CIC-5 and the V-ATPase is still debated. Two independent groups demonstrated the ability of CIC-5 to drive endosomal acidification independently of the V-ATPase (Scheel et al., 2005; Smith and Lippiat, 2010). On the other hand, several Authors endorse the hypothesis that CIC-5 provides a shunt conductance in early endosomes, enabling an efficient intraluminal acidification by the V-ATPase (Günther et al., 1998; Devuyt et al., 1999; Luyckx, 1998; Hara-Chikuma et al., 2005). Co-localization experiments demonstrated that CIC-5 expression largely overlaps with that of V-ATPase, supporting a close collaboration between the two proteins in this ion balancing act, thanks to the influx of Cl<sup>-</sup> induced by CIC-5 (Günther et al., 1998) (Fig. 2B). Such a cooperation was further supported in a recent paper by Satoh *et al.*, who found a reduced action of V-ATPase in a patient with Dent disease (Satoh, 2016).

#### 3.4. Renal expression of CIC-5

In the human kidney, CIC-5 is consistently expressed not only in PTCs but also in collecting duct  $\alpha$ -intercalated cells, and in epithelial cells of the thick ascending limb (TAL) of Henle's loop (Devuyt et al., 1999). This is a wider expression than in rat and mouse kidneys, where CIC-5 is expressed in PTCs, and in collecting duct  $\alpha$ - and  $\beta$ -intercalated cells (Günther et al., 1998; Obermüller et al., 1998; Sakamoto, 1999). In PTCs of all these species, CIC-5 is predominantly located in intracellular subapical endosomes, and in the brush border membrane (Günther et al., 1998; Devuyt et al., 1999; Sakamoto, 1999) (Fig. 3).

The prominent effects of CIC-5 in PTCs have overshadowed those on collecting duct and TAL even if CIC-5 expression in these segments is well-described (Günther et al., 1998; Devuyt et al., 1999; Luyckx, 1998; Sakamoto, 1999). In the collecting duct, CIC-5 is localized to the  $\alpha$ -intercalated cells that are crucial for acid-base homeostasis, and it colocalizes with the V-ATPase in the apical and subapical vesicles. Accordingly, CIC-5 might be important for insertion and recycling of these vesicles, and when CIC-5 function is lost, defective expression of V-ATPase may result causing impaired urinary acidification (Günther et al., 1998). The role of CIC-5 in TAL remains circumstantial and speculative (Pham, 2004). Studies suggest that endocytosis takes place in murine TAL where V-ATPase

is also present albeit at a lesser extent than in PTCs, thus suggesting a possible role for CIC-5 during endocytosis and exocytosis processes in this nephron segment (Bastani, 1997).

CIC-5 proximal tubular apical expression is fine-tuned by several proteins. In 2001, the Thakker group identified the interaction between the WW domain-containing protein 2 (WWP2) and a proline-rich stretch of amino acids in the CIC-5C-terminus. They also showed that WWP2 is needed to modulate CIC-5 retention in the plasma membrane (Schwake et al., 2001). In 2004, the Poronnik group added another piece to the puzzle, demonstrating the functional interaction of Nedd4-2 with CIC-5 (Hryciw, 2004) in Opossum kidney (OK) cells. WWP2 and the Nedd4-like proteins belong to the same ubiquitin-protein ligase family (Harvey and Kumar, 1999), which regulates membrane expression levels of target proteins. They remove specific proteins from the plasma membrane via the ubiquitination pathway, leading to the target protein's degradation into proteasomes (Schwake et al., 2001). Unfortunately, these findings were not confirmed in PTCs from *Clcn5<sup>-/-</sup>* mice (Rickheit, 2010). To complicate things further, the Thakker group demonstrated *in vivo* and *in vitro*, in both polarized and non-polarized OK cells, that the interaction between CIC-5 and KIF1B via the CIC-5 C-terminus is important for the plasma expression of CIC-5 as well (Reed et al., 2010). Wojciechowski *et al.* also recently reported that barttin plays a part in the trafficking and processing of CIC-5 too (Wojciechowski, 2018). These Authors made the point, however, that the interaction between barttin and CIC-5 probably occurs in the tubular segments where barttin is expressed, such as the thick ascending limb of Henle's loop and the intercalated cells of the collecting duct (Wojciechowski, 2018).

