A new macrocyclic antibiotic, fidaxomicin (OPT-80), causes less alteration to the bowel microbiota of *Clostridium difficile*-infected patients than does vancomycin

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**INTRODUCTION**

*Clostridium difficile* infection (CDI) is the most common identifiable cause of diarrhoea in hospitalized patients. Current therapies rely on the administration of metronidazole or vancomycin, which reduce vegetative populations of *C. difficile* in the bowel. Recurrence of the disease when treatment with these antibiotics ceases indicates that metronidazole and vancomycin affect not only *C. difficile* but also commensal populations that normally mediate competitive exclusion. Fidaxomicin is a new antibiotic that inhibits *C. difficile*. Our study shows that fidaxomicin had little effect on the composition of the faecal microbiota in terms of its major phylogenetic clusters. Notably, clostridial clusters XIVa and IV, and *Bifidobacterium*, were much less affected by fidaxomicin compared to vancomycin treatment. These findings help to explain the substantially reduced rates of relapse following treatment of CDI with fidaxomicin in recent clinical trials.

**METHODS**

**Faecal samples.** Faecal samples were analysed from 23 patients with a mild to moderate CDI, recruited for a phase 2 dose-ranging clinical trial (Louie et al., 2009b). The patients were adults with three or more loose, unformed bowel motions per day during the enrolment period, who were untreated, were without fever and had little abdominal pain. Patients were divided into three groups: eight patients administered 50 mg fidaxomicin twice daily for 10 days, seven patients administered 100 mg fidaxomicin twice daily for 10 days and eight patients administered 200 mg fidaxomicin twice daily for...
Twenty-three samples were collected on day 0 (prior to treatment of CDI), 22 on days 7, 10 and 21, and 9 on day 365 (one year post-treatment samples that were included as internal ‘normal’ controls). Additionally, faecal samples obtained from eight patients that were administered 125 mg vancomycin four times daily for 10 days were included in the analysis. These patients were matched demographically and symptomatically with the fidaxomicin patients (see Louie et al., 2009b for demographics) and faecal collections were made at days 0, 10 and 21. None of the C. difficile-infected patients received concomitant antibiotics. Faecal samples were also obtained from eight healthy subjects (single samples). The stool samples were frozen within approximately 1 h of collection and stored at -280°C prior to bacteriological analysis. Approval of the clinical work was obtained from the Conjoint Health Ethics Board, University of Calgary. Participants gave their informed consent.

**Generation and comparison of faecal microbiota profiles using temporal temperature gradient electrophoresis (TTGE).** Bacterial DNA was extracted from stool samples as described previously (Tannock et al., 2004). Universal bacterial primers HDA1-GC and HDA2 were used to amplify the V3 region of the 16S rRNA gene by PCR, as described previously (Tannock et al., 2004). Microbiota profiles were generated using the DCode universal mutation detection system apparatus (Bio-Rad) as described previously (Gore et al., 2008). A reference sample with fragments distributed throughout the whole gel was included in gel runs to permit normalization and comparison of profiles. Gelcompar II (Allied Maths) was used to compare TTGE profiles by multi-dimensional scaling (MDS). MDS uses the similarity matrix as input which can be applied directly to pairwise-compared profile patterns.

**Quantification of phylogenetic groups of bacteria in faeces by using fluorescent in situ hybridization and flow cytometry (FISH/FC).** The proportions of seven phylogenetic groups commonly detected in human faeces were determined using oligonucleotides Erec482, Clep866, Bac303, Bif164, Ato291, Enter1432 and Lab158. These probes detect bacterial members of clostridial cluster XIVa, clostridial cluster IV, Bacteroides–Prevotella, Bifidobacterium, Atopobium, enterobacteria and Enterococcaceae–Lactobacillaceae respectively. Details of these oligonucleotide probes were given by Lay et al. (2005). The proportions of each phylogenetic group were measured in comparison to the total bacterial community, which was determined using propidium iodide and probe Eub 338 covalently.
linked at the 5' end to FITC. The probes specific to particular bacterial groups were linked at the 5' end to the sulfoindocyanine dye indodicarbocyanine (Cy-5). Positive and negative control probes (Eub 338 and non-Eub 338) were labelled with Cy-5. Competitor oligonucleotides were unlabelled. The probes were purchased from MWG Biotech. FISH/FC procedures were performed as described previously (Lay et al., 2005). The Mann–Whitney test was used for statistical analysis.

