The role of enterocyte defects in the pathogenesis of congenital diarrheal disorders

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ABSTRACT

Congenital diarrheal disorders are rare, often fatal, diseases that are difficult to diagnose (often requiring biopsies) and that manifest in the first few weeks of life as chronic diarrhea and the malabsorption of nutrients. The etiology of congenital diarrheal disorders is diverse, but several are associated with defects in the predominant intestinal epithelial cell type, enterocytes. These particular congenital diarrheal disorders (CDDENT) include microvillus inclusion disease and congenital tufting enteropathy, and can feature in other diseases, such as hemophagocytic lymphohistiocytosis type 5 and trichohepatoenteric syndrome. Treatment options for most of these disorders are limited and an improved understanding of their molecular bases could help to drive the development of better therapies. Recently, mutations in genes that are involved in normal molecular bases could help to drive the development of better disorders are limited and an improved understanding of their molecular bases could help to drive the development of better therapies. Recently, mutations in genes that are involved in normal intestinal epithelial physiology have been associated with different CDDENT. Here, we review recent progress in understanding the cellular mechanisms of CDDENT. We highlight the potential of animal models and patient-specific stem-cell-based organoid cultures, as well as patient registries, to integrate basic and clinical research, with the aim of clarifying the pathogenesis of CDDENT and expediting the discovery of novel therapeutic strategies.

KEY WORDS: Brush border, Cell polarity, Congenital diarrheal disorder, Enterocyte, Intracellular trafficking, Microvillus inclusion diseases

Introduction

Congenital diarrheal disorders (CDDs) are a group of rare inherited intestinal disorders that are characterized by persistent life-threatening intractable diarrhea and nutrient malabsorption, which emerge during the first weeks of life. The etiology of CDDs is diverse, including defects in enteroendocrine cells, dysregulation of the intestinal immune response, or defects in the predominant cell type of the intestinal epithelium, the enterocyte (Canani et al., 2015).

CDDs associated with enterocyte defects (abbreviated as CDDENT) include disorders that can be treated with nutrition therapy. Other CDDENT require life-long total parenteral nutrition (TPN; see Box 1 for a glossary of clinical terms used in this article) to receive adequate nutrition, and are a leading indication for pediatric intestinal transplantsations (Halac et al., 2011). Most CDDENT are difficult to diagnose, and clinical management is restricted to the treatment of symptoms; there is currently no cure. If left untreated, CDDENT are invariably fatal.

Owing to the consanguinity of parents of affected children, genetic defects associated with CDDENT have recently been identified. The clinical consequences of some mutations – those affecting specific transporter proteins or certain enzymes – are relatively straightforward, such as in individuals with congenital lactase deficiency or sucrase-isomaltase deficiency caused by loss-of-function mutations in lactase (Behrendt et al., 2009; Kuokkanen et al., 2006) and sucrase-isomaltase (Ritz et al., 2003), respectively. Other mutations, however, are in genes that have less well-understood functions in intestinal epithelial physiology, such as in individuals with microvillus inclusion disease (MVID), congenital tufting enteropathy (CTE), familial hemophagocytic lymphohistiocytosis type 5 (FHL5) and trichohepatoenteric syndrome (THES) (Fabre et al., 2012; Hartley et al., 2010; Heinz-Erian et al., 2009; Müller et al., 2008; Sivagnanam et al., 2008; Szerpl et al., 2011; Wiegierink et al., 2014; zur Stadt et al., 2009). Table 1 summarizes CDDENT-associated genes, the proteins they encode and their function. Understanding the mechanisms by which these mutations lead to disease should pinpoint targets for improved diagnosis and therapeutic intervention.

The identification of genetic mutations in individuals with CDDENT has confirmed the autosomal recessive inheritance pattern of these diseases; thus, genetic counselling and prenatal diagnosis are important tools for heterozygote carriers. Because the histological hallmarks that characterize some CDDENT can be very subtle and easily missed, the identification of genetic defects contributes to a better and faster differential diagnosis, which is currently offered by several medical centers worldwide.

Here, we discuss the different CDDENT, recent discoveries concerning their underlying molecular and genetic mechanisms, and the model systems used in researching these disorders. Further, basic research is urgently needed to improve the diagnosis and management of these devastating diseases, and for developing new therapeutic strategies to combat them.

