Blastocystis Is Associated with Decrease of Fecal Microbiota Protective Bacteria: Comparative Analysis between Patients with Irritable Bowel Syndrome and Control Subjects

Céline Nourrisson, Julien Scanzi, Bruno Pereira, Christina Nkoudmongo, Ivan Wawrzyniak, Amandine Cian, Eric Viscogliosi, Valérie Livrelli, Frédéric Delbac, Michel Dapoigny, et al.

To cite this version:

Céline Nourrisson, Julien Scanzi, Bruno Pereira, Christina Nkoudmongo, Ivan Wawrzyniak, et al.. Blastocystis Is Associated with Decrease of Fecal Microbiota Protective Bacteria: Comparative Analysis between Patients with Irritable Bowel Syndrome and Control Subjects. PLoS ONE, Public Library of Science, 2014, 9 (11), pp.25365580. 10.1371/journal.pone.0111868. hal-01111985

HAL Id: hal-01111985
https://hal.archives-ouvertes.fr/hal-01111985
Submitted on 15 Nov 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Distributed under a Creative Commons Attribution - NonCommercial| 4.0 International License
Blastocystis Is Associated with Decrease of Fecal Microbiota Protective Bacteria: Comparative Analysis between Patients with Irritable Bowel Syndrome and Control Subjects

Céline Nourrisson1,2,3, Julien Scanzi4,5, Bruno Pereira6, Christina NkoudMongo1, Ivan Wawrzyniak2,3, Amandine Cian7, Eric Viscogliosi7, Valérie Livrelli1,8, Frédéric Delbac2,3, Michel Dapoigny4,5, Philippe Poirier1,2,3

1 CHU Clermont-Ferrand, Centre de Biologie, Laboratoire de Parasitologie-Mycologie, Hôpital G. Montpied, Clermont-Ferrand, France, 2 Clermont Université, Université Blaise Pascal, Laboratoire Microorganismes: Génome et Environnement, BP 10448, Clermont-Ferrand, France, 3 CNRS, UMR 6023, LMGE, Aubière, France, 4 CHU Clermont-Ferrand, Service de Médecine digestive et hépatobiliaire, Hôpital Estaing, Clermont-Ferrand, France, 5 Clermont Université, Université d’Auvergne, UMR 1107 INSERM, Neuro-Dol, Clermont-Ferrand, France, 6 CHU Clermont-Ferrand, DRCI, ‘Délegation Recherche Clinique et Innovation’, Clermont-Ferrand, France, 7 Université Lille Nord de France, INSERM U1019, CNRS UMR 8204, Centre d’Infection et d’Immunité de Lille (CIL), Institut Pasteur, Biologie et Diversité des Pathogènes Eucaryotes Emergents, Lille, France, 8 Clermont Université, Université d’Auvergne, Centre de Recherche en Nutrition Humaine Auvergne, M2iSH, ‘Microbes, Intestin, Inflammation et Susceptibilité de l’Hôte UMR INSERM/Université d’Auvergne U1071 USC-INRA 2018, BP 10448, Clermont-Ferrand, France

Abstract

Blastocystis is a protozoan parasite living in the digestive tract of many animals, including humans. This highly prevalent intestinal parasite is suspected to be linked to Irritable Bowel Syndrome (IBS), a chronic functional bowel disorder. Here, we first compared the prevalence of Blastocystis among 56 IBS patients (40 IBS with constipation (IBS-C), 9 IBS with diarrhea (IBS-D), 4 mixed IBS (IBS-M) and 3 unsubtyped IBS (IBS-U)) according to the Rome III criteria) and 56 control (i.e. without any diagnosed chronic or acute gastrointestinal disorder) subjects. The highest prevalence of Blastocystis spp. was observed in the IBS group, but was only statistically significant in men (36.8% in the IBS group versus 4.8% in the control group). We then conducted a meta-analysis including epidemiological studies attempting to determine whether Blastocystis carriage could be linked to IBS, and highlighted that IBS patients had a relative risk of 2.34 to be infected by Blastocystis when compared to non-IBS subjects. We also looked for Dientamoeba fragilis, which is often associated with IBS, and identified this parasite only in some IBS patients (n = 6/56). Several studies provided evidence for a major role of the gut microbiota in the pathophysiology of IBS. Thus, we investigated the possible impact of Blastocystis carriage on the enteric bacterial community through quantification of 8 major bacterial groups from the enteric flora. Our data indicated that men with IBS-C had a significant decrease in Bifidobacterium sp. when infected by Blastocystis. Interestingly, in control subjects (i.e. without any gastrointestinal disorder) positive for Blastocystis, Faecalibacterium prausnitzii, which is known for its anti-inflammatory properties, was significantly decreased in men. Our results support the hypothesis that Blastocystis might be linked to the pathophysiology of IBS-C and intestinal flora imbalance.

