Diversity of caecal bacteria is altered in interleukin-10 gene-deficient mice before and after colitis onset and when fed polyunsaturated fatty acids

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Interleukin-10 gene-deficient (Il10−/−) mice show a hyper-reaction to normal intestinal bacteria and develop spontaneous colitis similar to that of human Crohn’s disease when raised under conventional (but not germ-free) conditions. The lack of IL10 protein in these mice leads to changes in intestinal metabolic and signalling processes. The first aim of this study was to identify changes in the bacterial community of the caeca at 7 weeks of age (preclinical colitis) and at 12 weeks of age (when clinical signs of colitis are present), and establish if there were any changes that could be associated with the mouse genotype. We have previously shown that dietary n-3 and n-6 polyunsaturated fatty acids (PUFA) have anti-inflammatory effects and affect colonic gene expression profiles in Il10−/− mice; therefore, we also aimed to test the effect of the n-3 PUFA eicosapentaenoic acid (EPA) and the n-6 PUFA arachidonic acid (AA) on the bacterial community of caeca in both Il10−/− and C57 mice fed these diets. The lower number of caecal bacteria observed before colitis (7 weeks of age) in Il10−/− compared to C57 mice suggests differences in the intestinal bacteria that might be associated with the genotype, and this could contribute to the development of colitis in this mouse model. The number and diversity of caecal bacteria increased after the onset of colitis (12 weeks of age). The increase in caecal Escherichia coli numbers in both inflamed Il10−/− and healthy C57 mice might be attributed to the dietary PUFA (especially dietary AA), and thus not be a cause of colitis development. A possible protective effect of E. coli mediated by PUFA supplementation and associated changes in the bacterial environment could be a subject for further investigation to define the mode of action of PUFA in colitis.

INTRODUCTION

The interactions between intestinal bacteria and the mucosal immune system of a genetically susceptible host are important in the development of inflammatory bowel disease (IBD) such as Crohn’s disease (CD). There is evidence that an abnormal mucosal immune response to common intestinal bacteria underlies the mucosal inflammation in this disease in humans (Strober et al., 2007). Both human clinical studies and animal studies have shown differences in the bacterial communities of the intestine between disease and control subjects, which suggest the involvement of luminal bacteria and bacterial products in the initiation and progression of intestinal inflammation (Mangin et al., 2004; Bibiloni et al., 2005). Antibiotic
treatment decreased concentrations of intestinal bacteria and attenuated colitis in CD patients (Colombel et al., 1997; Gui et al., 1997) and in the Il10<sup>−/−</sup> mouse model of IBD (Madsen et al., 2000). Colonization studies with germ-free rodent models have also indicated that enteric bacteria vary in their ability to induce colitis and interact specifically with genetically susceptible hosts (Rath et al., 1999; Waidmann et al., 2003; Kim et al., 2005). Probiotic bacteria, such as Lactobacillus spp., were able to prevent colitis in Il10<sup>−/−</sup> mice (Madsen et al., 2000). Enterococcus spp. are common intestinal bacteria in healthy humans and animals (Jett et al., 1994; Sellon et al., 1998), but Enterococcus spp., especially Enterococcus faecalis, have been shown to induce intestinal inflammation in germ-free Il10<sup>−/−</sup> mice (Balish & Warner, 2002; Kim et al., 2005, 2007). Il10<sup>−/−</sup> mice carrying a null mutation in the gene that normally codes for the anti-inflammatory cytokine IL10 show a hyper-reaction to normal intestinal bacteria (loss of tolerance) and develop intestinal inflammation, unlike their wild-type counterparts (Kim et al., 2005). Intestinal inflammation does not occur when Il10<sup>−/−</sup> mice are born and maintained in germ-free conditions (Kim et al., 2005), but develops from 20 weeks of age in Il10<sup>−/−</sup> mice housed in specific pathogen free (SPF) conditions (McCarthy et al., 2003). These findings are supported by in vitro evidence that IL10, produced by T regulatory lymphocytes, is effective in controlling tolerance to commensal bacteria (Izcue et al., 2006).