Enterocytes: a brief overview

Enterocytes are the absorptive cells in the lining of the intestinal mucosa. Enterocytes originate from the intestinal stem cells that reside in the intestinal crypts (Sato et al., 2009), and differentiate and migrate within 3-4 days from the crypt to the villus tip, where they are extruded into the gut lumen. Enterocytes are arranged as a monolayer of polarized epithelial cells (Fig. 1) (Massey-Harroche, 2000). Their plasma membrane consists of a basal and a lateral domain, facing the underlying tissue and neighboring cells, respectively, and an apical domain, facing the gut lumen. Densely packed microvilli, supported by an actin filament meshwork,
Defects of brush-border-associated enzymes and transporter proteins

The majority of CDD\textsuperscript{ENT} are caused by autosomal recessive mutations in genes that encode brush-border-associated enzymes and transporter proteins (Canani et al., 2015) (Table 1). Depending on the type of mutation, these proteins are either not expressed, not correctly transported to the brush border membrane, or display defects in their activity, resulting in defective digestion, absorption and/or transport of nutrients, metabolites and/or electrolytes at the enterocyte brush border. Subsequent changes in the concentration of osmotically active compounds in the gut lumen cause diarrhea. Prototypical examples of these CDD\textsuperscript{ENT} are glucose-galactose malabsorption (caused by mutations in the Na\textsuperscript{+}/glucose cotransporter gene, SGLT1) (Martín et al., 1996), congenital lactase deficiency (mutations in the lactase gene, LCT) (Kuokkanen et al., 2006), sucrase-isomaltase (SI) deficiency (caused by mutations in the SI gene) (Ritz et al., 2003), congenital chloride diarrhea (caused by mutations in the solute carrier family 26 member 3 gene, SLC26A3) (Wedenoja et al., 2011); several other CDD\textsuperscript{ENT} can also be included in this category (Canani and Terrin, 2011) (Table 1).

Individuals with familial diarrhea syndrome have activating mutations in GLUCY2C, which encodes the guanylate cyclase 2C protein. Mutated guanylate cyclase 2C enhances cellular cGMP levels (Fiskerstrand et al., 2012). cGMP stimulates cystic fibrosis transmembrane conductance regulator (CFTR) activity in the brush border of enterocytes by stimulating its proper translocation, resulting in enhanced secretion of chloride and water (Golin-Bisello et al., 2005). CDD\textsuperscript{ENT} associated with functional defects of brush-border-associated enzymes and transporter proteins are typically not associated with abnormal enterocyte organization, as examined by histology.

Defects in intracellular protein transport

In other CDD\textsuperscript{ENT}, apical brush-border-associated enzymes and transporter proteins are collectively mislocalized in the enterocytes, indicative of general defects in intracellular protein transport. Examples of CDD\textsuperscript{ENT} characterized by this class of defect are described below.

Microvillus inclusion disease

Individuals with MVID suffer from persistent diarrhea, nutrient malabsorption and failure to thrive (Cutz et al., 1989). In most cases (95\%), symptoms develop within days after birth, but a late-onset variant, which manifests 2-3 months postnatally, has also been described (Cutz et al., 1989). Variable extra-intestinal symptoms include intrahepatic cholestasis and renal Fanconi syndrome (van der Velde et al., 2013) (see MVID case study in Box 2). Some individuals with MVID present less-severe digestive symptoms for reasons that are not clear (Perry et al., 2014).

MVID, which is diagnosed by intestinal biopsy, features villus atrophy, microvillus atrophy, and the redistribution of CD10 and periodic acid Schiff (PAS)-stained material from the brush border to intracellular sites (Phillips et al., 2000) in the enterocytes. Staining of the epithelial cell-cell adhesion protein EpCAM, aberrant in CTE, is normal (Martin et al., 2014). A definitive diagnosis is recommended prior to potential intestinal transplantation, and this includes analysis by electron microscopy (EM) for microvillus inclusions in the cytoplasm of enterocytes. The frequency of such inclusions can be very low and repeated rounds of EM analyses can be required, although semi-automated EM might help to increase the efficiency of screening (de Boer et al., 2015). Immuno-based detection of
### Table 1. Overview of CDD<sup>ENT</sup>, their associated genes and currently available model systems

