Molecular analysis of faecal and duodenal samples reveals significantly higher prevalence and numbers of *Pseudomonas aeruginosa* in irritable bowel syndrome

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INTRODUCTION

Irritable bowel syndrome (IBS) is a gastrointestinal disorder of unknown aetiology characterized by abdominal pain and change in bowel habit. Alteration in faecal microbiota composition and abnormal colonic fermentation imply that gastrointestinal microbiota may play a role in the pathogenesis of IBS (Spiller, 2007; Quigley, 2007). In 7–30% of IBS patients, acute gastrointestinal infection has been proposed as trigger of the onset of IBS symptoms, and the inflammatory response to the infection may cause persistent sensory-motor dysfunction (Madden & Hunter, 2002; Rodriguez & Ruigómez, 1999; Parry et al., 2003; Collins et al., 2001). Moreover, antibiotic therapy and probiotic supplementation have been shown to reduce IBS symptoms in a subset of IBS patients, by either eradication of small intestinal bacterial overgrowth or modulation of the composition of the microbiota (Pimentel et al., 2000; Nobaek et al., 2000; Niedzielin et al., 2001; O’Mahony et al., 2005). Antibiotic therapy may also be a risk factor for developing IBS symptoms due to changes in bowel microbiota and colonization of pathogenic bacteria (Maxwell et al., 2002). It is well recognized that the microbial community is significantly altered in IBS (King et al., 1998; Posserud et al., 2007). Conventional culturing methods have shown that faeces of IBS patients contain higher numbers of facultatively anaerobic bacteria and members of the Enterobacteriaceae and lower numbers of lactobacilli and bifidobacteria than those of healthy subjects (Malinen et al., 2005; Balsari et al., 1982; Madden & Hunter, 2002; Si et al., 2004).

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Detection and identification of gut bacteria by culturing is hampered by the limitations of culture conditions, and a large number of intestinal bacteria cannot be cultured (Mai & Morris, 2004; Furrie, 2006; Suau et al., 1999). Molecular techniques based on 16S rRNA gene analysis allow a more comprehensive assessment of this complex microbial ecosystem (Vaughan et al., 2000). Using PCR-based techniques, a significant difference in the predominant faecal groups has been reported in IBS patients (Malinen et al., 2005; Kassinen et al., 2007). Studies investigating the gut microbiota in IBS using molecular-based methods have been limited to the faecal microbiota and have not assessed mucosa-associated microbiota in the small intestine. The mucosa-associated bacteria are thought to have a stronger interaction than luminal bacteria with the host (Hooper & Gordon, 2001). The composition of luminal and mucosa-associated bacteria is not the same since the micro-environments are very different at the surface of the intestinal epithelium than in the lumen (Zoetendal et al., 2002; Lepage et al., 2005).

The aim of our research was to determine differences in mucosa-associated small intestinal and luminal faecal microbiota between IBS patients and healthy subjects using a molecular approach based on the sequence variability of the 16S rRNA gene.

**METHODS**

**Subjects.** Thirty-seven IBS patients who fulfilled Rome II criteria for IBS were included in this study. The IBS patient group consisted of 13 alternating IBS patients, 13 diarrhea-predominant IBS patients and 11 constipation-predominant IBS patients. Twenty healthy subjects (control group) had neither intestinal complaints nor a history of bowel resection. All subjects had to stop antibiotics at least 1 month before endoscopy. Use of probiotics, proton pump inhibitors and antisecretory medication had to be stopped at least 3 weeks prior to endoscopy. The standard preparation for an upper endoscopy in our hospital is fasting 12 h before the endoscopy. At the request of a subject, Xylocaine spray is used to anaesthetize the throat or a sedative (Dormicum 5 mg) is given. The Human Ethics Committee of the University Medical Centre Utrecht approved the study and all subjects gave written informed consent.

**Sampling, preparation and storage.** A sterile cytology brush (Uno-Brush; Prince Médical) sheathed in a sterile catheter was placed through the endoscope biopsy channel and advanced under direct vision out beyond the endoscope tip (León-Bartía et al., 1993). The duodenal mucosa was brushed three times to obtain mucosa-associated bacteria. Brush samples from each subject were obtained from the descending and horizontal part of the duodenum. After brushing, the brush was pulled back into the sheath of the catheter, which was removed and the brush was immediately cut off the catheter and placed into a sterile tube in liquid nitrogen and stored at −80 °C until analysis.