CIC-5 is not only expressed by tubular cells in the kidney. We recently found it expressed in human glomeruli as well, identifying these CIC-5-positive cells as podocytes. In particular, CIC-5 was found overexpressed in the glomeruli of patients with proteinuric nephropathies, at both mRNA and protein level, suggesting a role for this protein in albumin endocytosis by podocytes (Ceol, 2012). Prabakaran *et al.* demonstrated human podocyte positivity for both megalin and cubilin too, supporting the likelihood of a functional role for CIC-5 at glomerular level (Prabakaran, 2011; Prabakaran et al., 2012) (Fig. 3). Further *in vitro* studies on human podocytes confirmed the presence of CIC-5 (Gianesello, 2017; Solanki, 2018), and showed that protein overload can modulate the protein uptake macromolecular complex, inducing an increase in the gene expression of *CLCN5*, *CUBN*, and *AMN*, and in the protein expression of CIC-5 (Gianesello, 2017).

Podocytes are not the only type of glomerular cell expressing the protein uptake complex. We recently showed that human parietal epithelial cells (PECs) also express CIC-5, megalin and cubilin (Gianesello, et al., 2018) (Fig. 3). This evidence confirmed previous findings in kidneys of diabetic rats (Zhao et al., 2019). Zhao et al. also demonstrated that album intake by rat PECs via megalin led to an increase in CD44 (Zhao et al., 2019). The cluster of differentiation 44 (CD44) is a glycoprotein localized on the cell surface that plays a role in several cellular processes, such as cell differentiation, cell migration, cell-matrix binding, leukocyte trafficking, and scar formation (Nakamura et al., 2005). CD44 is now used to identify PECs directed towards a profibrotic phenotype and ultimately leading to glomerulosclerosis and kidney failure (Lim et al., 2016). Dent disease patients are now

known to have focal segmental glomerulosclerosis (FSGS) and/or focal global glomerulosclerosis (Wang, 2016), so the expression of CIC-5 and its protein partners in PECs points to an active involvement of these cells in the onset of the glomerular damage.

#### 4. *CLCN5* and Dent disease 1

The term Dent's disease was first introduced in the 1990s (Wrong et al., Aug. 1994). It identifies a group of X-linked recessive renal disorders characterized by LMW proteinuria and variable degrees of hypercalciuria, nephrocalcinosis and/or nephrolithiasis (Lloyd, 1996; Thakker, 2000; Dent and Friedman, 1964). Mutations in the *CLCN5* gene are the most common cause of the disease (responsible for about 65% of cases), which is now called Dent disease type 1 (DD1; MIM#300009) (Jentsch et al., 1995; Thakker, 1997; Waldegger and Jentsch, 2000). Dent disease type 2 (DD2; MIM#300555) is due to mutations in the *OCRL* gene (Hoopes et al., 2005), identified in about 10–15% of Dent disease patients (Lieske et al., 1993). The remaining 25–35% of patients have neither of these mutations, and were classified as cases of Dent disease type 3 (DD3) (Anglani, 2015).

Several studies tried to identify other genes responsible for the phenotype observed in DD3 patients. In 2009, the Thakker and Anglani groups screened Dent disease patients for mutations in the genes encoding for cofilin and collectrin, but none came to light (Wu, et al., 2009; Tosetto, Oct. 2009). After technological advances in next-generation sequencing, a couple of studies tried to fill the gap between the DD3 phenotype and its genetic origin, but to no avail (Gianesello, 2020; Zhang et al., 2017; Anglani, 2018). Collectively, these studies give the impression that DD3 patients' phenotypes might be explained by a number of hypotheses: (i) they could be the result of defects in more than one gene; (ii) they may be atypical phenotypes of known hereditary nephropathies; or (iii) they may be blended phenotypes.