<table>
<thead>
<tr>
<th>Disease name</th>
<th>Gene</th>
<th>Protein</th>
<th>Protein function</th>
<th>Cell models</th>
<th>Animal models</th>
<th>Patient-specific models</th>
</tr>
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<tbody>
<tr>
<td>Glucose-galactose malabsorption</td>
<td>SGLT1</td>
<td>Na&lt;sup&gt;+&lt;/sup&gt;/glucose cotransporter</td>
<td>Glucose and galactose transport</td>
<td>–</td>
<td>SGLT1 KO mouse</td>
<td>–</td>
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<tr>
<td>Congenital lactase deficiency</td>
<td>LCT</td>
<td>Lactase</td>
<td>Lactose digestion</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td>Sucrase-isomaltase (SI) deficiency</td>
<td>SI</td>
<td>Sucrase-isomaltase</td>
<td>Carbohydrate digestion</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Congenital chloride diarrhea</td>
<td>SLC26A3</td>
<td>Solute carrier family 26 member 3</td>
<td>Chloride and bicarbonate exchange</td>
<td>–</td>
<td>SLC26A3 KO mouse (Wang et al., 2004)</td>
<td>–</td>
</tr>
<tr>
<td>Familial diarrhea syndrome</td>
<td>GUCY2C</td>
<td>Guanylate cyclase 2C</td>
<td>Enterotoxin receptor</td>
<td>–</td>
<td>GUCY2C KO mouse</td>
<td>–</td>
</tr>
<tr>
<td>Acrodermatitis enteropathica</td>
<td>SLC39A4</td>
<td>Solute carrier family 39 member 42</td>
<td>Zn&lt;sup&gt;2+&lt;/sup&gt; transport</td>
<td>–</td>
<td>Conditional and global SLC39A4 KO mouse</td>
<td>–</td>
</tr>
<tr>
<td>Fanconi-Bickel syndrome</td>
<td>SLC2A2</td>
<td>Solute carrier family 2 member 2</td>
<td>Glucose transport</td>
<td>–</td>
<td>SLC2A2 KO mouse</td>
<td>–</td>
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<tr>
<td>Lysinuric protein intolerance</td>
<td>SLC7A7</td>
<td>Solute carrier family 7 member 7</td>
<td>Amino acid transport</td>
<td>–</td>
<td>SLC7A7 KO mouse</td>
<td>–</td>
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<tr>
<td>Maltase-glucoamylase deficiency</td>
<td>MGAM</td>
<td>Maltase-glucoamylase</td>
<td>Carbohydrate digestion</td>
<td>–</td>
<td>MGAM KO mouse</td>
<td>–</td>
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<tr>
<td>Primary bile acid diarrhea</td>
<td>SLC10A2</td>
<td>Solute carrier family 10 member 2</td>
<td>Bile acid transport</td>
<td>–</td>
<td>SLC10A2 KO mouse</td>
<td>–</td>
</tr>
<tr>
<td>MVID</td>
<td>MYOSB</td>
<td>Myosin Vb</td>
<td>Molecular motor, plasma membrane recycling</td>
<td>Caco-2 cells (RNAi) (Dhekne et al., 2014; Knowles et al., 2014)</td>
<td>Myo5B KO mouse; conditional Rab11a KO mouse; conditional Cdc42 KO mouse (Cartón-García et al., 2015; Melendez et al., 2013; Sakamori et al., 2012; Sato et al., 2007; Sobajima et al., 2014).</td>
<td>Explant culture (Rhoads et al., 1991)</td>
</tr>
<tr>
<td>Atypical MVID</td>
<td>STX3</td>
<td>Syntaxin-3</td>
<td>Apical plasma membrane fusion</td>
<td>Caco-2 cells (mutant Stx3 overexpression) (Wegerinck et al., 2014)</td>
<td>–</td>
<td>Intestinal organoid (Wegerinck et al., 2014)</td>
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<tr>
<td>FHL5</td>
<td>STXB2P2</td>
<td>Munc18-2</td>
<td>Apical plasma membrane fusion</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>THES</td>
<td>TTC37</td>
<td>TRP37</td>
<td>mRNA processing and decay</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>SKIV2L</td>
<td>Helicase SKI2W</td>
<td>mRNA processing and decay</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>CMRD</td>
<td>SAR1B</td>
<td>Sar1b</td>
<td>Chylomicron transport vesicle fusion</td>
<td>–</td>
<td>Sar1b-knockdown zebrafish (Levic et al., 2015)</td>
<td>–</td>
</tr>
</tbody>
</table>

Continued
villin, which marks microvillus inclusions, has been proposed to be a useful adjunct in MVID diagnosis (Shillingford et al., 2015). Notably, microvillus inclusions are also present in rectal biopsies, facilitating diagnosis if a duodenal biopsy is not feasible. Some individuals with clinical symptoms typical of MVID show no microvillus inclusions but do show the other enterocyte abnormalities, suggesting that MVID is a heterogeneous disease (Mierau et al., 2001).

MVID and variants of MVID are associated with MYO5B, STXBP2 and STX3 mutations (Table 1) (Müller et al., 2008; Ruemmele et al., 2010; Stepensky et al., 2013; Szperl et al., 2011; Wiegerinck et al., 2014). Deletion of the Myo5B gene in mice

