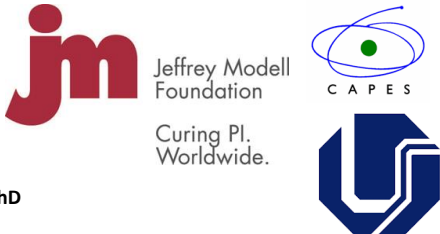


Clinical-molecular characteristics of very early-onset inflammatory bowel disease in Brazilian children



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1. Introduction

Inflammatory bowel disease (IBD) is a multifactorial disease caused by the combination of genetic predisposition, exposure factors (environmental and dietary), immune status, and dysbiosis, and it could present at any age, ranging from newborns to the elderly. Very early onset inflammatory bowel disease (VEOIBD) represents 4 to 10% of pediatric IBD and is characterized by the presence of symptoms onset before the age of 6 years. Unlike older children and adults, who mostly have polygenic involvement in pathogenesis, VEOIBD has mono- or oligogenic involvement. Recent studies have shown an annual increase in incidence of 7% in children under 5 years old with IBD diagnosis over the past decades. Due to the importance of monogenic causes in patients with VEOIBD and their close relationship with IEI, this study aims to identify variants that may be associated with VEOIBD using a molecular panel developed for IEI diagnosis

2. Methods

This is a cross-sectional study with participants aged 0 to 18 years, with IBD onset before age 6, recruited between April 2022 and January 2024. Saliva samples were collected for genetic testing using oral swabs for analysis by INVITAE. The Fleury Genomics laboratory also analyzed a small portion of the samples. Both use NGS techniques via the Illumina platform, based on the GRCh37 version of the Human Genome for variant detection and analysis. The selected genetic panel contains 426 genes. The data generated by sequencing were analyzed through customized bioinformatics processes (pipeline v3.10). The variants were classified according to the American College of Medical Genetics (ACMG) as pathogenic, likely pathogenic, and of uncertain significance (Figure 1)

3. Results

The study included 32 VEOIBD patients, predominantly female, with an average symptom onset at 2 years and 3 months. 37.5% had symptoms before age 2, and diagnostic confirmation took about 11 months. Clinical data and all IBD characteristics are described in Table 1. Lymphocyte counts and immunoglobulin levels are demonstrated in Table 2.

Table 3 describes clinical, endoscopic, laboratory, and genetic findings in patients with pathogenic/likely pathogenic/ or VUS variants in the genes previously associated with VEOIBD. Table 4 describes the same characteristics for patients with variants associated with an increased risk of developing IBD. Table 5 describes findings in patients with variants we considered with probable association with IBD.

Figure 1: Screening of variants through the evaluation of the phenotype previously described for the gene in question (ClinVar, Medgen, OMIM) and the clinical manifestations presented by the patient, also considering inheritance, zygosity, and alterations in the encoded protein

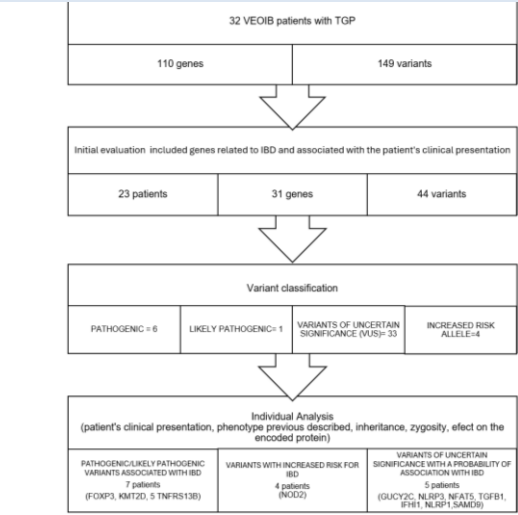


Table 3: Genotypic and phenotypic characterization of patients with pathogenic/ likely pathogenic/ VUS variants associated with IBD

