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*TOPIC HIGHLIGHT*

**WJG 20th Anniversary Special Issues (3): Inflammatory bowel disease**

# **Inflammatory bowel disease in pediatric and adolescent patients: A biomolecular and histopathological review**

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## **Abstract**

Crohn's disease (CD) and ulcerative colitis (UC) are the two main forms of inflammatory bowel disease (IBD) with both overlapping and distinct clinical, pathological and biomolecular features. It has been suggested that pediatric IBD is a distinct disease entity, with probably different disease subtypes.The aim of this study is to review and summarize the evolution of the current concept of pediatric IBD. The results of this review reinforce the idea that pediatric CD and UC may be further classified in various clinicopathologic entities. For clinicians and pathologists convenience, practical algorithms for the distinction of the various subphenotypes of pediatric IBD are also provided.

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**Key words:** Pediatric inflammatory bowel disease; Crohn's disease; Ulcerative disease; Histopathology; Molecular biology

**Core tip:** The review contains the most recent data of the literature and suggests a clinical- pathological heterogeneity of the inflammatory bowel disease (IBD) in childhood. It provides diagrams that display the main anatomo-clinical and biomolecular correlations and that may be encountered in IBD children. These diagnostic patterns and correlations may be useful in clinical practice for pediatric IBD.

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## **INTRODUCTION**

Inflammatory bowel disease (IBD) represents a group of idiopathic, chronic, inflammatory intestinal conditions in which complex interactions among genetic, immune, and environmental factors are involved. Crohn's disease (CD) and ulcerative colitis (UC) are the two most common forms of IBD with both overlapping and distinct clinical, pathological and biomolecular features. Traditionally, UC is defined as a disease involving the colonic mucosa in a diffuse, continuous manner, always affecting the rectum. In contrast, CD may involve any part of the gastrointestinal tract and frequently shows discontinuous or segmental involvement. However, IBD may be better considered as a syndrome of complex disorders with a significant heterogeneity in disease presentation and course[1-5]. It has also been suggested that pediatric IBD is characterized by distinct phenotypic differences including disease type, disease location, disease behaviour, gender preponderance and genetically attributable risk, compared to adult-onset  $IBD<sup>[6-11]</sup>$ . The incidence of  $IBD$ in childhood is rising worldwide<sup>[12,13]</sup>. Rates are highest in North America and Europe, with rapid increases noted in developing nations adopting a Westernized lifestyle.



Childhood and adolescent IBD accounts for nearly 30% of total cases<sup>[14-17]</sup>. Pediatric IBD demonstrates a pattern with CD predominating over UC. In particular, the incidence of CD has risen markedly, while a rather stable incidence of pediatric onset UC has been reported<sup>[18]</sup>. A recent study based on the Swedish population found that the incidence of CD was 9.2 per 100000 per person years. The incidence of UC in children over the same time period was 2.8 per 100000 per person years<sup>[19]</sup>. Similar rates have been reported by other studies<sup>[20-24]</sup>.

Recent population based studies have demonstrated a significant male excess in incidence of pediatric  $CD^{[25]}$ . Pediatric CD more often involves the ileocolonic/colonic regions, whereas adult CD does not demonstrate a high proportion of colonic disease $[7]$ . Furthermore, a variety of phenotypic characteristics have been described in pediatric UC thanks to increasing diagnostic  $accuracy^{[26,27]}$ . Reflecting these trends, IBD classification has been changed from the Vienna statement<sup>[28]</sup>, through the Montreal classification<sup>[29]</sup> to the recent pediatric Paris  $classification^{[30]}$ .

Although the precise etiology of IBD remains elusive, both animals and human studies point towards a strong genetic susceptibility. Genome wide association studies (GWAS) identified over 160 susceptibility loci/ genes that are significantly associated with IBD<sup>[31-33]</sup>. However, newer genomics technologies are now beginning to complement GWAS findings and add to our understanding of the molecular genetic universe of IBD. Genetic studies have provided detailed appreciation of the molecular architecture of IBD, and, in particular, the areas of overlap between CD and UC (such as Th17 pathways) and the pathways which are disease-specific. Moreover, the genes implicated in childhood-onset and adult-onset IBD often overlap, suggesting similar contributory genetic predisposition and pathophysiological pathways. For CD*,* gene discoveries have focused on defective processing of intracellular bacteria, autophagy, and innate immunity. For UC, the focus has been on barrier function.

A further addition to the complexity of understanding disease mechanisms is that a susceptibility allele often requires other genetic and non-genetic cues to manifest the disease<sup>[34]</sup>. The variable concordance rate in monozygotic twins of 27%-50% in CD compared with 15%-19% in UC suggests that non-genetic factors may have an even more important role in UC than in  $CD^{[35,36]}$ .

In the present review, we summarize current knowledge concerning the correlation between clinicopathologic features and genetic profiles of pediatric IBD in order to offer practical algorithms for the categorization of the vast majority in this group of lesions.