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**Table 1. Continued**

<table>
<thead>
<tr>
<th>Disease name</th>
<th>Gene</th>
<th>Protein</th>
<th>Protein function</th>
<th>Cell models</th>
<th>Animal models</th>
<th>Patient-specific models</th>
</tr>
</thead>
<tbody>
<tr>
<td>Familial hypobetalipoproteinemia</td>
<td>APOB</td>
<td>ApoB</td>
<td>Chylomicron formation</td>
<td>–</td>
<td>Modified ApoB allele in mouse</td>
<td>–</td>
</tr>
<tr>
<td>Abetalipoproteinemia</td>
<td>MTTP</td>
<td>Microsomal triglyceride transfer protein</td>
<td>Chylomicron formation</td>
<td>–</td>
<td>Conditional and global MTTP KO mouse</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>DGAT1</td>
<td>Acyl CoA: diacylglycerol acyltransferase 1</td>
<td>Triglyceride synthesis</td>
<td>–</td>
<td>DGAT1 KO mouse</td>
<td>–</td>
</tr>
<tr>
<td>CTE</td>
<td>EPCAM</td>
<td>EpCAM</td>
<td>Cell-cell adhesion, differentiation and proliferation</td>
<td>T84 cells (RNAi) (Kozan et al., 2015)</td>
<td>Global EPCAM KO mouse (Guerra et al., 2012; Kozan et al., 2015)</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>SPINT2</td>
<td>Kunitz-type serine protease inhibitor</td>
<td>Serine protease inhibitor</td>
<td>–</td>
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<td>–</td>
</tr>
</tbody>
</table>

CMRD, chylomicron retention disease; CTE, congenital tufting enteropathy; FHL5, familial hemophagocytic lymphohistiocytosis type 5; KO, knockout; MVID, microvillus inclusion disease; THES, trichohepatoenteric syndrome.

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**Fig. 1. Schematic overview of tissue and cellular characteristics of healthy intestinal epithelium and enterocytes.** In healthy enterocytes, the apical recycling endosome (ARE; green) is located sub-apically, and is important for transporting apically residing proteins (depicted in red) to the apical membrane (brush border), via mechanisms that are not well understood that involve the small GTPases Rab11a and Rab8, and the effector protein myosin Vb (MyoVb; see text). At the apical membrane, syntaxin-3 (STX3) and Munc18-2 (STXBP2) are involved in the fusion of the membrane-bound apical vesicle (orange), β-catenin (β-cat) and EpCAM mediate cell-cell adhesion. Other organelles and common trafficking routes are shown in light gray (not discussed here). AEE, apical early endosome; AQP7, aquaporin-7; BEE, basolateral early endosome; CRE, common recycling endosome; LE, late endosome; Lys, lysosome; NHE, sodium/hydrogen exchanger; NIS, Na/I symporter; TJ, tight junction.
causes the development of early-onset MVID (Cartón-García et al., 2015). MYOSB encodes the actin-based motor protein myosin Vb, which consists of an N-terminal actin-binding motor domain and a C-terminal tail domain that includes the cargo-binding domain. Based on crystal structures of the myosin Vb protein, mutations in MYOSB have been functionally categorized (van der Velde et al., 2013). The myosin Vb cargo-binding domain binds selectively to small Rab GTPases, including RAB11A and RAB8A. Myosin Vb, RAB11A and RAB8A associate with apical recycling endosomes (AREs) in polarized epithelial cells, where they control the activity of the small GTPase CDC42 (Bryant et al., 2010), and both myosin Vb and RAB11A are mislocalized in MVID enterocytes (Fig. 2) (Dhekne et al., 2014; Szerpel et al., 2011). Accordingly, in addition to Myosb knockout (KO) mice (Cartón-García et al., 2015), mice in which the intestinal Rab8a, Rab11a or Cdc42 genes have been individually deleted also develop the cellular hallmarks of MVID (Melendez et al., 2013; Sakamori et al., 2012; Sato et al., 2007; Sobajima et al., 2014). However, diarrhea is not observed in Rab11a or Cdc42 KO mice, and Rab8a KO mice survive for approximately 5 weeks after birth, thus more closely resembling the phenotype of late-onset MVID. Mutagenesis of residues in myosin Vb that mediate this protein’s interaction with either RAB11A or RAB8A, and the subsequent introduction of these mutant forms into myosin Vb-silenced human Caco-2 cells (Caucasian colon adenocarcinoma), revealed that the uncoupling of myosin Vb from both RAB11A and RAB8A forms the basis of MVID pathogenesis (Knowles et al., 2014).

Rab11a- and Rab8a-positive AREs play a pivotal role in epithelial polarity development (Bryant et al., 2010; Golachowska et al., 2010; Overeem et al., 2015; Wakabayashi et al., 2005). Rab11a-positive AREs localize in close proximity to the apical brush border surface in enterocytes and harbor signaling molecules, including: phosphoinositide-dependent protein kinase-1 (PDK1) (Dhekne et al., 2014; Kravtsov et al., 2014); the PDK1 target, atypical protein kinase C-iota; and the ezrin-phosphorylating kinase, Ms4 (Dhekne et al., 2014). Myosin Vb is required for the polarized, subapical localization of Rab11a-positive AREs (Szerpel et al., 2011), which, in turn, is required for efficient Ms4-mediated phosphorylation of ezrin and for ezrin-controlled microvilli development (Dhekne et al., 2014). Myosin-Vb-controlled AREs might thus function as a subapical signaling platform that regulates the absorptive surface area of enterocytes (Dhekne et al., 2014). Interestingly, ezrin depletion in the mouse intestine leads to a disorganized subapical actin filament web and causes microvillus atrophy (Saotome et al., 2004), similar to that seen in individuals with MVID. The presence of ezrin at the intestinal brush border correlates with the expression and function of the Na⁺/H⁺ hydrogen exchanger (NHE)-3, which regulates sodium absorption, and loss of Nhe-3 in mice leads to diarrhea (Ledoussal et al., 2001). MVID enterocytes show reduced NHE-3 expression (Ameen and Salas, 2000), and MVID jejunal explants revealed a net secretory state of the jejenum (Rhoads et al., 1991).