##### 4.1. Allelic heterogeneity

Allelic heterogeneity is a characteristic of DD1. To date, 266 different *CLCN5* pathogenic variants have been described (Table S1) (Mansour-Hendili, 2015; Gianesello, 2020; Bitsori et al., 2019; Tang, 2016; Li, 2016; Wong et al., 2017; Guven, 2017; Günthner et al., 2018; Sancakli et al., 2018; Bignon, 2018; Wen et al., 2018; Matsumoto, 2018; Ye et al., 2019; Hoopes et al., 2004; Bhardwaj et al., 2016; Armanet et al., 2015; Danyel et al., 2019; Zaniew, 2017; Tosetto, 2009; Güngör, 2020). A few pathogenic variants were found in more than one family (Lieske et al., 1993): 48% were truncating (nonsense, frameshift or complex); 37% were non-truncating (missense or in-frame insertions/deletions); 10% were splice site mutations; and 5% were other types (large deletions, Alu insertions or 5'UTR mutations). In particular, the majority of the reported mutations were missense (with 93 different mutations) or frameshift (83), followed by nonsense mutations (44), splicing mutations (26), and large deletions (10) (Fig. 4).

The spectrum of pathogenic *CLCN5* variants shows great variety, and de novo pathogenic variants are common. They are scattered throughout the gene's coding sequence, generating truncated or absent CIC-5 protein in approximately 60% of cases (Lieske et al., 1993). Most pathogenic *CLCN5* variants have not been fully investigated in functional terms. DD1



phenotypic variability may be due to different degrees of the altered CIC-5 protein's function loss. Functional investigations on wild-type and mutant CIC-5 in *Xenopus* oocytes (Lloyd, 1996; Lloyd, 1997), in human embryonic kidney cells (HEK) (Smith and Lippiat, 2010; Grand et al., 2011), in conditionally immortalized proximal-tubular epithelial cell lines (ciPTEC) from patients with DD1 (Gorvin et al., 2013), and *in vivo* in mice harboring induced CIC-5 mutations (Novarino et al., 2010) have enabled *CLCN5* variants to be classified according to their functional consequences as follows (Lourdell et al., 2012; D'Antonio et al., 2013; Lieske et al., 1993; Smith et al., 2009; Ludwig et al., 2005).

*Class 1:* pathogenic variants that impair processing and folding, leading to the mutated protein's retention in the endoplasmic reticulum, and its degradation by proteasomes. This results in the mutant proteins being improperly N-glycosylated, and non-functioning due to a defective trafficking to the cell surface and to the early endosomes;

*Class 2:* pathogenic variants that generate a functionally defective protein, devoid of electric currents, and resulting in the failure of endosomal acidification;

*Class 3:* pathogenic variants that cause an abnormal subcellular localization of the mature protein;

*Class 4:* pathogenic variants generating a protein that normally targets the plasma membrane correctly, but exhibits reduced membrane currents.

The above evidences indicate that the mechanisms by which CIC-5 mutations lead to DD1 vary and are not necessarily linked to a primary defect in the endosomal acidification.

#### 4.2. Clinical description

Since DD1 is an X-linked recessive disorder, males are more frequently affected than females. Females carriers are usually asymptomatic (Lieske et al., 1993). The clinical signs in patients with DD1 are the consequence of an involvement of both the tubular and the glomerular compartments. These signs generally appear in childhood or early adulthood. The signs of DD1 can vary, but always include proteinuria (Anglani, 2015). DD1 patients may also reveal a significantly reduced cubilin and megalin expression in PTCs, probably due to a disturbed intracellular trafficking of the receptors (Gianesello, 2020; Christensen et al., 2013); this is probably one of the reasons behind the onset of proteinuria.

Proximal renal tubular dysfunction is characterized by LMW proteinuria (LMWP), hypercalciuria, nephrocalcinosis and/or nephrolithiasis. Additional tubular defects, such as hyperphosphaturia, glycosuria and aminoaciduria, may sometimes appear too, but are less prominent features (Devuyst and Thakker, 2010; Hodgkin et al., 2008). Males under ten years old may manifest only LMWP and/or hypercalciuria. Hypophosphatemia and bone disorders (rickets or osteomalacia) have also been reported, as well as growth restriction and short stature (Bökenkamp, 2009), usually without a complete Fanconi syndrome or metabolic acidosis (Reinhart et al., 1995) (Fig. 5).