Fig. 3. Quantification of bacterial populations in faeces by FISH/FC. Results are the means of multiple individuals in each sampling group. Error bars in (a) and (b) represent standard error. (a, c) Results from fidaxomicin-treated patients (pooled data from all doses). The numbers of faecal samples per sampling time were 23 at day 0, 22 at days 7, 10 and 21, and 9 at day 365. (b, d) Results obtained from the eight vancomycin-treated patients. (c, d) Graphs were plotted to produce area fill curves (GraphPad Prism, Graphpad software) that emphasize outgrowth of enterobacteria (light shading) coincident with decrease in proportion of clostridial cluster XIVa (dark shading) during treatment with vancomycin. (e) Data from eight healthy subjects. Oligonucleotide probes used to determine the groups are labelled 1–6: 1, Erec482 detects members of clostridial cluster XIVa; 2, Clep866, clostridial cluster IV; 3, Bac303, Bacteroides–Prevotella; 4, Bif164, Bifidobacterium; 5, Ato291, Atopobium; 6, Enter1432, enterobacteria.

Quantification of C. difficile in faeces using quantitative PCR. Real-time quantitative PCR was carried out using an ABI 7500 Fast System in MicroAmp Fast Optical 96-well plates with optical adhesive film (Applied Biosystems). Primers targeting the C. difficile 16S rRNA gene were those previously described by Rinttilä et al. (2004) and were purchased from Invitrogen. All reactions were carried out in a final volume of 20 µl containing 1 × Fast SYBR Green PCR Mastermix (Applied Biosystems) and 300 nM of each primer. Template DNA
was extracted from stool samples as described above and further cleaned using Qiagen DNeasy blood and tissue spin columns (Qiagen); 5 µl of the DNA was then added to the Mastermix. The thermocycling profile consisted of an initial activation of the polymerase at 95 °C for 30 s, followed by 40 cycles of 95 °C for 10 s and 60 °C for 30 s. Fluorescence levels were measured after the 60 °C annealing/extension step. A melt curve was generated to analyse product specificity. Standard curves were generated using genomic DNA isolated from *Clostridium perfringens* ATCC 9689T by using the Gram-positive bacteria protocol of the Qiagen DNeasy blood and tissue kit. The standard DNA was quantified spectrophotometrically using a Nanodrop 1000 (Thermo Scientific) and diluted in 10-fold steps from $5 \times 10^6$ to $5 \times 10^1$ genomes per reaction, which were calculated on the basis of one copy of the target gene per genome. All reactions were carried out in duplicate and were run twice on separate plates. No-template controls and a further negative control containing $5 \times 10^1$ genomes of *Clostridium perfringens* ATCC 13124T DNA were also included on each plate.

## RESULTS

### Comparison of TTGE profiles

Measurement of the similarity between profiles by MDS analysis did not reveal any clustering of the microbiota profiles of samples collected from fidaxomicin-treated patients at days 0, 7, 10 or 21 (Fig. 1a). MDS analysis showed that the profiles of samples from fidaxomicin-treated patients, vancomycin-treated patients and untreated controls tended to cluster separately, although profiles from fidaxomicin-treated subjects were more loosely distributed (Fig. 1b). Overall, MDS analysis indicated that the composition of the faecal microbiota was differentially altered by antibiotic treatment relative to healthy and day 365 sample controls.

### Alterations in microbiota compositions detected by FISH/FC

The compositions of the faecal microbiota of patients administered different doses of fidaxomicin were similar for all phylogenetic clusters ($P>0.05$); data for clostridial cluster XIVa as a proportion of the total microbiota in these patients are shown as an example in Fig. 2. Data obtained from fidaxomicin-treated patient samples were therefore pooled (all three doses) for simplicity because all doses of fidaxomicin affected microbiota composition in the same way. Pooled results are shown in Fig. 3(a) and Table 1. Clostridial cluster XIVa and clostridial cluster IV populations increased during and after the fidaxomicin treatment period. Clostridial cluster XIVa populations attained levels similar to those of the control faeces by day 10 (Fig. 3a, c, e; $P>0.05$). In contrast, vancomycin treatment greatly reduced the proportions of the clostridial clusters, and also of bifidobacteria, by day 10 of the treatment period ($P<0.05$). Outgrowth of enterobacteria coincided with the decrease in other phylogenetic groups (Fig. 3b, d). Samples from fidaxomicin-treated patients that had been administered the antibiotic one year previously had a bacterial composition resembling that of the control faeces (Fig. 3a, e). Bacteria detected by the Lab 158 probe include mainly lactobacilli and enterococci. The proportions of these bacteria did not vary during the fidaxomicin treatment period, but increased during vancomycin treatment ($P<0.05$), coincident with the decrease in proportions of clostridial clusters and bifidobacteria (Table 1). Overall, vancomycin treatment was characterized by a decrease in the proportions of obligately anaerobic bacteria that normally populate the human colon, and an outgrowth of facultatively anaerobic and microaerobic bacterial groups during the treatment period.