## **PARIS CLASSIFICATION**

The issue of subclassification of IBD by phenotype has

been reviewed in recent years. The World Congress of Gastroenterology in Vienna, in 1998, considered age of onset (A), disease location (L), and disease behaviour (B) as predominant phenotypic elements<sup>[28]</sup>. The Montreal revision of the Vienna classification did not changed the three predominant parameters of age at diagnosis, location, and behaviour, but modification within each of these categories was made<sup>[29]</sup>. However, the criteria of Montreal Classification has inherent limitations with respect to classification of pediatric IBD. In the pediatric Paris classification[30] growth failure in the patient at any time was added as G1 *vs* G0 (never growth failure) to classic phenotypic elements (age at diagnosis, disease location, and disease behaviour). The comparisons between the Montreal and Paris classifications for CD and UC are shown in Tables 1 and 2, respectively.

## **IBD UNCLASSIFIEDAND "INDETERMINATE" COLITIS**

The term "indeterminate colitis" was originally coined for IBD resections with features of both UC and CD, usually in the setting of severe acute or "fulminant" colitis<sup>[37]</sup>. Over the years the term has been adopted by clinicians to describe patients in whom a diagnosis of UC or CD cannot be made based on standard clinical testing, including colonoscopy, imaging, laboratory tests and biopsy<sup>[38]</sup>. However, this term has been used incorrectly with considerable confusion among clinicians and pathologists. Recently, it has been recommended that the term "indeterminate colitis" be reserved only for patients for whom a surgical specimen is available and the term "colonic IBD type unclassified" (IBD-U) for patients with no surgical specimen available and for whom endoscopy is inconclusive and histological changes do not fit with either CD or  $UC^{[29]}$ . It remains controversial whether IBD-U constitutes a problem of classification or an IBD subtype distinct from CD and UC. Some authors believe that IBD-U is not a third form of IBD with specific diagnostic criteria, being a provisional diagnosis of exclusion used until a diagnosis of UC or CD is made with certainty<sup>[39,40]</sup>. Instead, other authors consider IBD-U as a distinct phenotype of IBD for the following reasons: (1) A recent meta-analysis showed that IBD-U is more common in children accounting for 12.7% of all cases of IBD  $\nu s$  6% in adults<sup>[41]</sup>; (2) Children with IBD-U have a disease that rapidly progresses to pancolitis $[42,43]$ ; (3) Although many patients with IBD-U will be reclassified as having CD or UC on long-term follow-up evaluation, a significant proportion of them will still carry the diagnosis of indeterminate colitis<sup>[44]</sup>; (4) Epidemiologic data have shown that clinical course and prognosis of IBD-U could be worse compared with UC, especially concerning outcome of surgery with greater risk of pouchitis<sup>[45]</sup>; and (5) As will be discussed in the next section, IBD-U is diagnosed in a large subgroup of patients at a very





#### **Table 2 Montreal and Paris classifications for ulcerative colitis**



early age (0-2 years, infantile IBD)<sup>[30-46]</sup>.

## **AGE OF ONSET**

An important modification recommended by the Paris classification<sup>[30]</sup> includes age at onset as A1a (0 to  $\leq 10$ ) years) and A1b (10 to  $\leq$  17 years). In both the Montreal<sup>[29]</sup> and Paris<sup>[30]</sup> Classification systems, A2 and A3 account for age of diagnosis at  $17-40$  years, and  $> 40$ years, respectively.

Although rare, IBD may occur before the age of 2 years. Therefore, the Paris classification<sup>[30]</sup> suggested the possibility of distinguishing a separate group of children diagnosed with IBD at a very early age (0-2 years, infantile IBD)*.* This subgroup is characterized by a high rate of consanguinity, more severe disease course, association with primary immunodeficiency and resistance to immunosuppressive treatment<sup>[45,46]</sup>. Abscess formation, anal fissures and enterocutaneous or rectovaginal fistulae complicate the disease and frequently require partial or total colectomy[30,47].

The suspicion of a monogenetic cause of these early onset forms was recently confirmed by the discovery of mutations in the genes coding for one of the two IL10 receptors causing impaired IL10 signalling<sup>[48-52]</sup>.

The region encoding IL10 was originally identified by a German GWAS in UC, and the association docu-

mented with non-coding variants upstream of the IL10 gene<sup>[53]</sup>. Subsequently, an international GWAS metaanalysis showed that this region is associated with  $CD^{[54]}$ . Through a genetic-linkage analysis and candidate-gene sequencing on samples from two unrelated consanguineous families with children affected by early-onset IBD, Glocker *et al*<sup>[55]</sup> identified three distinct homozygous mutations in genes IL10RA and ILRB. These genes encode the IL10R1 and IL10R2 proteins, respectively, which form a heterotetramer to make up the IL10 receptor. Functional experiments have shown that the *IL10RA* and *ILRB* gene mutations abrogate IL10 signalling and lead to severe intestinal inflammation. Loss of function mutation in IL10 and IL10R was also identified in 66 patients with very early onset IBD. In this study, it has been found that in 5 patients with IL10R deficiency, the allogenic hematopoietic stem cell transplantation induced sustained clinical remission with a median follow-up time of 2 years<sup>[49]</sup>. Recently, Moran *et al*<sup>[50]</sup> have identified a novel homozygous, splice-site point mutation in IL10RA in an infantile-onset IBD Caucasian female. The patient was also affected by significant arthritis and folliculitis. The mutation caused a premature stop codon (P206X) and IL10 insensitivity. Moreover, 188 children with earlyonset IBD and 188 healthy subjects have been studied. In the discovery cohort, five IL10RA polymorphisms associated with UC have been found<sup>[50]</sup>. These studies