Patient	Gene(s)	Variant(s)	DNA effect	Effect on the encoded protein	Zygosity	Inheritance	ACMG classification	Associated phenotype (ClinVar, Medgen, OMIM)	Sex	Age at diagnosis (months)	FH	IBD Diagnostic	Symptoms	Internal findings	Additional findings	Treatment required
7	IRF1	c.418C>T (p.Arg140Cys)	missense	like to be tolerated	heterozygous	AD	VUS	Immunodeficiency-12B selective susceptibility to enterobacterial infections	M	24	Yes	CD	Bloody diarrhea, Weight deficit, Perianal Disease	Proctitis with large elevated-edge ulcers, intense inflammatory infiltrate with granuloma tissue. Chondritis with villous atrophy	Alopecia, eczema, recurrent infections, hypogammaglobulinemia (IgG), reduced CD19 lymphocytes	EEN for 3 weeks. Inadequate from the start (Top-down), monthly Gastrostomy for nutritional recovery
	KMT2D	c.1018T_1020Tdel (p.Val1398_Ala1403del)	insertion	like to be disruptive	heterozygous	AD	VUS	Kohls syndrome: peculiar facies, dental abnormalities, intellectual disability, growth failure, eczema. Association with IBD								
	TTC7A	Deletion (Exon 1-5)	deletion	disrupted protein (LOF)	heterozygous	AR	Pathogenic	Immunodeficiencies with multiple defects, severe diarrhea, colitis								
13	FOXP3*	c.1250G>A (p.Arg417Gln)	missense	like to be disruptive	heterozygous	X linked	VUS	FOXP3 polyautoimmune; enteropathy, dysregulation, DM, dermatitis, eczema	M	23	No	UC	Bloody diarrhea, Abdominal pain	Macroscopic proctitis, intense inflammatory infiltrate, cryptitis, abscesses	Reduced CD19 lymphocytes	Mesalazine
17	SOD3	c.143C>T p.(Pro46Leu)	missense	like to be tolerated	heterozygous	AD	VUS	Familial autoimmune-inflammatory syndrome: cystitis, hemolytic anemia, thrombocytopenia, lymphadenopathy. It may be associated with CD	F	4	Yes	CD	Bloody diarrhea, Weight deficit, Perianal disease	Proctitis with serous ulcers, mucosal erythema, intense inflammatory infiltrate with eosinophils and lymphoid accumulations, fissures	anemia, leukocytosis, eczema, infections de repousse from the start (Top-down), monthly Gastrostomy for nutritional recovery	EEN for 3 weeks. Inadequate from the start (Top-down), monthly Gastrostomy for nutritional recovery
	TNFRSF1B	c.110T>C p.(Cys104Arg)	missense	disrupted protein (LOF)	heterozygous	AD/AR	Pathogenic	TAC1 deficiency: recurrent infections, autoimmune manifestations Association with IBD and CVID								
20	TNFRSF1B	c.118T>C p.(Tyr40Leu)	missense	deleterious in silico	heterozygous	AD/AR	VUS	TAC1 deficiency: recurrent infections, autoimmune manifestations Association with IBD and CVID	M	18	No	UC	Bloody diarrhea, Abdominal pain	Proctitis, intense inflammatory infiltrate with eosinophils and eosinophils	Anemia, reduction of T lymphocytes, CD4, CD8 and CD8	Azathioprine
21	TNFRSF1B	c.110T>C p.(Cys104Arg)	missense	disrupted protein (LOF)	heterozygous	AD/AR	Pathogenic	TAC1 deficiency: recurrent infections, autoimmune manifestations Association with IBD and CVID	M	3	No	CD	Bloody diarrhea, Weight deficit	Ulcerative proctitis, infiltrate with neutrophils/eosinophils, architectural distortion, Erythrocytic debris/Chondritis	Elevated IgE, lymphocytosis, reduction in T lymphocytes, CD4, autoimmune manifestations	Azathioprine, stepped up to infliximab
22	TNFRSF1B	c.110T>C p.(Cys104Arg)	missense	disrupted protein (LOF)	heterozygous	AD/AR	Pathogenic	TAC1 deficiency: recurrent infections, autoimmune manifestations Association with IBD and CVID	F	<1	Yes	IBD/U	Bloody diarrhea	Enteric proctitis with neutrophilic inflammatory infiltrate	Anemia, recurrent infections, lymphocytosis, hypogammaglobulinemia (IgM/IgG)	Intensive immunoglobulin
25	TNFRSF1B	c.110T>C p.(Cys104Arg)	missense	disrupted protein (LOF)	heterozygous	AD/AR	Pathogenic	TAC1 deficiency: recurrent infections, autoimmune manifestations It may be associated with IBD and CVID	F	34	No	UC	Bloody diarrhea, Weight deficit	Enteric proctitis, intense inflammatory infiltrate, neutrophils, crypt distortion	Anemia, hypothyroidism, reduction in T lymphocytes CD1/CD4	Azathioprine, stepped up to infliximab