Effects of dietary lipids on gastrointestinal bacteria have only been reported in a few human studies investigating faecal bacteria (Cummins et al., 1978; Endo et al., 1991; Eastwood & Allgood, 1995; Farnworth et al., 2007). To our knowledge there have been no studies on the potential effects of dietary lipids such as polyunsaturated fatty acids (PUFA) on the bacterial profiles of the caeca of inflamed Il10<sup>−/−</sup> mice. Anti-inflammatory actions of the n-3 PUFA eicosapentaenoic acid (EPA) have mainly been attributed to the substitution of arachidonic acid (AA) in cell membranes, which results in the decreased production of AA-derived pro-inflammatory eicosanoids (Calder, 2006). Long-chain PUFA also show antibiotic-like and growth inhibitory actions against pathogenic bacteria and can enhance the beneficial actions of probiotics, e.g. Lactobacillus spp., on the mucosal surface and aid probiotics in colonizing the gastrointestinal tract (Das, 2002).

Since the lack of IL10 protein leads to significant changes in metabolic and signalling processes in the colon of Il10<sup>−/−</sup> mice (Knoch et al., 2010a), the first aim of this study was to examine changes in the bacterial community of the caecum at 7 weeks of age (preclinical colitis) and 12 weeks of age (when clinical signs of colitis are present) that may be associated with the mouse genotype. As we previously showed that dietary n-3 and n-6 PUFA exerted anti-inflammatory effects and affected colonic gene expression profiles in Il10<sup>−/−</sup> mice (Knoch et al., 2009, 2010b), we aimed to test the effect of dietary n-3 EPA and n-6 AA on the bacterial community of the caecum as a function of the host genotype.

**METHODS**

**Animal experiments.** The studies were approved by the AgResearch Ruakura Animal Ethics Committee in Hamilton, New Zealand, according to the Animal Protection Act (1960) and the Animal Protection Regulations (1987) and Amendments; animal ethics application nos. 10642 and 10587. The experimental design of study 1 (time-course; Knoch et al., 2010a) and study 2 (PUFA intervention; Knoch et al., 2009, 2010b) has been previously described. Briefly, male Il10<sup>−/−</sup> mice (C57BL/6J background, formal designation B6.129P2-Il10<sup>−/−</sup>; Il10<sup>−/−</sup>tm1Cgn/J) raised under SPF conditions (Park et al., 1997). In study 1, five or six mice were euthanized at 7, 8.5, 10, 12 and 14 weeks of age. Histological signs of colitis were assessed at all time points as described by Knoch et al. (2010a). The two time points used for gene and protein expression profiling (Knoch et al., 2010a) were also selected for profiling the bacterial community of the caeca; these were based on histopathological assessment to obtain groups of individuals with no (7 weeks of age) or severe (12 weeks of age) colitis: Il10<sup>−/−</sup> mice 7 weeks of age (three mice), Il10<sup>−/−</sup> mice 12 weeks of age (four mice), C57 mice 7 weeks of age (four mice) and C57 mice 12 weeks of age (four mice). One 7-week-old Il10<sup>−/−</sup> mouse died of unknown causes and two others showed moderate colitis; these mice were excluded from the analysis. In study 2, four to six Il10<sup>−/−</sup> and C57 mice were euthanized at 11 weeks of age. This time was selected based on study 1, where all bacterially inoculated Il10<sup>−/−</sup> mice developed colitis. One Il10<sup>−/−</sup> mouse in the OA diet group and two Il10<sup>−/−</sup> mice in the EPA diet group died of unknown causes. One caecal sample of C57 mice on the AIN-76A diet, OA, EPA or AA diet and one sample of an Il10<sup>−/−</sup> mouse on the AA diet were excluded because of degraded bacterial DNA. From each group, caeca including the digesta were snap-frozen in liquid nitrogen and stored at −80°C until analyses were carried out.

**Molecular analysis of caecal bacteria.** Bacterial genomic DNA from frozen caecal samples (caecum and digesta) was isolated using a QIAamp DNA Stool mini kit (Qiagen) according to manufacturer’s instructions. The extracted DNA was used as a template in PCRs, using the HDAl-GC (GC-clamp) and HDAl universal primers to amplify the variable V2–V3 regions of the bacterial 16S rRNA genes (Tannock et al., 2000). PCR amplifications were performed using a GeneAmp PCR System 9700 thermal cycler (Applied Biosystems). The PCR products, 200 bp in length, were checked on 2% agarose gels before performing denaturing gradient gel electrophoresis (DGGE), which has been described previously (Nones et al., 2009).
Digital images of the DGGE gels were analysed to detect DNA bands using the band-searching algorithm of BioNumerics software (Applied Maths). After normalization of the gels relative to the control sample, differences and similarities between the profiles within the same gel were analysed for the presence and absence of bands using the unweighted pair-group method of arithmetic averages (UPGMA) with the Dice similarity coefficient ($D_{sc}$). The position tolerance was set to 3% for all analyses.

