

began in a LD state transitioned to a non-LD state after antibiotics. 12 controls were in an NLD state at baseline, of these 11 remained NLD at the second time point. 44 controls started in an LD state and all remained in LD at the second time point.

**Conclusion.** In the short term, metronidazole results in a transition of the VMB from a NLD to a *L. iners*-dominated state. There was little impact of non-nitroimidazole antibiotics on the VMB. Studies assessing longer-term impact of antibiotics on the composition of the VMB are needed.

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

### 2573. Impact of Anaerobic Antibacterial Spectrum on Cystic Fibrosis Lung Microbiome Diversity and Pulmonary Function

Michael Jason. Bozzella, DO, MS<sup>1</sup>; Hollis Chaney, MD<sup>1</sup>; Iman Sami, MD<sup>1</sup>; Geovanny Perez, MD<sup>1</sup>; Anastassios Koumbourlis, MD, MPH<sup>1</sup>; James Bost, PhD<sup>1</sup>; Robert Freishtat, MD, MPH<sup>1</sup>; Keith Crandall, PhD<sup>2</sup>; Andrea Hahn, MD, MS<sup>1</sup>; <sup>1</sup>Children's National Health System, Washington, DC; <sup>2</sup>George Washington University, Washington, DC

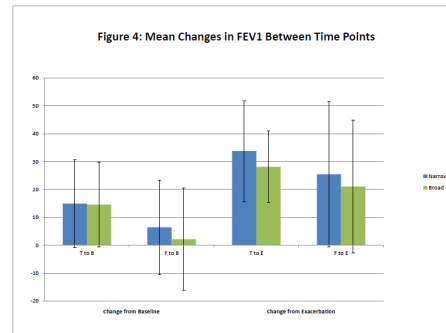
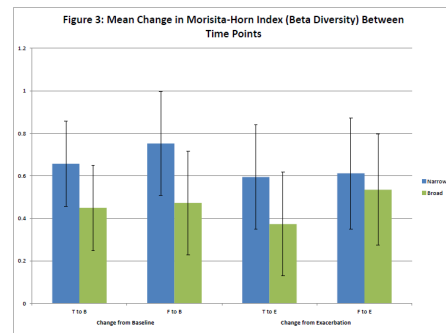
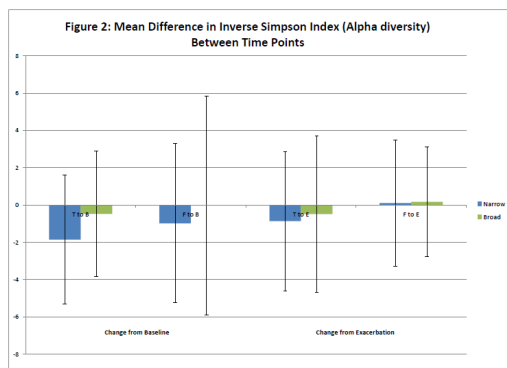
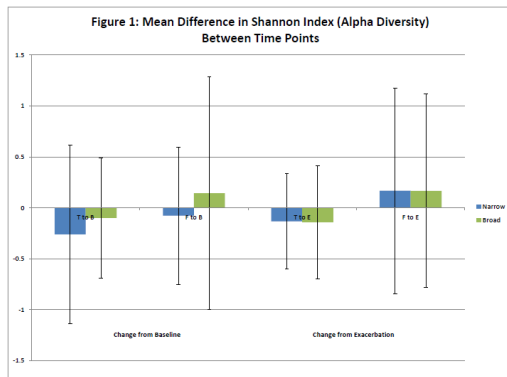
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**Background.** Next-generation sequencing has shown the cystic fibrosis (CF) lung microbiome to be a complex polymicrobial community. Anaerobic bacteria decrease in relative abundance with older age and disease progression, and may impact host inflammatory state. Persons with CF suffer from recurrent pulmonary exacerbations (PEs) that are treated with broad-spectrum antibiotics. Our objectives were to examine the effect of broad-spectrum (BS) vs narrow-spectrum (NS) anaerobic antibacterial treatment on bacterial diversity, and on pulmonary function recovery.

**Methods.** Pulmonary function tests (PFTs) and respiratory samples were collected as part of a prospective 18 month longitudinal study in CF patients at 4 time points, baseline (B), pulmonary exacerbation (E), end of exacerbation treatment (T), and follow-up (F). Treatment antibiotics were classified as broad or narrow based on anaerobic activity. 16S rRNA sequencing generated operational taxonomic units for analysis. Alpha diversity (relative abundance) was calculated via Shannon Index and Inverse Simpson formulas and  $\beta$  diversity (similarity in community composition) by Morisita-Horn (MH). Differences in diversity indices and PFTs were compared with regard to BS vs NS anaerobic activity, and statistical significance determined by GLS regression.

