

SYN-004 (ribaxamase)
PREVENTED Clostridium
difficile INFECTION IN
PATIENTS BEING TREATED
WITH BETA-LACTAM
ANTIBITOICS

John F. Kokai-Kun

6th International C. difficile Symposium

Bled, Slovania

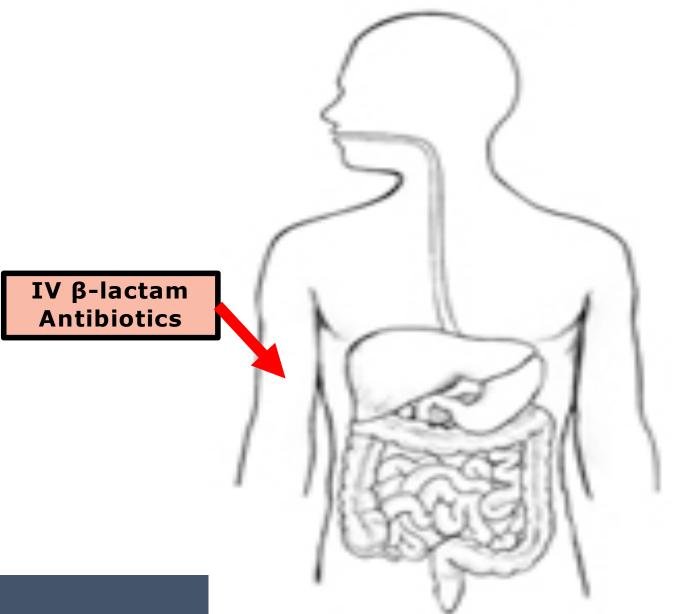
September 12, 2018

# **Forward-Looking Statements**

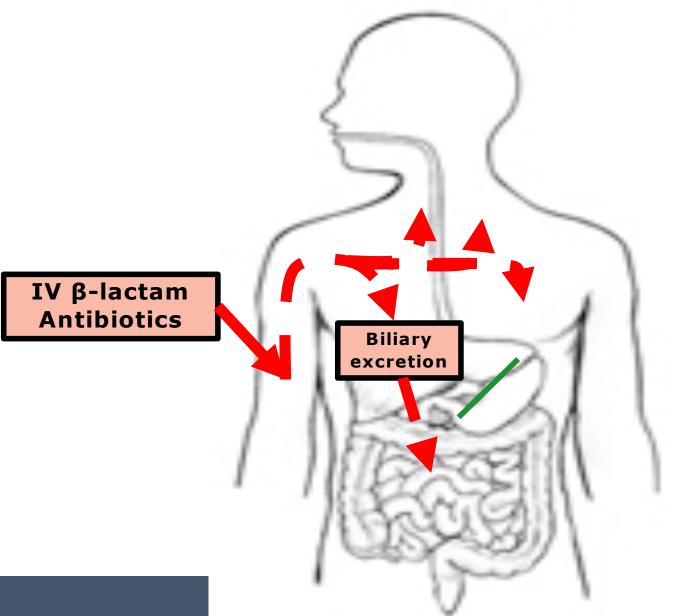
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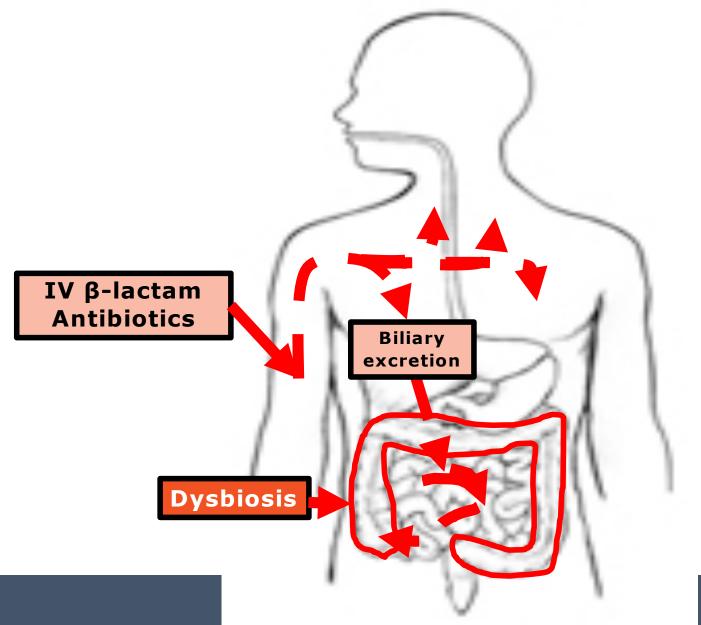