Introduction

Blastocystis sp. is an anaerobic protistan parasite found in the intestinal tract of humans and various animals, with a widespread distribution and characterized by extensive genetic diversity [1]. At least 17 subtypes (STs) have been described on the basis of the sequence of the gene encoding the 18S rRNA, the ST1 to ST9 being recovered from human stool samples [1,2]. Its prevalence in humans widely varies between countries according to hygienic conditions and sanitary practices [1]. A recent study indicated that this prevalence can reach 100% in a Senegalese population [3]. However, the clinical relevance of Blastocystis sp. remains controversial because most cases of infection are asymptomatic [1]. Interest of the scientific and medical communities in Blastocystis increased these last few years since epidemiological surveys highlighted a higher prevalence of this parasite in patients suffering from the Irritable Bowel Syndrome (IBS) compared to healthy populations or to patients suffering from other gastrointestinal disorders [4]. IBS is a functional chronic disorder characterized by abdominal pain, bloating and alteration of bowel...
In our work, we first aimed to evaluate the prevalence of both *Blastocystis* and *D. fragilis* in an IBS population from a westernized country. A meta-analysis including all previous studies reporting prevalence of *Blastocystis* in IBS patients was also performed. In a second part we quantified 8 major bacterial groups from the enteric flora to identify bacterial changes associated to the presence of *Blastocystis*.

### Results

#### IBS and control cohorts

56 patients fulfilling Rome III criteria for IBS were recruited (see details in Table 1). Most of them were classified as IBS-C (71.4%), the other were IBS-D (16.1%), IBS-M (7.1%) and IBS-U (5.4%). The control group also included 56 subjects without any history of chronic or acute digestive disease.

#### Prevalence of *Blastocystis* sp.

*Blastocystis* was detected by qPCR in 23.2% (13/56) of patients with IBS and 16.1% (9/56) of control subjects (Table 1 and Figure 1). Interestingly, when considering only males, the prevalence of the parasite in the IBS group (36.8%, 7/19) was significantly higher (*p* = 0.017) than in the control group (4.8%, 1/21). In contrast, the prevalence of *Blastocystis* sp. in females did not significantly differ between both groups (*p* = 0.559). Similar results were observed when considering only the IBS-C subgroup (see Table 1 and Figure 1).

#### Prevalence of *Dientamoeba fragilis*

We found that all the 56 control subjects were negative for *D. fragilis* whereas 6 patients (4 women and 2 men) with IBS were positive for the parasite (Figure 1 and Table 1). Three of these patients were also co-infected with *Blastocystis*. However, the number of patients was too low to calculate *p*-values according to subject sex.

#### *Blastocystis* subtyping

In the control group, all the 9 *Blastocystis* positive subjects were infected by ST4, including one that was co-infected with ST2 (Table 1). ST4 was also the predominant ST found in *Blastocystis*-positive IBS patients (6/13, Table 1). Among the 7 other patients with IBS, 1 was infected by ST1, 2 by ST2, 3 by ST3 and 1 was co-infected by both ST2 and ST3. However, statistical analysis revealed that the distribution of *Blastocystis* subtypes did not significantly differ between IBS and control groups.

#### Meta-analysis of *Blastocystis* prevalence in IBS patients

A systematic review and meta-analysis was conducted of the 11 published studies to assess the prevalence of *Blastocystis* in patients with IBS. This meta-analysis included 1728 IBS patients and 1292 control subjects (Table S1). IBS patients had a relative risk of 2.336 when compared to non-IBS subjects (Figure 2). However, we were unable to perform this analysis when considering only males or females because of numerous missing data in the selected studies.