For sequence analysis, DGGE bands were excised from the gel matrix and eluted in sterile water at 4°C overnight. After reamplification with the HDA1/2 primers, the amplicons were purified using the QIAquick PCR purification kit (Qiagen) according to the manufacturer’s instructions, cloned into the plasmid vector pCR 2.1 and transformed into Escherichia coli TOP10 competent cells using the TOPO-TA cloning system (Invitrogen) according to the manufacturer’s instructions. After reamplification with the HDA1-GC/HDA2 primers, the position of the clone-band in a DGGE gel was compared with the original gel band. Clones that migrated to the same position as the original band were sequenced using the vector-specific M13 forward primer (5' - CCCAGTCAC-GACGTGGTAAAAGC-3') at the Allan Wilson Centre Genome Service at Massey University, Palmerston North, New Zealand. The sequences were compared against 16S rRNA gene sequences available from the online database of the NCBI to identify the most closely related bacterial species.

**Real-time PCR quantification of total bacteria and selected bacterial groups.** The primers used in the real-time quantification of total bacteria, Bacteroides–Prevotella–Porphyromonas spp., Enterococcus spp., Clostridium perfringens, E. coli and Bacteroides vulgatus, using the caecal DNA from Il10–/– and C57 mice, are listed in Table 1. The bacterial strains used for standard curves were as follows: E. coli ATCC 35150, Bacteroides fragilis NZRM 964, Ent. faecalis AGR 991, C. perfringens ATCC 13124 and Lactobacillus reuteri DPC 16. B. vulgatus DSM 1447 was used in a species-specific PCR. All bacterial strains were grown anaerobically overnight at 37°C. Tryptone Soy Broth (Oxoid) was used for growth of E. coli, de Man–Rogosa–Sharpe (MRS) broth (Oxoid) for L. reuteri, Todd–Hevitt broth (Oxoid) for Ent. faecalis; and Brain Heart Infusion broth (Oxoid) for B. fragilis, B. vulgatus and C. perfringens. Bacterial cells were counted using a Neubauer haemocytometer after 18 h incubation.

The standard curves were prepared using a 10-fold dilution series (1 x 10^4 to 1 x 10^9 c.f.u. ml⁻¹) of genomic DNA extracted from each bacterial reference strain. The real-time quantitative PCR (qPCR) analysis was carried out in triplicate on a LightCycler 480 instrument (Roche Diagnostics), as described by Nones et al. (2009), using LightCycler 480 SYBR Green I Master Mix (Roche Diagnostics). PCR amplicons were checked on 1% agarose gels. The interpretations of the bacterial quantities were based on the assumption that the analysed community represented a similar mean number of 16S rRNA gene copies per bacterial cell. The qPCR results (number of cells per g wet caecum content) were log-transformed, and statistical analysis was performed using two-way ANOVA, followed by the least-significant-difference post hoc test in GenStat (11th edition, VSN International). $P<0.05$ was considered significant. All caecal samples were also tested for the presence of Helicobacter spp. by conventional PCR using primers H267F/H676R (5'-CTATG-ACGGGTATCCGAGC-3' / R 1996) and HotStarTaq DNA polymerase (Qiagen), as described by Nones et al. (2009). PCR amplicons were checked on 2% agarose gels.

## RESULTS

**DGGE profiles of murine caecum before and after onset of colitis**

Global bacterial changes in the caecum of 7- and 12-week-old mice were monitored using DGGE. Individual Il10–/– or C57 mice in both age groups showed similar profiles for the predominant DNA fragments, while more variation was seen for the less dominant DNA fragments. To support these observations, a similarity matrix analysis was conducted, using the $D_{sc}$ for the DGGE profiles of individual mice at 7 and 12 weeks of age (Fig. 1, Table 2). This analysis showed similarities (81.4–91.0%) in DGGE profiles between individual mice within each age group and also within each mouse genotype. The profiles of the 7- and 12-week-old Il10–/– mice were more similar (81.4% and 82%, respectively) than the profiles of the 7- and 12-week-old C57 mice (86% and 91%, respectively). At 7 weeks of age, the profiles of the Il10–/– mice were more