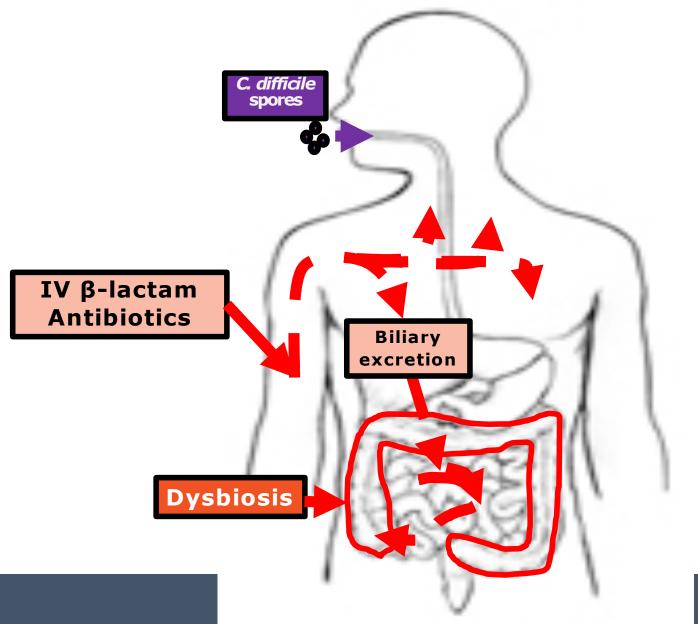




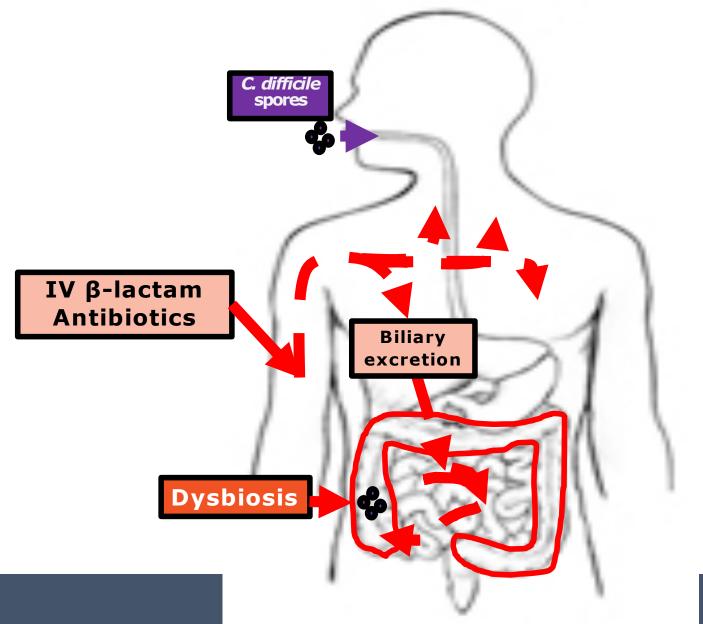




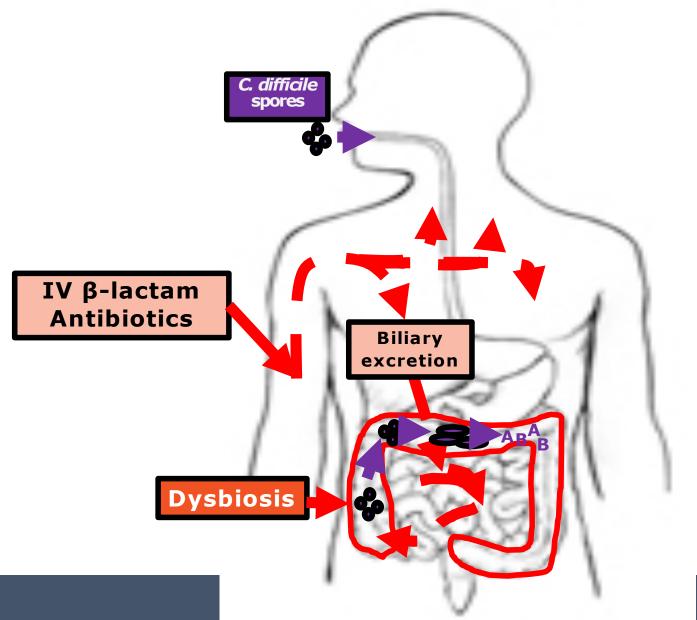




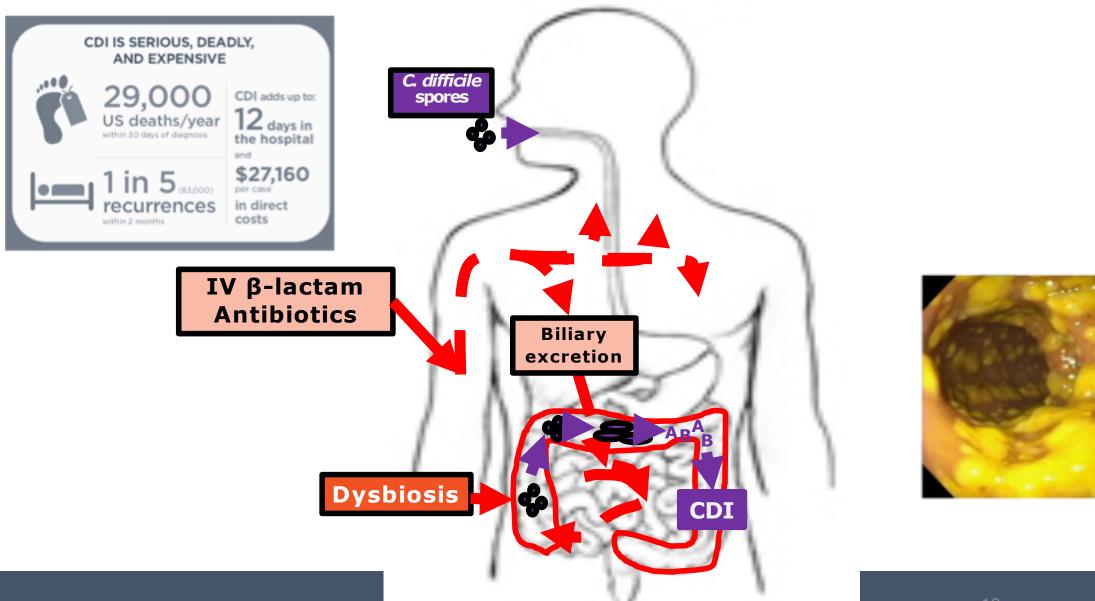




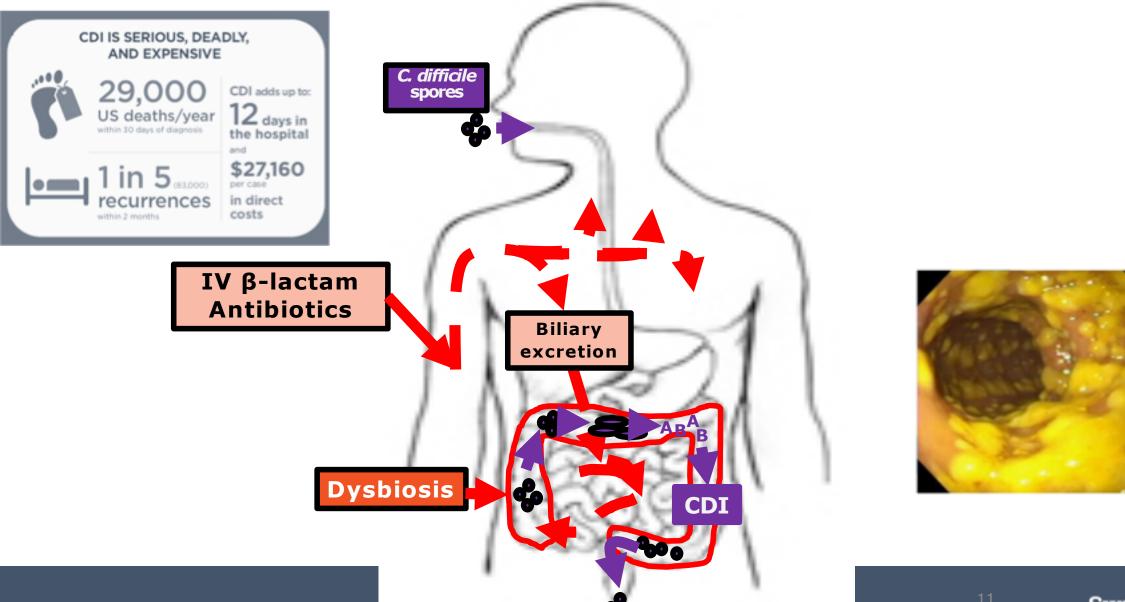




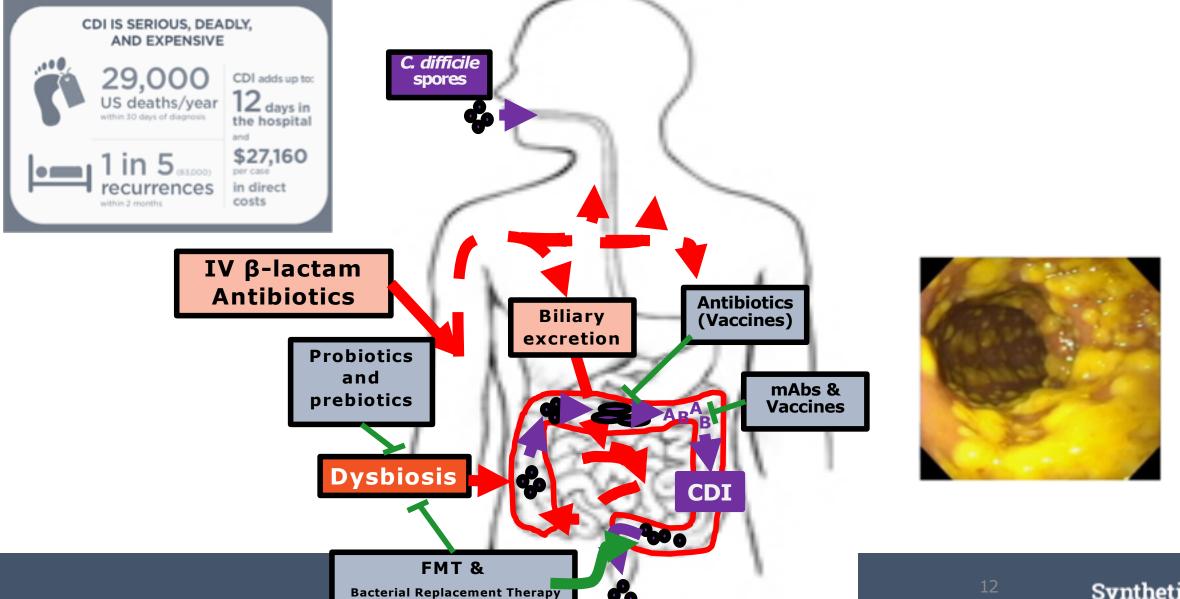




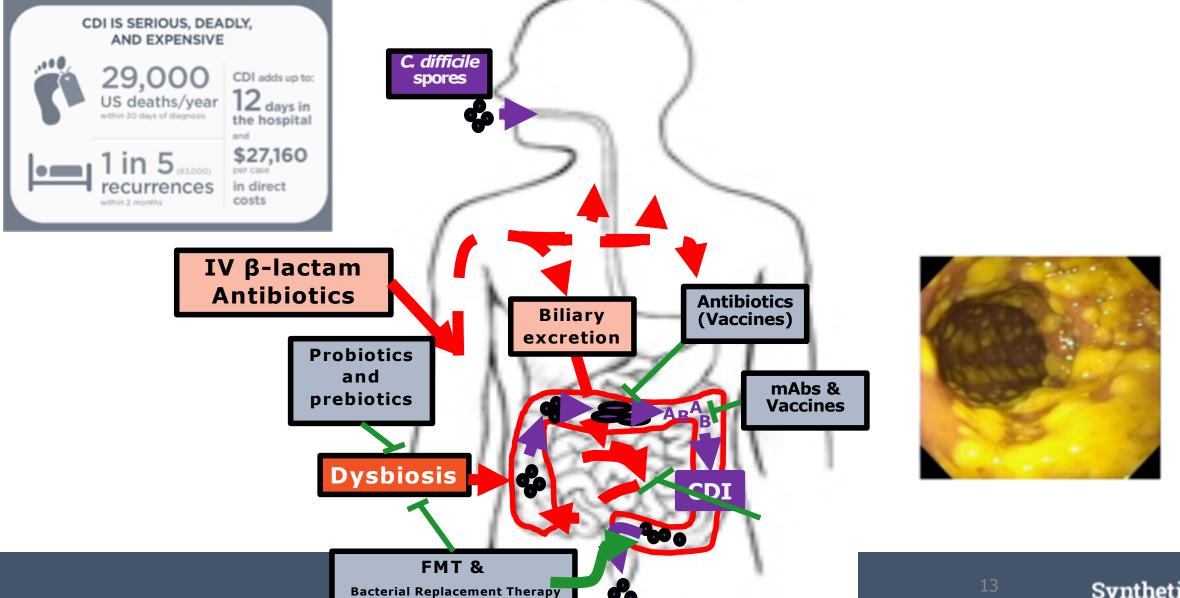




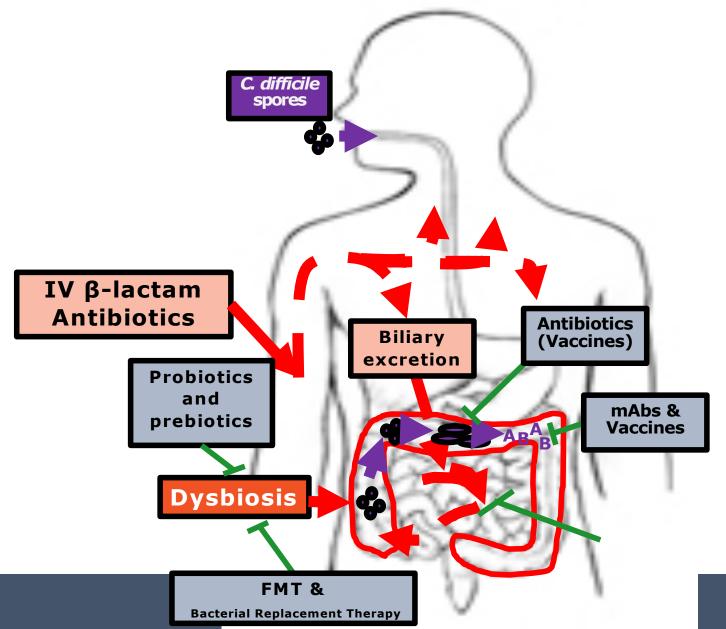




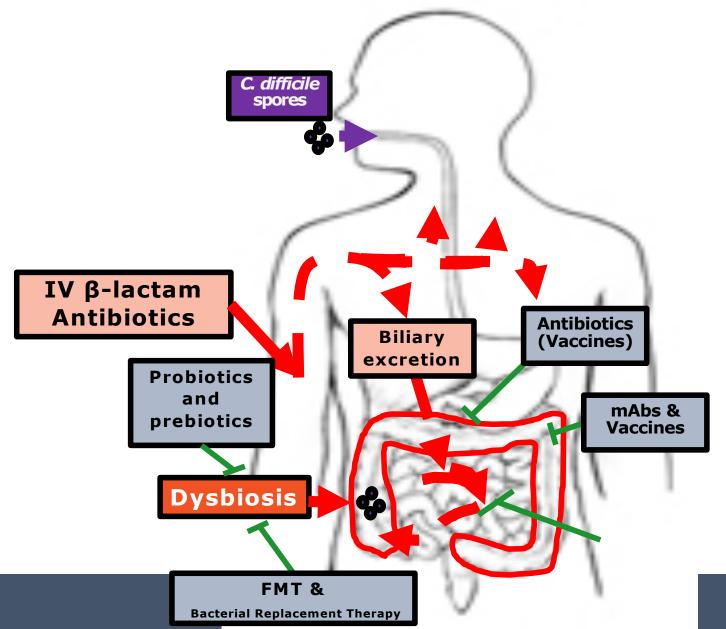




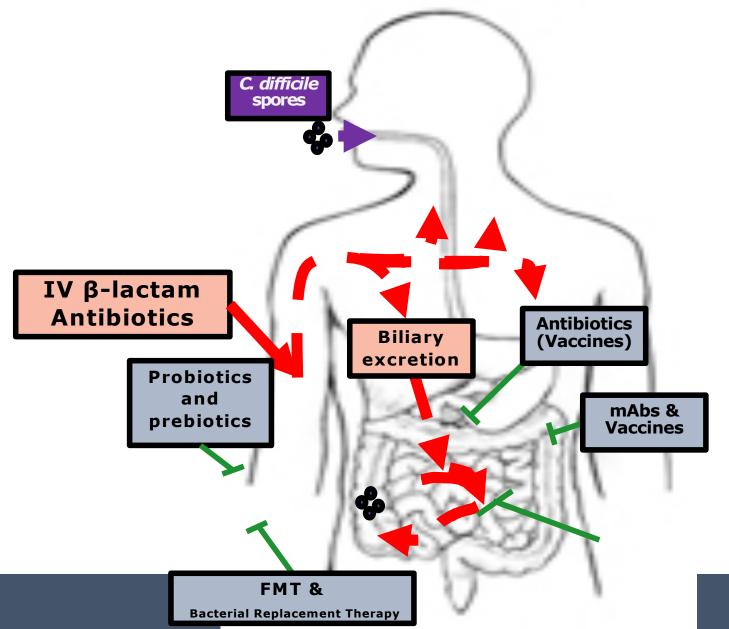




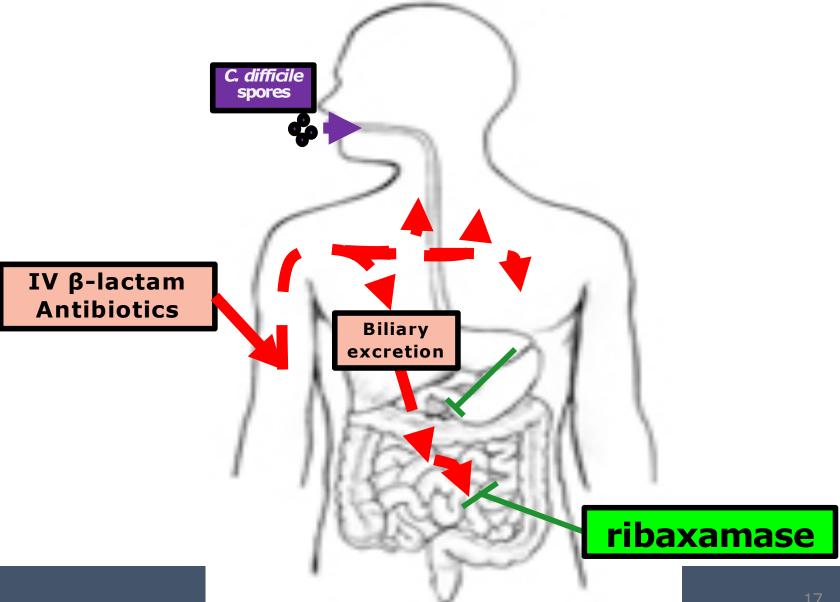














# SYN-004 (ribaxamase) rye bak' sa mase

 An orally administered, β-lactamase (an enzyme of 29 kDa) that is designed to degrade penicillins and cephalosporins

- Formulated for pH-dependent release at ≥ 5.5 (proximal small intestine)
- Expected to be orally administered during and after administration of intravenous (IV)  $\beta$ -lactam-containing antibiotics like ceftriaxone
- Intended to degrade the excess antibiotics that are excreted into the small intestine via the bile (ribaxamase is stable in human intestinal chyme)
- Designed to prevent disruption of the gut microbiome and thus protect from opportunistic GI pathogens like C. difficile



