the three groups. At presentation, disease severity was similar in all groups; however, patients in GI1 were more likely to have detectable toxin A/B by ELA compared with GI and GI1I (53% vs. 23%, P = 0.015) and higher treatment failure rates (56%) when compared with GI (15% P = 0.007) and GI1I (16%, P = 0.004). Bacteremia was more common in GI1I (28%) compared with GI (0%) P = 0.041 and GI1I 7% P = 0.007. Patients in GI had fewer complications when compared with those in GI1I 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 CFI due to GI1I ribotypes are more likely to exacerbate toxin A/B and fail conventional therapy. In contrast, patients in GI and GI1I were more likely to respond to therapy. GI was associated with fewer complications. Of interest, GI1I was associated with bacteremia. Evaluation of C. difficile ribotypes is clinically relevant in cancer patients with CFI.

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1266. Bezlotoxumab (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, MS3; Mary E. Hanson, PhD4 and Mary Beth Dorr, PhD1; Tufts Medical Center, Boston, Massachusetts, 1University of Texas School of Public Health, Houston, Texas, 2Baylor St. Luke’s Medical Center, Houston, Texas, 3Hospital Dr. Fernando Fonseca, EPE – Amadora/Sintra, Amadora/Sintra, Portugal, 4Merck & Co., Inc., Kendworth, New Jersey.

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

Methods. MODIFY IIi mITT populations were pooled to estimate initial clinical cure (IC), rCDI, and mortality through 12 weeks. Estimated glomerular filtration rate (eGFR) was calculated with the Modified Diet in Renal Disease (MDRD) method. SRI was defined as eGFR <60 mL/minute/1.73 m2.

Results. Of the included 1554 patients, 1101 had no SRI (≥90; n = 612; 60 to <90; n = 489); 430 had SRI (30 to 60; n = 290; 15 to <30; n = 71; <15; n = 69); 23 had unknown eGFR. 87% of SRI patients had ≥1 risk factor for rCDI. Relative to patients without SRI, more patients with SRI were ≤65 years (69% vs. 44%), immunocompromised (25 vs. 20%), had ribotype 027 (25% vs. 17%), and used concomitant antibiotics during SoC (41% vs. 31%) or after SoC (36% vs. 28%). SRI patients had more severe CDI (21% vs. 14%), lower CDI cure (78.4% vs. 80.1%), higher rCDI (31.6% vs. 27.8%), and death (11.6% vs. 5.3%). In the SRI cohort, more BEZ vs. PBO patients were inpatients (81% vs. 72%), ≥65 years (72% vs. 65%), immunocompromised (28 vs. 22%), and used systemic antibiotics after SoC ended (40% vs. 32%). The rate of ICC was similar between treatment groups and the rCDI rate was significantly less the BEZ vs. PBO group (Table).

Conclusion. SRI was associated with worse CDI outcomes. BEZ given with SoC significantly reduced rCDI in patients with SRI and could benefit this hard to treat population.

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1267. Successful Response to Microbiota-Based Drug RBX2660 in Patients with Recurrent Clostridium difficile Infection is Associated with More Pronounced Alterations in Microbiome Profile Sahil Khanna, MBBS, MS1; Ken Blount, PhD2; Courtney Jones, BS3; Bill Shannon, PhD, MBA4; and Sharrina Carter, PhD5; 1Gastroenterology and Hepatology, Mayo Clinic, Rochester, Minnesota, 2Rebiotix, Roseville, Minnesota, 3BioRankings LLC, St. Louis, Missouri.

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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 receive 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 were 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.

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

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1268. Changes to the Composition of the Gastrointestinal Microbiome after Probiotics for Clostridium difficile Infection in Adults Shoshannah Eggers, BS1; Travis De Wolfe, MS2; Anna Barker, BA3; Megan Duster, MT(ASCP); Kimberly Dill-McFarland, PhD1; Garret Suen, PhD2 and Nasia Safdar, MD, PhD, FISHEA,1; 1Department of Population Health Sciences, School of Medicine and Public Health, University of Wisconsin – Madison, Madison, Wisconsin, 2Department of Food Science, University of Wisconsin – Madison, Madison, Wisconsin, Division of Infectious Diseases, School of Medicine and Public Health, University of Wisconsin – Madison, Madison, Wisconsin, 3Department of Bacteriology, College of Agriculture and Life Sciences, University of Wisconsin – Madison, Madison, Wisconsin.

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