### Table 1. Primers used for bacterial quantification by real-time PCR

<table>
<thead>
<tr>
<th>Bacterial group</th>
<th>Primers (5’–3’)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total bacteria</td>
<td>ACTCCTACGGGAGGCGACGAGT</td>
<td>Tannock et al. (2000)</td>
</tr>
<tr>
<td></td>
<td>GTATTACGGCCGCTGCTGCGC</td>
<td></td>
</tr>
<tr>
<td>Porphyromonas spp.</td>
<td>CGCA(C/T)GAAGGGCGCGTGC</td>
<td>Rinttilä et al. (2004)</td>
</tr>
<tr>
<td>Enterococcus spp.</td>
<td>CTTTATTTGTGATGTTGCACTATTT</td>
<td>Rinttilä et al. (2004)</td>
</tr>
<tr>
<td>Clostridium perfringens</td>
<td>ATGCAAGTCGAGGAG(C/T)G</td>
<td>Rinttilä et al. (2004)</td>
</tr>
<tr>
<td></td>
<td>TATCCGAGTAATACTT(C/T)CTTT</td>
<td></td>
</tr>
<tr>
<td>Escherichia coli</td>
<td>CATGCCGGGTGTTGAGAAGA</td>
<td>Huijsdens et al. (2002)</td>
</tr>
<tr>
<td>Bacteroides vulgatus</td>
<td>CGGTTACGTCATAGGCGAA</td>
<td>Wang et al. (1996)</td>
</tr>
<tr>
<td></td>
<td>GCCGATCGGTCGCTGCTGCT</td>
<td></td>
</tr>
<tr>
<td></td>
<td>TCCATACGGCCTTATTCCCT</td>
<td></td>
</tr>
</tbody>
</table>
similar to those of the C57 mice (81.4 % and 86 %, respectively) than when they were at 12 weeks of age (82 % and 91 %, respectively).

When excised, purified and sequenced, the closest sequence match in BLAST of bands 1–6 and 9–16 from the DGGE profiles of 7- and 12-week-old Il10−/− and C57 mice was to uncultured strains (Fig. 1, Table 3). Bands 7 and 8 from the caecal profiles of 7- and 12-week-old immunocompetent non-inflamed C57 mice were identified as Helicobacter pullorum (GenBank accession FJ236465, 99–100 % identity). This particular species appeared to be mostly absent in the Il10−/− mice. This suggests that this species could belong to the resident murine microflora in control mice, as observed in the stools of healthy subjects (Ceelen et al., 2006). As it has been shown that Helicobacter spp. can induce intestinal inflammation (Burnens et al., 1994; Fox et al., 1999; Varon et al., 2009) the bacterial DNA isolated from the caecum of all Il10−/− and C57 mice was tested for the presence of Helicobacter spp. by genus-specific conventional PCR (data not shown). As expected, the result was positive for all mice. Whether H. pullorum or other Helicobacter spp. play a role in inducing colitis in the conventional Il10−/− mice requires further investigation.

Real-time PCR quantification of bacterial groups found in murine caecum before and after onset of colitis

Cell numbers of total bacteria, Bacteroides–Prevotella–Porphyromonas and Enterococcus spp. were determined by real-time PCR in 7- and 12-week-old Il10−/− and C57 mice (Fig. 2). The total number of bacteria was higher in the caecum of 12-week-old Il10−/− mice compared to 7-week-old Il10−/− mice (P=0.008), and was lower in 7-week-old Il10−/− mice compared to 7-week-old C57 mice (P<0.001). At 12 weeks of age, the total bacterial number was higher in the caecum of C57 compared to Il10−/− mice (P=0.02) (Fig. 2a). The bacterial cell number of the Bacteroides–Prevotella–Porphyromonas spp. was higher in 7-week-old C57 mice compared to Il10−/− mice at the same age (P=0.003). An increase in the cell number of Bacteroides–Prevotella–Porphyromonas spp. was also observed from 7 weeks to 12 weeks of age in the caecum of Il10−/− mice (P=0.05) (Fig. 2b). While there was an increase in the total bacterial cell number from 7 weeks to 12 weeks of age in Il10−/− mice, the cell number of Enterococcus spp. decreased from 7 weeks to 12 weeks of age in the caecum of Il10−/− mice (P=0.001). More Enterococcus spp. cells were present in Il10−/− mice compared to C57 mice at 7 weeks (P=0.0005) and 12 weeks (P=0.03) of age (Fig. 2c).