# **Early Phase Clinical Studies**

#### Phase 1 and Phase 2a

- Phase 1 two studies in normal, healthy volunteers
  - Well tolerated up to 750 mg single dose and 300 mg q.i.d. for 7 days
  - Not systemically absorbed and no anti-drug antibodies were detected
  - Roberts et al. 2016. Clinical Drug Investigation 36: 725-734
- Phase 2 two studies in subjects with functioning ileostomies, administered IV ceftriaxone ± oral ribaxamase
  - Ribaxamase degraded ceftriaxone to below the level of detection in the intestine
  - Ribaxamase did not affect the plasma PK of the ceftriaxone
  - Ribaxamase can be administered in the presence of proton pump inhibitors
  - Kokai-Kun et al. 2017. Antimicrobial Agents and Chemotherapy. 41(3):e02197-16.



# Ribaxamase: Phase 2b Proof-of-Concept Study

#### **84 Multinational Clinical Sites**

Patients admitted to the hospital for treatment of a lower respiratory tract infection

**Modified intent to treat = 412 patients** 

1:1

Ceftriaxone +

(plus a macrolide)

Ribaxamase

Ceftriaxone + Placebo (plus a macrolide)

# **Primary Endpoint:**

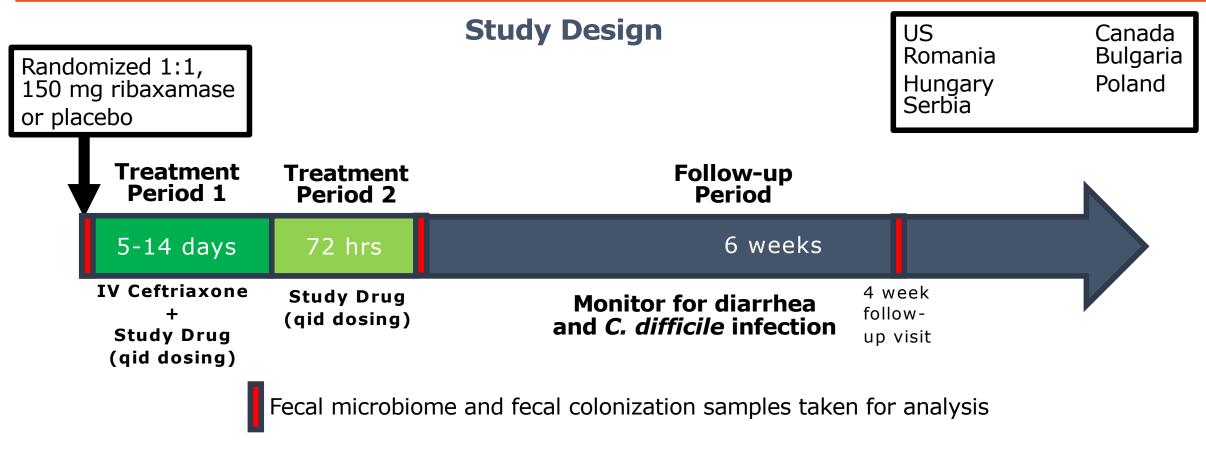
Prevention of
 C. difficile infection (CDI)