Abbreviations: ACMG, American College of Medical Genetics and Genomics; AD, autosomal dominant; AR, autosomal recessive; CD, Crohn's disease; CVID, common variable immunodeficiency; DM, diabetes mellitus; FH, family history of IBD; IBD, inflammatory bowel disease; UC, ulcerative colitis; VEOIBD, very early onset IBD; VUS, variant of uncertain significance

Table 4: Genotypic and phenotypic characterization of patients with variants associated with an increased risk of developing IBD

Patient	Gene(s)	Variant(s)	DNA effect	Effect on the encoded protein	Zygosity	Inheritance	ACMG classification	Associated phenotype (ClinVar, Medgen, OMIM)	Sex	Age at diagnosis (months)	FH	IBD Diagnostic	Symptoms	Internal findings	Additional findings	Treatment required
4	NOD2	c.218AC>T (p.Arg70Tyr)	missense	like to be tolerated	heterozygous	AD	Increased Risk Allele	NOD2: expressed in intestinal cells of the small intestine, mediates antibacterial effects, releases cytokines with T cell activation. Increased risk for CD	F	10	Yes	UC	Bloody diarrhea	Chronic erosive proctitis with moderate inflammatory infiltrate	Elevated IgE, lymphocytosis	Azathioprine
	PEPD	c.682_684del (p.Tyr231del)	deletion	like to be disruptive	heterozygous	AR	Likely pathogenic	Protease deficiency: autoimmune diseases, skin ulcers, eczema, infections.								
	AKK1	c.1384G>C (p.Lys458Asn)	missense	like to be tolerated	heterozygous	AD	VUS	Autoinflammation, immune dysregulation, eosinophilia, may be present with eosinophilic colitis								
9	LZBA	c.3508G>A (p.Gln1158Lys)	missense	like to be tolerated	heterozygous	AR	VUS	TAC1 deficiency: recurrent infections, autoimmune manifestations Can be associated with VEOIBD	F	72	No	UC	Bloody diarrhea, Abdominal pain	Enteritis with moderate inflammatory infiltrate, with the presence of cryptitis	Anemia, recurrent infections, lymphocytosis, hypogammaglobulinemia (IgM/IgG)	Azathioprine, stepped up to infliximab
	NOD2	c.218AC>T (p.Arg70Tyr)	missense	like to be tolerated	heterozygous	AD	Increased Risk Allele	NOD2: expressed in intestinal cells of the small intestine, mediates antibacterial effects, releases cytokines with T cell activation. Increased risk for CD								
	NOD2	c.2722G>C (p.Gly908Arg)	missense	like to be tolerated	heterozygous	AD	Increased Risk Allele	NOD2: expressed in intestinal cells of the small intestine, mediates antibacterial effects, releases cytokines with T cell activation. Increased risk for CD								
11	NOD2	c.697C>T (p.Gln233*)	stop sign	disrupted protein (LOF)	heterozygous	AD	VUS	Bleu syndrome: vesitis, granulomatous pyoderitis, rash, 30% develop CD	M	48	Yes	CD	Bloody diarrhea, Weight deficit	Proctitis with moderate inflammatory infiltrate, with the presence of cryptitis	Anemia, hypoproteinemia, hypogammaglobulinemia (IgG)	Azathioprine, stepped up to infliximab
	GRA21	c.778G>A (p.Arg259His)	missense	inconclusive	heterozygous	AR	VUS	Immunodeficiency 9: recurrent infections, myopathy, ectodermal dysplasia								
	ZAP70	c.572C>T (p.Pro191Leu)	missense	like to be tolerated	heterozygous	AR	VUS	Immunodeficiency 60: inflammatory bowel disease and recurrent mucocutaneous infections								
	BACK2	c.879G>A (p.Val293Thr)	missense	like to be tolerated	heterozygous	AD	VUS	Immunodeficiency 60: inflammatory bowel disease and recurrent mucocutaneous infections								
13	NFAT5	c.358AC>T (p.Ser119Phe)	missense	like to be tolerated	heterozygous	AD	VUS	Autoimmune enteropathy with immunodeficiency, may be associated with CVID					Abdominal pain, Weight loss	Enteritis with moderate inflammatory infiltrate with eosinophils and eosinophils, with anal involvement	Recurrent oral ulcers, increased IgE, reduced CD19 cells	Mesalazine
	NOD2	c.3011del (p.Tyr1047Profs 72)	stop sign	like to be disruptive	heterozygous	AD	Increased Risk Allele	NOD2: expressed in intestinal cells of the small intestine, mediates antibacterial effects, releases cytokines with T cell activation. Increased risk for CD	F	72	No	UC				
	RELA	c.917A>G (p.Tyr306Cys)	missense	like to be tolerated	heterozygous	AD	VUS	Beckwith-Wiedemann syndrome: predisposition to childhood cancer								
	RTLE1	c.978>A-G (p.Tyr326Cys)	splice site	like to be tolerated	heterozygous	AD	VUS	Compensated dyskeratosis and dystrophic skin papulosis, neonatal leukopenia, colitis, enteropathy								

