

Cytokine gene polymorphisms in *Blastocystis* carriers

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The Irritable Bowel Syndrome pathogenesis (IBS) is considered to be multifactorial, some are:

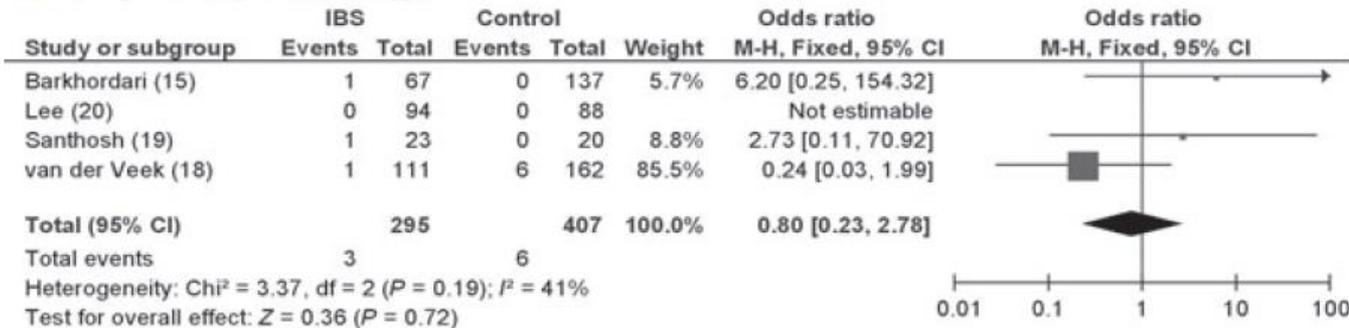
- ❖ Psychological distress
- ❖ Gastrointestinal dysmotility
- ❖ Visceral hypersensitivity
- ❖ Microbiota
 - Bacterial overgrowth
 - Altered microbiota
- ❖ Infections: Post-infective (PI)-IBS
 - Episode of gastroenteritis can trigger IBS symptoms
- ❖ The immune activation in the Intestinal wall: Low-grade inflammation
 - ↑ numbers of T cells in lymphoid compartments of the small or large intestine in IBS patients.
 - ↑ proinflammatory cytokines such as interleukin (IL)-1 β , IL-6, IL-8 and tumor necrosis factor (TNF)- α in serum of IBS patients.
- ❖ Genetics
 - Familiar aggregation (\approx 33% IBS patients reported a family history of IBS Vs 2% of the control group)
 - SNPs (Single Nucleotide Polymorphisms)** gene polymorphisms that encoding proteins with immunomodulatory and neuromodulatory features

Cytokine gene polymorphisms are associated with irritable bowel syndrome: a systematic review and meta-analysis