Figure 1 Distinct clinicopathological and biomolecular features of the pediatric colonic inflammatory bowel disease. IBD: Inflammatory bowel disease; CD: Crohn's disease; UC: Ulcerative colitis.

show the role of immune pathways in early onset IBD pathogenesis. Indeed, IL10 is an anti-inflammatory cytokine secreted by a variety of cell types and is critical for maintaining immune homeostasis in the gastrointestinal (GI) tract. IL10 restricts excessive immune response<sup>[56]</sup>. In particular, IL10 limits the secretion of proinflammatory cytokines, such as tumour necrosis factor  $\alpha$  (TNF- $\alpha$ ) and  $IL12^{57}$ . Moreover, the assembly of  $IL10R1$  results in the activation of the receptor-associated Janus tyrosine kinases, JAK1 and Tyk2, leading to the phosphorylation of STAT3 (signal transducer and activator of transcription 3) and the induction of STAT3-dependent genes<sup>[58]</sup>. A severe enterocolitis has been found in mice that are deficient in either IL10 or IL10R2. These data underline the pivotal role of IL10 in the mediation of signalling that controls inflammation in the gut.

Other monogenic primary immunodeficiencies showing IBD-like gastrointestinal pathology include Wiskott-Aldrich syndrome<sup>[47]</sup>, chronic granulomatous disease<sup>[47]</sup>, XIAP deficiency<sup>[55,59]</sup>, X-linked (IPEX) syndrome<sup>[60]</sup> and nuclear factor kB essential modulator (NEMO) deficiency<sup>[61]</sup>. It is also noteworthy that a large subgroup of these patients have IBD- $U^{[30,42]}$ . Therefore, we think that IBD-U is an IBD subtype distinct from CD and UC as it constitutes a histopathological substrate of a clinicopathologic entity with characteristic epidemiological (< 2 years old), clinical ( severe clinical course with pancolitis), and genetic features (*i.e.*, mutation in interleukin-10 receptor and interleukin gene or other primary immunodeficiencies). It is, therefore, plausible that infantile IBD (< 2 years) may be incorporated into future modifications of the Paris classification. Figure 1 summarizes the main clinicopathologic characteristics of infantile IBD.

## **CD**

#### *Disease location*

According to the Paris classification<sup>[30]</sup>, CD location is categorized as follows: (L1) involvement of the terminal ileum only, with limited or no cecal disease; (L2) colonic involvement only; (L3) involvement of both the terminal ileum and colon; (L4) isolated upper gastrointestinal disease. L4 is further separated into esophagogastroduodenal disease (L4A), jejuna/proximal ileal disease (L4B), or both L4A and L4B. Adolescents more often present with ileal disease (L1), whereas children have a tendency to present with isolated colonic disease (L2). Pediatric patients with L2 disease are less likely to have esophagogastroduodenal involvement or stricturing disease behaviour than patients with L1 and L3 disease<sup>[62]</sup>. These data support the existence of discrete subtypes of CD, which are, in part, defined by the predominant anatomical location of disease<sup>[7]</sup> and summarized in Table 3 and Figure 2.

## *Paneth cells are protagonist in the L1CD*

Histologic, immunologic and biomolecular evidence strongly suggests a key role for Paneth cells in L1 CD. Histologically, Paneth cells are abundant in the small







IBD: Inflammatory bowel disease; CD: Crohn's disease; UC: Ulcerative colitis.

intestine and are occasionally found in the cecum and proximal ascending colon<sup>[63]</sup>. In parallel, L1 (distal  $1/3$ ileum ± limited cecal disease) CD location corresponds to the normal distribution of Paneth cells.