Abbreviations: ACMG, American College of Medical Genetics and Genomics; AD, autosomal dominant; AR, autosomal recessive; CD, Crohn's disease; CVID, common variable immunodeficiency; FH, family history of IBD; IBD, inflammatory bowel disease; LOF, loss of function; UC, ulcerative colitis; VEOIBD, very early onset IBD; VUS, variant of uncertain significance

Table 5: Genotypic and phenotypic characterization of patients with variants of uncertain significance with probable association with IBD

Patient	Gene(s)	Variant(s)	DNA effect	Effect on the encoded protein	Zygosity	Inheritance	ACMG classification	Associated phenotype (ClinVar, Medgen, OMIM)	Sex	Age at diagnosis (months)	FH	IBD Diagnostic	Symptoms	Internal findings	Additional findings	Treatment required
1	GUCY2C	c.1489G>A (p.Arg497Gln)	missense	like to be disruptive	heterozygous	AD	VUS	Congenital familial diabetes Susceptibility to VEOIBD	M	33	No	UC	Bloody diarrhea	Proctitis with ileocecal valve involvement		Mesalazine
	NLRP3	Exonic coding sequence	copy number gain	like to be tolerated	heterozygous	AD	VUS	Autoinflammation, autoinflammation, autoinflammation, autoinflammation Susceptibility to IBD								
	NFAT5	c.338C>T (p.Pro113Leu)	missense	like to be tolerated	heterozygous	AD	VUS	Autoimmune enteropathy with CVID								
10	TGFB1	Exon 1, c.85G>A (p.Gly28Asp)	missense	like to be tolerated	heterozygous	AD	VUS	Severe colitis, association with IBD, recurrent infections, macrophagopathy	F	60	No	DC	Bloody diarrhea, Weight loss	Enteritis with moderate inflammatory infiltrate, with the presence of cryptitis	Significant increase in IgE, reduced CD19 lymphocytes and NK cells	Azathioprine, stepped up to infliximab, monthly
18	IFIH1	c.1211T>C p.(Val404Asn)	missense	deleterious in silico	heterozygous	AD/AR	VUS	MDA5 deficiency: characterized by increased susceptibility to infectious and VEOIBD	F	36	No	CD	Bloody diarrhea, Abdominal pain, Weight loss	Enteritis with moderate inflammatory infiltrate, ileocecal involvement, ileitis, ileocolitis, ileocolitis, ileocolitis	Ileal ulcers, IgA and IgG+ PPT, reduction in CD19 lymphocytes and NK cells	Azathioprine, stepped up to infliximab
29	NLRP3	c.1531A>G p.(Lys510Gln)	missense	inconclusive	heterozygous	AD/AR	VUS	Autoinflammation, dyskeratosis, enteritis, autoinflammation Susceptibility to IBD	M	72	No	UC	Bloody diarrhea	Proctitis with moderate neutrophilic infiltrate, architectural distortion, and goblet cell depletion. Villi slightly distorted and enlarged in the small intestine		Azathioprine