### *C. difficile* populations in faeces

*C. difficile* populations were detected in 19 out of the 23 fidaxomicin-treated patients and seven out of the eight vancomycin-treated patients at day 0 (Fig. 4). One patient treated with vancomycin had detectable *C. difficile* at day 10, whereas four or five patients treated with fidaxomicin harboured these bacteria at days 7, 10 and 21. Three of these patients had received the lowest dose (50 mg) of fidaxomicin. This observation vindicated the selection of the higher dosage of 200 mg fidaxomicin twice daily for clinical usage. Both vancomycin and fidaxomicin are not absorbed from the bowel and observation of 1100 patients administered 400 mg fidaxomicin daily has not revealed adverse effects (Louie *et al.*, 2009b; T. Louie, unpublished clinical observations).

### Table 1. Quantification of *Enterococcaceae–Lactobacillaceae* (probe Lab158) as a proportion of the total faecal microbiota

Data are means ± SE of percentage values. ND, No samples; NA, not applicable.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Percentage of total faecal microbiota on day:</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>0</td>
</tr>
<tr>
<td>Fidaxomicin</td>
<td>4.06 ± 1.37</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>6.04 ± 2.66</td>
</tr>
<tr>
<td>None (healthy controls)</td>
<td>4.72 ± 1.50</td>
</tr>
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Clustering XIVa and IV and bifidobacteria than does vancomycin. Emphasis, to date, has been placed on the lack of antibacterial activity of fidaxomicin against Gram-negative bacteria (Louie et al., 2009a) but our study has shown that Gram-positive commensals are also relatively unaffected. By sparing the normally predominant members of the microbiota, fidaxomicin treatment appears to minimize the disruption of competitive exclusion: in phase 3 trials of the antibiotic, fidaxomicin patients had a 47% lower recurrence rate of CDI versus vancomycin (P=0.004) (Miller, 2010). Moreover, the bowel microbiota is highly interactive with the host, which can have important physiological outcomes (Hooper, 2004; Bäckhed et al., 2004). Therefore, antibiotics that produce a cure while having minimal effects on the composition of the microbiota are desirable. Their use should ensure that normal physiological processes are restored quickly with minimal consequences to the human–microbe balance that underpins the healthy bowel biome. Overall, our observations affirm the hypothesis that fidaxomicin is a narrow-spectrum and directed therapeutic agent for CDI. As shown in phase 3 trials, the antibiotic meets both end-point requirements of treatment: cure and an absence of recurrent disease in a large proportion of patients.

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**REFERENCES**


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**DISCUSSION**

The composition of the faecal microbiota is considered to reflect microbiological phenomena occurring in the distal human colon (Moore et al., 1978). The colonic microbiota has a relatively stable composition due to the self-regulatory activities of the bacterial community and the ability of its members to obtain carbon and energy sources from a wide variety of substrates that may vary in availability from day to day (Gill et al., 2006). *C. difficile* infection results in marked diarrhoea that may become life threatening. Broad-spectrum antibiotic treatment that predisposes patients to CDI, and the purging action of diarrhoea, diminish the numbers of bacteria in the colon and, as shown in our day 0 data, reduces the proportions of the clostridial groups that normally predominate in the human bowel. Vancomycin effectively inhibits the growth of *C. difficile*, resulting in the recovery of the patient, but it also has devastating effects on the composition of the microbiota. Such perturbations of bacterial communities are likely to provide vacant niches that can be filled by otherwise subdominant species. Thus, in some patients, the effects produced by vancomycin on the bowel microbiota allow the germination of *C. difficile* spores and proliferation of vegetative cells in the bowel, causing a re-emergence of *C. difficile* populations and, hence, a recurrence of diarrhoeal disease as recorded in clinical studies (Rubin et al., 2009b). Stool transplantation has been proposed as a means of quickly ‘normalizing’ the bowel microbiota but thorough investigations have not yet been completed (Rubin et al., 2009). Fidaxomicin, as reported here, has a much less marked effect on the members of clostridial clusters XIVa and IV and bifidobacteria than does vancomycin. Emphasis, to date, has been placed on the lack of antibacterial activity of fidaxomicin against Gram-negative bacteria (Louie et al., 2009a) but our study has shown that Gram-positive commensals are also relatively unaffected. By sparing the normally predominant members of the microbiota, fidaxomicin treatment appears to minimize the disruption of competitive exclusion: in phase 3 trials of the antibiotic, fidaxomicin patients had a 47% lower recurrence rate of CDI versus vancomycin (P=0.004) (Miller, 2010). Moreover, the bowel microbiota is highly interactive with the host, which can have important physiological outcomes (Hooper, 2004; Bäckhed et al., 2004). Therefore, antibiotics that produce a cure while having minimal effects on the composition of the microbiota are desirable. Their use should ensure that normal physiological processes are restored quickly with minimal consequences to the human–microbe balance that underpins the healthy bowel biome. Overall, our observations affirm the hypothesis that fidaxomicin is a narrow-spectrum and directed therapeutic agent for CDI. As shown in phase 3 trials, the antibiotic meets both end-point requirements of treatment: cure and an absence of recurrent disease in a large proportion of patients.


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