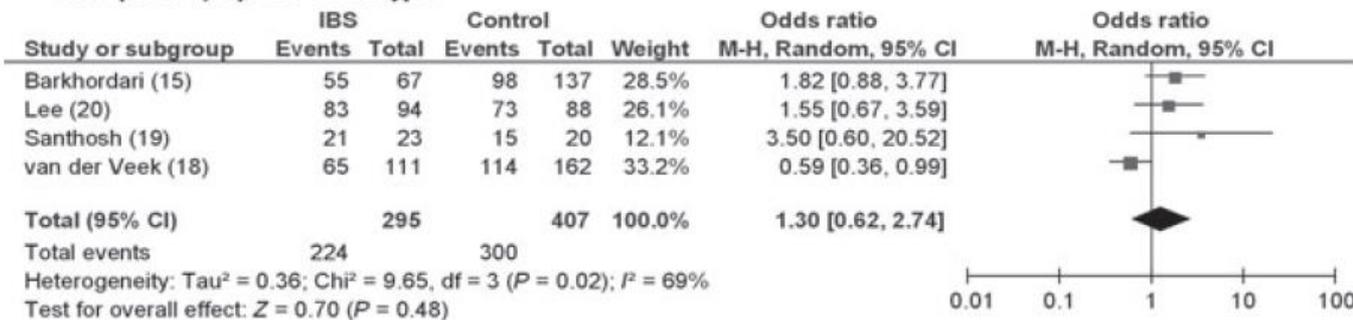
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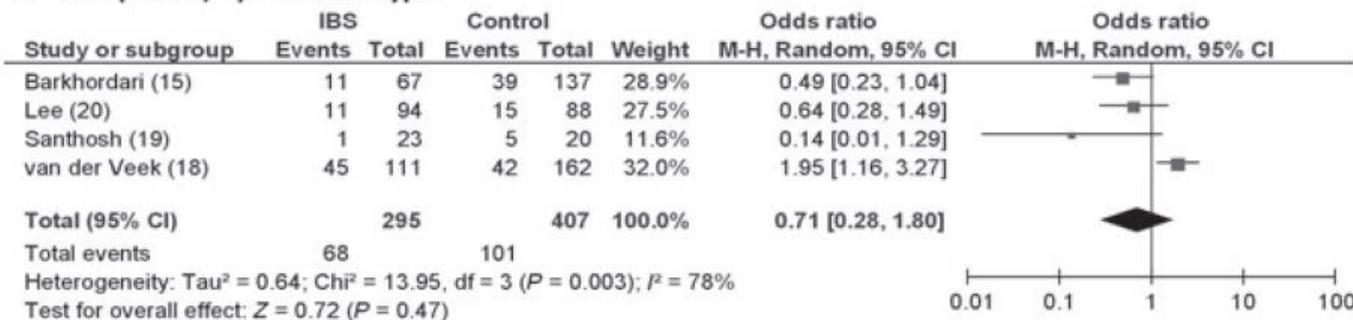
A TNF (-308G/A): AA Genotype