Faecal samples were collected before the endoscopy and were stored at −80 °C until analysis. Both faecal and brush samples were shipped in dry ice to the microbiological laboratory for analysis.

**DNA extraction and PCR amplification.** Faecal samples were thawed and DNA extraction was performed using the Fast DNA Spin kit (Qbiogene) from approximately 0.1 g faecal material. The frozen brush samples were thawed and suspended in 180 μl ATL buffer (Qiagen) and vigorously vortexed to extract the attached bacteria. Subsequently, DNA was isolated from the mucosa-associated bacteria using the DNeasy Blood & Tissue kit (Qiagen) according to the manufacturer's instructions. The isolated DNA solutions from both faeces and brush samples were stored at −20 °C.

The extracted DNA was used as a template to amplify the V6–V8 regions of the 16S rRNA gene with primers U968-GC-F (5′-CCG GGG GGC GGC CCC CGG GGC GGC GGC GCA CGG GAA CGC GAA GAA CCT TAC-3′), which contains at its 5′-end a 40-base GC clamp, and U1401-r (Muyzer et al., 1993; Muyzer & Smalla, 1998). PCRs were performed using a Taq DNA polymerase kit from Invitrogen. The reaction mixture consisted of 1 × PCR buffer, 3 mM MgCl₂, 50 μM each deoxynucleotide triphosphate, 1.25 U Taq polymerase, 10 pmol each primer and 1 μl appropriately diluted template DNA in a final volume of 50 μl. Samples were amplified in a PTC-200 PCR system (MJ Research) with the following thermocycling program: 94 °C for 5 min; 10 cycles of denaturation at 94 °C for 1 min, annealing at 65–56 °C for 1 min (reduction of 1 °C for each cycle) and extension at 68 °C for 3 min; 33 cycles for faecal and 43 cycles for brush samples of 94 °C for 1 min, 56 °C for 1 min and 68 °C for 3 min. Aliquots of 5 μl PCR product were analysed by electrophoresis on a 1.5 % (w/v) agarose gel containing ethidium bromide (0.04 %, w/v).

**Denaturing gradient gel electrophoresis analysis of PCR amplicons.** PCR amplicons were separated by denaturing gradient gel electrophoresis (DGGE) based on the protocol of Muyzer & Smalla (1998) using the DGGE Decode system (Bio-Rad Laboratories) with the following modifications. Polyacrylamide gels consisted of 8 % (v/v) polyacrylamide (ratio of acrylamide/bisacrylamide, 37.5:1) and 0.5 × Tris/acetate-EDTA (TAE; pH 8.0) buffer. Denaturing acrylamide of 100 % was defined as 7 M urea and 40 % formamide. The polyacrylamide gels were made with a denaturing gradient ranging from 32.5 to 72.5 %. The gels were poured from the top using a gradient maker and a pump (Econo gradient pump; Bio-Rad Laboratories) at a speed of 3 ml min⁻¹. Prior to the polymerization of the denaturing gel (gradient volume, 28 ml), a 7.5 ml stacking gel without denaturing chemicals was added, and the appropriate comb was subsequently inserted. Electrophoresis was performed first for 5 min at 200 V and then at 80 V for 17 h in 0.5 × TAE buffer at a constant temperature of 60 °C. The gels were stained with AgNO₃ as described by Sanguinetti et al. (1994) and dried overnight at 50 °C.

**Analysis of the DGGE profiles and generation of pooled profiles.** The average curve feature 'show average curve' of GelCompar software (Applied Maths) was used to create averaged fingerprints. This script generates an averaged fingerprint using the densitometric and location results from the bands in the original gels. The intensity of the band in the average IBS patient or healthy subject profile is calculated by the intensity of the original bands in the average gels from the IBS patient samples we created the healthy subject samples we created the healthy subject profiles. Percentage similarity between the averaged IBS profile and the averaged healthy subject profile is based on the number of identical bands and the numeric values of the band intensity (with 5 % background subtraction) found in the two profiles. Similar band positions are removed, generating a graph with unique bands for healthy subjects and unique bands for IBS patients. Band differences in these average computer-generated profiles were determined and the bands which were unique for either group were localized in the individual original DGGE profiles. The most intense bands in the individual profiles were cut from the original gels. The DNA from