32	SAMD9	c.400TT>C p.(L>C404>C1>C44>C>C2>C4)	missense	deleterious in silico	heterozygous	AD	VUS	MEPAGE syndrome: myelodysplasia, infections, growth retardation, adrenal hypoplasia, genital abnormalities, enteropathy	F	36	No	UC	Bloody diarrhea	Enteritis with moderate inflammatory infiltrate rich in eosinophils and neutrophils, lymphoid aggregates, architectural distortion, Dyskeratosis and chronic proctitis	Elevated IgE, reduction in CD19 lymphocytes and NK cells	Azathioprine, stepped up to infliximab

Abbreviations: ACMG, American College of Medical Genetics and Genomics; AD, autosomal dominant; AR, autosomal recessive; CD, Crohn's disease; CVID, common variable immunodeficiency; FH, family history of IBD; IBD, inflammatory bowel disease; UC, ulcerative colitis; VUS, variant of uncertain significance

Table 1: Characterization of Brazilian patients with Very Early Onset Inflammatory Bowel Disease (VEOIBD)

Mean age at diagnosis (months)	50.3±34.24
Median time to diagnostic confirmation (months)	10.50 (6 - 17)
Sex N (% female)	21 (65.63%)
Family history of IBD N (%)	7 (21.88%)
Clinical symptoms N (%)	
Bloody diarrhea	17 (57.12%)
Abdominal pain	15 (46.87%)
Weight loss	14 (43.75%)
Non-bloody diarrhea	4 (12.50%)
Perianal disease	3 (9.38%)
Extraintestinal manifestations N (%)	13 (40.62%)
Laboratorial findings (mean±SD)	
Hemoglobin level (g/dl)	10.71±2.49
Hematocrit (%)	33.45±6.67
Platelets	477.058±197.438
ESR (mm/h)	41.1±36.60
CRP (mg/dl)	13.51±16.82
Calprotectin (µg/g)	1690 (600-5657)
Disease location N (%)	
Pancolonic	26 (81.25%)
Ileal involvement	7 (21.87%)
Left Colon	5 (15.63%)
Rectum only	1 (3.13%)
Upper gastrointestinal tract involvement	14 (43.75%)
Initial diagnosis N(%)	
Crohn's disease	13 (40.63%)
Ulcerative colitis	16 (50.00%)
Inflammatory bowel disease unclassified	3 (9.38%)
Moderate to severe disease (PUCAI/PCDAI)	27 (84.38%)
Endoscopic findings consistent with VEOIB N (%)	
Focal chronic inflammation	18 (56.25%)
Architectural distortion	16 (50.0%)
Basal lymphoplasmacytosis	14 (43.75%)
Lymphoid accumulation	13 (40.63%)
Increased eosinophils	9 (28.13%)
Increased neutrophils	8 (25.00%)
Nonspecific infiltrate	4 (12.50%)
Granulomas	1 (3.13%)
Perianal disease	3 (9.38%)
Villous atrophy	3 (9.38%)
Moderate to severe histological activity N(%)	21 (77.77%)
Initial therapeutic choice N(%)	
Exclusive Enteral Nutrition (EEN)	3 (9.38%)
Corticosteroids in induction therapy	32 (100%)
Immunosuppressants (Thiopurines)	26 (81.25%)
Mesalazine	3 (9.38%)
Biologic therapy as first choice (top-down)	2 (6.25%)
Progression to anti-TNF	16 (50%)
18 (59.34%)	
Other Therapies (Immunoglobulins)	1 (3.13%)
Therapeutic failure N(%)	17 (59.37%)