DGGE profiles of murine caecum in response to dietary PUFA

Global bacterial changes in the caecum of mice fed n-3 and n-6 PUFA diets monitored with DGGE are shown in Fig. 3, and the Dsc values from the similarity analysis of the DGGE profiles within dietary groups are listed in Table 2. The similarity analysis showed that caecal profiles of individual Il10−/− mice fed the EPA diet were less similar (67.5 %) to each other than were the profiles between individual mice.
in the other dietary groups (79.3–87.0%). Changes were observed in the individual DGGE profiles that seem to be associated not only with the mouse genotype but also with dietary PUFA. The DGGE profiles of \(10^{15} \) mice on the AIN-76A, EPA and OA diets showed a lower number and diversity of caecal bacteria than those of C57 mice on the same diets, which may be related to the mouse genotype. In contrast, the AA diet caused a significant shift in the bacterial pattern in C57 mice, whose profiles appeared of similar complexity to those of the AA-fed \(10^{15} \) mice.

**B. vulgatus** (99–100% identity) was identified from bands A and B in the DGGE profiles of \(10^{15} \) mice fed PUFA or control diets, but not in the profiles of C57 mice (Table 4). The DNA fragments excised from bands G and H were identified as *E. coli* (EU555536, 100% identity), and were present in profiles of AA-fed C57 mice and in EPA-, AA- or AIN-76A-fed \(10^{15} \) mice. This band was not observed in the profile of \(10^{15} \) mice fed the OA diet. DNA fragments (bands K and L) identified as *C. perfringens* (FN356962, 100% identity) were present in DGGE profiles of \(10^{15} \) mice fed the control diets, whereas an uncultured *Clostridium* spp. (bands M and N, EF710221, 98 and 100% identities) was identified in profiles of \(10^{15} \) mice fed the PUFA diets. Other DNA fragments (bands C–F, I, J and O–R) were identified as uncultured bacteria and their closest relatives are listed in Table 4.

**Real-time PCR quantification of bacterial groups found in murine caecum in response to dietary PUFA**

The quantitative analyses revealing the numbers of cells of total bacteria, *Bacteroides–Prevotella–Porphyromonas* spp., *E. coli*, *C. perfringens*, *Enterococcus* spp. and *B. vulgatus* are shown in Fig. 4. The qPCR data suggest a significant effect of diet on cell numbers of total bacteria, *E. coli* and *B. vulgatus* \((P<0.05)\); a significant effect of mouse genotype on cell numbers of total bacteria, *C. perfringens* and *B. vulgatus* \((P<0.01)\); and a significant interaction between mouse genotype and diet affecting *E. coli* \((P<0.01)\); all based on the copy numbers of caecal bacteria in \(10^{15} \) and C57 mice. There was a lower cell number of total bacteria in the OA-fed \(10^{15} \) mice compared to the OA-fed C57 mice \((P=0.008)\). The reduction in total bacterial cell numbers in AA-fed C57 mice relative to OA- or EPA-fed C57 mice (Fig. 4a) tends to support the apparent reduced abundance of bands in DGGE profiles in response to dietary AA.

Cell numbers of *C. perfringens* were increased in the caecum of \(10^{15} \) mice on all diets compared to C57 mice fed the same diets, suggesting a mouse genotype effect. The only dietary effect on *C. perfringens* was observed in AA-fed compared to OA-fed C57 mice (Fig. 4b). The qPCR results showed a clear diet effect on *E. coli* in the caecum of \(10^{15} \) mice. The number of *E. coli* cells was higher in AA-fed compared to OA-fed \(10^{15} \) mice \((P<0.001)\) and higher in AA-fed compared to OA-fed C57 mice \((P=0.01)\). The EPA diet also increased the number of *E. coli* cells in the caecum of \(10^{15} \) mice, when compared to the OA diet. The number of *E. coli* cells was lower in EPA-fed C57 mice compared to AA-fed C57 mice (Fig. 4c). There was no significant effect of diet or mouse genotype on the number of cells of *Enterococcus* spp. in the caecum of \(10^{15} \) or C57 mice (Fig. 4d).

