the three groups. At presentation, disease severity was similar in all groups. However, patients in GI were more likely to have detectable toxin A/B and C. difficile infection compared with GI and GII (53% vs. 23%, P = 0.015) and higher treatment failure rates (56%) when compared with GI (15% P = 0.007) and GII (6%, P = 0.004). Bacteremia was more common in GII (28%) compared with GI (0%) P = 0.041 and GII 6% P = 0.007. Patients in GI had fewer complications when compared with those in GII P = 0.025. No differences in sustained clinical response, recurrence, ICU stay or all-cause 90-day mortality were found between the groups.

Conclusion. Cancer patients with CDI due to GII ribotypes are more likely to exceed fecal toxin A/B and fail conventional therapy. In contrast, patients in GI and GII were more likely to respond to therapy. GI was associated with fewer complications. Of interest, GII was associated with bacteremia. Evaluation of C. difficile ribotypes is clinically relevant in cancer patients with CDI.

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1266. Bezloeotham (BEZ) for Prevention of Clostridium Difficile Infection (CDI) Recurrence (rCDI): Outcomes in Patients with Substantial Renal Impairment (SRI) Yoav Golan, MD1-2; Herbert L. DuPont, MD3; Fernando Aldomiro, MD3; Erin H. Jensen, MS4; Mary E. Hanson, PhD4 and Mary Beth Dorf, PhD4; Tufts Medical Center, Boston, Massachusetts, University of Texas School of Public Health, Houston, Texas, Baylor St. Luke's Medical Center, Houston, Texas, Hospital Dr. Fernando Fonseca, EPE – Amadora/Sintra, Amadora/Sintra, Portugal, Merck & Co., Inc., Kendworth, New Jersey

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

Background. CDI in patients with SRI is harder to treat and is associated with higher recurrence. MODIFY I/II found that BEZ, a monoclonal antibody against C. difficile toxin B, is superior to placebo (PBO) at preventing rCDI in patients receiving standard care antibiotics (SoC). This post hoc analysis assessed efficacy of BEZ in patients with SRI in the MODIFY studies.

Methods. Patients with baseline eGFR < 60 mL/min/1.73 m2 at baseline and 7 days post-treatment in responders but not in non-responders (Figure 1). Microbiome changes in responders were a larger shift from baseline microbiome was seen in responders to RBX2660 compared with non-responders.

Results. Baseline patient microbiomes were similar across response groups. RBX2660 treatment shifted the relative microbiome densities with taxa-specific increase in Bacteroidia, Clostridia, and decrease in Gamma-proteobacteria abundance. A larger shift from baseline microbiome was seen in responders to RBX2660 compared with non-responders (Figure 1). Microbiome changes in responders were durable to 60 days. RBX2660 treatment increased Shannon and Simpson diversity at 7 days post-treatment in responders but not in non-responders (P < 0.05).

Conclusion. RBX2660 treatment shifts patient intestinal microbiomes with greater alterations seen in those with a successful clinical outcome.

Funded by Rebiotix Inc., Roseville, MN.

Figure 1. Responders to RBX2660 have a greater change in taxa abundance from baseline relative to non-responders at 30 days. Dirichlet-Multinomial distribution parameter α/2 presented as mean (95% CI).

Disclosures. S. Khanna, Rebiotix, Inc.: Scientific Advisor, Consulting fee; K. Blount, Rebiotix, Inc.: Employee, Salary; C. Jones, Rebiotix, Inc.: Employee, Salary; B. Shannon, Rebiotix, Inc.: Research Contractor, Consulting fee; S. Carter, Rebiotix, Inc.: Research Contractor, Consulting fee.

1267. Successful Response to Microbiota-Based Drug RBX2660 in Patients with Recurrent Clostridium difficile Infection is Associated with More Pronounced Alterations in Microbiome Profile

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

Background. Recurrent Clostridium difficile infections (rCDI) are associated with decreased diversity and altered intestinal microbiome compared with healthy patients. RBX2660, a standardized microbiota-based drug, is designed to restore microbiome diversity and composition in patients. The effect of RBX2660 on CDI patient microbiomes was evaluated by comparing pre- and post-treatment samples from PUNCH CD 2—a randomized, double-blind, placebo-controlled study.

Methods. rCDI subjects were randomized to blinded treatments of 2 doses of RBX2660 (Group A), 2 doses of placebo (Group B), or 1 dose each of RBX2660 and placebo (Group C), by enema 7 days apart. Subjects submitted stool samples at baseline, day 7, 30, and 60 after treatment. Stool samples from responders to RBX2660 treatment per protocol defined as the absence of CDI for 8 weeks after treatment compared with non-responders.

Relative taxonomic abundances at the class level were determined using 16s rRNA sequencing analysis for 94 stool samples from 45 patients in Groups A and C. Relative abundance data were grouped longitudinally using Bray-Curtis dissimilarity index. Analyses were performed based on the Dirichlet-Multinomial distribution to compare group mean relative taxonomic abundances; Simpson and Shannon diversity indices were compared among groups longitudinally.