The ectopic expression of the myosin Vb tail domain, which acts as a dominant-negative mutant by competing with endogenous myosin Vb for the Rab proteins, can disrupt the delivery of proteins from Rab11a-positive AREs to the apical plasma membrane (Golachowska et al., 2010). The mechanism by which myosin Vb controls apical-surface-directed transport of proteins from AREs is not fully understood. Interestingly, individuals with mutations in either STX3 (Wiegerinck et al., 2014), which encodes the transmembrane protein syntaxin-3, or STXBP2 (Stepensky et al., 2013), which encodes Munc18-2, develop the clinical symptoms and cellular characteristics of MVID. Mutations in STX3 or STXBP2 give rise to disorders termed atypical MVID and FHL5, respectively (Fig. 2). In enterocytes, syntaxin-3 resides at the apical cell-surface domain, where it, in concert with SNAP23 and Munc18-2, mediates the fusion of transport vesicles with the apical plasma membrane (Riento et al., 2000). MVID-associated STX3 mutations cause the depletion of syntaxin-3 or the expression of a syntaxin-3 protein that lacks the transmembrane domain (Wiegerinck et al., 2014), disrupting its function. STXBP2 mutations abolish the interaction of Munc18-2 with syntaxin proteins (zur Stadt et al., 2009). Interestingly, enterocytes of conditional Rab11 KO mice show altered localization of syntaxin-3 (Knowles et al., 2015). It is possible that myosin Vb mediates the apical trafficking of syntaxin-3 via AREs, and protein delivery to the apical cell surface. However, the effect of myosin Vb mutations on the apical membrane fusion machinery in MVID remains to be demonstrated. It should be noted that a homozygous mutation in STX3 was also reported in an individual with autosomal recessive congenital cataracts and intellectual disability phenotype, without mention of intestinal symptoms (Chogran et al., 2015); thus, further investigation into genotype-phenotype correlation of the different STX3 mutations is warranted.

Taken together, the available data suggest that defects in ARE function result in brush border microvillus atrophy and in the
intracellular retention of enzymes and transporters that are required for the absorption of nutrients and ions by villus enterocytes, leading to the clinical phenotype of malabsorption and diarrhea in MVID (Dheke et al., 2014; Knowles et al., 2014) (Fig. 2).

Trichohepatoenteric syndrome

Individuals with THES present with intractable diarrhea in the first months of life accompanied by nutrient malabsorption and failure to thrive (Hartley et al., 2010). THES is associated with facial dysmorphism, hair abnormalities and, in some cases, skin abnormalities and immune disorders (Goulet et al., 2008). Some individuals with THES display trichoiodystrophy, liver disease, hepatomegaly and siderosis (see Box 1). Affected individuals are prone to infections, might fail to produce antibodies upon vaccination, or present with low immunoglobulin levels. Mild intellectual deficiency is a feature of ~50% of all cases. THES can present as very-early-onset inflammatory bowel disease (Kammermeier et al., 2015). Although MIA is not a CDD, these findings implicated in a different disorder: multiple intestinal atresia (MIA) (Fabre et al., 2012). TTC37, but not SKIV2L, is highly co-expressed with two genes involved in apical trafficking (SCAMP1 and EXOC4; http://coxpresdb.jp/cgi-bin/coex_list.cgi?gene=9652&sp=Hsa2). The mechanism underlying THES is currently unknown, so further studies are needed to elucidate potential relationships between TTC37/ SKIV2L, the Ski complex and the trafficking of apical transporter proteins.

Interestingly, another tetratricopeptide repeat protein, TTC7A, is implicated in a different disorder: multiple intestinal atresia (MIA). Stem-cell-derived intestinal organoids from a MIA individual show enterocyte polarity defects that are rescued by pharmacological inhibition of the small GTPase RhoA (Bigorgne et al., 2014; Overeem et al., 2015). Although MIA is not a CDD, these findings further accentuate the role of tetratricopeptide-repeat proteins in functional enterocyte polarity and associated intestinal disorders.