B TNF (-308G/A): GG Genotype

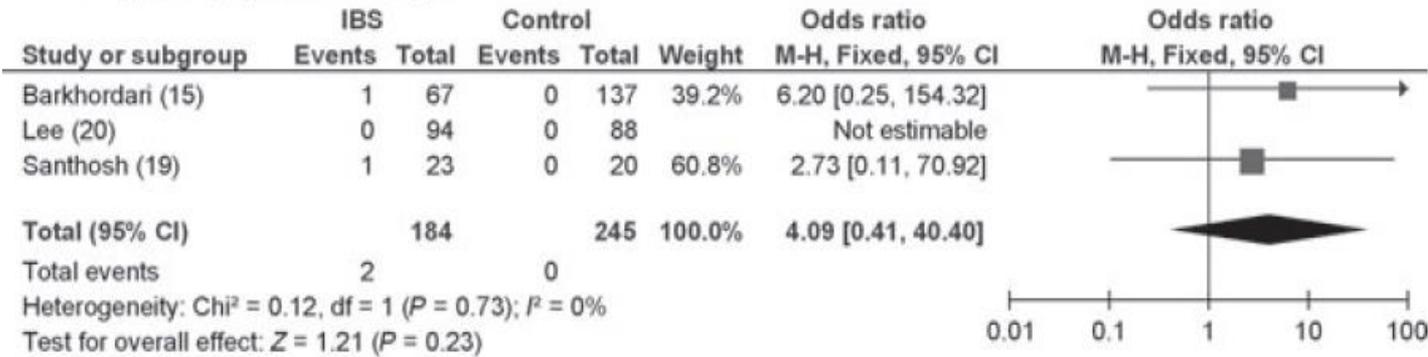


C TNF (-308G/A): GA Genotype

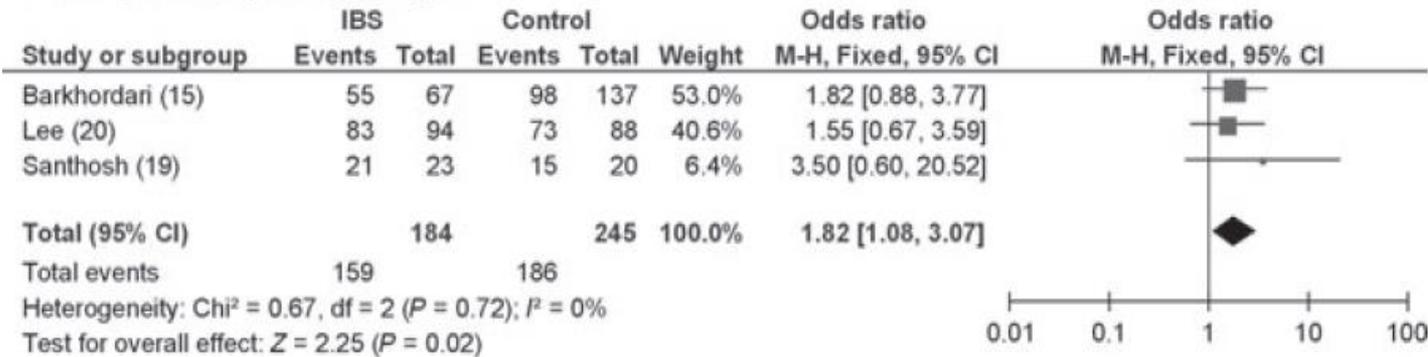


For pooled studies

A TNF (-308G/A): AA Genotype



B TNF (-308G/A): GG Genotype

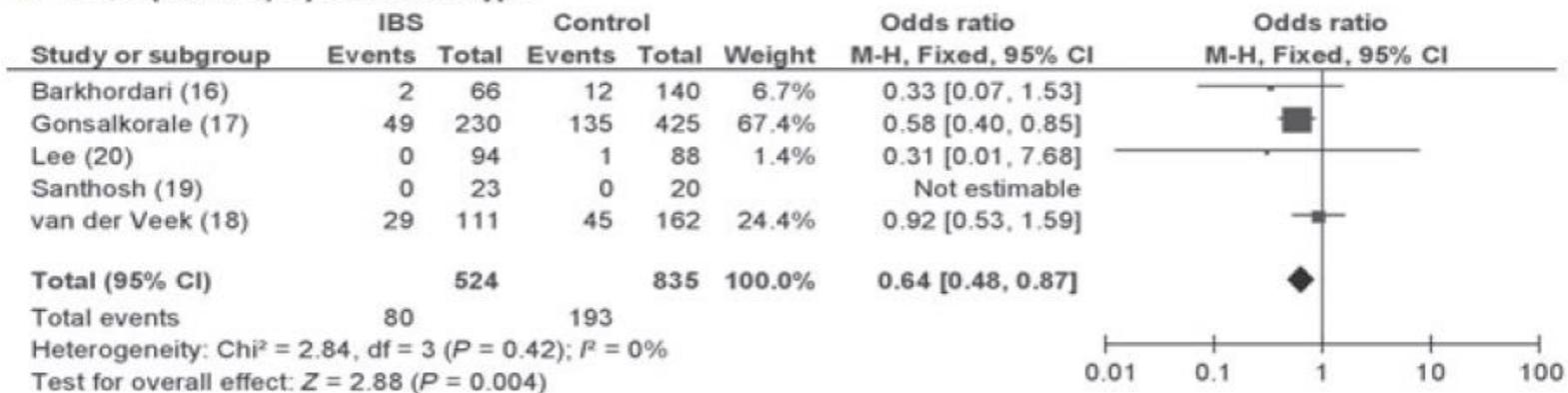


C TNF (-308G/A): GA Genotype



For studies in Asian patients

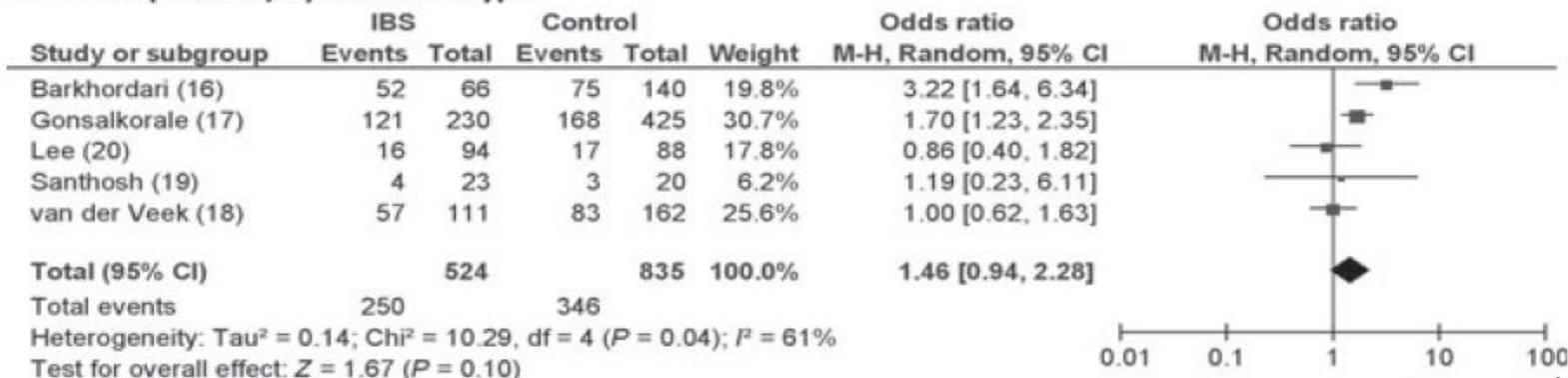
A IL-10 (-1082G/A): GG Genotype



B IL-10 (-1082G/A): AA Genotype



C IL-10 (-1082G/A): GA Genotype



For pooled studies

Proinflammatory Cytokine Gene Polymorphisms in Irritable Bowel Syndrome

J Clin Immunol (2010) 30:74–79

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Maryam Alighardashi • Hamid Reza Ahmadi-Ashtiani • Mahdi Mahmoudi •
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Cytokine	Position	Allele	Patients (<i>n</i> =71) <i>n</i> (%)	Controls (<i>n</i> =140) <i>n</i> (%)	<i>P</i> value	Odds ratio (95% confidence interval)
IL-6	-174	C	27 (20.76%)	101 (36.3%)	0.002	0.46 (0.27–0.77)
		G	103 (79.23%)	177 (63.7%)		2.18 (1.30–3.66)