This huge variability in the clinical phenotype of DD1 was further confirmed in two murine *Clcn5* knock-out models (Wang, 2000; Piwon et al., 2000; Silva et al., 2003; Günther et al.,

Jan. 2003): both models showed LMWP, polyuria, phosphaturia, and normal serum PTH; the Guggino model also revealed hypercalciuria, nephrocalcinosis, and an increase in serum 1,25(OH)<sub>2</sub>D (Anglani et al., Nov. 2019).

Dent disease progresses to chronic kidney disease (CKD) between the 3rd and 5th decades of life in 30–80% of male patients. In adult cases, the disease is usually suspected in the presence of nephrocalcinosis/nephrolithiasis or unexplained CKD in individuals with hypercalciuria, or in the context of familial cases of CKD and/or nephrolithiasis (Edvardsson et al., 2013; Ferraro et al., 2013).

In several case reports, DD1 patients had not only LMWP, but also severe proteinuria (even in the nephrotic range), suggesting the possibility of glomerular as well as tubular damage. This hypothesis was confirmed by histological findings of focal global and/or focal segmental glomerulosclerosis or mesangial proliferative glomerulonephritis, in addition to episodic evidences of isolated proximal tubular dysfunction (Wang, 2016; Zaniew, 2017; Copelovitch et al., 2007; Frishberg et al., 2009; Kaneko et al., 2010; Cramer et al., 2014; Bao et al., 2019; Fervenza, 2013). These histological signs suggest that there could be misdiagnosed cases of DD1 among patients diagnosed with FSGS. The recent study by Beara-Lasic *et al.* on pediatric FSGS and CKD cohorts found no *CLCN5* mutations in these children, however (Beara-Lasic *et al.*, 2019).

### 4.3. Atypical phenotypes

DD1 is rarely associated with extrarenal symptoms, which are more common in DD2 due its overlapping features with Lowe syndrome that is also caused by mutations in the *OCRL* gene (De Matteis et al., 2017). In fact, a case of DD1 associated with ocular anomalies, bone disease, and mild mental impairment was described as being caused by the coinheritance of mutations in both the *CLCN5* and the *OCRL* genes (Addis et al., 2013). DD1 is considered an exclusively renal disease, given that CIC-5 is expressed mainly in the kidney. Some reported cases of DD1 were associated with unusual symptoms, such as: night blindness (Sethi et al., 2009; Becker-Cohen et al., 2012); growth hormone deficiency (Samardzic et al., 2011; Sheffer-Babila et al., 2008); and, in one instance, growth hormone deficiency complicated by Budd-Chiari syndrome (Platt et al., 2014).

A blended phenotype should be suspected for DD1 associated with a Bartter-like phenotype. Bartter's syndrome (BS; MIM #: type I, 601678; type II, 241200; type III, 607364; type IV, 602522; type IVb, 613090) and Gitelman's syndrome (GS; MIM # 263800) are autosomal recessive tubular disorders with characteristic sets of metabolic abnormalities, including: hypokalemia; metabolic alkalosis; hyperreninemia; hyperplasia of the juxtaglomerular apparatus; and hyperaldosteronism. They are caused by mutations in genes encoding proteins involved in renal electrolyte homeostasis in the thick ascending limbs of Henle's loop, and in the distal convolute tubule (Blanchard et al., 2017). DD1 and BS may be clinically diagnosed in the same patient, albeit rarely (Besbas et al., 2005; Bogdanovi et al., 2010; Okamoto et al., 2012). It is currently hard to say whether this blended phenotype is the outcome of mutations in both the *CLCN5* and the BS or GS genes, or rather an expansion of the DD1 phenotype because of the role of CIC-5 in the other tubular segments of the nephron, which however has yet to be clarified. In fact, if on one hand not all of the BS and

GS genes were screened in these patients, on the other it was very recently reported that barttin, the protein impaired in Bartter's syndrome type 4 (which is an essential subunit of the CIC-Ka and CIC-Kb chloride channels), appears to regulate the subcellular localization and posttranslational modification of CIC-5 (Wojciechowski, 2018). The Authors hypothesized that abnormal barttin-CIC-5 interactions in the thick ascending limbs of Henle's loop and the collecting duct might contribute to the Bartter's phenotype seen in some DD1 patients.