From an immunological viewpoint, Paneth cells, by virtue of their vast repertoire of effector molecules, are multifunctional cells. They produce antimicrobial proteins such as alpha-defensins HD5 and HD6, lysozyme, secretory phospholypase A2 and the lectinReg $\text{I\!I} \gamma^{[64]}.$  Wehkamp *et al*<sup>[65]</sup> showed that ileal (L1) but not isolated colonic (L2) CD is associated with a diminished synthesis of Paneth cell defensins. Wehkamp and Stange<sup>[66]</sup>, therefore, proposed the term "Paneth's disease" to describe a complex disease in which Paneth cells might explain the poor antimicrobial capability of (L1) CD. Paneth cells have also been shown to contain TNF- $\alpha$  transcripts. With ultrastructural immunogold methods, Beil *et al*<sup>[67]</sup> showed TNF- $\alpha$  in mature and immature secretory granules of Paneth cells. One of the major biological roles of  $TNF-\alpha$  is in the host defence to bacterial, viral and parasitic infections, and Paneth cells are considered to be the major source of TNF- $\alpha$  in the normal bowel<sup>[67]</sup>. Clinical and molecular studies implicate TNF- $\alpha$  as a key mediator in the initiation and propagation of  $CD^{68}$ . This is evidenced by an increased amount of TNF in inflammatory cells infiltrating ileal tissue (eosinophils, mast cells, neutrophils, macrophages, fibroblasts) and a marked clinical response of TNF- $\alpha$  antagonists in patients with active CD<sup>[69]</sup>. Therefore, abnormal production of TNF- $\alpha$  protein by Paneth cell may be involved in the pathogenesis of L1  $CD^{[69]}$ .

From a histopathological viewpoint, Paneth cell depletion occurs in the most heavily inflamed areas of the ileal mucosa<sup>[70]</sup>. Recently, Günther *et al*<sup>[71]</sup> showed a significant decrease in the number of Paneth cells and a high number of dying cells with shrunken eosinophilic cytoplasm at the crypt base in histological samples from terminal ileum of patients with active CD. Paneth cells showed ultrastructural signs of non-apoptotic cell death, such as organelle swelling, vacuole formation and the lack of blebbing. The data of Günther *et al*<sup> $71$ </sup> suggest that necroptosis (a form of non-apoptotic cell death) of Paneth cells might be involved in the pathogenesis of CD.

Recently, VanDussen *et al*<sup>[72]</sup> have studied the correlation between Paneth cell phenotype (based on lysozymepositive secretory granule morphology) and NOD2 and ATG16L1 genotype. They observed an inverse correlation between abnormal Paneth cells (with disordered, diminished, diffuse, or excluded granule phenotypes) and the presence of granulomas $^{[72]}$ . The cumulative number of NOD2 and ATG16L1 risk alleles had an additive effect on the proportion of abnormal Paneth cells. Moreover, high proportions of abnormal Paneth cells were associated with shorter time to disease recurrence after surgery. VanDussen *et al*<sup>[72]</sup> suggest stratifying CD based on Paneth cell phenotypes rather than the presence of granulomas. In fact, granulomas could be sparse and more likely to be undersampled, especially in biopsy specimens, whereas Paneth cell phenotypes are more easily analyzed within limited samples. Therefore, these authors concluded that histologic analysis of Paneth cell phenotypes can be used to divide patients with CD into subgroups with distinct pathognomonic and clinical features<sup>[49]</sup>. However, further correlative histopathologic and biomolecular studies are necessary to clarify the role of necroptosis and/or granule changes of Paneth cells in L1 CD characterized by abundant or few granulomas (so-called granuloma-rich or granuloma-poor CD).

## *Biomolecular studies of antimicrobial function in Paneth cells*

Defective antimicrobial function in Paneth cells has been described by a variety of mechanisms including mutations in the innate immune receptor NOD 2, defensins, Toll-like receptors (TLRs), the autophagy protein AT-G16L1, *IRGM* gene.

### *NOD2 gene*

With the pivotal study of Hugot *et al*<sup>[73]</sup>, who discovered the very first and also strongest susceptibility gene for CD in NOD2/CARD15, "IBD gene hunting" was opened. NOD2 is an intracytoplasmic member of the family of intracellular NLR (NOD like receptors) able to recognize pathogen associated molecular patterns (PAMPs) and to modulate an inflammatory response through enhanced NF- $\kappa$ B activation<sup>[74,75]</sup>. NOD2 is highly expressed in cells of the phagocyte system and is involved in the production of defensins in response to gut microbiota. Three single nucleotide polimorphisms (SNPs) within the NOD2/CARD15 gene (R702W, G908R, and 1007fsinsC) have been established as independent risk factors for CD in Caucasians<sup>[76,77]</sup> and they represent 82% of the mutations in NOD2[78]. Interestingly, the NOD2/CARD15 mutations are absent or very rare in Asians, Arabs, Africans, and African Americans<sup>[79]</sup>. NOD2/CARD15 variants have been associated to more severe CD, a greater need for surgery and a younger age at onset<sup>[80]</sup>. In children, a correlation with ileal  $(L1)$  localization<sup>[81-87]</sup>, stricturing behavior<sup>[82,83,87]</sup>, early surgery<sup>[83]</sup>, growth delay<sup>[83,84]</sup> and higher disease activity<sup>[83,88]</sup> has been found. However, these results have not been confirmed by other studies<sup>[89-91]</sup>. The precise mechanistic relationship between NOD2/CARD15 and CD remains controversial. Interestingly, a study by Zelinkova *et al*<sup>92]</sup> suggested that NOD2 mutations may result in perpetuation of mucosal inflammation through insufficient pathogen elimination.