Defects in intracellular lipid transport and metabolism

In addition to defects in the intracellular transport of proteins, defects in the intracellular transport of lipids, summarized in Fig. 4, have been associated with CDDs. Our current understanding of the molecular mechanisms underlying this class of CDDs is summarized below.
Two other CDD ENT have been associated with defects in intestinal fat absorption and chylomicron assembly. Familial hypobetalipoproteinemia (FHBL), the only CDD ENT that is dominantly inherited, is associated with mutations in the APOB gene, encoding apolipoprotein B (Young et al., 1990), which, together with triglycerides and other lipids, makes up the nascent chylomicron (Fig. 4). Abetalipoproteinemia is associated with mutations in the MTTP gene, which encodes microsomal triglyceride transfer protein (MTTP). MTTP catalyzes the transfer of triglycerides to nascent ApoB particles in the endoplasmic reticulum. Abetalipoproteinemia-associated mutations reduce MTTP activity, the synthesis of very-low-density lipoproteins, and lipid absorption in the intestine. To date, there have been two known cases of congenital diarrhea associated with mutations in DGAT1, which encodes acyl CoA:diacylglycerol acyltransferase 1, an enzyme that is involved in triglyceride synthesis and is highly expressed in the intestine (Haas et al., 2012). The mechanism by which DGAT1 mutations cause diarrhea is unclear, but is likely to involve the build-up of DGAT1 lipid substrates in the enterocytes or in the gut lumen (Haas et al., 2012). Dgat1 KO mice do not develop diarrhea, and it has been proposed that this is due to compensatory Dgat2 expression in the mouse intestine (Buhman et al., 2002). The observation that the overexpression of Sar1b in human Caco-2 cells stimulated DGAT and MTTP activity (Levy et al., 2011) underscores the fact that all currently known CDD ENT that are associated with defective lipid absorption originate in defects in the triglyceride-rich lipoprotein assembly pathway.

**Familial hypobetalipoproteinemia and abetalipoproteinemia**

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**Defects in intestinal barrier function**

The barrier function of the intestine is important for fluid homeostasis and critically depends on cell-cell adhesions. Defects in the intestinal barrier function have been associated with at least one CDD.

**Congenital tufting enteropathy**

Congenital tufting enteropathy (CTE) is characterized by persistent diarrhea that presents immediately or shortly after birth, despite bowel rest and total parenteral nutrition (TPN) (Goulet et al., 2007). Some affected individuals display a milder phenotype than others, and these can sometimes be progressively weaned off TPN (Lemalle et al., 2011). A subset of individuals with CTE display a syndromic form of the disease [congenital sodium diarrhea (CSD)] that includes dysmorphic features, woolly hair, punctate keratitis, atresias, reduced body size and immune deficiency (see Box 1). Like THES, CTE can present as very-early-onset inflammatory bowel disease (Kammermeier et al., 2014).

Histological analysis of the intestine in the context of CTE reveals various degrees of villous atrophy, basement membrane abnormalities, disorganization of enterocytes, and focal crowding at the villus tips, resembling tufts (Fig. 5). There is no evidence for abnormalities in epithelial cell polarization; the enterocyte brush border appears normal, and the staining pattern of the brush-border-associated metalloproteinase CD10 is normal (Martin et al., 2014), but expression of desmogleins, a family of cadherins, is enhanced (Goulet et al., 2007). The major diagnostic marker is the absence of epithelial cell adhesion molecule (EpCAM) staining in CTE enterocytes (Martin et al., 2014). Furthermore, immune cell infiltration into the lamina propria is absent. In some cases, however, increased numbers of inflammatory cells have been reported in the lamina propria, indicating that their presence does not preclude the diagnosis of CTE (Kammermeier et al., 2014).

CTE is associated with **EPCAM** or **SPINT2** mutations. EpCAM is a multifunctional transmembrane glycoprotein involved in cell-cell adhesion, proliferation and differentiation (Schnell et al., 2013b). In individuals with CTE, EpCAM protein levels in the intestine are decreased (Sivagnanam et al., 2008) and all CTE-associated **EPCAM** mutations lead to loss of cell-surface EpCAM (Fig. 5) (Schnell et al., 2013a), either because of impaired plasma membrane targeting or because of truncation of the protein, both of which result in its secretion. Both Epcam KO mice and mice in which exon 4 of Epcam is deleted develop CTE (Guerra et al., 2012; Kozan et al., 2015). In the Epcam KO mouse intestine, E-cadherin and β-catenin, two adherens-junction-associated proteins, are also mislocalized, leading to disorganized transition from crypts to villi (Guerra et al., 2012). Mice with reduced EpCAM levels and Caco-2 cells depleted of EpCAM show decreased expression of tight-junction proteins, increased permeability and decreased ion transport (Kozan et al., 2015). EpCAM interacts with the tight-junction proteins claudin-7 and claudin-1 (reviewed in Schnell et al., 2013b). Conceivably, loss of EpCAM expression and/or function leads to the increased permeability of the intestinal barrier by disrupting tight junctions (Fig. 5), resulting in diarrhea.