#### 4.4. Clinical management

There is no specific therapy for patients with DD1, so it is usual clinical practice to treat patients symptomatically. Pharmacological intervention generally aims to reduce proteinuria, hypercalciuria or rickets, or may be to prevent nephrolithiasis or nephrocalcinosis. Many of the therapeutic options available have not been tested in randomized clinical trials.

Thiazide diuretics have proved effective against hypercalciuria in DD1 patients (Raja et al., 2002), but the Authors recommended using hydrochlorothiazide only in those who were recurrent stone formers. This was the starting point for the first clinical trial on DD1 patients, conducted in France from 2003 to 2008 ([ClinicalTrials.gov Identifier: NCT00638482](https://clinicaltrials.gov/ct2/show/study/NCT00638482)), to examine whether high doses of thiazides could prevent nephrocalcinosis in children with Dent disease. The Authors found the treatment associated with a lower calcium excretion, but also with significant adverse events (which prompted the trial to be stopped early), so they recommended caution in the use of diuretics in pediatric patients with Dent disease (Lieske et al., 1993; Blanchard et al., 2008).

The presence of proteinuria usually induces physicians to treat DD1 patients with ACE and/or angiotensin II receptor blockers. Theoretically, drugs inhibiting the renin-angiotensin-aldosterone system (RAAS) should not be effective for tubular proteinuria, but the glomerular damage present in some DD1 patients could explain the positive effects of this treatment (Zaniew, 2017; Blanchard et al., 2016). Only a small percentage of DD1 patients have glomerular damage, however, and this would explain the discrepant results obtained with RAAS inhibition in such patients (van Berkel et al., 2017).

Studies on *Clcn5*<sup>-/-</sup> mice revealed that a high-citrate diet could reduce hypercalciuria and slow renal disease progression, even in the absence of nephrolithiasis (Cebotaru et al., 2005), but this has yet to be confirmed in humans. Nonetheless, DD1 patients are often prescribed citrates (usually potassium citrate) to prevent nephrolithiasis, improve acidosis, and thus slow CKD progression (Lieske et al., 1993; Zaniew, 2017).

Bone disease was found to respond to vitamin D supplementation in patients with high serum alkaline phosphatase levels (Wrong et al., 1994). Treatment with vitamin D requires close monitoring, however, because it can exacerbate hypercalciuria, and may increase the risk of nephrocalcinosis. That is why some authors recommend monitoring calcemia, calciuria and 25-hydroxyvitamin D to prevent this from happening (Blanchard et al., 2016).

Finally, phosphate supplementation could be used to treat hypophosphatemia or bone disease (Lieske et al., 1993; Zaniew, 2017). The most recent clinical trial focusing on this

issue was carried out at the Mayo Clinic in Minnesota from 2014 to 2019 ([ClinicalTrials.gov Identifier: NCT02016235](https://clinicaltrials.gov/ct2/show/study/NCT02016235)), the aim being to establish whether supplementation with phosphorus could reduce hypercalciuria. The results of this study have yet to be published.

## 5. Conclusions

In conclusion, proteinuria is an important clinical sign that should not be underestimated. It is well-known that the CIC-5 channel, encoded by the *CLCN5* gene, has a pivotal role in protein re-uptake by PTCs. Studies on Dent disease patients have expanded the picture, disclosing how widely the CIC-5 channel is expressed throughout the kidney, and how many processes are affected by its malfunctioning. Taken together, these data demonstrate that Dent disease type 1 should now be considered as a disorder affecting not only PTCs, but the whole kidney.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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## Abbreviations:

