Background. *Clostridium difficile* infections (CDI) in the US have markedly increased. Disturbances to the gastrointestinal (GI) microbiome due to antibiotic use predisposes patients to CDI. Probiotics are recommended to prevent GI microbiota changes during CDI antibiotic treatment, but efficacy is unknown. We conducted a randomized, double-blinded, placebo-controlled, examination of clinical and GI microbiota changes in subjects administered probiotics during a primary episode of CDI.

Methods. 33 subjects with a primary episode of CDI were randomized to once daily oral probiotic, consisting of four different bacterial strains, or placebo 4 weeks (week 0–4) concurrent to antibiotic treatment. Subjects completed a daily stool diary, and stool samples were collected at enrollment (week 0), at the end of the probiotic or placebo adjournment (week 4) and 4 weeks post-treatment (week 8). DNA was extracted for 165 rRNA sequencing with Illumina MiSeq, and subject’s GI microbiota community structure was compared using analysis of variance and permutation analysis of variance. Similarity percentage analysis identified the operational taxonomic units driving the variation in β diversity.

Results. The duration of diarrhea (P = 0.039) and total days of diarrhea (P = 0.005) both decreased in the probiotic group compared with the placebo group. Analysis of community structure showed significant differences between treatment groups overall (P = 0.017) and in both groups over time (P = 0.007), but not between groups at each individual time point. Subjects in the probiotic group had a higher abundance of the family *Lachnospiraceae* at week 4 than subjects in the placebo group. By week 8 the abundance of *Lachnospiraceae* did not differ between subjects administered probiotic or placebo.

Conclusion. Lack of difference in overall community structure between groups at each time point is likely due to concurrent antibiotic therapy. The differential abundance of *Lachnospiraceae* likely contributes to the differences in the diarrheal outcomes observed between groups, as it has previously been associated with attenuated *C. difficile* pathogenicity. Shortening the duration of diarrhea from an initial CDI may reduce the spread of *C. difficile* and improve clinical outcomes.

Disclosures. All authors: No reported disclosures.

1269. Endogenous Serum IgG Antibodies to *Clostridium difficile* Toxin B Are Associated with Protection against *C. difficile* Infection Recurrence

Ciaran P. Kelly, MD1; Ian R. Poxton, PhD, DSc2; Judong Shen, PhD3; Xiaoyun Li, MS4; Marina加强对C. difficile pathogenicity. Shortening the duration of diarrhea from an initial CDI may reduce the spread of *C. difficile* and improve clinical outcomes.

Disclosures. All authors: No reported disclosures.

1270. Comparative Effectiveness of Vancomycin vs. Metronidazole in Mild *Clostridium difficile* Infections, and Potential Impact on Subsequent Vancomycin-Resistant Enterococcus (VRE) Isolation

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Session 148. C. difficile: From the Bench to Bedside Friday, October 6, 2017: 12:30 PM

Background. The epidemiology and clinical characteristics of *Clostridium difficile* infections (CDI) have evolved dramatically in the past decade. Vancomycin is the treatment of choice for moderate to severe CDI, and with superior cure rates compared to traditional comparators. However, controlled comparative efficacy data pertaining to mild CDI is lacking. Furthermore, the potential impact of vancomycin treatment on subsequent Vancomycin-Resistant Enterococcus (VRE) isolation rates remains unknown at the individual patient level.

Methods. A retrospective cohort analysis was executed at the Assaf Haroef Medical Center, Israel, from 2010 to 2015. Adult patients (>18 years) with a first episode of acute CDI, determined per pre-established criteria, were enrolled. The efficacy of vancomycin vs. metronidazole was evaluated in the subset of patients with mild CDI. The outcomes of patients, who received vancomycin or metronidazole (but not both), were compared by Cox regression. A prediction score was used to control for possible confounders associated with being treated with vancomycin. The independent association of oral vancomycin treatment during the acute CDI and later (up to 18 months) VRE isolation was analyzed using Cox regression.

Results. A total of 413 patients with CDI were included in the study. The majority were elderly (median age 75 years, range 19–120), and had extensive comorbidities (mean Charlson’s combined condition score 6.7 ± 3.4) and significant acute illness indices (35% with severe to fulminating Illness). Among 126 patients with mild disease, no differences were observed in terms of clinical outcomes between vancomycin or metronidazole treatment. Metronidazole remained non-inferior even after incorporating a prediction score to control for confounders associated with being a “vancomycin case”. Ten patients had new post-CDI VRE isolation. In multivariable analysis, oral vancomycin treatment during the acute CDI was the strongest independent predictor for later isolation of VRE (aOR=6.57, P = 0.04).

Conclusion. Our study suggests that metronidazole should remain the recommended treatment of choice for mild CDI, due to clinical non-inferiority and an apparent association between vancomycin therapy and subsequent VRE isolation in an individual patient level analysis.

Disclosures. All authors: No reported disclosures.

1271. Belzotuxumab (BEZ) for Prevention of *Clostridium difficile* Infection (CDI) Recurrence (rCDI): Distinguishing Relapse from Reinfection with Whole Genome Sequencing (WGS)

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Session 148. C. difficile: From the Bench to Bedside Friday, October 6, 2017: 12:30 PM

Background. Belzotuxumab (BEZ) and actoxumab (ACT) are monoclonal antibodies against *C. difficile* toxins B and A, respectively. Patients receiving a single infusion of BEZ alone or with ACT in the MODIFY II/III trials showed an absolute 10% (relative ~40%) reduction in rCDI over 12-weeks compared with placebo (PBO). The addition of ACT did not improve efficacy. This post hoc analysis investigated whether BEZ prevented relapse with the same strain and/or reinfection with a new strain.

Methods. *C. difficile* strains isolated from patient stool samples were typed by PCR ribotyping. PCR free library construction and illumina whole genome