IL-6	nt565	A	25 (19.23%)	50 (18.0%)	0.868	1.09 (0.62–1.91)
		G	105 (80.76%)	228 (82.0%)		0.92 (0.52–1.63)
TNF- α	-308	A	13 (9.7%)	39 (14.2%)	0.257	0.65 (0.31–1.31)
		G	121 (90.29%)	235 (85.8%)		1.54 (0.76–3.18)
TNF- α	-238	A	8 (5.97%)	59 (21.5%)	<0.001	0.23 (0.10–0.52)
		G	126 (94.02%)	215 (78.5%)		4.32 (1.92–10.13)
IL-1 α	-889	C	97 (68.3%)	186 (68.4%)	0.923	1.00 (0.63–1.58)
		T	45 (31.7%)	86 (31.6%)		1.00 (0.63–1.59)
IL-1 β	-511	C	71 (50%)	154 (55.4%)	0.344	0.81 (0.53–1.23)
		T	71 (50%)	124 (44.6%)		1.24 (0.81–1.90)
IL-1 β	+3962	C	96 (67%)	198 (70.7%)	0.586	0.86 (0.55–1.37)
		T	46 (32%)	82 (29.3%)		1.16 (0.81–1.90)
IL-1R	Pst-I 1970	C	104 (74%)	174 (62.1%)	0.017	1.76 (1.10–2.83)
		T	36 (26%)	106 (44.2%)		0.57 (0.35–0.91)
IL-1RA	Mspa-I 11100	C	27 (19%)	64 (22.9%)	0.521	0.82 (0.48–1.40)
		T	111 (80%)	216 (77.1%)		1.22 (0.71–2.08)

Objective: To evaluate the role of SNP for IL -6, 8, 10 and tumor necrosis factor-alpha (TNF- α) in IBS patients and controls, with or without *Blastocystis* infection.