# **Exploratory Endpoints:**

 Evaluate ability to limit disruption of the gut microbiome



# **Phase 2b-Proof of Concept Study**



Diarrhea = 3 or more loose or watery stools in a 24 hour period, samples are collected CDI = local lab results for presence of *C. difficile* toxins A and/or B by an approved test (confirmed at a central lab by toxin ELISA)



# **Study Demographics and Safety Outcomes**

- 206 patients per group in mITT
- Average age of patients ~70 years old
- ~2/3 males in each group
- ~1/3 of patients in each group also received macrolides
- ~1/3 patients received concurrent drugs for stomach acidity (PPIs)

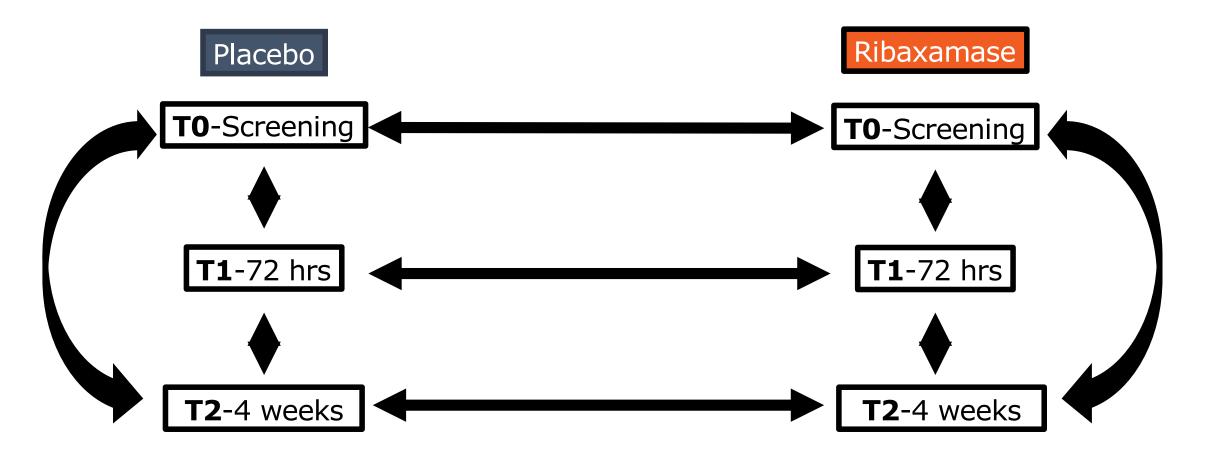
#### Adverse Events

- Percentage of subjects reporting at least one treatment emergent adverse event (TEAE) was similar between ribaxamase and placebo groups (40.8% vs. 44.2%)
- SAEs, including fatal AEs, were not considered drug-related by investigators at the clinical sites, or by an independent third-party expert, each of whom determined that SAEs were attributable to disparities in underlying health and comorbidities between the groups
- PI's assessment of **resolution of the LRTI was equivalent** in both groups at 2 weeks post treatment