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Fig. 1. DGGE analysis of the duodenal mucosa-associated and faecal bacteria. No evident clusters were shown in the clustering tree of the silver-stained DGGE gel of the V6–V8 regions of the 16S rRNA gene, obtained from duodenal samples (a) and faecal samples (b) of 20 healthy subjects (HS), 11 diarrhoea-predominant IBS patients (IBS-D), 13 alternating IBS patients (IBS-C).
(IBS-A) and 10 constipation-predominant IBS patients (IBS-C). Dendrograms based on the DGGE gel for each individual were generated by using the Pearson correlation index for each pair of lanes within a gel and were used as a measure of similarity between the fingerprints. The scale bar indicates the DGGE similarity between profiles. The clustering of patterns was calculated using the unweighted-pair group method using average linkages.
these bands was used for a second DGGE analysis using a 46–51.6 %
gradient. Bands of interest were subjected to sequencing as described
below.

**DGGE band sequence analysis.** To identify the bacteria, a small
piece from the middle of the selected band was cut from the DGGE
gel with a sterile scalpel and then incubated in 50 μl sterile MilliQ
water for 24 h at 4 °C to allow diffusion. The eluent containing DNA
fragments was used for PCR reamplification with the same primers
used earlier. To check whether the DNA of interest on the first DGGE
gel and the reamplified DNA migrated to the same position, we
carried out a second DGGE in order to compare the two samples.
When the two bands co-migrated, DNA fragments were purified with the
GenElute PCR DNA Purification kit (Sigma) and thereafter
ligated into the pCR2.1-TOPO vector and transformed into
Escherichia coli One Shot TOP10 competent cells (Invitrogen).
Plasmids from colonies of kanamycin-resistant transformants were
extracted with the Qiagen Plasmid Midi Purification kit. The
plasmids were screened for inserts of the correct size by
performing a PCR with the M13 forward and reverse primers as well
as with the 968f and 1401r primers. Insert PCR amplicons of selected
transformants were purified and subjected to DNA sequence analysis
(Baseclear). Sequence similarities of the clones were checked with the
Basic Local Alignment Search Tool (BLAST) at the NCBI database

**Quantitative real-time PCR analysis.** Quantitative real-time PCR
(q-PCR) was performed to determine the percentage of Pseudomonas
aeruginosa in brush and faecal samples. Measurement of P. aeruginosa
was performed as described by Pirnay et al. (2000) with some slight
modifications. The detection limit of the assay was 10³ c.f.u. g⁻¹
and 1–10 c.f.u. per reaction (Pirnay et al., 2000). The fluorescent labels
were changed from LC Red 640 to 6FAM and from fluorescein to TAMRA
while the other ingredients and conditions for the described q-PCR
stayed the same. The fluorescence signal was measured in the annealing
phase on the ABI 7900HT Fast system (Applied Biosystems). The total
bacterial load was determined as described by Nadkarni et al. (2002).
The relative percentage of P. aeruginosa was subsequently calculated
according to Liu & Saint (2002a, b). The efficiency of each
amplification curve was calculated separately and used to determine
the initial relative amounts of DNA. The amount used was in general
between 100 and 200 ng DNA per reaction. Finally, the obtained ratios
between the initial amounts of DNA were normalized against a
monoculture of the same species, which was set at 100 %.

**Statistical analysis.** DGGE data were analysed by GelCompar II
software (Applied Maths). Cluster analysis and calculation of the
similarity indices between the different banding patterns were
performed using Pearson product-moment correlation and the
unweighted-pair group method using arithmetic averages.

P. aeruginosa levels in IBS patients and healthy subjects were analysed
using independent samples t-test. P. aeruginosa levels in IBS
subgroups were analysed using one-way ANOVA with Bonferroni
correction. Data are expressed as mean ± SEM. SPSS 12.0.1 for Windows
was used for analysis.

**RESULTS**

**Study population**

Healthy subjects (5 men, 15 women) were significantly
(P=0.005) younger (32 ± 2.6 years) than the IBS patients
(11 men, 26 women; 42 ± 2.3 years). No differences
between both groups in gender distribution were observed.