Recruiting of IBS patients (according to the Rome III criteria*) and controls, previous informed consent

*Recurrent abdominal pain or discomfort for at least 3 d per month in the last 3 mo associated with two or more of the following

- Improvement with defecation
- Onset associated with a change in frequency of stool
- Onset associated with a change in form (appearance) of stool

Obtaining feces samples by colonoscopy and blood samples of all participants

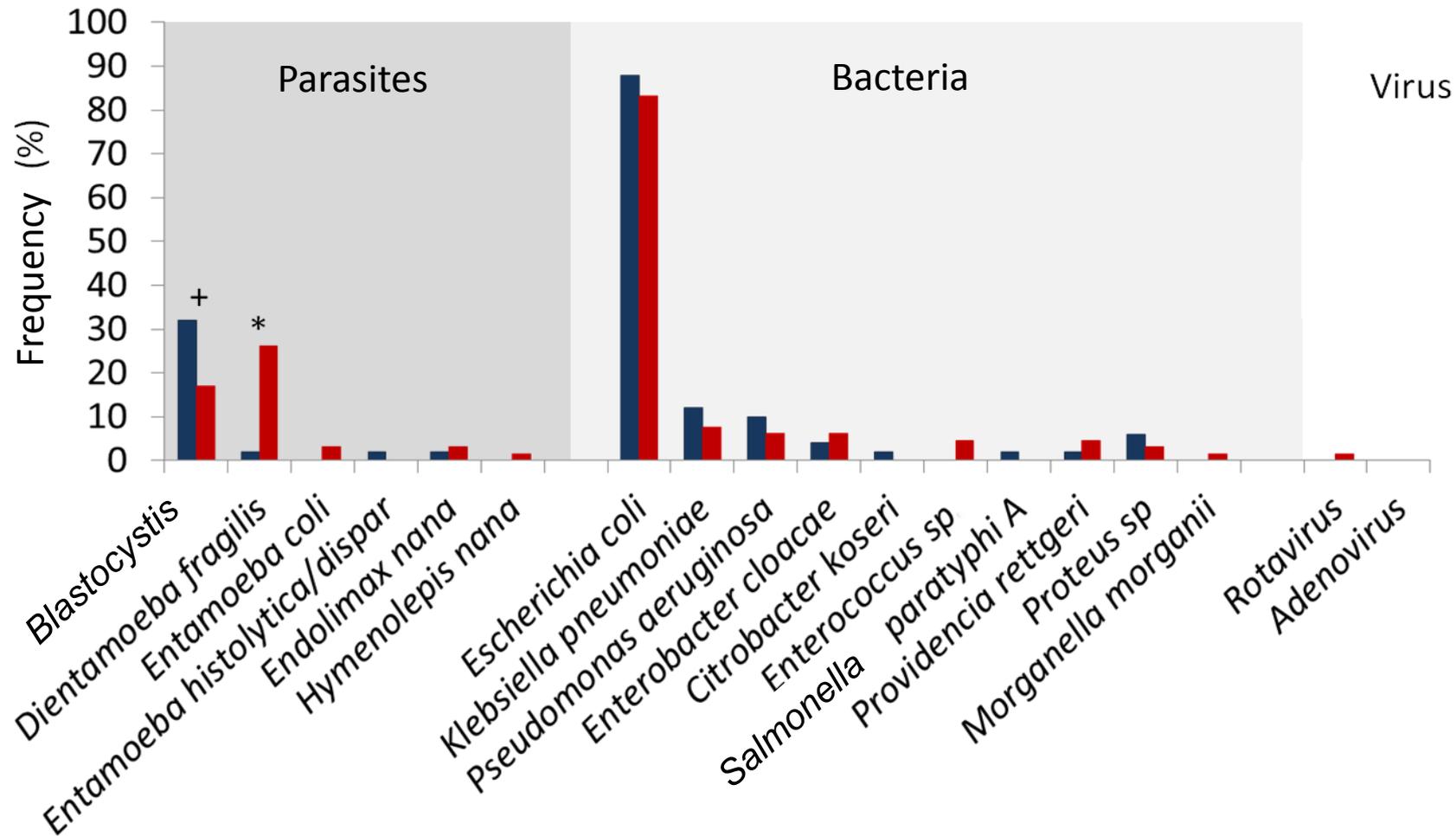
Coprolological assays for search of helminths ova and protozoa cysts, PCR for *Blastocystis* subtypes and for *Dientamoeba fragilis*