# **Analysis of Changes in the Gut Microbiome**

16S rRNA sequencing of DNA extracted from fecal samples



652 samples sequenced, 229 patients, 187 full-3 sample sets

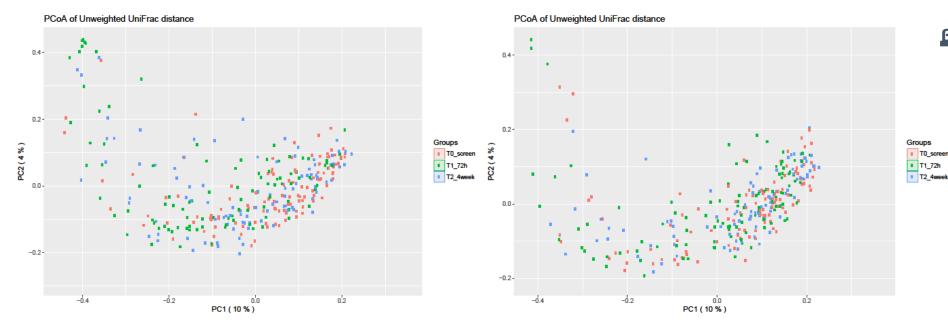


Prevented ceftriaxone-mediated loss of  $\beta$ -diversity and enhanced microbiome recovery

**Placebo** 

Ribaxamase

# Beta diversity compares the community composition of two different sample sets



Principle coordinate analysis of the  $\beta$ -diversity (unweighted Unifrac) of patient samples.  $\beta$ -diversity is the community composition of two different samples. Each dot represents one patient sample.

#### **B-diversity**

- Bray-Curtis
- Unweighted Unifrac

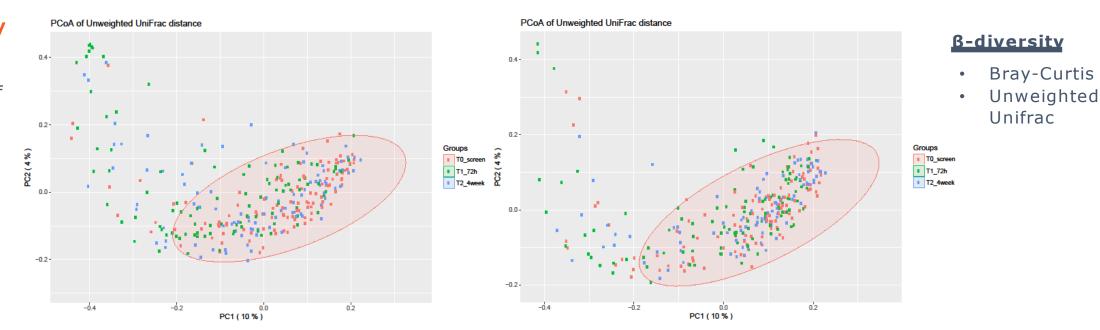


Prevented ceftriaxone-mediated loss of  $\beta$ -diversity and enhanced microbiome recovery

Placebo TO

Ribaxamase TO

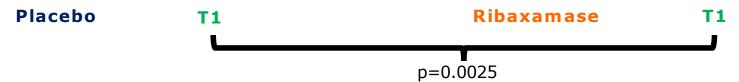
Beta diversity
compares the
community
composition of
two different
sample sets



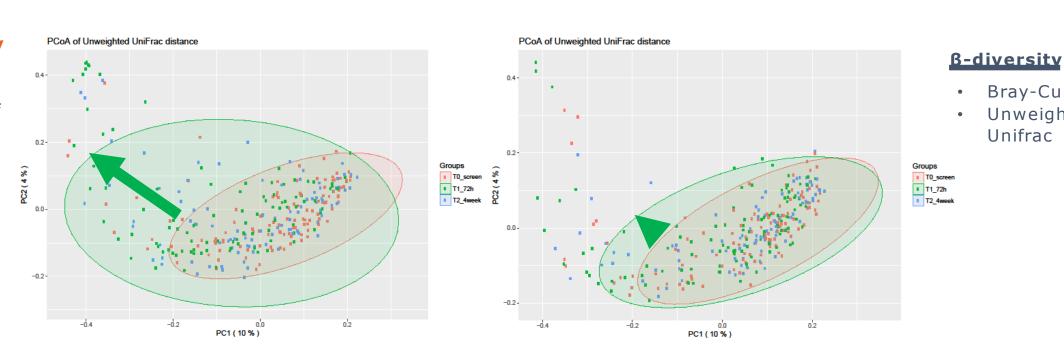
Screening samples are similar with regards to  $\beta$ -diversity in both groups



Prevented ceftriaxone-mediated loss of  $\beta$ -diversity and enhanced microbiome recovery



#### **Beta diversity** compares the community composition of two different sample sets



Placebo samples display a significant loss of β-diversity as compared with ribaxamase

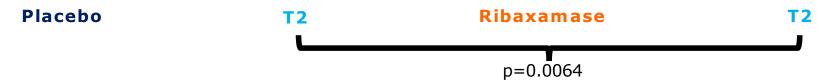


**Bray-Curtis** 

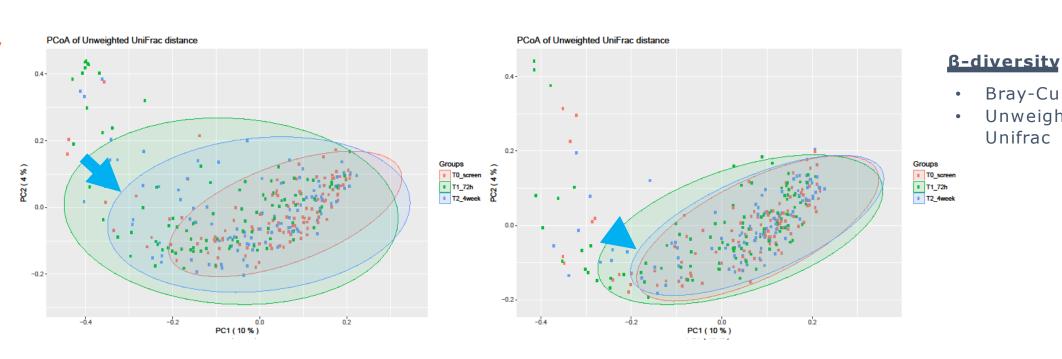
Unweighted

Unifrac

Prevented ceftriaxone-mediated loss of  $\beta$ -diversity and enhanced microbiome recovery



#### **Beta diversity** compares the community composition of two different sample sets



By T2, the ribaxamase samples have recovered to their starting diversity, but the placebo samples still display a significant loss of diversity as compared with screening