**Bacterial diversity of the dominant microbiota as assessed by DGGE**

DGGE analysis of the PCR-amplified fragments of the V6–
V8 region of the 16S rRNA gene of both duodenal mucosa-
associated bacteria (Fig. 1a) and faecal bacteria (Fig. 1b)
from IBS patients and healthy subjects was performed,
showing no evident clusters between healthy subjects and
IBS subgroup patients. Comparing the fingerprints of
faecal and small intestinal samples for all subjects, a clear
clustering was observed independently from the disease
state (data not shown), indicating that the mucosa-
associated microbiota is significantly different from the
faecal microbiota, as also observed in a previous study
(Zoetendal et al., 2002). Based on the DGGE profiles, no
clear difference between the IBS patients and healthy
subjects could be detected for the most abundant micro-
bacteria at any sampling location. Moreover, statistical analysis
of the DGGE profiles from both sampling sites (duodenal
brush and faecal samples) did not reveal any specific core
microbiota that could be distinguished between healthy
subjects, IBS patients or IBS subgroup patients. However,
some subclusters could be identified, suggesting overlap
of specific microbial components. To identify possible micro-
bacterial components specifically associated with healthy
subjects or with IBS patients, the DGGE profiles generated from
all IBS patients and those from healthy subjects were pooled
in average profiles (Figs 2 and 3).

Comparing the generated average duodenal fingerprints of
healthy subjects and IBS patients, 14 (78.2 %) of the bands
were identical for both groups, 6 bands were specific for IBS
patients (10 % of all IBS bands) while 27 bands were
specific for healthy subjects (34 % of all healthy subject
bands) (see Fig. 2). The band location and intensity in the
average profiles were used to generate Fig. 2.

Fig. 3 shows the average faecal fingerprints of both groups,
in which 21 (86.25 %) of the bands were identical, 33 bands
were confined to healthy subjects (21 % of all healthy subject
bands) and 17 bands were confined to IBS patients
(10 % of all IBS bands). The DGGE band fragments that
were of interest were further characterized by sequence
analysis.

**Sequence analysis of the dominant microbiota**

The 16S rRNA genes from the isolated bands from the
DGGE profiles of faecal and duodenal samples from the
healthy subjects and IBS patients were amplified and
cloned in E. coli. The V6–V8 region of the cloned 16S
rRNA gene fragments from the cell lysates of transformants
was amplified. In this way, 51 clones were generated, the
plasmid DNA from the corresponding clones was purified
and, subsequently, the nucleotide sequence inserts were
determined and compared to the 16S rRNA databases
using the BLAST tool (Zhang et al., 2000). From the
duodenal samples, a total of 19 clones, comprising 15
clones recovered from 4 unique bands from the IBS
patients and 4 clones from 1 unique band from the healthy subjects, were generated. A total of 32 clones retrieved from faecal samples, comprising 24 clones from 3 unique bands from IBS patients and 8 clones from 1 unique band from healthy subjects, were obtained.

Among the 51 sequenced clones retrieved from both groups, 35 shared 95 % or less 16S rRNA sequence identity with their nearest relatives based on a BLAST search. This indicated that the majority of the sequences were derived from new, as yet undescribed, phylotypes. Most cloned sequences retrieved from the IBS patients could be assigned to the class Gammaproteobacteria mainly to Pseudomonas species, and other clones retrieved essentially from the faecal samples were assigned to Clostridium nexile. However, in the healthy subjects, the cloned sequences were allocated to the two major phylotypes commonly encountered in human faecal clone libraries, namely Clostridium cluster XIVa and Bacteroidetes.

Brush samples. Out of the 15 clones retrieved from the brush samples from IBS patients, seven cloned sequences were affiliated with different Pseudomonas species with a sequence similarity ranging from 94 to 99 %. Remarkably, one cloned sequence was almost identical to P. aeruginosa (99 % sequence similarity). Three clones were closely related to Klebsiella pneumonieae with 96–97 % sequence similarity, one clone was almost identical to Oribacterium sinus (99 % sequence similarity) and there were two new phylotypes (90–96 % sequence similarity to an uncultured bacterium clone, rc2-18, isolated from rat faeces; Brooks et al., 2003). In addition, one clone showed 96 % sequence similarity with an uncultured Neisseria sp. clone isolated from P. aeruginosa-colonized patients (Flanagan et al., 2007) and shared only 91 % similarity with the closest cultured relative, i.e. Kingella kingae strain ATCC 23330. Another clone was related to uncultured Neisseria sp. clone 101C07 isolated from the oral cavity with only 91 % sequence similarity.

The four cloned sequences obtained from the healthy subjects were identified as Serratia sp., Acinetobacter sp., Pantoea sp. and an uncultured Clostridiales bacterium with 99, 98, 91 and 95 % sequence similarity, respectively.