#### Quantification of major bacterial groups from the enteric flora

In order to compare the 8 major bacterial communities between IBS-C and control groups, only *Blastocystis*-negative subjects were first considered. *Bacteroides* sp. were significantly increased in patients with IBS-C (*p* < 0.001) compared with control group, whereas *Bifidobacterium* sp. (*p* < 0.001), *Desulfovibrio* sp.
Table 1. Demographic and epidemiological characteristics of IBS and control groups.

<table>
<thead>
<tr>
<th>Populations</th>
<th>Control group</th>
<th>Overall</th>
<th>IBS-C</th>
<th>IBS-D</th>
<th>IBS-M</th>
<th>IBS-U</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number</td>
<td>56</td>
<td>56</td>
<td>40</td>
<td>9</td>
<td>4</td>
<td>3</td>
</tr>
<tr>
<td>Male</td>
<td>21</td>
<td>19</td>
<td>12</td>
<td>4</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Female</td>
<td>35</td>
<td>37</td>
<td>28</td>
<td>5</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>Age, years (mean±SD)</td>
<td>53.3±16.3</td>
<td>53.6±16.0</td>
<td>55.1±16.4</td>
<td>50.2±16.2</td>
<td>45.0±12.0</td>
<td>55.3±15.6</td>
</tr>
</tbody>
</table>

**Blastocystis-positive**

| Number/total (p-value) | 9/56 (p=0.476) | 13/56 (p=0.583) | 11/40 (p=0.583) | 1/9 | 1/4 | 0/3 |
| Male/Total (p-value)   | 1/21 (p=0.017) | 7/19 (p=0.037)  | 5/12 (p=0.037)  | 1/4 | 1/1 | n.a. |
| Female/Total (p-value) | 8/35 (p=0.359) | 6/37 (p=0.745)  | 6/28 (p=0.745)  | 0/4 | 0/3 | n.a. |
| Age, years (mean±SD)   | 55.3±19.8      | 52.5±16.4       | 51.6±17.7       | 62  | 52  | n.a. |

**Subtype distribution**

| ST1 | 0 | 1 | 1 | 0 | 0 | n.a. |
| ST2 | 0 | 2 | 2 | 0 | 0 | n.a. |
| ST3 | 0 | 3 | 3 | 0 | 0 | n.a. |
| ST4 | 8 | 6 | 4 | 1 | 1 | n.a. |

**Dientamoeba fragilis-positive**

| Number/total (p-value) | 0/56 | 6/56 (p=0.027) | 4/40 | 1/9 | 1/4 | 0/3 |
| Age, years (mean±SD)   | n.a. | 55.8±16.4       | 58.3±19.0 | 61  | 41  | n.a. |

Overall: males plus females, S.D.: standard deviation, n.a.: not applicable, ST: subtype. P-values of 0.05 or below were considered as significant (two-sided). doi:10.1371/journal.pone.0111868.t001
\( p = 0.011 \), \( C. \) leptum \( p = 0.001 \) and \( F. \) prausnitzii \( p = 0.004 \) were significantly decreased (Table S2). Statistical analyses after a clustering per sex revealed that \( Bacteroides \) sp. significantly increased in males \( p = 0.046 \) and females \( p = 0.001 \), whereas \( F. \) prausnitzii significantly decreased only in males \( p = 0.008 \), (Figure 3, Table S2) and both \( Bifidobacterium \) sp. and \( C. \) leptum decreased only in females \( p < 0.001 \) and \( p = 0.004 \) respectively.

When considering \( Blastocystis \)-positive IBS-C patients, only \( Bifidobacterium \) sp. were significantly decreased in males \( p = 0.008 \), (Figure 3, Table S2). No difference was observed for the other bacterial groups.

In the overall control group (i.e. without any gastrointestinal disorder), no significant difference between both \( Blastocystis \)-positive and \( Blastocystis \)-negative patients was observed (Table S2).

\( (p = 0.011) \), \( C. \) leptum \( (p = 0.001) \) and \( F. \) prausnitzii \( (p = 0.004) \) were significantly decreased (Table S2). Statistical analyses after a clustering per sex revealed that \( Bacteroides \) sp. significantly increased in males \( (p = 0.046) \) and females \( (p = 0.001) \), whereas \( F. \) prausnitzii significantly decreased only in males \( (p = 0.008) \), (Figure 3, Table S2) and both \( Bifidobacterium \) sp. and \( C. \) leptum decreased only in females \( (p < 0.001 \) and \( p = 0.004 \) respectively).