### Table 3. Species identified from excised bands in study 1

<table>
<thead>
<tr>
<th>Band</th>
<th>No. of clones sequenced per band</th>
<th>Species identified by sequencing</th>
<th>GenBank ID (Identity)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1, 2</td>
<td>3</td>
<td>Uncultured bacterium clone H83N4₈₉₉₀₂, isolated from mouse caecum</td>
<td>EU458036 (99–100%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Closest known cultured relative – <em>Bacteroides fragilis</em></td>
<td>ABZ01000006 (95%)</td>
</tr>
<tr>
<td>3, 4</td>
<td>3</td>
<td>Uncultured bacterium clone R-8325, isolated from faeces of rats fed wheat bran</td>
<td>FJI881325 (100%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Closest known cultured relative – <em>Bacteroides uniformis</em> ATCC 8492</td>
<td>N₉₋₉₄₉₀₂₀₀₀₀₂₉ (95%)</td>
</tr>
<tr>
<td>5, 6</td>
<td>3</td>
<td>Uncultured bacterium clone MMP7 + + 82, isolated from MMP7 + + mouse distal small intestine</td>
<td>EU791198 (98–100%)</td>
</tr>
<tr>
<td>7, 8</td>
<td>3</td>
<td>Closest known cultured relative – <em>Verminephrobacter eiseniae</em> EF01-2</td>
<td>NC₀₀₈₈₇₈₆ (87–88%)</td>
</tr>
<tr>
<td>9, 10</td>
<td>3</td>
<td>Uncultured bacterium clone OF2A10, isolated from stool sample</td>
<td>GQ285980 (99–100%)</td>
</tr>
<tr>
<td>11, 12</td>
<td>3</td>
<td>Closest known cultured relative – <em>Bacteroides capillosus</em> ATCC 29799</td>
<td>NZ₋₉₄₉₀2₀₀₀₀₃₇ (96%)</td>
</tr>
<tr>
<td>13, 14</td>
<td>3</td>
<td>Uncultured bacterium clone Y000363F09, isolated from Salmonella-infected mouse caecum</td>
<td>EU656022 (100%)</td>
</tr>
<tr>
<td>15, 16</td>
<td>2</td>
<td>Closest known cultured relative – <em>Bryantella formatexogens</em> DSM 14469</td>
<td>ACCL02000018 (93%)</td>
</tr>
</tbody>
</table>

*Numbers correspond to bands labelled in Fig. 1.*
A significant effect of mouse genotype ($P < 0.001$) and diet ($P = 0.04$) was observed for $B. vulgatus$. Cell numbers of $B. vulgatus$ (a member of the Bacteroides–Prevotella–Porphyromonas spp. group) were significantly higher in the caecum of $Il10^{-/-}$ mice fed the AIN-76A ($P = 0.05$) and OA ($P = 0.003$) control diets or the AA ($P = 0.02$) diet, compared with C57 mice on the same diets. The EPA diet increased the number of $B. vulgatus$ in the caecum of C57 mice compared with OA-fed C57 mice (Fig. 4f).

**DISCUSSION**

This study describes the use of DGGE and qPCR analysis of 16S rRNA genes to investigate differences in the bacterial community in the caeca of $Il10^{-/-}$ and C57 mice, and the impact of the onset of colitis and dietary PUFA. The findings show shifts in bacterial profiles of the caecal intestine upon progression from preclinical colitis to clinical colitis in $Il10^{-/-}$ mice. Some of these shifts were shown to be affected by dietary PUFA, especially AA, and were also influenced by the mouse genotype. A limitation of this type of study is that only a limited number of DGGE band-derived amplicons (in this case 34 bands) can be sequenced, providing an incomplete view of the complex, and bacteria-dense, caecal community. Next-generation sequencing technologies allow vast numbers of partial 16S rRNA genes from uncultured bacteria to be sequenced (Claesson et al., 2009). While DGGE analysis misses these shifts in bacterial community composition, it is a method that, when combined with quantification, gives reproducible results revealing the most abundant bacterial changes.