Faecal samples. Out of the 24 clones retrieved from faecal samples from IBS patients, 11 cloned sequences were affiliated with different Pseudomonas species with a sequence similarity ranging from 85 to 100 %. Noticeably, one cloned sequence showed a perfect match with P. aeruginosa and three other sequences shared 88–95 % similarity with the same species. Furthermore, eight clones were affiliated with different Clostridium species. Among these, six clones were closely related to C. nexile with sequence similarity varying from 93 to 97 %, and two clones were identified as Clostridium sp. with sequence similarity varying from 92 % to 96 %. One clone was identified as Desulfovibrio vulgaris (98 % similarity), and one clone was related to an uncultured faecal bacterium clone isolated by Li et al. (2008) with 94 % sequence similarity. In addition, two clones shared only 92 % and 91 % sequence similarity with Burkholderia mallei and finally one cloned sequence was related to Alcaligenes faecalis with 92 % sequence similarity.

Out of the eight clones from the faecal samples from healthy subjects, five cloned sequences were affiliated with different Bacteroides species with a sequence similarity ranging from 95 to 99 %, with the closest culturable species being Bacteroides ovatus (97 % sequence similarity), Bacteroides vulgatus (96 % sequence similarity) and Bacteroides coprophilus (99 % sequence similarity). Furthermore, one clone was almost identical to Prevotella corporis (99 % sequence similarity), one clone shared 95 % sequence similarity with Prevotella aurorium and one clone shared 97 % sequence similarity with Clostridium butyricum.

Quantification of P. aeruginosa using real-time PCR

Since the majority of IBS unique bands belonged to the genus Pseudomonas, of which P. aeruginosa was the most frequently identified species, real-time PCR was used to quantify P. aeruginosa in the brush and faecal samples. The data in Fig. 4(a) show that the relative abundance of P. aeruginosa (% of total bacterial load) was significantly (P<0.001) higher in IBS patients (8.3 % ± 0.950) than in healthy subjects (0.1 % ± 0.069). The Ct value of the positive controls, negative control (water), all IBS patients and healthy controls was <22, >45, 30.4 (SEM 0.84) and 36.6 (SEM 0.83), respectively. Moreover, the prevalence of P. aeruginosa in the duodenal samples was 97.3 % in IBS patients and only 40 % in healthy subjects.

The results illustrated in Fig. 4(b) reveal that the percentage of P. aeruginosa in faecal samples was also significantly higher (P<0.001) in IBS patients (2.34 % ± 0.31) than in healthy subjects (0.003 % ± 0.0027). We also found that P. aeruginosa was detected in 97.2 % of the faecal samples from IBS patients whereas only 15.8 % of the healthy subjects were positive carriers of P. aeruginosa. No differences related to the abundance and prevalence of P. aeruginosa between IBS subgroups were detected in both sampling sites.

DISCUSSION

This study shows clearly that, analysing the entire faecal and small intestinal microbiota population using DGGE, there are specific DGGE bands for healthy subjects and specific bands for IBS patients. Focusuing on the specific bands showed that most clones belonged to the genus Pseudomonas, of which P. aeruginosa was the predominant species. The most important finding of this study is the higher prevalence and levels of P. aeruginosa
in small intestinal and faecal samples from IBS patients than in those from healthy subjects, analysed by q-PCR.

Previously, Kassinen et al. (2007) also showed distinct microbiota based on their mol% G+C fractions in faecal samples from IBS subtypes and from controls using molecular tools. After faecal microbial genomes of IBS subtypes and controls were pooled, differences in the *Firmicutes*, *Bacteroidetes*, *Actinobacteria* and *Proteobacteria* were shown (Kassinen et al., 2007). Our sequence analysis data showed that members of the *Proteobacteria* and *Firmicutes* were specific for IBS patients. *Pseudomonas* sp. was the most prevalent and q-PCR analysis showed a higher prevalence and levels of *P. aeruginosa* in small intestinal mucosa-associated and faecal samples from IBS patients than in those from healthy subjects.