When considering \( Blastocystis \)-positive IBS-C patients, only \( Bifidobacterium \) sp. were significantly decreased in males \( (p = 0.008) \), (Figure 3, Table S2). No difference was observed for the other bacterial groups.

In the overall control group (i.e. without any gastrointestinal disorder), no significant difference between both \( Blastocystis \)-positive and \( Blastocystis \)-negative patients was observed (Table S2).


\( \text{Figure 1. Prevalence of } Blastocystis \text{ and } Dientamoeba fragilis \text{ in both control and IBS groups. } \) Overall: males plus females; *, $: p$-value $p < 0.05$. The \( p \)-values are determined by reference to control group.

doi:10.1371/journal.pone.0111868.g001

\( \text{Figure 2. Forest plot of relative risk and 95\% confidence interval for } Blastocystis \text{ carriage in IBS subjects. } \) The horizontal lines represent the 95\% confidence interval (CI) of the relative risk (RR) for IBS subjects compared to non-IBS subjects in each study. The black box in the middle of the CI represents the single best estimate of RR in that study. The width of the CI is related to the power of the study and inversely associated with sample size. In addition, the pooled or combined RR results of the meta-analysis are represented by a diamond, the width of which is the CI for the pooled data. The vertical line is typically displayed to indicate no effect when RR = 1. When the CI crosses the vertical line of no effect, we must accept the null hypothesis of no difference between two groups. Only if the CI remains clear of the vertical line of no effect can we reject the null hypothesis.

In our study, the RR for IBS subjects to carry \( Blastocystis \) was 2.336 \( (p = 0.001) \).

doi:10.1371/journal.pone.0111868.g002
However, 3 bacterial groups were shown to be significantly modified in males (Figure 3). Indeed, a significant increase in Lactobacilli was observed in Blastocystis-positive; *: $p < 0.001$ and F. prausnitzii (#): $p = 0.002$ were significantly decreased (Figure 3).

**Discussion**

Various human diseases are associated with an imbalance of bacteria in the gut, termed dysbiosis, and studies reporting changes in microbiota composition among subgroups of patients with IBS are increasing [10,16,17]. Also, intestinal eukaryotic parasites such as Blastocystis or Dientamoeba fragilis have been shown to be more prevalent in patients suffering from IBS [20–25]. However, the role of these parasites in the pathophysiology of IBS is still debated [1,31]. In addition, most of the studies exploring the prevalence of both Blastocystis and D. fragilis in IBS cohorts were conducted in Middle-East, Asia or South-America. Because data from westernized countries were missing, we conducted a prospective study in a French cohort. We recruited 56 IBS patients fulfilling Rome III criteria and 56 control subjects and carried out the detection/quantification of both Blastocystis and D. fragilis by qPCR [36,37]. Although a higher prevalence of Blastocystis was found in IBS patients (23.2% versus 16.1% in the control group), this difference was not statistically significant (Figure 1). We then performed a systematic review of the literature and a meta-analysis including previous epidemiological studies in IBS cohorts. Results from this meta-analysis revealed that infection by Blastocystis occurs 2.34 times more frequently in patients with IBS than in non-IBS subjects ($p < 0.01$, Figure 2). When we compared the prevalence of Blastocystis within male and female subgroups (with or without IBS), we observed that the difference was only significant in the males (36.8% for IBS males versus 4.8% for control males, Figure 1). This result was confirmed by the multivariate analysis. Among the 56 IBS patients, 40 were IBS-C, 9 IBS-D, 4 IBS-M and 3 unclassified-IBS (Table 1). IBS subgroup is an important parameter to take into account when considering parasite prevalence, as it is thought that causes underlying this syndrome could be different as symptoms appear heterogeneous. Using conventional PCR, Yakoob et al. previously reported a higher prevalence of Blastocystis in an IBS-D cohort from Pakistan (44% versus 21% in controls, $p < 0.001$) [23]. In our study, we did not observe any difference in Blastocystis carriage between controls and IBS-D/M/U (Figure 1), but the number of patients in these subgroups was too low (Table 1). Since most patients with IBS were subtyped as IBS-C (71.4%), we decided to focus our attention on the prevalence of Blastocystis within this subgroup. Here again only significant differences in the prevalence of Blastocystis were observed when comparing IBS-C males and control males (41.7% versus 4.8%, respectively, see Figure 1). However, because the detailed descriptions of the cohorts were often lacking in other published studies, the meta-analysis did not confirm this difference in Blastocystis prevalence between men and women suffering from IBS. Thus, we hypothesized that men could be more exposed to the parasite than women (via an environmental reservoir, work, different eating habits ...). Nevertheless, we cannot exclude that men suffering from IBS could be more susceptible to the infection by Blastocystis since this difference was not observed in the control group. This result is intriguing as women are twice as likely to suffer from IBS than men [38]. This gender disparity is not well understood but likely implies physical, hormonal, social and emotional differences [39]. Thus, the discrepancy between IBS sex-ratio and the distribution of Blastocystis in our study remains to be determined.