Coproculture for pathogen bacteria and examination for virus (rotavirus and adenovirus)

Profile of genetic polymorphisms of SNP for TNF α , IL-6, IL-8 e IL-10 \ddagger by PCR-dot blot and PCR RFLP

Data Analysis

\ddagger -174 for IL-6; -251, +396, +781, +1633 for IL-8; -1082, -819, -592 for IL-10, as well as -238 and -308 for TNF- α



Frequency of microorganisms identified by CPS, coproculture, virus screening and PCR for *Blastocystis sp.* ($p=0.048$) and *D. fragilis* ($p=0.0004$)

Blastocystis subtypes

Group/Subtype	ST 1	ST 2	ST 3	ST 1/3	ST 2/3	Total
IBS	2	1	2	10	1	16
Control	0	0	3	7	1	11

Some associations between variables

Association	χ^2	<i>p</i>	OR	95% CI
<i>Blastocystis</i> /IBS	3.57	0.048	2.31	1.113-5.567
ST2/IBS	6.072	0.065	12	1.027-140.192
<i>Blastocystis</i> / <i>P. aeruginosa</i>	2.996	0.083	0	0-1.87
<i>Blastocystis</i> / <i>K. pneumoniae</i>	3.071	0.079	0.187	0.024-1.488
<i>Dientamoeba</i> /IBS	13.53	0.0004	0.05	0-0.52

Statistical differences within SNPs

Relationship	Alleles or genotypes	<i>p</i>	OR (95%CI) ^b	EF ^c
IBS vs. control	Allele			
	IL-8+396 (G)	0.0437	1.78 (1.01-3.12)	0.291
	IL-10-1082 (A)*	0.0267	1.99 (1.08-3.69)	0.358
	Genotypes			
	IL-8+396(GG)	<0.0001	10.13 (2.73-37.55)	0.313
	IL-8+781(CT)	0.0248	2.45 (1.11-5.39)	0.348
	IL-10-1082(AA)*	0.0039	3.64 (1.49-8.89)	0.353
Presence or absence of <i>Blastocystis</i>	Allele			
	IL-8+781 (T)	0.0448	2.00 (1.01-3.97)	0.228
	Genotype			
	IL-8+396(GG)	0.0025	4.64 (1.63-13.19)	0.290
IBS and <i>Blastocystis</i> carrier vs. IBS and absence of <i>Blastocystis</i>	Allele			
	IL-10-592 (C)†	0.0166	3.28 (1.22-8.79)	0.454
	Genotype			
	IL-8+396(GG)	0.0272	4.22 (1.15-15.5)	0.429
Control and <i>Blastocystis</i> carrier vs. control and absence of <i>Blastocystis</i>	Genotype			
	IL-10-819 (CC)†	0.0426 ^d	0.12 (0.01-1.05)	-

^a Mantel–Haenszel test; ^b Odds ratio (95% confidence interval); ^c Etiologic fraction; ^d Fisher's exact test

*Allele A has been associated as low producer of IL-10; † Allele A has been associated as higher producer of IL-10.