The important role of NOD2 in the pathogenesis of CD has been underlined by recent studies on microR-NAs (miRNAs)<sup>[93]</sup>. miRNAs are short non-coding RNAs that have emerged as key modulators of various cellular processes at the post-transcriptional level<sup>[94-96]</sup>. There are recent reports on their role in the regulation of intestinal permeability as the loss of intestinal miRNAs impairs the epithelial barrier function, and causes acute inflammation<sup>[97]</sup>. Some Authors showed that miRNA-122 regulates intestinal permeability tight junctions (TJ) by targeting occluding mRNA degradation<sup>[98-102]</sup>. Moreover, Chen  $e\bar{t}$   $a\bar{t}^{102}$  found that NOD2 is a functional target of miRNA-122.

Other mechanisms have been proposed for NOD2/ CARD15 mutations in recent years, ranging from abnormal Paneth cell function with reduced defensin secretion, altered modulation of Toll-like receptor signaling and a reduced ability to trigger autophagy<sup>[103]</sup>. Several studies have shown the role of defensins in the pathogenesis of  $CD^{[104-107]}$ . In particular, ileal (L1) and ileal colonic (L3) CD is characterized by a specific decrease in small intestinal Paneth cell human α-defensin HD-5 and-6<sup>[106-108]</sup>. In a group of pediatric CD, Perminow  $et al^{[109]}$  studied the role of HD5 and TCF-4, a Wnt-signaling transcription factor which controls Paneth cell defensin expression. They showed a low intestinal expression of HD5 and TCF4 mRNA in ileal CD, confirming the important role of antimicrobial host defense in pediatric patients.

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Toll-like receptors (TLRs) have an important role in the pathogenesis of CD. They are crucial components of innate immunity and cell surface molecules that also detect normal and pathogenic microbial agents and can trigger antimicrobial host defense responses. TLRs are abundantly expressed on the surface of monocytes, macrophages, and dendritic and epithelial cells<sup>[110]</sup>. In IBD mucosa, dendritic cells are activated and there are increased levels of TLR2 and TLR4. These TLRs mediate the recognition of bacterial lipoproteins and LPS, respectively. An association has been described between the TLR4 D299G SNP and IBD, in UC as well as CD patients<sup>[111]</sup>. This SNP is associated with impaired LPS signaling and increased susceptibility to gram-negative infections, thus supporting the role of gram-negative bacteria in the pathogenesis of IBD. Polymorphisms have been described in IBD with regard to the TLR9 gene, but their functional significance is still unclear<sup>[112]</sup>.

#### *Genes of the autophagy: A key role in IBD*

The autophagy 16-like 1 (*ATG16L1*), immunity-related guanosine triphosphate M (IRGM), and leucine-rich repeat kinase 2 (*LRRK*2) genes, which regulate autophagy, have been associated with CD in  $GWAS^{[113,114]}.$ 

Autophagy describes the sequestration of intracellular material such as obsolete organelles or large unfolded protein within membranes, and their trafficking to fuse with lysosome with a subsequent degradation of the contents. Autophagy is now recognized as playing a key role in innate immunity against intracellular microorganisms.

 ATG16L1 is essential for all forms of autophagy as it has a role in the clearance of intracellular bacteria<sup>[115]</sup>. It interacts with two other autophagy proteins, ATG5 and ATG12, to forms a complex essential for the process of autophagy<sup>[116]</sup>. The association at ATG16L1 with CD seems to be entirely accounted for by the *T300A* coding variant which maps to a highly conserved part of the gene adjacent to the coiled-coil domain. ATGL16L1 mutations cause a deficiency of the correspondent protein and disrupt the recruitment of the ATG12-ATG5. Therefore, autophagosome formation and degradation of proteins with a long half-life are severely impaired in ATG16L1-deficient cells<sup>[117,118]</sup>. The decreased autophagy impairs immune tolerance by autoantigen presentation on major histocompatibility complex class Ⅱ molecules and causes immune inflammation $[119]$ .

*ATG16L1* gene mutations could also impair the mechanisms that involve autophagy and apoptosis as there is an acceleration in the rate of epithelial cell apoptosis and an inhibition of inflammatory cell apoptosis in CD and UC<sup>[120,121]</sup>. Several studies have been performed on the role of *ATG16L1* gene in the pathogenesis of IBD.

The *T300A* allele was correlated with the incidence of CD in three populations from Germany, Hungary and the Netherlands<sup>[122]</sup>. In contrast, no correlation between T300A allele and UC was detected. However, the results of other studies on the association of T300A

allele with predisposition to CD and UC, are inconsistent<sup>[122]</sup>, also in child-onset IBD cases<sup>[123]</sup>. Recently, a meta-analysis performed on twenty-five studies of CD, 14 of which involved cases of  $UC^{[124]}$  showed that the T300A allele confers a susceptibility to CD and to UC. However, ATG6L1 was associated with the risk of childonset CD, but not with child-onset UC probably because there are few studies on pediatric UC. Recently, a functional link between NOD2/CARD15, ATG16L1 and autophagy has been provided<sup>[125-128]</sup>.