*P. aeruginosa*, a Gram-negative aerobic rod, is known to predominantly infect immunosuppressed and cystic fibrosis patients (Oliver et al., 2000; Fichtenbaum et al., 1994; Baron & Hollander, 1993). The 15.8% prevalence of *P. aeruginosa* in faecal samples from healthy subjects in this study is within the range of 0–24% reported in other studies (Bonten et al., 1999; Speert et al., 1993; Kessner & Lepper, 1967; Bleday et al., 1993; Levy, 2000). Higher prevalence (97%) and levels of *P. aeruginosa* in IBS patients have not been reported in the literature to our knowledge. However, in functional dyspepsia patients, *Pseudomonas* was cultured as the predominant bacterium in the small intestine (León-Barúa et al., 1993). Previous studies using molecular-based methods to determine the quantity of faecal microbiota in IBS patients and healthy subjects showed differences in microbiota composition (Kassinen et al., 2007; Malinen et al., 2005). However, *P. aeruginosa* levels were not tested in these studies.

The age differences between the healthy subjects and IBS patients in our study might be a confounding factor. The effect of the age difference between healthy subjects (mean age 32 years) and IBS patients (mean age 42 years) on bacterial DNA load, prevalence and quantity of *P. aeruginosa* is not known. Current literature does describe change in faecal microbiota composition in subjects older
than 65 years of age compared to younger adults (Hopkins & Macfarlane, 2002; Woodmansey et al., 2004; Mueller et al., 2006). To evaluate the effect of age difference in adult subjects on microbiota composition, further investigations are needed.

The question arises whether differences in prevalence and quantity of *P. aeruginosa* might be epiphenomenal or be the cause of IBS symptoms. First of all, it is known that *P. aeruginosa* may occur as the sole potential pathogen in patients with diarrhoea and *P. aeruginosa* induces signs and symptoms of enteritis in antibiotic-treated rats (Adlard et al., 1998). Also, a causative relationship between *P. aeruginosa* and diarrhoea has been found in immuno-compromised individuals (Adlard et al., 1998). However, in our study, *P. aeruginosa* was increased not only in diarrhoea-predominant IBS patients, but also in constipation-predominant and alternating IBS patients.

Secondly, proteases of *P. aeruginosa* are known to disable protease-activated receptor-2 (PAR-2) in the respiratory tract (Dulon et al., 2005). The effect of *P. aeruginosa* proteases on PAR-2 in the gastrointestinal tract is unknown. PAR-2 activation in the gastrointestinal tract has been shown to modify motility patterns, inflammatory mediator release, intestinal barrier integrity, ion transport and nociceptive functions, all functions which are part of gut physiology involved in generation of IBS symptoms (Vergnolle, 2005).

Indication that increased *P. aeruginosa* might be epiphenomenal is reported in a recent study which showed high levels of *Pseudomonas* species in pouchitis patients in remission. If the normal microbiota of the gastrointestinal tract is altered, potential pathogens can colonize or resident pathogens can multiply. The remission of the pouchitis patients was induced by antibiotic therapy (Kühbacher et al., 2006). It has been shown that antibiotic treatment of mice increases the colonization potential of *Pseudomonas* species (George et al., 1989). *P. aeruginosa* is naturally resistant to many antibiotics due to the permeability barrier of its outer membrane lipopolysaccharide, tendency to colonize surfaces in a biofilm form and maintenance of antibiotic-resistance plasmids (Mah et al., 2003; Walters et al., 2003; Masuda et al., 1999; Livermore, 1992). Antibiotics and probiotics used more than a month before the start of the study are unlikely to have had an effect on the *P. aeruginosa* colonization since stabilization of the intestinal microbiota within 1–2 weeks after antibiotic therapy has been reported (Woodmansey et al., 2004; Edlund & Nord, 2000; Hentges et al., 1985; Levison, 1973; Gorbach et al., 1988).

In a previous study, we showed a lower *Bifidobacterium catenulatum* level in both faecal and duodenal brush samples from IBS patients than in those from healthy subjects (Kerckhoffs et al., 2009). This decrease in normal microbiota might give *P. aeruginosa* the opportunity to multiply. A major obstacle in relating microbial composition with a role in IBS pathophysiology is the fact that each individual is inhabited by a specific microbial community shaped by host and environmental factors (Eckburg et al., 2005).

In conclusion, our data show no apparent difference in the diversity of predominant microbiota profiles between IBS patients and healthy subjects. However, using the pooled average profiles of the PCR-DGGE fingerprints allowed us to isolate and sequence specific bands from IBS patients and healthy subjects. IBS-specific bands were predominantly members of the genus *Pseudomonas*. q-PCR analysis confirmed that *P. aeruginosa* is found more frequently and in higher levels in IBS patients than in healthy subjects. Therefore, we propose that *P. aeruginosa* may be involved in the pathophysiology of IBS.

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