At least 17 subtypes of Blastocystis have been identified, ST1 to ST9 being recovered from human stools with ST3 as the predominant human ST [1]. Some studies suggested the existence of more virulent STs, including ST1 and ST4 [23,40]. Interestingly, a consistent link between ST1 and IBS-D was identified in a cohort from Pakistan [23]. However, there is no clear evidence between one Blastocystis ST and pathogenicity. Further, in our study, the multivariate analysis did not show any association between ST and IBS. Nevertheless, ST4 appeared to be the most prevalent ST in our study (59.1%, Table 1). This high prevalence of ST4 was comparable to that observed (63%) in a previous study.
we conducted among patients with hematological malignancies [36].

Like Blastocystis, the clinical significance of the intestinal protozoa D. fragilis remains uncertain as it is commonly isolated from both symptomatic and asymptomatic individuals [31], and it is often associated with IBS [23]. In our study, D. fragilis was only detected in some patients with IBS (n=6, Figure 1). Three of the six D. fragilis positive patients were also infected by Blastocystis, confirming the frequently reported occurrence of D. fragilis and fecal-oral transmitted parasites co-infections [1,41].

Gut microbiota modifications reported from IBS subjects primarily associated an increase of Enterobacteriaceae with a decrease of both Lactobacilli and Bifidobacteria [10,16,17]. While no standard pattern has been associated to one subgroup of IBS, it was shown that fecal flora composition in patients with IBS-D significantly diverged from controls but also from other IBS subgroups [42]. Consequently, we focused our analysis on quantification of the gut microbiota in the IBS-C subgroup as it represents the majority of our IBS patients (71.4%). To strengthen statistical analyses, 13 additional control patients positive for Blastocystis were added to the control group and all D. fragilis positive patients were excluded. Eight major bacterial groups as representative of the enteric flora, Enterobacteriaceae, Lactobacillus sp., Bacteroides sp., Bifidobacterium sp., D. fragilis sp., Clostridium cocoides, Clostridium leptum and Faecalibacterium prausnitzii were quantified by qPCR (Table S2). We first considered Blastocystis-negative subjects in both IBS-C and control groups. Our results in IBS-C patients were consistent with those of other studies [43] including a significant increase of Bacteroides sp. while the Enterobacteriaceae were increased in patients with IBS-C, the difference with control subjects was not statistically significant (Table S2). Bifidobacteria, C. leptum group as well as F. prausnitzii were shown to significantly decrease in IBS-C Blastocystis-negative subjects. Chassard et al. recently reported a significant increase of Desulfovibrio in IBS-C patients using a FISH method [44]. Desulfovibrio sp. belongs to the sulphate reducing bacteria (SRB) producing H$_2$S. H2S is known to have various biological effects, and its role in gut homeostasis is still debated [11]. In contrast, we observed that Desulfovibrio sp. was significantly decreased in our IBS-C patients. We hypothesized that this discrepancy may be the result of the different methods used for bacterial quantifications. Indeed, discordances in the detection of Bifidobacteria have been reported whether using qPCR or fluorescent in situ hybridization [43].