The mechanism by which mutations in **SPINT2** lead to CTE phenotypes, however, is not clear. SPINT2 encodes the transmembrane Kunitz-type 2 serine-protease inhibitor. Spint2 KO mice are embryonically lethal owing to developmental defects that are unrelated to the intestine (Szabo et al., 2009), and are therefore unsuitable for studying the intestinal symptoms of CTE. Interestingly, two of the target enzymes of Spint2 are the serine proteases matriptase and prostatin (Szabo et al., 2009), which are primary effector proteases of tight-junction assembly in intestinal epithelial cells (Buzza et al., 2010). The Y163C mutation in Spint2 results in a complete loss of the ability of Spint2 to inhibit prostatin and another intestinal protease, the transmembrane protease serine 13 (Tmprss13) (Faller et al., 2014). Further investigation is needed to determine the role of Spint2 and other proteases in the regulation of cell-cell junctions in the pathogenesis of CTE.

The inhibition of trypsin-family serine peptidases, such as that encoded by **SPINT2**, abolishes the constitutive stimulation of apical Na⁺ transport by nonvoltage-gated sodium channel-1-alpha (Scnn1a) in polarized intestinal epithelial cells (Planèes and Caughey, 2007), which could contribute to secretory diarrhea. It is possible that such a mechanism forms the basis of the syndromic form of congenital sodium diarrhea that is associated with **SPINT2** mutations (Faller et al., 2014; Heinz-Erian et al., 2009).

Publicly available bioinformatics gene co-expression databases show that the **EPCAM** and **SPINT2** genes are strongly co-expressed in humans (http://coxpresdb.jp/cgi-bin/coex_list.cgi?gene=4072&sp=Hsa, and http://coxpresdb.jp/cgi-bin/coex_list.cgi?gene=10653&sp=Hsa), which suggests that they either share a transcriptional regulatory program, are functionally related, or are members of the same pathway or protein complex. Interestingly, **ST14**, the gene that encodes matriptase, is strongly co-expressed with both **EPCAM** and **SPINT2**, further underscoring the need to study its involvement in the pathogenesis of CTE.

**Outlook and future perspectives**

Establishing a molecular diagnosis for CDDENT is becoming feasible in most cases, and can be a key contributor to clinical decision making. At the moment, the prognosis and survival of individuals with CDDENT depend on early TPN and successful bowel transplantation, but survival is generally poor. A variety of extra-intestinal symptoms are associated with CDDENT. Of these, renal
Fanconi syndrome in MVID disappears after bowel transplantation (Golachowska et al., 2012), whereas intrahepatic cholestasis in MVID is aggravated after bowel transplantation (Girard et al., 2014; Halac et al., 2011). It remains unclear whether these symptoms are iatrogenic, i.e. complications of treatment, and/or are linked to particular CDD\textsuperscript{ENT}-associated gene mutations or the genetic background of the patient. Prospective patient registries, animal models, and stem-cell-based organoid technology combined with novel gene-editing tools, such as CRISPR, will address these current shortcomings in our knowledge, as discussed below (see Box 3).

**Patient registries and databases**

Dedicated patient registries are crucial resources for correlating the genotype, phenotype and clinical presentation of individuals with CDD\textsuperscript{ENT}. Thus far, only a registry of patients with MVID and associated genotype, phenotype and clinical presentation of individuals with CDD\textsuperscript{ENT} patients, including a prospective set-up that allows the course of disease to be recorded together with the influence of therapeutic interventions, is expected to improve disease diagnosis, prognosis and counseling.

**Vertebrate and invertebrate model organisms for CDD\textsuperscript{ENT}**

Intestinal epithelial cell lines cannot recapitulate all of the phenotypes associated with CDD\textsuperscript{ENT}, such as those related to the different states of proliferation and differentiation in enterocytes as they migrate from the crypts to the villus tips in the intestine. This is important for understanding the cellular defects seen in MVID and CTE, which are more pronounced in the villus than they are in the crypt region (Groisman et al., 1993; Phillips et al., 2000; Thoeni et al., 2014). Cell lines also do not form villi, precluding the study of villus defects, villus atrophy and villus tufts. Finally, studies in intestinal cell lines do not take into account effects beyond the intestine.

Animal models offer a useful system for determining causal relationships between genes and CDD\textsuperscript{ENT} for investigating disease pathogenesis, and for evaluating treatment options preclinically. KO animals are useful for studying the function of the targeted gene and for modeling CDD\textsuperscript{ENT} individuals with homozygous mutations, and gene-editing techniques such as CRISPR-Cas can be used to introduce patient-relevant homozygous and compound heterozygous missense mutations both in animal and cell-line models.