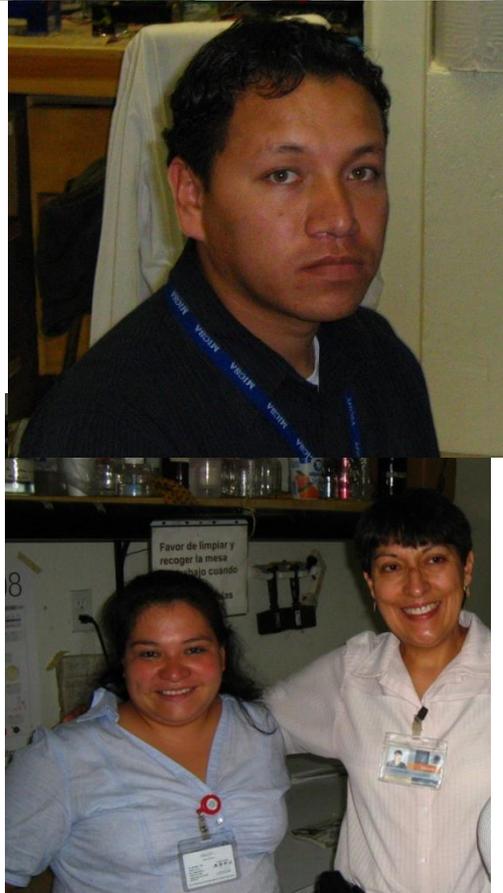
Discussion

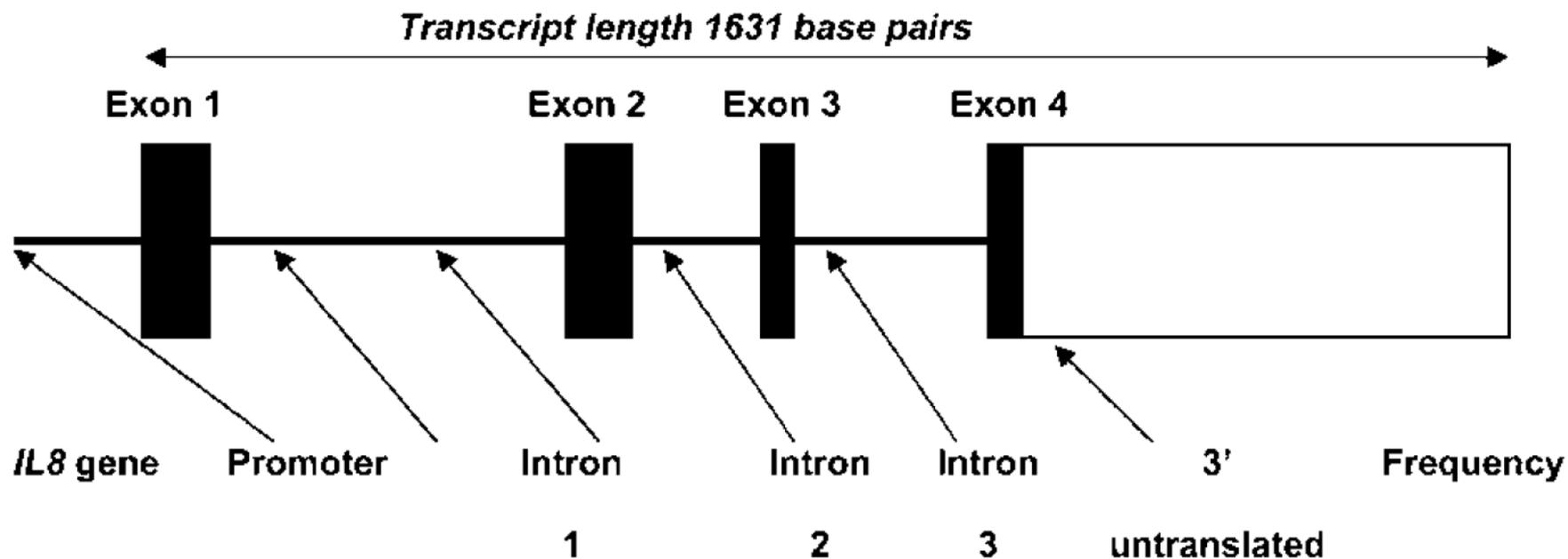
- ✓ An association between *Blastocystis* infection and development of IBS was identified, supports its pathogenic role.
- ✓ *Blastocystis* subtypes 1 and 3 were the most frequent, according with other studies; interestingly, many cases with co-infection were observed.
- ✓ No associations among *Blastocystis* and symptoms, presence with other microorganisms, age and gender were found.
- ✓ Polymorphisms in SNP of IL-6 and TNF- α promoters might not contribute for the susceptibility to IBS in our population.

- ✓ In contrast, we found that alleles G and A, as well as the homozygous variant for IL-8 at position +396 and IL-10 at position -1082, respectively, were relevant to develop IBS.
- ✓ Association between IL-8 and IL-10 gene polymorphisms to the pair IBS–*Blastocystis* carrier suggests their individual or additive role as significant factors in the etiology of this disease.
- ✓ Finally, *Dientamoeba fragilis* showed a prevalence of 2% in IBS patients and 28% in controls, it is probably that this phenomenon is due to a selection bias as IBS patients are multi-treated



Thank you!!!!