Table 2: Immunological screening of patients, including immunoglobulin levels and lymphocyte typing, based on references for the Brazilian population.

Immunoglobulin (mg/dL)*	Median (25-75)	<P3	P3-50	P50-97	>P97
IgA (N=26)	158.5 (105.2 - 210.0)	1 (3.8%)	5 (19.2%)	14 (53.8%)	6 (23.1%)
IgM (N=22)	127.0 (98.0 - 206.2)	1 (4.5%)	8 (36.4%)	3 (13.6%)	10 (38.5%)
IgG (N=24)	1176.5 (951.7 - 1278.0)	1 (4.2%)	2 (8.3%)	14 (58.3%)	7 (26.9%)
IgE (N=24)	31.8 (11.85 - 64.15)	-	-	-	-
Lymphocyte immunophenotyping (cells/µL)	Median (25-75)	<P10	P10-50	P50-90	>P90
CD3 (N=23)	2736.0 (1683.6 - 3673.5)	4 (17.4%)	5 (21.7%)	7 (30.4%)	7 (30.4%)
CD4 (N=20)	1379.2 (992.2 - 1975.2)	4 (20.0%)	2 (10.0%)	4 (20.0%)	10 (50.0%)
CD8 (N=20)	867.5 (572.7 - 1627.2)	2 (10.0%)	3 (15.0%)	10 (50.0%)	5 (25.0%)
CD19 (N=17)	616.0 (353 - 1116.0)	9 (52.9%)	0 (0.0%)	2 (11.8%)	6 (35.3%)
CD56 (N=17)	225.0 (90.0 - 725.0)	7 (41.2%)	2 (11.8%)	2 (11.8%)	6 (35.3%)

*Source: Fujimura MD, 1991

*Source: Moraes-Pinto MI et al, 2005

4. Conclusions

In this study, it was possible to establish a well-defined genetic diagnosis in 11 patients (34.4%), including 7 patients (21.8%) with monogenic disease, who presented pathogenic or likely pathogenic variants for IBD, and 4 patients (12.8%) with increased risk variants for IBD. Five Patients presented suspicious variants, included in Table 5, that we considered were probably associated with VEOIBD.

In our study, we have found 149 variants that were analyzed in a monogenic disease perspective, excluding them according to previous relation with VEOIBD, zygosity, and potential pathogenicity. On the other hand, recent studies have shown that the interaction between variants, some considered benign when isolated, can be associated with diseases when present together with other variants of the same immune pathway or acting synergistically. Gene variant interaction is a new challenge for understanding the influence of genetics on inflammatory diseases. Pediatric IBD represents a spectrum that can range from extreme monogenic variants to complex polygenic variants, and new AI tools could improve the way to study these interactions.

In conclusion, the genetic evaluation of patients with VEOIBD with target genetic panels to immunologic genes can improve the understanding and the treatment of patients.

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