The potential use of model organisms other than mice for CDD\textsuperscript{ENT} research has not been fully explored. Intestinal brush border proteins are normally apically localized in invertebrate nematode Caenorhabditis elegans worms that lack Hum2, the ortholog of MYO5 (Winter et al., 2012). Conceivably, this reflects the distinct physiology and cellular architecture of the worm intestine. In developing larvae of the fly Drosophila melanogaster, myosin-V deficiency interferes with apical protein secretion in the hindgut (Massarwa et al., 2009). This suggests a problem with apical protein delivery and warrants further research to examine the potential of myosin-V-deficient flies as a model for CDD\textsuperscript{ENT}. Other CDD\textsuperscript{ENT}-associated genes have not yet been examined in worms or flies.

The ability to perform high-throughput assays and intravitral imaging in vertebrate zebrafish (van Ham et al., 2014) make these animals a promising model for studying the effect of genetic manipulations and pharmacological treatment. Intestinal anatomy and architecture in zebrafish closely resemble the anatomy and architecture of the mammalian small intestine (Yang et al., 2014) and have been used to study enteropathies such as congenital short bowel syndrome (Van Der Werf et al., 2012). Zebrafish could therefore make a useful addition to current CDD\textsuperscript{ENT} models. Indeed, sar1b-deficient zebrafish display phenotypes resembling CMRD (Levic et al., 2015). The absence of the myosin-V ortholog in zebrafish results in an abnormal epidermal tissue structure. In the study reporting this mutant, inclusion bodies in the intestine are mentioned (Sonal et al., 2014). epcam-deficient zebrafish have aberrant epidermal development; however, intestinal defects have not been reported (Slanchev et al., 2009).

**Stem-cell-based organoids**

Advances in stem cell technology provide new models for studying CDD\textsuperscript{ENT}. Generating three-dimensional cultures of stem-cell-derived intestinal cells that resemble to some extent the intestinal tissue (so-called organoids) enables disease modeling that better resembles the in vivo situation while still retaining experimental versatility and the ability to genetically manipulate cells. Organoids allow for patient-specific personalized disease modeling. Promisingly, intestinal organoids generated from STX3-mutation-carrying individuals with MVID recapitulate most of the in vivo phenotypes (Wiegerinck et al., 2014).

Intestinal organoids can be generated from adult stem cells and by differentiating induced pluripotent stem cells (iPSCs) into intestinal cell lines (Forster et al., 2014; Sato et al., 2009; Spence et al., 2011). Although both adult-stem-cell- and iPSC-derived intestinal tissue structures are referred to as organoids, notable differences exist between the two. Organoids obtained from iPSCs, but not from adult stem cells, contain supporting mesenchymal cells. Moreover, iPSC-derived organoids are relatively immature with fetal-like characteristics, although transplantation of iPSC-derived immature organoids under the kidney capsule of mice results in the development of mature, engrafted intestinal tissue that develops villi and crypts (Watson et al., 2014). From adult stem cells, only genomically engineered organoids that contain tumorigenic mutations have undergone successful engraftment under the mouse kidney capsule, suggesting that mesenchymal cells are required for organoid maturation outside of the intestinal niche (Matano et al., 2015). However, adult-stem-cell-derived organoids have been reported to engraft in the chemically injured mouse colon, to contribute to tissue regeneration, and to be indiscernible from host epithelium (Yui et al., 2012).

These differences are important to consider when organoids are used to study CDD\textsuperscript{ENT}. The investigation of phenotypes that manifest at a multicellular level, such as the structural villi abnormalities in MVID and CTE, requires a model that forms villi and crypts. The maturity of organoids is also relevant because CDD\textsuperscript{ENT} phenotypes do not always manifest immediately after birth.
(e.g. late-onset forms). A practical consideration is that adult-stem-cell-derived organoid culture requires invasive biopsies, whereas the somatic cells to generate iPSCs can be non-invasively acquired.

Organoid technology uniquely allows the creation of patient-specific disease models. Despite harboring mutations in the same protein, many individuals with CDDENT often vary in the range and severity of their symptoms. This suggests that different mutations could have a varying effect on protein function, and thus on disease outcome. Other potential factors that could influence such variation are the genetic background of a patient and any adverse effects of treatment. Organoids from affected individuals with varying symptoms exclude confounding environmental factors and provide a model in which phenotypes are tissue-autonomous and solely dependent on patient genotype. The use of gene-editing tools, such as CRISPR, in organoid cultures could provide a valuable tool for making definitive genotype-phenotype correlations. Finally, organoids created from different organs of the same patient could provide additional insights into the genetic relationship of extra-intestinal symptoms associated with CDDENT.

Although diagnostic tools for CDDENT have improved over the last few years, a cure for CDDENT is desperately needed. Organoid transplantation and/or cell-replacement strategies can lead to the restoration of the intestinal epithelium in mice (Yui et al., 2012). This raises the exciting possibility of investigating whether CRISPR-based correction of mutations in patient stem cells and transplantation of genetically corrected organoids could represent a regenerative medicine approach to cure CDDENT.

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