<b>5'UTR</b>	5' untranslated region
<b>BS</b>	Bartter's syndrome
<b>CKD</b>	chronic kidney disease
<b>ciPTEC</b>	conditionally immortalized proximal-tubular epithelial cell lines
<b>CSB</b>	cystathionine beta-synthase
<b>DD1</b>	Dent disease type 1
<b>DD2</b>	Dent disease type 2
<b>DD3</b>	Dent disease type 3
<b>FSGS</b>	focal segmental glomerulosclerosis
<b>GBM</b>	glomerular basement membrane
<b>GFB</b>	glomerular filtration barrier

<b>GS</b>	Gitelman's syndrome
<b>HEK</b>	human embryonic kidney cells
<b>LMW</b>	low-molecular-weight
<b>LMWP</b>	low-molecular-weight proteinuria
<b>NHERF2</b>	Na <sup>+</sup> -H <sup>+</sup> exchanger regulatory factor 2
<b>NHE3</b>	Na <sup>+</sup> -H <sup>+</sup> exchanger isoform 3
<b>OK</b>	Opossum kidney
<b>PEC</b>	parietal epithelial cell
<b>PTCs</b>	proximal tubular cells
<b>RAAS</b>	renin-angiotensin-aldosterone system
<b>TAL</b>	thick ascending limb
<b>V-ATPase</b>	electrogenic vacuolar H <sup>+</sup> -ATPase
<b>WWP2</b>	WW domain-containing protein 2