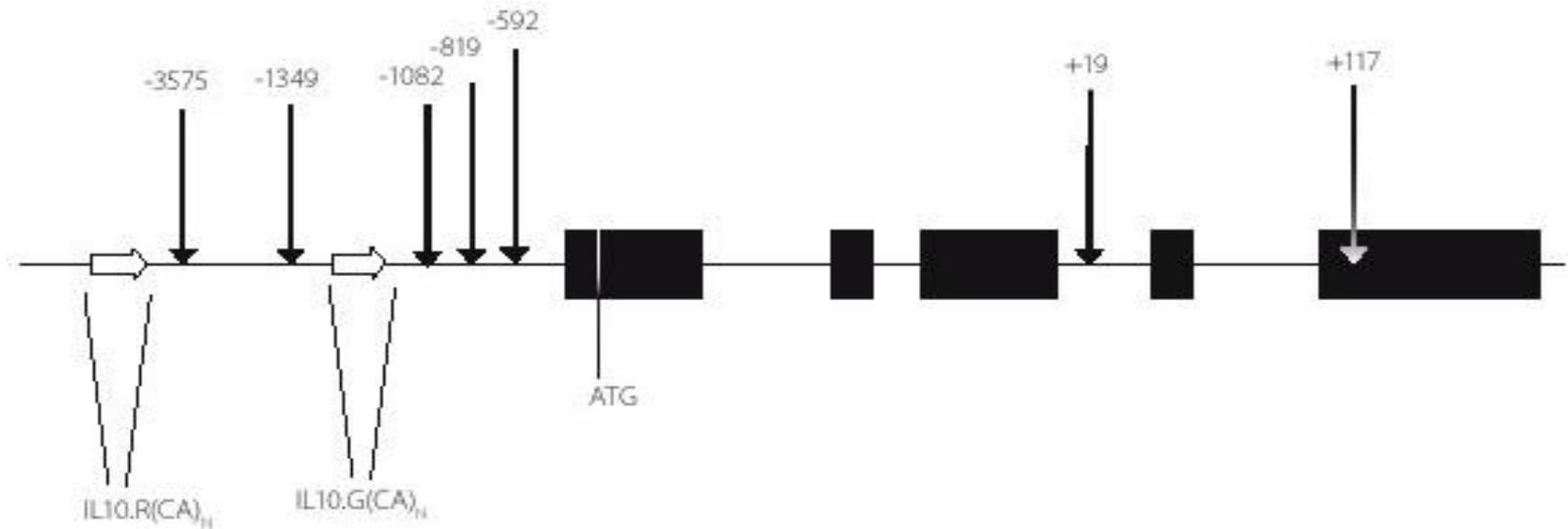
		1	2	3	untranslated	
SNP	-251	+396	+781	+1238	+1633	+2767
Haplotype 1	T	T	C	C		0.52

Genes Immun. 2004 Jun;5(4):274-82.

Haplotypes	IBS group (<i>n</i> = 45; %)	Control group (<i>n</i> = 137; %)	<i>P</i> value	<i>P_c</i> value ^c	OR (95 % CI) ^d
IL-8 ^a					
AGCT	21.34	22.16	0.896	6.272	0.95 (0.47–1.94)
TTCC	3.48	19.09	0.003	0.025	0.15 (0.03–0.63)
AGTT	8.24	9.02	0.898	6.289	0.93 (0.32–2.68)

^c Bonferroni correction

IL-10 SNPs



SNP	-1082	-819	-592			
Haplotypes	IBS group (<i>n</i> = 45; %)	Control group (<i>n</i> = 137; %)	<i>P</i> value	<i>P_c</i> value ^c	OR (95 % CI) ^d	
IL-10 ^b						
ATA	32.7	28.3	0.498	3.486	1.19 (0.71–1.99)	
GCC	17.71	31.84	0.011	0.075	0.46 (0.26–0.84)	
ACC	26.43	7.94	<0.001	<0.001	4.17 (2.19–7.89)	

^c Bonferroni correction