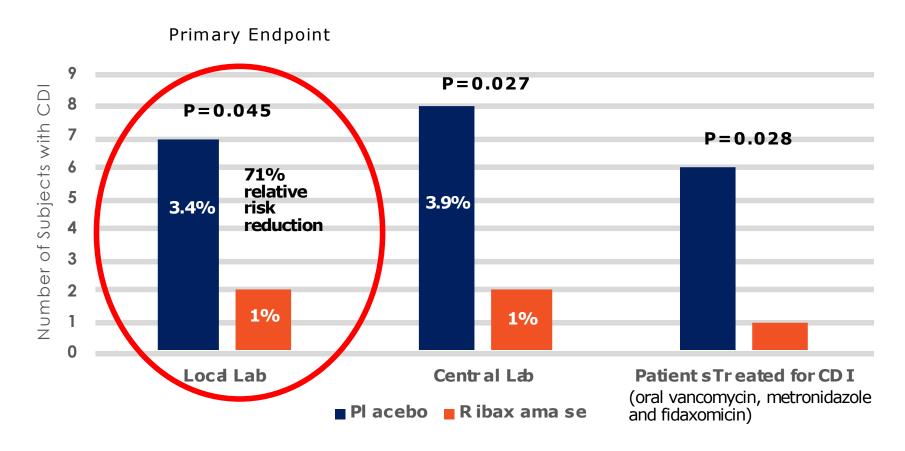


**Bray-Curtis** 

Unweighted

Unifrac

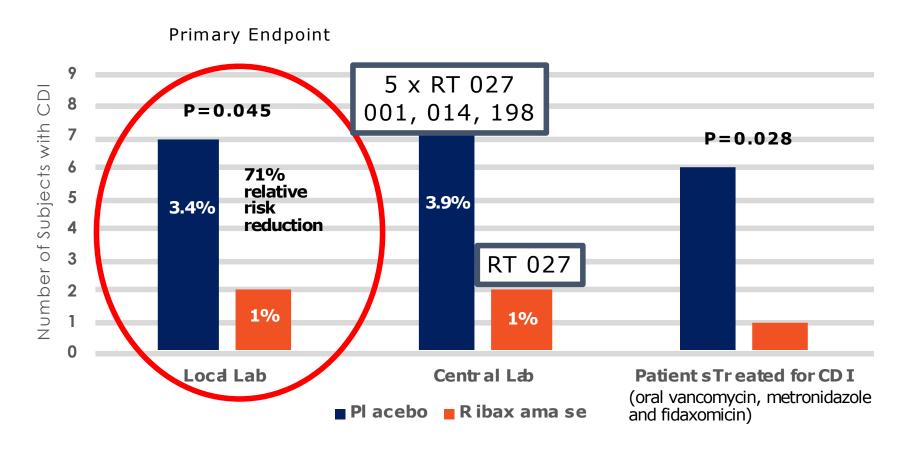
# Clostridium difficile Infection (CDI)



- No CDI patients reported previous CDI
- P-values are 1-sided based on the pre-specified Z-test
- The study was powered at 80% with 1-sided alpha=0.05



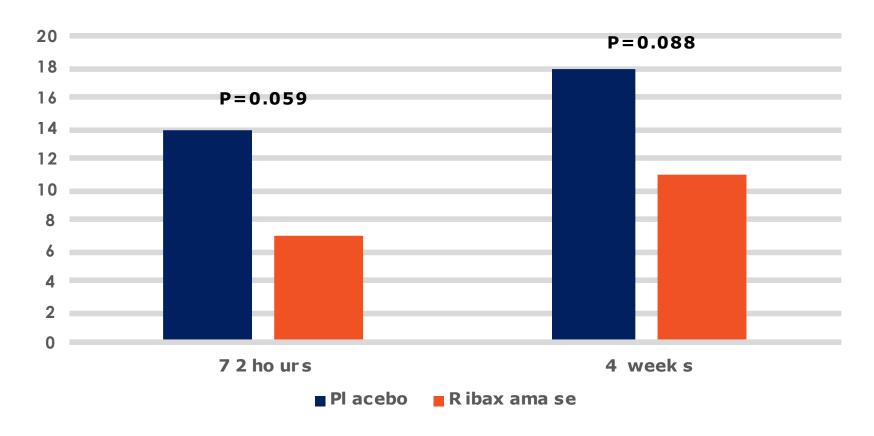
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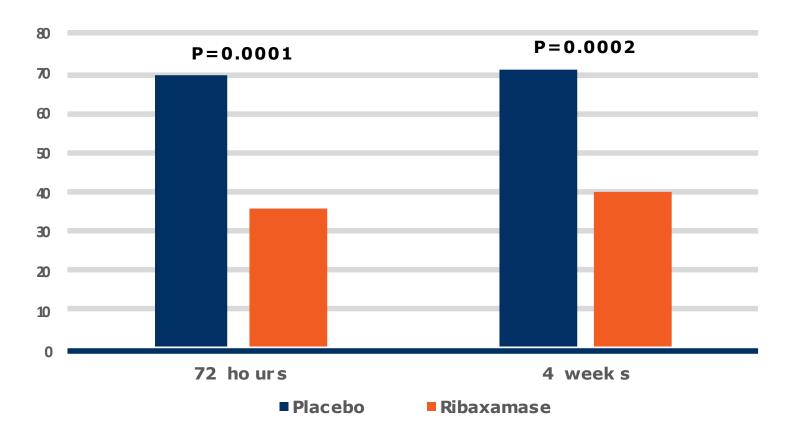
#### New C. difficile Colonization at 72 hrs & 4 weeks



- New colonization is negative on screening and then positive on a subsequent sample
  P-values are 1-sided based on the pre-specified Z-test