The presence of Blastocystis in both IBS-C and control males was associated with a decrease in Bifidobacteria (Figure 3). F. prausnitzii was also significantly reduced in Blastocystis-positive males within the control group (Figure 3). As mentioned previously, F. prausnitzii was significantly decreased in IBS-C Blastocystis-negative subjects. However, we did not observe a supplementary decrease in presence of Blastocystis. We supposed that F. prausnitzii was probably already strongly decreased in the context of IBS thus preventing to see a significant difference between Blastocystis-positive and Blastocystis-negative IBS patients. F. prausnitzii belongs to the group of C. leptum and represents about 5% of the fecal microbiota [45]. A decrease of F. prausnitzii was reported from gastrointestinal disorders such as inflammatory bowel diseases (IBD) and IBS. F. prausnitzii is considered as an indicator of intestinal health since in vitro and in vivo assays demonstrated anti-inflammatory effects of this bacteria [18]. Bifidobacteria are widely used as probiotics for their protective effect due to anti-carcinogenic and immunostimulatory properties [46]. Then, both F. prausnitzii and Bifidobacteria are considered as protective bacteria. Consumption of Bifidobacteria (as probiotic) could induce in return an increase of F. prausnitzii suggesting a putative cross feeding between these bacteria [47]. Their decrease in males in the presence of Blastocystis is rather intriguing and suggests that Blastocystis carriage could be associated with inflammatory environment. One of the key roles of the gut microbiota is to protect against pathogens. We can assume that the modifications we reported may have favoured the establishment of Blastocystis. We recently summarized the hypotheses supporting the association between Blastocystis and IBS [4]. Since genomic data from Blastocystis ST7 reported the presence of genes encoding a polyketide synthase (PKS) and 2 non ribosomal peptide synthase (NRPS), we hypothesized that Blastocystis may have an impact on gut microbiota [4,48]. Indeed, PKS and NRPS are known to produce a variety of highly effective molecules such as antibiotics [49]. Thus Blastocystis may potentially interact with gut microbiota and induce changes in its composition. In their work, Verma et al. also reported a depletion of major microbiota genera after infection by Entamoeba histolytica [50]. In that field, animal models may probably provide crucial informations. Indeed, the use of gnotobiotic animals would enable to evaluate the direct impact of Blastocystis on microbiota composition, or favouring effect of altered microbiota on the establishment of Blastocystis.

In summary, we confirmed in a meta-analysis that Blastocystis is two times more prevalent in IBS patients than in non-IBS subjects. In our study, this concern was only true in males and associated to significant changes in gut microbiota composition with a decrease of some protective bacteria in IBS-C patients. Nevertheless, our results are self-limited by the method we used. Thus, next generation sequencing tools could be more appropriate to explore whole gut microbiota changes associated to the presence of Blastocystis. Even if we cannot conclude whether observed changes in the gut flora were a cause or a consequence of the high prevalence of Blastocystis in IBS patients, our results suggest that Blastocystis may be used as an indicator of microbiota changes.

**Material and Methods**

**Patients and stool samples**

Stool samples from 56 patients suffering from IBS were prospectively collected during medical consultation in the Gastroenterology unit at the teaching hospital of Clermont-Ferrand (France) from January 2012 to July 2013. The clinical study was approved by the research ethics committees of the Clermont-Ferrand Hospital (“Comité de Protection des Personnes Sud‐Est 6”, France) with the reference number 2014/CE29 and which had decided that informed consent from all subjects was not necessary as experiments did not induce additional constraints for patients. IBS diagnosis and symptom-based subgroups of IBS (IBS-C/D/M/U) were established according to the Rome III classification [6]. The control group included 56 patients living in the same geographical area than the group of patients suffering from IBS, and without any history of chronic intestinal disorder nor acute digestive infection at the time of sampling. The stool samples were prospectively collected during the initial systematic screening for digestive colonization with multidrug-resistant bacterial strains. Stool samples from 13 supplementary Blastocystis-positive subjects without any history of chronic intestinal disorder were included in the study for the quantification of bacterial groups in order to increase statistical power. All experiments were performed in accordance with relevant guidelines and regulations.
DNA extraction

Total DNA from 200 mg of each stool sample was extracted using the DNA stool mini kit (Qiagen) according to the manufacturer’s recommendations. DNA extracts were stored at −20°C until PCR or qPCR analyses.

Detection and subotyping of Blastocystis sp.