## *IRGM gene*

In the Wellcome Trust Case-Control Consortium (WTCCC) GWA scan, a highly significant association between variant flanking IRGM and susceptibility to CD has been shown. The *IRGM* gene is located on chromosome 5q33.1, and is required during the initiation phase of autophagy, when it localizes to bacteria- containing autophagic vacuoles. IRGM and autophagy are involved in clearance of intracellular organisms such as *M. tubercolusis*<sup>[129,130]</sup> and the CD-associated IRGM variant is predicted to affect autophagic control of Salmonella typhimurium<sup>[131]</sup>.

The IRGM risk alleles for CD are non-coding and appear to affect mRNA transcription or stability. Over the last 5 years three distinct mechanisms have been identified which might explain the impact on IRGM expression. Cooney *et al*<sup>[131]</sup> discovered a large copy number variant upstream of IRGM which correlated with tissuespecific expression effects. Prescott *et al*<sup>[132]</sup> reported a disruption of a transcription factor binding site in the IRGM promoter. Most recently, Brest et al<sup>[133]</sup> found that a synonymous coding variant of IRGM alters the binding domain of miRNA196, a family of miRNAs, hence affecting mRNA stability and gene translation. In this study, it has been shown that microRNA196 is overexpressed in CD patients and that it downregulates an IRGM protective variant but not the risk-associated allele.

Lapaquette *et al*<sup>[134]</sup> found that the reduced *IRGM* gene expression correlated with impaired clearance by macrophages of CD-associated adherent-invasive *Escherichia*   $\text{coli. A recent Italian study}$ <sup>[135]</sup> reported the association between CD and two risk SNPs (rs1000113 and rs4958847) for IRGM, irrespective of age, but not in UC. In addition, a trend to B3 (penetrating) disease behavior in patients with IRGM SNPs was suggested<sup>[135]</sup>. Moon *et al*<sup>[136]</sup> showed that IRGM SNP rs10065172 was significantly associated with CD susceptibility. They also reported a protective role of SNP rs72553867.

By suppressive subtractive hybridization (SSH) technique, Sim *et al*<sup>[137]</sup> studied the differential expression gene profiles in ileal biopsies from CD children. Twentyeight genes previously reported in association with adult CD, and 47 new genes were identified. It is significant that some adult CD genes have also been found in earlyonset CD. Indeed, it underlines that, in some cases, there is a common genetic pathway between pediatric and

adult CD cases. Several genes reported in the study are involved in microbial pathogenesis, antigen presentation, inflammation, regulation of epithelial barrier function, vesicular transport or cell differentiation and proliferation. Recent studies have found that IL33 expression is enhanced in the inflamed colonic mucosa of IBD, especially in UC<sup>[138,139]</sup>, and the IL33/IL1RL1 signalling axis has been implicated in the IBD pathogenesis $[140]$ . Recently, new genes have been identified by GWAS in IBD<sup>[141-150]</sup>. In particular, in 2008, Kugathasan *et al*<sup>[141]</sup> performed the first GWAS in a cohort with pediatric disease onset, identifying two new loci on 20q13 and 21q22. This paper reported the associations with two intronic SNPs (rs2315008 and rs4809330) at the 20q13 locus. These two SNPs map to the zinc finger CCCH-type with G patch domain (ZGPAT) gene which is located in a region containing eight potential candidate genes for CD. Moreover, an association, at the 21q22 region, of CD with the intergenic SNP rs2836878 has been shown that implicated the nearby PSMG1 gene $^{[141]}$ .

A follow-up scan on an extended cohort of 3426 childhood-onset IBD (European/North America collaboration) identified five more new loci associated with pediatric IBD<sup>[147]</sup>. These loci included 16p11 near the cytokine gene IL27, 22q12, 10q22, 2q37 and 19q13.11. The results of this study showed that IL27 is a promising candidate gene for pediatric CD. Recently, Latiano *et al*[149] have studied a large Italian cohort of adult and early-onset IBD to verify the role of new genes involved in the immune response and inflammation (PTGER4, HLA-BTNL2, TNFSF15, NKX2-3, ZNF365, IFNG, PTPN2, and PSMG1).

## *Role of colonic epithelial cells producing* β*-defensins in colonic (L2) CD location.*

Since Paneth cells are rare in the colon, the contribution of α-defensins to antimicrobial defence in the large intestine is only limited. In contrast, β-defensins HDB1-3 are secreted by columnar and goblet cells in the colon[151,152]. A deficiency of β-defensin HDBD2 has been shown by molecular biology in L2 (colonic) CD and confirmed on the protein level by immunohistochemistry[104]. This observed colonic defect of the antimicrobial barrier caused by a diminished expression of β-defensins may allow luminal microbes to attach to and invade the mucosa triggering the inflammation<sup>[153]</sup>.