#### New VRE Colonization at 72 hrs & 4 weeks

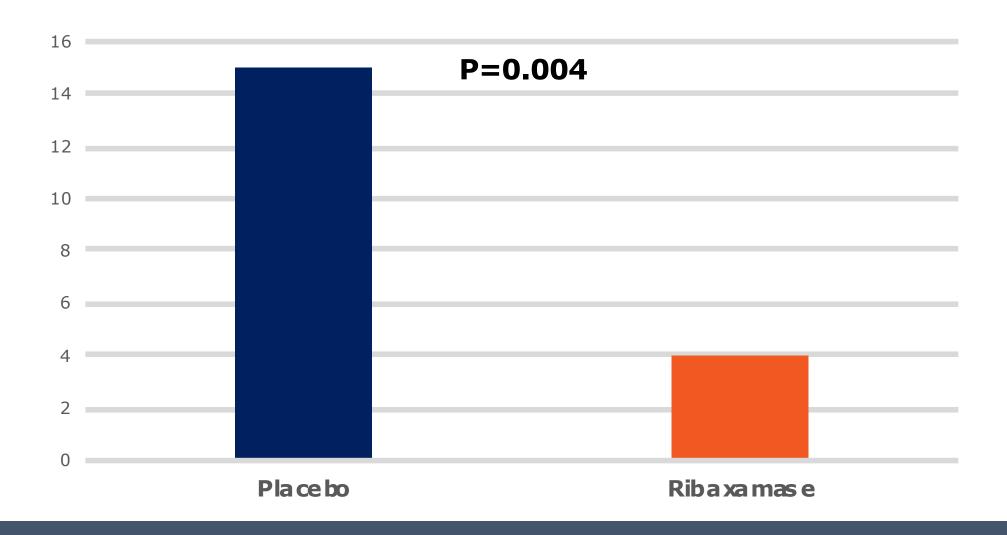


• P-values are 1-sided based on the pre-specified Z-test



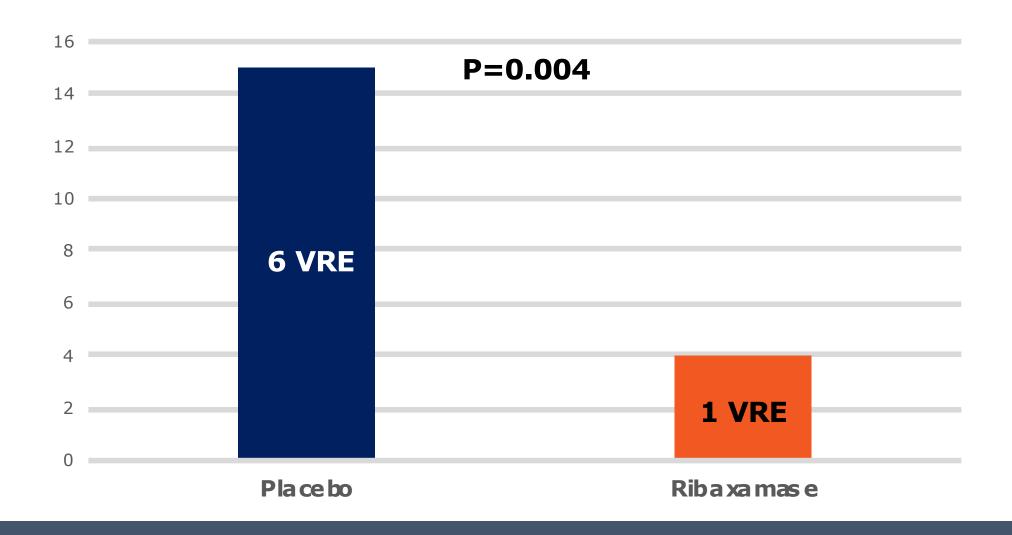
# **Comparison of Patients with Enterococcal Mono-domination**

> 30% of taxa present were enterococci at T1 or T2 based on 16S sequencing



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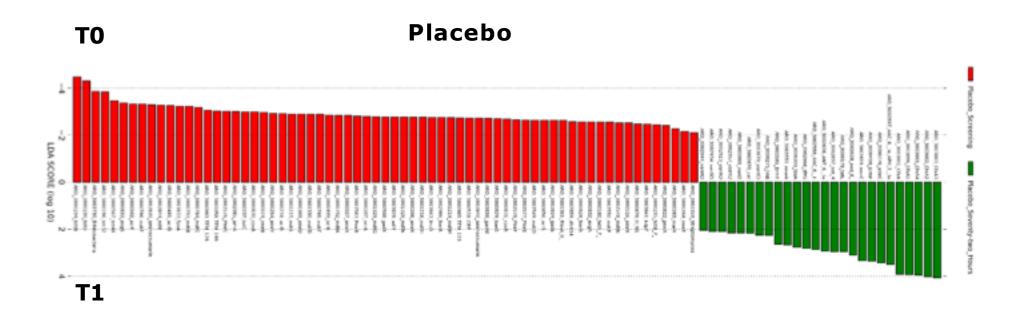


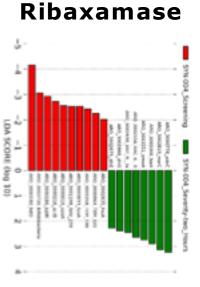


# **Resistome Analysis of Longitudinal Fecal Samples**

- DNA extracted from 350 fecal samples sequenced by whole genome shotgun sequencing (Diversigen, Houston, TX)
- Interrogated against the CARD database
- 21,000,000 DNA matches
- 1300 AMR genes identified with ~60,000 matches per sample
- Total hits per AMR gene ranged from 1 to 2.3M (tetQ, tetW)
- Including many genes of interest, β-lactamases, vancomycin and macrolide resistance genes
- Statistical analysis was performed to determine which genes significantly changed from the screening sample (T0) to the post antibiotic sample (T1) in the placebo vs. the ribaxamase patients