Specific quantitative PCR (qPCR) to detect and subtype Blastocystis was carried out using BL18SPPF1/BL18SR2PP primers (Table S3) which target a conserved region of the SSU rRNA gene as previously described [36]. PCR products from each positive sample were purified using the Wizard SV Gel and PCR cleanup system (Promega) and sequenced directly (without cloning) by MWG eurofins (Germany) to identify the subtype. In some samples, sequence chromatogram analysis revealed the presence of double traces, suggesting a co-infection by different Blastocystis STs. For these samples, a second PCR was performed to amplify and clone a partial sequence of a rDNA marker from the mitochondria-like organelle genome (MLOsrRNA) (Table S3) as recently described [51]. Briefly, the resulting PCR products were purified, cloned in the pGEM-T easy vector (Promega) and transfected into E. coli DH5α. Five clones of each sample were arbitrarily sequenced by GATC Biotech (Germany). Sequences were analyzed using the Basic Local Alignment Search Tool (BLAST; http://blast.ncbi.nlm.nih.gov/).

Detection of Dientamoeba fragilis

Specific qPCR to detect Dientamoeba fragilis was performed using DF3/DF4 primers and a TaqMan probe (Table S3) based on the sequence of the SSU rRNA gene as previously described [37].

Bacterial quantifications in stool samples

Most of the recruited IBS patients were classified as IBS-C (n = 40/56). As number of patients from IBS-D, IBS-M or IBS-U groups was too low to reach acceptable statistical power, we only considered IBS-C patients for the microbial quantifications. The aim of the study was to analyse changes in bacterial flora associated with the presence of Blastocystis, the 4 IBS-C patients infected with D. fragilis were excluded. Then, qPCR experiments for bacterial quantifications were carried out for the 36 remaining IBS-C patients, including 3 patients infected with Blastocystis. The control group (i.e. without IBS) included the 56 subjects previously described (Table 1) and samples from 13 supplementary Blastocystis positive patients without any history of chronic digestive disorder of a French multicentric study (personal communication). Eight bacterial groups (Enterobacteriaceae, Lactobacillus, Bacteroides, Bifidobacterium, Desulfovibrio, Clostridium cocoides, Clostridium leptum and Faecalibacterium prausnitzii) were quantified by specific qPCR as previously described (see primers and probes in Table S3) [52–56]. Total bacteria were also quantified by qPCR by targeting the gene encoding the 16S rRNA. All qPCR reactions were run in duplicate. Means of Ct of 16S rRNA qPCR were used to normalize bacterial quantifications by using the ΔΔCt methods. Results were expressed as Ln(2^ΔΔCt) for graphical representations.

Statistical analyses

All analyses were performed using the Stata statistical software (version 13, StataCorp, College Station, US). Qualitative data (including “sex” and “PCR +/-”) were expressed in numbers and associated frequencies, whereas quantitative data (“age” and bacterial quantifications) were expressed as mean (and associated standard deviation) according to the statistical distribution. Considering the non-normality distribution of several bacterial quantifications, a log-transformation was proposed. Then, comparisons between independent groups (“IBS patients”/“control subjects”) were performed by Chi-squared or Fisher’s exact tests for qualitative parameters and by Student’s t or Mann-Whitney tests when conditions of the t test were not respected (homoscedasticity studied by the Fisher-Snedecor test and normality by the Shapiro-Wilk test). The multivariate analysis (linear or logistic regression according to statistical distribution of dependent variable) was used to study the interaction “sex”×“IBS group”. P-values of 0.05 or below were considered as significant (two-sided). Due to multiple comparisons, the type-I-error inflation was considered when appropriate. Finally, Comprehensive Meta-analysis (version 2, Biostat Corporation) [57] was used with Stata software to conduct the meta-analytical statistical analysis. Heterogeneity in the study results was evaluated by examining forest plots, confidence intervals and using formal tests for homogeneity based on the I² statistics. Random effects meta-analyses were conducted when data could be pooled. Forest plot graph was presented.

Supporting Information

Table S1 Meta-analysis of prevalence of Blastocystis in both IBS and control subjects.

Table S2 Quantification of bacterial groups.

Table S3 Primer and probe sequences used in qPCR assays.

Acknowledgments

We would like to thank Jonathan Thevenot for providing primers and for its helpful advices in bacterial quantifications.

Author Contributions

Conceived and designed the experiments: CN JS MD PP. Performed the experiments: CN PP CNM IW. Analyzed the data: CN BP PP IW. Contributed reagents/materials/analysis tools: AC EV VL. Wrote the paper: CN PP FD.

References