## *CD behaviour*

The Montreal classification<sup>[29]</sup> describes three behaviours for CD: nonstricturing nonpenetrating disease (B1), stricturing disease (B2), penetrating/fistulizing disease  $(B3)$ . In addition, the Paris classification<sup>[30]</sup> proposes a new classification B2B3 to identify patients with both B2 and B3 phenotypes (either at the same or different times). Disease locations are the most important factor identified in determining the risk of developing either a structuring or penetrating complication (more complications with ileal, less with colonic disease)<sup>[154]</sup>. To date,

L1 CD Location: Involvement of the terminal ileum only, with limited or no cecal disease Diagnosis: After the age of 10 years old Gene: NOD2 and ATG16L1 Pathology: Abnormal paneth cells, granulomapoor

 $12 CD$ Location: Colonal involvement only Diagnosis: Before the age of 10 years old Gene:  $\beta$ -defensins Pathology: Granuloma-rich Perianal CD Location: Perianal and L1 or L3 Diagnosis: After the age of 10 years old Gene: NCF4

## **Figure 2 Subtypes of Crohn's disease.** CD: Crohn's disease.

there have been few pediatric studies that have evaluated the association between CD behavior and genotype with prolonged follow-up. In a study by Shaoul *et al*<sup>[155]</sup>, pediatric CD at the end of follow-up (mean 4.9 years) was classified as inflammatory (78%), stricturing (17%) and penetrating (7%). Moreover, a role for NOD2 in CD behavior (as opposed to location) was not supported in this study. NOD2 genotype was clearly associated with ileal involvement (L1), but not as an independent risk factor for stricturing, penetrating disease or a need for surgery<sup>[155]</sup>. A recent study showed that L1 CD and stricturing disease behavior are more common in children diagnosed after 10 years of age than in younger patients $^{[39]}$ .

Approximately 10% of newly diagnosed pediatric patients shows perianal CD at time of diagnosis<sup>[156]</sup>. The Vienna classification did not distinguish luminal and perianal fistulising disease into different categories<sup>[28]</sup>. Subsequent evidence suggested that perianal and luminal fistulae often occur completely independently of each other. According to the Montreal and Paris classifications<sup>[29,30]</sup>, a separate perianal modifier was added that can coexist with any disease behaviour. Perianal CD is defined as inflammation at or near the anus, including tags, fissures, fistulae, abscesses, or stenosis. A recent study by Eglinton *et*  $aI^{157}$  suggests specific associations with perianal CD patients compared with patients without perianal involvement. These associations include younger age at diagnosis, male gender, ileal (L1 or L3) location, and complicated disease behaviour (B2 + B3). In addition, an association with the NCF4 gene was demonstrated<sup>[157]</sup>. Taken together, literature data suggest that perianal CD represents a distinct disease phenotype, summarized in Figure 2.

## **UC**

UC is classically defined as a chronic inflammation characterized by a continuous involvement of the colonic mucosa without granulomas on biopsy, affecting the rectum and a variable extent of the colon in continuity, and characterized by a relapsing, remittent course<sup>[158]</sup>. However, several studies suggest that pediatric UC may present with atypical phenotypes, such as macroscopical rectal sparing, macroscopic skip lesions in the colon, periappendiceal inflammation, backwash ileitis, limited upper gastrointestinal inflammation, and extensive colitis with less severe and less diffuse architectural abnormalities $^{[159,160]}$ . Thus, diagnosis of UC in pediatric patients may be particularly difficult. The recent Paris classification<sup>[30]</sup>, which examined this issue, adds a new category (E4) for pancolitis (inflammation extending proximal to the hepatic flexure) (Table 2). Moreover, a disease behavior classification of S0 or S1 was adopted, with the latter denoting the presence of severe disease at any time in patient history (Table 2). The classification of UC based on anatomical extent has clinical relevance, as it affects the choice of therapy and the mode of delivery of drugs. For example, oral therapy is the first choice for UC extending above the splenic flexure<sup>[161]</sup>.

Primary sclerosing cholangitis (PSC) is a cholestatic liver disease of unknown etiology, commonly associated with IBD and characterized by inflammation, fibrosis, and stenoses of the biliary tree leading to liver cirrhosis<sup>[162]</sup>. In most patients (80%-90%) the IBD can be classified as UC. Several features of UC in PSC differ from those of a general UC population (increased frequency of pancolitis, "backwash ileitis", rectal sparing and colorectal carcinoma), and these observations have led to the hypothesis that UC in PSC may represent a specific phenotypic entity (PSC-UC)<sup>[163]</sup>. There are a few studies on PSC-UC in pediatric patients. Ordonez  $et \, al^{164}$  studied twenty-eight consecutive children with UC associated with PSC, celiac disease, or autoimmune hepatitis comparing them with a matched control group of 27 children with isolated UC. At diagnosis, pancolitis was seen in 18/28 UC associated with autoimmunity patients compared with 8/27 in UC. Pathological findings were also different from isolated UC: (1) major lesions predominantly located in the right colon; (2) pseudovillous appearance of the mucosa, and strong infiltration

with eosinophils; and (3) mild glandular lesions. Evolution in UC associated with autoimmune disease was less aggressive, requiring less corticosteroids/immunomodulators<sup>[164]</sup>. In conclusion, clinical, histological, and molecular analyses reveal marked differences between pediatric patients with isolated UC and those with associated autoimmune phenomena, supporting the hypothesis of a distinct autoimmune presentation of UC (Figure 1).