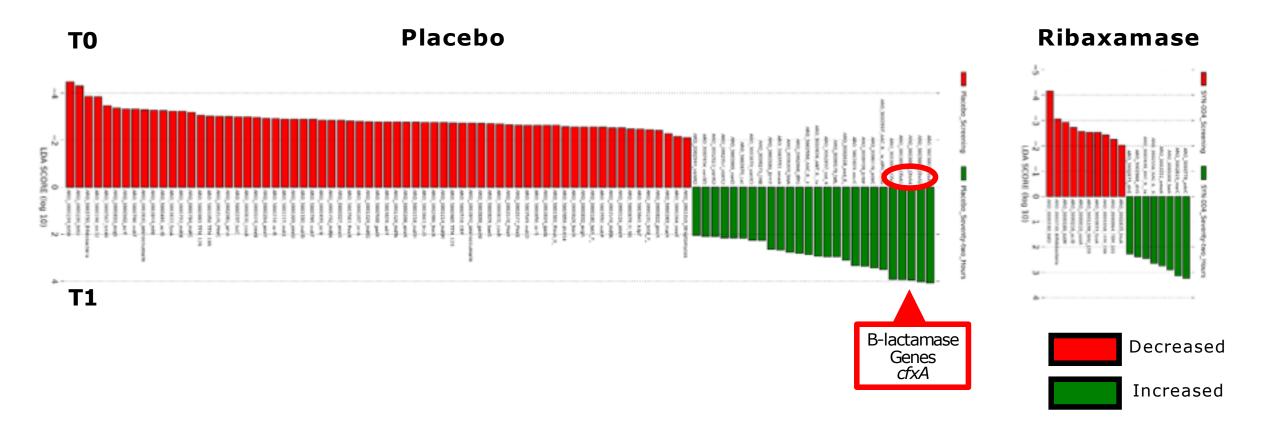




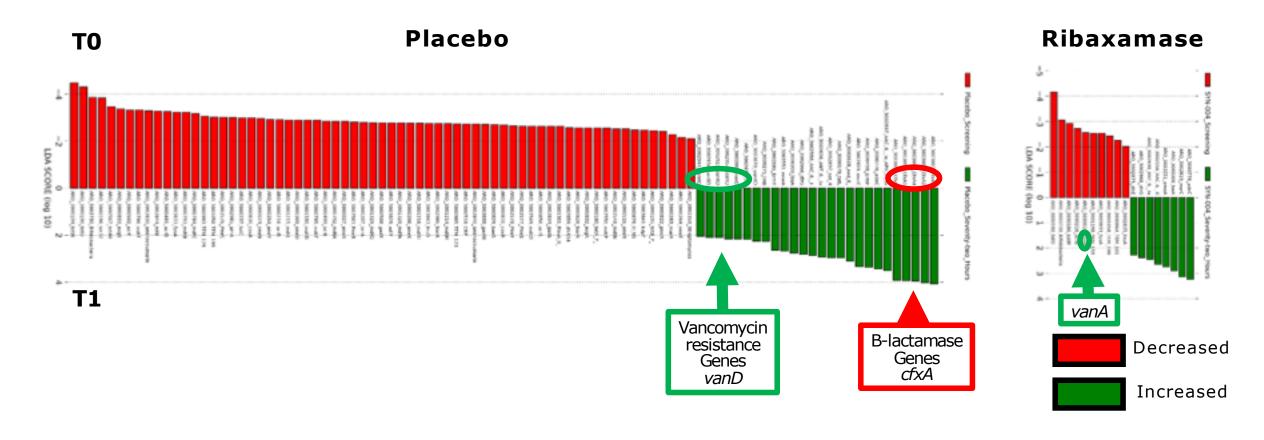




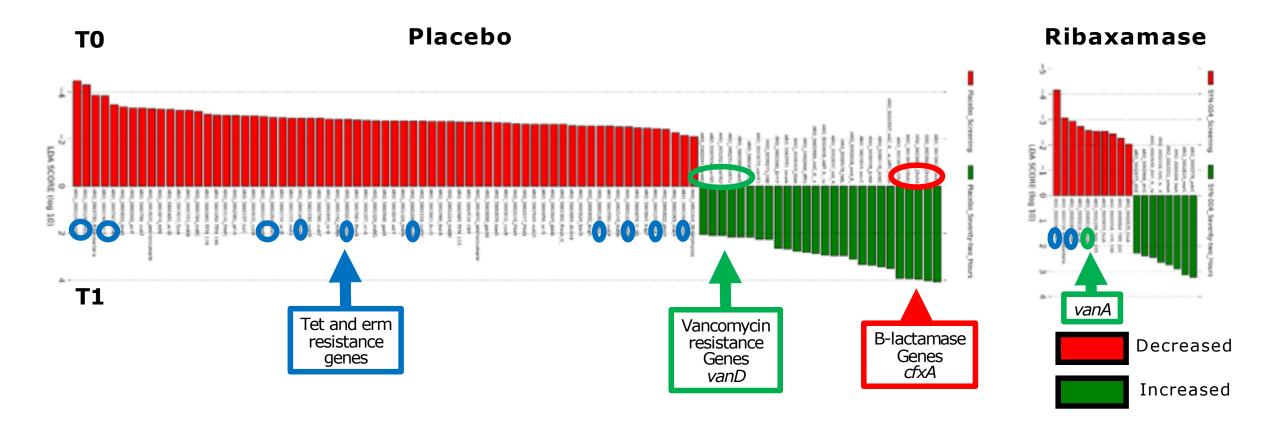






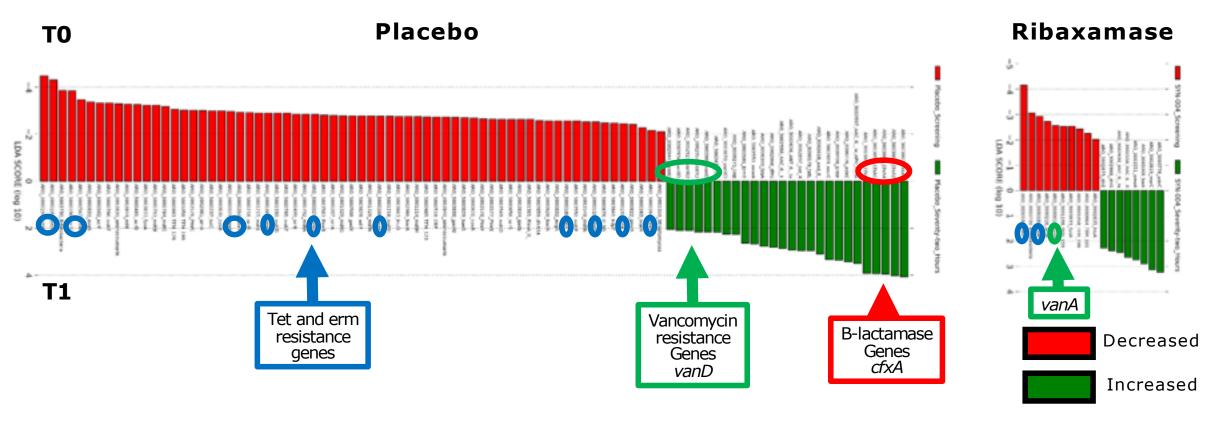








Collection point T0 to T1, Placebo vs. Ribaxamase-treated patients



Confirmed by qPCR analysis of cfxA1 and vanRD



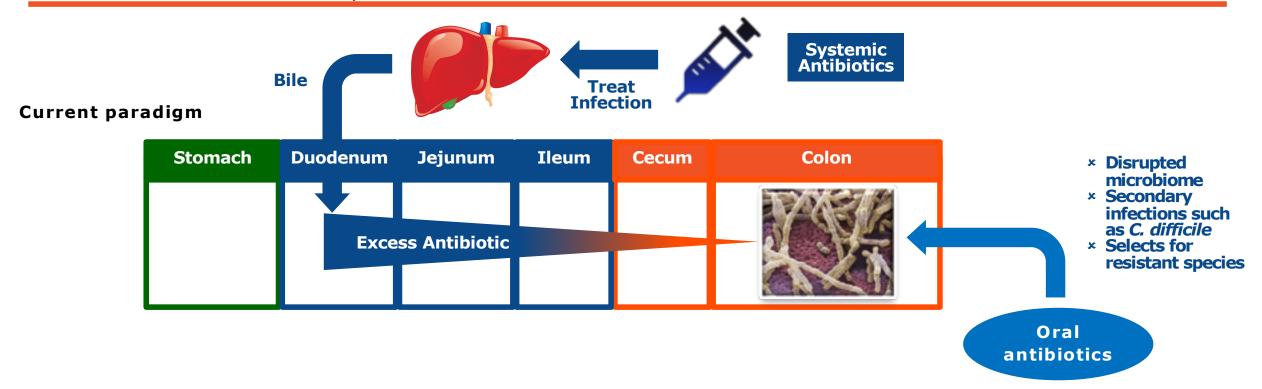
#### **Conclusions**

- Ribaxamase reduced the incidence of new onset CDI by 71% as compared with placebo (confirmed at the central lab), p=0.045
- Ribaxamase protected the diversity of the gut microbiome
- Ribaxamase appeared to be well-tolerated and not affect the cure rate for the primary infection
- Ribaxamase reduced new colonization with C. difficile and VRE, (p=0.0002), reduced enterococcal mono-domination
- Ribaxamase reduced ceftriaxone-induced changes in the gut resistome which could result in a general reduction of AMR



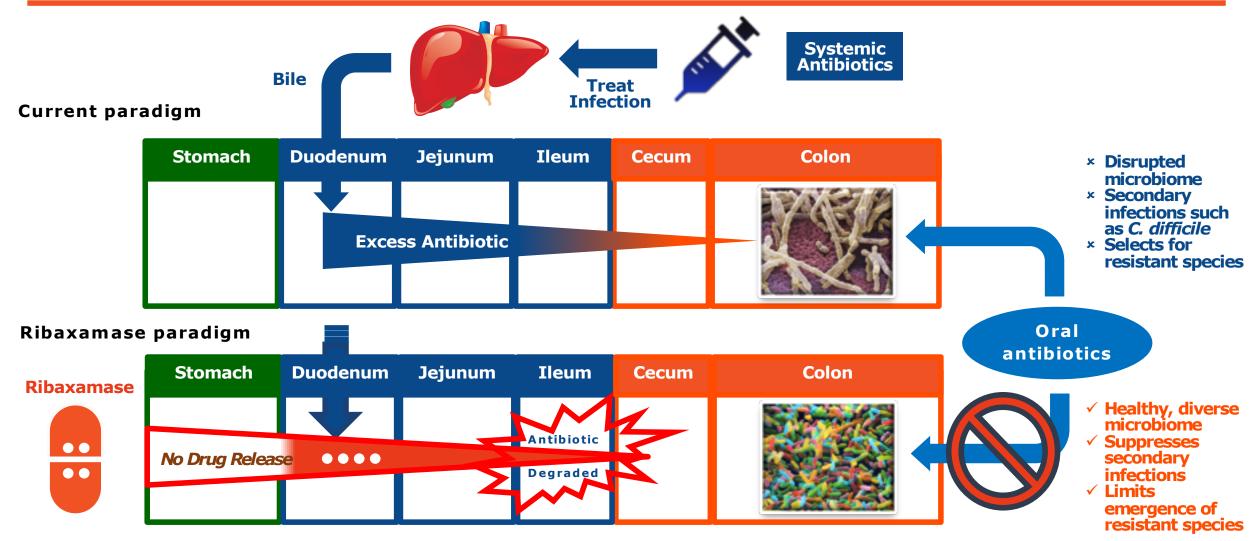
# Ribaxamase Represents a Paradigm Shift

In the Use of Intravenous  $\beta$ -lactam Antibiotics



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**Questions?**