**Effect of host genotype on caecal bacteria**

Studies with mice (Vahtovuo et al., 2001, 2003; Zoetendal et al., 2001; Nones et al., 2009), human IBD patients and healthy subjects (Frank et al., 2007) have shown that the host genotype affects the composition of the bacterial community of the intestine. The reduced number of caecal bacteria observed in $Il10^{-/-}$ compared to C57 mice, before clinical signs of colitis, is likely to be associated with the genotype. A reduction in bacterial number and diversity was reported with inflamed $Il10^{-/-}$ mice on the 129/SvEv background compared to the wild-type counterpart (Wohlgemuth et al., 2009). From 7 to 12 weeks of age there was an increase in the number of caecal bacteria in $Il10^{-/-}$ mice, suggesting that inflammation changes the intestinal environment. As two out of five $Il10^{-/-}$ mice had already developed histological signs of moderate colitis at 7
weeks of age (Knoch et al., 2010a), it seems likely that non-clinical inflammation was present in 7-week-old Il10–/– mice, implying an increased leakiness of the intestinal epithelium, an impaired barrier function, and a consequent accumulation of bacteria in the mucosa. It remains unclear whether the bacteria are responding to inflammation, or are a causative agent when accumulating due to the leaky epithelial barrier membrane; it is also unclear which bacterial species might be involved.

The only known bacterial species in the inoculum used here that is proven to be associated with IBD development in Il10–/– mice was Ent. faecalis (Balish & Warner, 2002). Whether the enterococci quantified here were the specific inoculated strains was not investigated. Nevertheless, the decreased cell number of enterococci in the caecum of 12-week-old inflamed Il10–/– mice suggests that other bacteria in the inflamed large intestine might have affected the number of Enterococcus spp. by competing with and displacing them. No enterococci could be detected in the caecum or colon of conventionally housed, inflamed Il10–/– mice (129/SvEv background) or the respective wild-type mice (Wohlgemuth et al., 2009), indicating that bacteria other than enterococci trigger colitis in the 129/SvEv Il10–/– mice. Similarly, the differences in caecal E. coli cell numbers observed between Il10–/– and C57 mice (measured in study 2 only) might not be related to colitis development. Wohlgemuth et al. (2009) found no correlation between increasing E. coli cell numbers in Il10–/– mice and colitis severity. Another study showed no increase in E. coli numbers in germ-free Il10–/– mice colonized with faecal bacteria from healthy wild-type mice (Bibiloni et al., 2005).

The increase in total cell numbers of Bacteroides–Prevotella–Porphyromonas spp. in caeca from 7- to 12-week-old Il10–/– mice indicates the potential involvement of these bacteria in colitis development. These species have been detected in colitis models (Rath et al., 1999) and in human IBD patients (Swidsinski et al., 2005). Although B. vulgatus is known to be associated with colitis (Rath et al., 1999; Kishi et al., 2000), mono-colonization of germ-free Il10–/– mice with B. vulgatus did not lead to colitis (Kim et al., 2007), indicating the importance of bacterial community composition in the induction of colitis in a genetically susceptible host.

**Fig. 3.** DGGE profiles of caecal bacteria from individual Il10–/– and C57 mice fed PUFA diets. C, control sample, used only to compare profiles between gels. Arrows indicate the positions in the gel where bands were excised for DNA recovery and sequencing. Letters match the sequencing results in Table 4.

Associated effects of dietary PUFA and genotype on caecal bacteria

Changes in bacterial profiles can be attributed to factors other than genotype, such as age, diet or the composition and interaction of the bacteria in a particular community. The present results show, we believe for the first time, that changes in dietary fatty acid composition, i.e. diet enrichment with pure ethyl esters of EPA and in particular
AA, can alter the number and diversity of bacteria in the caecum of healthy C57 and inflamed Il10<sup>–/–</sup> mice. Previously, we reported that dietary AA tended to decrease colonic and systemic inflammation levels, and reduced the expression levels of some genes associated with cellular stress, inflammatory and immune responses in colonic and systemic inflammation levels, and reduced the protective effect of dietary PUFA and the associated changes in gut mediated by dietary PUFA and the associated changes in gut mediators, such as TLR2-deficient mice. Knoch et al. (2010b) reported that non-virulent EM0 (a human faecal strain) and virulent JM105 K-12 E. coli strains protected germ-free C3H/HeOuJ mice against Salmonella infection. Accumulation of E. coli in inflamed ileal tissue, as a result of epithelial barrier damage, has been reported in C57BL/6 mice susceptible to oral infection with Toxoplasma gondii (Heimesaat et al., 2005). The protective effect of some E. coli against other Enterobacteriaceae occurs via biofilm formation that limits the ability of pathogens to bind to the epithelium (Hudault et al., 2001). Similarly, Kankaanpää et al. (2001) also suggested a beneficial effect of PUFA on the adherence of probiotics.