Results. Baseline patient microbiomes were similar across response groups. RBX2660 treatment shifted the relative microbiome densities with taxa-specific increase in Bacteroidia, Clostridia, and decrease in Gamma-proteobacteria abundance. A larger shift from baseline microbiome was seen in responders to RBX2660 compared with non-responders (Figure 1). Microbiome changes in responders were durable to 60 days. RBX2660 treatment increased Shannon and Simpson diversity at 7 days post-treatment in responders but not in non-responders (P < 0.05).

Conclusion. RBX2660 treatment shifts patient intestinal microbiomes with greater alterations seen in those with a successful clinical outcome.

Funded by Rebiotix Inc., Roseville, MN.

Figure 1. Responders to RBX2660 have a greater change in taxa abundance from baseline relative to non-responders at 30 days. Dirichlet-Multinomial distribution parameter α/2 presented as mean (95% CI).

Disclosures. S. Khanna, Rebiotix, Inc.: Scientific Advisor, Consulting fee; K. Blount, Rebiotix, Inc.: Employee, Salary; C. Jones, Rebiotix, Inc.: Employee, Salary; B. Shannon, Rebiotix, Inc.: Research Contractor, Consulting fee; S. Carter, Rebiotix, Inc.: Research Contractor, Consulting fee.

1268. Changes to the Composition of the Gastrointestinal Microbiome after Probiotics for Clostridium difficile Infection in Adults

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

Background. Probiotic use has been associated with a decrease in Clostridium difficile infections (CDI) and recurrence. A previous study demonstrated the effect of RBX2660, a novel probiotic, on the intestinal microbiome in CDI patients. This study focuses on the microbiome changes after RBX2660 and placebo in CDI patients in a randomized, double-blind, placebo-controlled treatment.

Methods. A total of 80 patients with a history of CDI were randomized to receive 2 doses of RBX2660 or placebo within 90 days after CDI. The primary endpoint was the proportion of responders (defined as diarrhea and toxigenic C. difficile isolated from stool samples after 7 days of study). The secondary endpoint was comparison of baseline and end-of-treatment microbiome changes using the Dirichlet-Multinomial distribution. The study was designed to detect a difference of 10% in the proportion of responders between the two groups with 80% power at an α level of 0.05.

Results. The study was completed in 2017, and the final results were presented at the American Society for Microbiology Conference in 2018. The study found that RBX2660 compared with placebo significantly reduced rCDI in patients with SRI and could benefit this hard to treat population.

Conclusion. RBX2660 treatment shifted the relative microbiome densities with taxa-specific increase in Bacteroidia, Clostridia, and decrease in Gamma-proteobacteria abundance. A larger shift from baseline microbiome was seen in responders to RBX2660 compared with non-responders. Relative taxonomic abundances at the class level were determined using 16s rRNA sequencing analysis for 94 stool samples from 45 patients in Groups A and C. Relative abundance data were grouped longitudinally using Bray-Curtis dissimilarity index. Analyses were performed based on the Dirichlet-Multinomial distribution to compare group mean relative taxonomic abundances; Simpson and Shannon diversity indices were compared among groups longitudinally.

Results. Baseline patient microbiomes were similar across response groups. RBX2660 treatment shifted the relative microbiome densities with taxa-specific increase in Bacteroidia, Clostridia, and decrease in Gamma-proteobacteria abundance. A larger shift from baseline microbiome was seen in responders to RBX2660 compared with non-responders (Figure 1). Microbiome changes in responders were durable to 60 days. RBX2660 treatment increased Shannon and Simpson diversity at 7 days post-treatment in responders but not in non-responders (P < 0.05).

Conclusion. RBX2660 treatment shifts patient intestinal microbiomes with greater alterations seen in those with a successful clinical outcome.

Funded by Rebiotix Inc., Roseville, MN.

Figure 1. Responders to RBX2660 have a greater change in taxa abundance from baseline relative to non-responders at 30 days. Dirichlet-Multinomial distribution parameter α/2 presented as mean (95% CI).
**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 different bacterial strains, or placebo for 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 adjunct regimen (week 4), and 4 weeks post-treatment (week 8). DNA was extracted for 16S rRNA sequencing with Illumina MiSeq, and microbiome 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.

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

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Session: 148. C. difficile: From the Bench to Bedside

Friday, October 6, 2017: 12:30 PM

**Background.** MODIFY I/II were global trials of the efficacy and safety of bezlotoxumab (BEZ), a monoclonal antibody (mAb) against *C. difficile* toxin B, alone and with actoxumab (ACT), a mAb against *C. difficile* toxin A. BEZ was superior to placebo (PBO) at preventing recurrent CDI (rCDI) in patients (patients) receiving anti-

**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 signifie-

**Conclusion.** Our study suggests that metronidazole should remain the recom-

**Disclosures.** All authors: no reported disclosures.

1271. Bezlotoxumab (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.** 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 I/II trials showed a 70% (relative – 39%) reduction in rCDI overall 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