### *Goblet cells as protagonist in the UC*

Mucus produced by goblet cells forms a key component of the mucosal barrier. Gel-forming mucins of intestinal mucus are arranged into a bilayer with a firm inner layer devoid of bacteria and a looser outer layer with MUC2 being major constituent of both<sup>[165]</sup>. The mucus layer has a crucial role in intestinal homeostasis, as decreased levels of goblet cells, leading to reduced mucin secretion, are a hallmark of human  $UC^{[166]}$ . The thickness of the mucus layer in the healthy colon is between 100 and 300 µm, increasing from the ascending colon to the rectum, whereas in UC, this mucus layer is thinner, more variable and in part denuded<sup>[167-169]</sup>. Taken together, several lines of evidence strongly suggest a key role for goblet cells in UC.

### *Molecular biology of UC*

GWAS and candidate gene association studies identified several UC susceptibility loci, including 7 that overlap with CD (*e.g.*, IL23 pathways genes, NKX2-3 and  $|{\rm L10}\rangle^{[170]}$ . In a recent study, three new UC specific loci (*HNF4A*, *CDH1* and *LAMB1*) has been found that are involved in the regulation of barrier function $[171]$ .

An association was seen at rs6017342 SNP which maps within a recombination hotspot on chromosome 20q13 in which the 3' untraslated region (UTR) of the HNF4A gene is located. This gene encodes the transcription factor hepatocyte nuclear factor 4  $\alpha$  which regulates the expression of multiple components within the adherens junction, the tight junction and desmosome<sup>[172]</sup>.

Cell-cell junctions have an important role on epithelial organization and barrier function. Moreover, in the embryonic age, the *HNF4A* gene participates in the development of mammalian gastrointestinal tract<sup>[173]</sup>. *CDH1* gene which encodes E-cadherin has been located on chromosome 16q22. E-cadherin is a transmembrane glycoprotein, a key component of the adherens junction and mediates intercellular adhesion in the intestinal epithelium<sup>[171]</sup>. It also participates in processes of epithelial restitution and repair following the damage of mucosa. Indeed, there is a significant reduced expression of CDH1 in areas of active  $UC^{[174]}$ . Interestingly, two CDH1 variants associated with  $UC^{[171]}$  have also been associated with colorectal cancer<sup>[175]</sup>, a possible complication of UC. The recent hypothesis is that HNF4A and E-cadherin co-participate to maintain the integrity of the epithelial intestinal barrier. *LAMB1* gene is located on chromosome  $7q31^{[171]}$  and encodes the laminin β 1 subunit, which is detected in laminins-1, -2 and-10. In UC, the expression of laminins in the intestinal basement membrane is downregulated<sup>[171]</sup>.

In 2011, Anderson *et*  $a l^{176}$  identified 29 additional UC risk loci from a meta-analysis and IL1R2, IL8RA/B, IL7R, IL12B, DAP, PRDM1, JAK2, IRF5, GNA12 and LSP1 were proposed as new important candidate genes in UC pathogenesis. Several genes were associated with cytokines and cytokine receptors, key regulators of citokyne-mediated signalling pathways, innate and adaptive immune response, macrophage activation and regulation of apoptosis. Interestingly, an association with *DAP*  gene (death-associated protein) has been found. The expression of DAP kinase increases with inflammation in  $UC^{[177]}$  and is a negative regulator of autophagy<sup>[178]</sup>. Therefore, the association with DAP suggests a possible link between autophagy and UC.

*PRDM1*, *IRF5* and *NKX2-3* genes could have a key role for transcriptional regulation in UC pathogenesis. GNA12 which plays a fundamental role in the tight junction assembly in epithelial cells has been identified at the  $7p22$  locus<sup>[179]</sup>. It is the most likely UC candidate gene from those described in the meta-analysis of Anderson et al<sup>[176]</sup>. Barrier integrity is important in UC pathogenesis given previous associations to *HNF4A*, *CDH1* and *LAMB1* genes<sup>[171]</sup>. Further studies are, however, need to verify the role of the genes in pediatric UC. The salient histopathological and biomolecular features of pediatric IBD are shown in Table 3.

## **CONCLUSION**

In conclusion, our review reinforce the idea that pediatric UC and CD may be further classified into various clinicopathologic entities, based on genotype-phenotype correlation reported in recent literature. Therapy for complex genetic diseases such as IBD is difficult. For example, treatment with ant-TNF- $\alpha$  monoclonal antibodies does not induce remission in the majority of CD cases. It is becoming increasingly apparent that novel strategies to define and stratify IBD patients, that are based on serum, DNA and histopathology, will be needed to progress towards improved diagnostics, prognostics and therapeuthics.

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