**Results.** Changes in alpha diversity for BS vs NS were not significantly different ( $P > 0.05$ ) (Figures 1 and 2). Community composition measured by MH was consistently more similar for NS than BS (T-B: 0.66 vs. 0.45,  $P = 0.04$ ; F-B: 0.75 vs. 0.47,  $P < 0.01$ ) (Figure 3). Recovery of forced expiratory volume in 1 second (FEV1) from E to F was significantly higher in the NS group (25.4 vs. 21.0,  $P < 0.01$ ) (Figure 4).

**Conclusion.** While antibiotic spectrum did not influence bacterial abundance, BS therapy led to higher changes in community composition from B and E onset following antibiotic administration compared with NS therapy. The differences in  $\beta$  diversity suggest BS therapy can have a lasting impact on community composition. As those receiving NS therapy had similar or better recovery of pulmonary function than those with BS, there is no indication that NS therapy leads to worse clinical outcomes. A limitation may be that children receiving BS therapy tended to have more severe disease.



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

### 2574. Temporal Changes in the Vaginal Microbiome During Treatment for Bacterial Vaginosis: Is *Lactobacillus Iners* an Important Player?

Elizabeth O. Shay, BA<sup>1</sup>; Oluwatosin Goje, MD<sup>2</sup>; Roshan Padmanabhan, PhD<sup>3</sup>; Charis Eng, MD, PhD<sup>2</sup>; <sup>1</sup>Cleveland Clinic Lerner College of Medicine, Cleveland, Ohio; <sup>2</sup>Cleveland Clinic Foundation, Cleveland, Ohio; <sup>3</sup>Lerner Research Institute, Cleveland, Ohio

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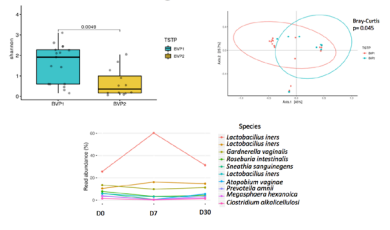
**Background.** Bacterial vaginosis (BV) is the most common vaginal condition affecting women of reproductive age and yet it remains poorly understood. Recurrent BV causes significant emotional and psychological distress and can prove difficult to resolve with currently available treatments. We aimed to investigate the microbiome of recurrent BV patients at various time points in relation to oral Metronidazole treatment.

**Methods.** Women aged 18–40 years, with recurrent BV, were prospectively enrolled. Vaginal samples (lavage) were collected at baseline (D0), at 7–10 days (D7) and 30–40 days (D30) after initiation of oral metronidazole treatment (500 mg BID, 7 days). DNA was extracted, amplified using primers targeting the V3-V4 region of the 16 srRNA, and then sequenced and processed through a hybrid Qiime MICCA bioinformatics pipeline.

**Results.** Seventeen recurrent BV patients were enrolled. Alpha diversity decreased ( $P = 0.0049$ ) after the first week of treatment with oral metronidazole, but increased ( $P = 0.0062$ ) to near baseline by D30. *Lactobacillus iners*, was the dominant *Lactobacillus*, with transient increase in this species corresponding with metronidazole treatment. There was also a decrease in *Gardnerella vaginalis* that re-normalized to baseline at 30 days. Of the 10 recurrent BV patients with data for all three time points, 4 relapsed by D30.  $\beta$  diversity differed significantly between patients that relapsed and those that did not ( $p = 0.044$ ). Alpha diversity did not differ between the groups ( $p = 0.07$ ).

**Conclusion.** The dominant *Lactobacillus* pretreatment in this cohort was *L.iners*. Oral metronidazole was associated with a decrease in alpha diversity, decrease in *G. vaginalis* and increase in *L. iners*. Although *L. iners* increased after metronidazole treatment, this increase was not sustained by D30. Treatment with metronidazole, only temporarily altered the microbiome. Further studies are needed to clarify the role of *L. iners* in recurrent BV.

#### Metronidazole Use Alters the Microbiome of Recurrent Bacterial Vaginosis Patients



Alpha diversity decreases after metronidazole treatment ( $p = 0.0049$ ). (B) Beta diversity significantly differs for recurrent bacterial patients before and after treatment with metronidazole ( $p = 0.044$ ). (C) *Lactobacillus iners* abundance increases after metronidazole treatment but eventually returns to near baseline by day 30.

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