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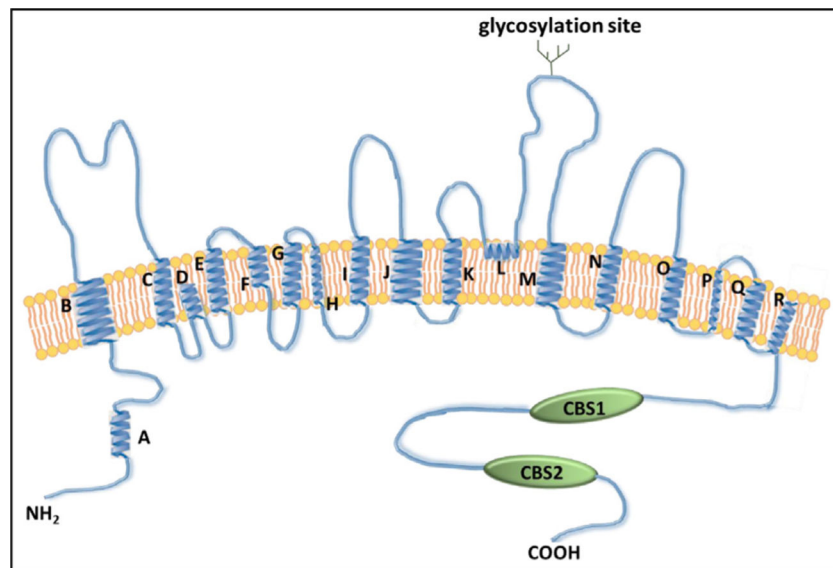
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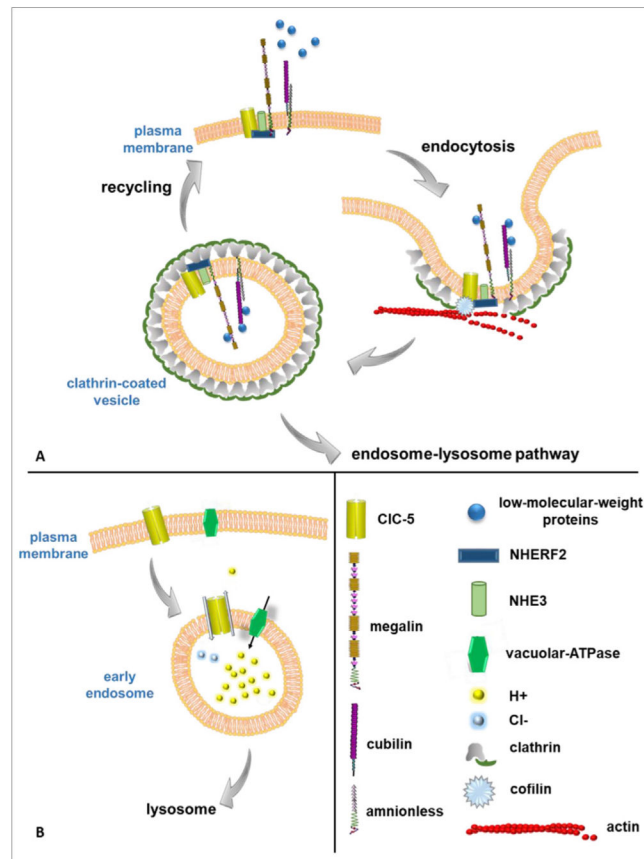
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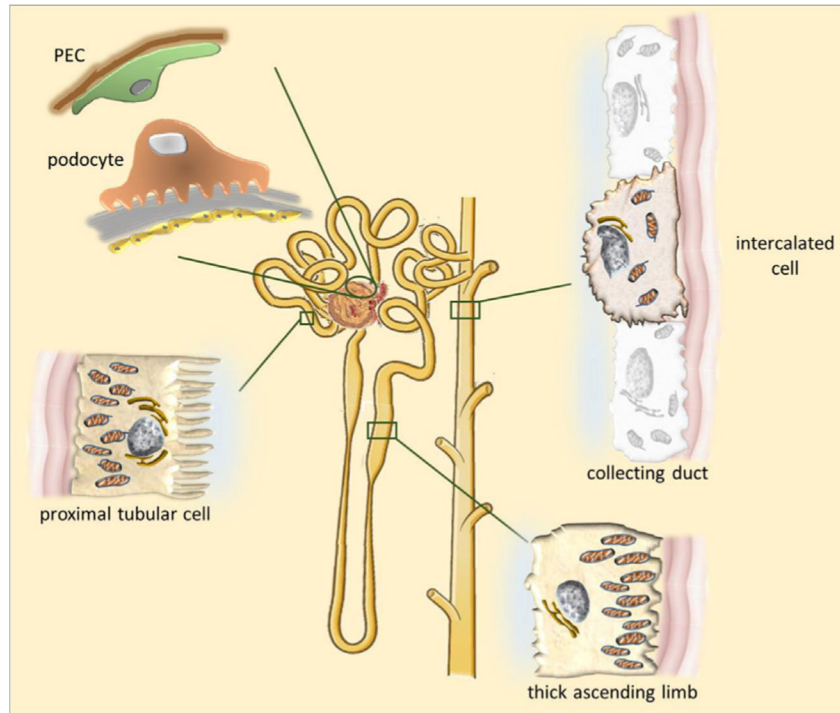
**Fig. 1. CIC-5 protein structure.** Schematic representation of the CIC-5 protein showing the 18 alpha-helices (from A to R), the two CBS domains, and the main glycosylation site.



**Fig. 2. CIC-5 and its protein partners.**

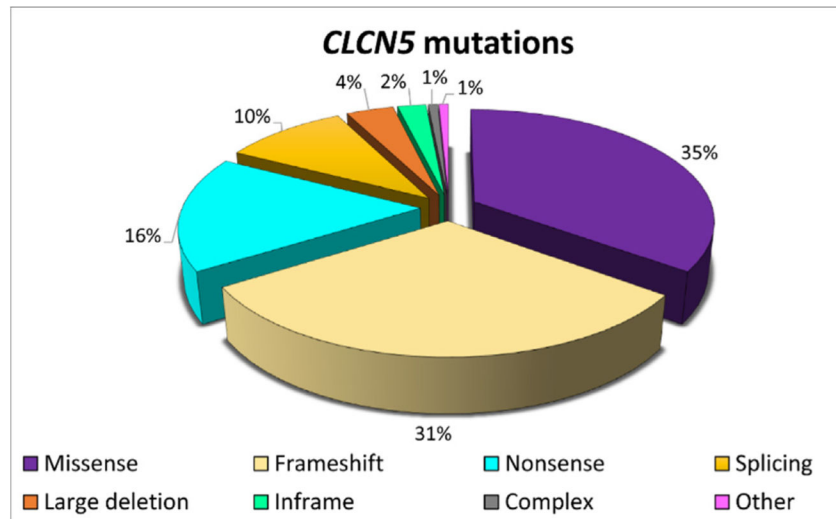
CIC-5 is involved in two different processes conducted by PTCs: the endocytosis of low-molecular-weight proteins (A); and endosomal-lysosomal acidification (B). These two processes are closely connected, and require collaboration between CIC-5 and several other actors with distinctive features.