In conclusion, the differences in bacterial composition of the caeca between the mouse strains might be, at least partly, associated with the genotype. An association between particular bacterial species and colitis could not be made due to the complexity and heterogeneity of the bacteria present in the large intestine. Colonization studies of germ-free Il10<sup>–/–</sup> mice with an individual bacterium, or a defined mix of commensal bacteria, will be required to make clear associations between bacterial species and colitis development. A possible protective effect of E. coli strains mediated by dietary PUFA and the associated changes in the bacterial environment could be a subject for further study.

### Table 4. Species identified from excised bands in study 2

<table>
<thead>
<tr>
<th>Band excised&lt;sup&gt;a&lt;/sup&gt;</th>
<th>No. of clones sequenced per band</th>
<th>Species identified by sequencing</th>
<th>GenBank ID (identity)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A, B</td>
<td>3</td>
<td>Uncultured Bacteroidales bacterium clone Fhc31, isolated from human and animal faeces</td>
<td>EU913590 (99–100 %)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Closest known cultured relative – Bacteroides vulgatus ATCC 8482</td>
<td>NC_009614 (99–100 %)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Closest known cultured relative – Porphyromonas uenonis 60-3 deg111864099623</td>
<td>NZ_ACLR010000152 (89 %)</td>
</tr>
<tr>
<td>C, D</td>
<td>3</td>
<td>Uncultured bacterium clone 2.77F, isolated from mouse faeces</td>
<td>EU655985 (100 %)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Closest known cultured relative – Clostridium perfringens partial, isolate colony 3, isolated from canine faeces</td>
<td>NZ_AAXG02000037 (96 %)</td>
</tr>
<tr>
<td>E, F</td>
<td>2</td>
<td>Uncultured bacterium clone Y00272E02, isolated from streptomycin-treated Salmonella-infected murine ileum</td>
<td>FJ838603 (100 %)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Closest known cultured relative – Denitrovibrio acetiphilus DSM 12809</td>
<td>NZ_ABTN01000006 (87 %)</td>
</tr>
<tr>
<td>G, H</td>
<td>3</td>
<td>Escherichia coli strain CNM 477-02</td>
<td>EU555536 (100 %)</td>
</tr>
<tr>
<td>I, J</td>
<td>3</td>
<td>Uncultured bacterium clone OF2A10, isolated from stool of healthy human</td>
<td>GQ285980 (100 %)</td>
</tr>
<tr>
<td>K, L</td>
<td>2</td>
<td>Uncultured Clostridium sp. clone MS213A1_H11, isolated after gastrointestinal resection of IBD patient</td>
<td>EF710221 (98 and 100 %)</td>
</tr>
<tr>
<td>M, N</td>
<td>2</td>
<td>Uncultured bacterium clone mcbcl20, isolated from caecum of TLR2-deficient mice</td>
<td>AM932646 (99–100 %)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Closest known cultured relative – Clostridium species</td>
<td>ACDK010000101 (98 and 100 %)</td>
</tr>
<tr>
<td>O, P</td>
<td>3</td>
<td>Uncultured bacterium clone mcbl20, isolated from caecum of TLR2-deficient mice</td>
<td>AM932646 (99–100 %)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Closest known cultured relative – Desulfobivio desulfuricans subsp. desulfuricans ATCC 27774</td>
<td>NC_011883 (95–96 %)</td>
</tr>
<tr>
<td>Q, R</td>
<td>3</td>
<td>Uncultured bacterium clone Y00360E03, isolated from streptomycin-treated Salmonella-infected murine ileum</td>
<td>FJ837456 (100 %)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Closest known cultured relative – Bryantella formatexigens DSM 14469</td>
<td>ACCL02000018 (93 %)</td>
</tr>
</tbody>
</table>

<sup>a</sup>Numbers correspond to bands labelled in Fig. 3.
investigation to define the mode of action of dietary PUFA during colitis.

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