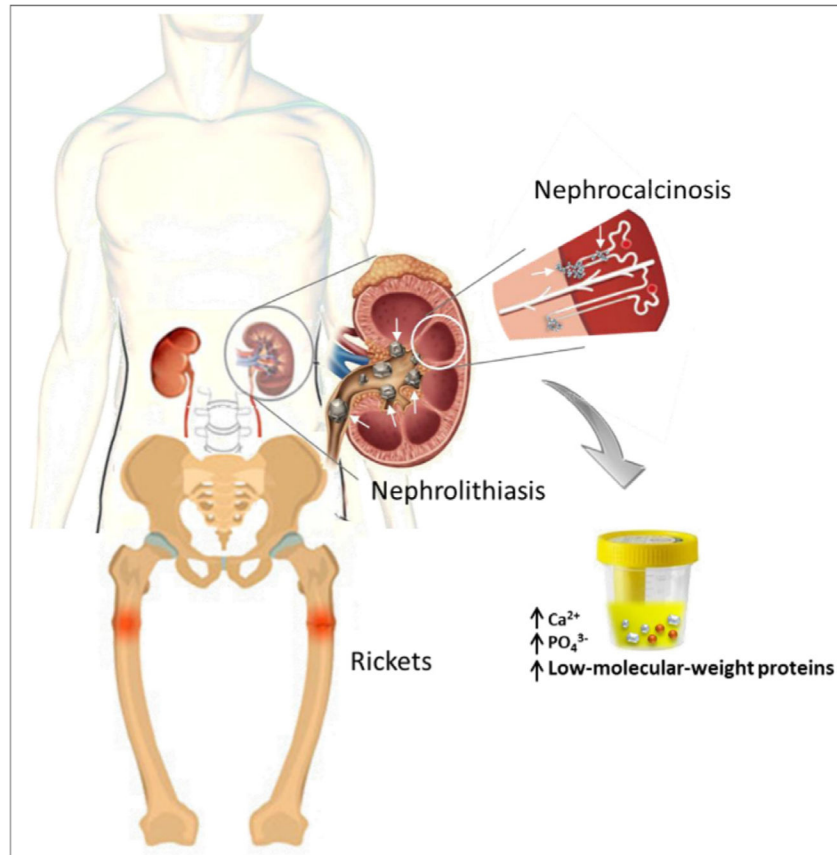
**Fig. 3. CIC-5 expression in the kidney.**

CIC-5 is expressed in various tubular segments (proximal tubule, thick ascending limb of Henle's loop, alpha-intercalated cells of the collecting duct), and in glomerular cells (podocytes and parietal epithelial cells [PECs]).



**Fig. 4. Distribution of CLCN5 gene mutations.**

The graph shows the proportions of the different *CLCN5* mutations identified. Other: Alu insertion and 5'UTR mutations.



**Fig. 5. Dent disease 1, clinical phenotype.**

DD1 is associated with the variable presence of a number of clinical signs.

**Table 1**Basic properties of *CLCN5* and its protein product CIC-5.

	<i>Homo sapiens</i>	<i>Mus musculus</i>
<b>Gene symbol</b>	<i>CLCN5</i>	<i>CLCN5</i>
<b>Chromosome</b>	Xp11.23	X A1.1; X 3.21
<b>Ensembl ID</b>	ENSG00000171365	ENSMUSG00000004317
<b>Uniprot ID</b>	P51795	Q9WVD4
<b>Exon numbers</b>	12, coding exons: 11	12, coding exons: 11
<b>Protein length (in aa's)</b>	746	746
<b>Protein mass (kDa)</b>	83	83

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