2575. Dramatic Time-Dependent Changes of Bacterial and Fungal Taxonomic Signatures in 4 Body Regions of ICU Patients

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Background: It has been hypothesized that intensive care unit (ICU)-related complications like nosocomial pneumonia or gastrointestinal dysfunction are associated with disturbances of normal host microorganisms. However, these alterations are largely unknown in ICU patients. The bacterio- and mycobiota in 4 body regions in 14 ICU patients was investigated after admission until death or discharge to other wards.

Methods: Medical ICU patients were sampled with pharyngeal swabs, endotracheal aspirates, gastric secretions and stools or rectal swabs (in constipated patients). V1-V2 (16S rRNA gene) and eukaryoitic ITS sequencing was performed as previously described as well as denoizing, transformation into amplicon sequence variants and analysis using qiime2 and LEfSe (LDA Score > 3.0, P-value < 0.05). For sequence classification databases SILVA 132 (16S) and UNITE version 7.2 (ITS) were used.

Results: Samples were obtained at multiple time points from day 1 up to day 47 with a median of 11 samples per patient (range 2 to 17). In 11 patients all intended body regions were sampled (stool was missing in two patients and gastric secretion in two patients). The length of ICU stay and number of antibiotics administered during ICU stay was associated with loss of diversity in all investigated body sites. Taxonomic profiling showed a significant reduction of physiological members from the oral and fecal microbial community (e.g., *Clostridiales*, *Bacteroidales*, *Faecalibacterium* spp. etc.) after 2 weeks at the ICU. In contrast, *Enterococcus* spp. and *Staphylococcus* spp. were enriched in the gastric and fecal microbiota. *Candida* spp. dominated fungal communities of all body sites investigated. *Staphylococcus aureus* was associated with ITS positive, *Candida* spp. dominated samples throughout all body sites, while *Pseudomonas aeruginosa* was associated with ITS-negative samples.

Conclusion: The length of the ICU stay and the number of different antibiotics administered during the stay at the ICU are associated with severe intestinal dysbiosis, determined by loss of physiological microbes, decreased bacterial richness and domination of low-diversity fecal microbiota. Early colonization of *Candida* spp. might favor a co-existance of a *Staphylococcus* spp.-dominated microbiota in the ICU.

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

2576. The Microbiome of Recurrent Bacterial Vaginosis Compared with Asymptomatic Controls

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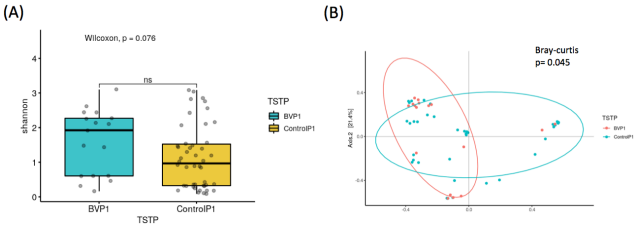
Background: Bacterial vaginosis (BV) affects nearly 1 in 3 women in the United States and is poorly understood. The study of the vaginal microbiome, using 16S rRNA-gene amplicon sequencing, has increased our knowledge of BV. We aimed to characterize the vaginal microbiome of women with recurrent BV firstly in comparison to controls, and secondly in comparison to a sub-population of our asymptomatic controls, positive for *Gardnerella vaginalis* via a vaginal pathogens DNA direct probe test (DNA probe).

Methods: Women aged 18–40 years, with recurrent BV, and asymptomatic controls were prospectively enrolled. Vaginal samples were collected from each participant. DNA was extracted, amplified using primers targeting the V3-V4 variable region of the 16S rRNA-gene, and then sequenced and processed through a hybrid Qiime MICCA bioinformatics pipeline. We also tested for G. vaginalis using the DNA probe.

Results: Seventeen recurrent BV patients and 46 controls were enrolled. B diversity (P = 0.045), but not alpha diversity (P = 0.076) differed between groups. The genera *Gardnerella* and *Prevotella* were relatively more abundant, while Lactobacillus was relatively less abundant in recurrent BV vs. control groups. Of the patients for whom results of the DNA probe for *Gardnerella vaginalis* were available, 11 (69%) recurrent BV patients and 14 (35%) controls were positive. Control patients, negative by the DNA probe test, showed decreased alpha diversity (P = 0.0001) and significantly different β diversity (P = 0.001) compared with recurrent BV patients. Neither alpha (P = 0.31) nor β (P = 0.096) diversity differed between recurrent BV patients and controls that were *G. vaginalis* positive.

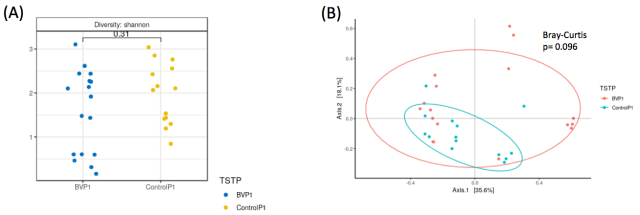
Conclusion: The microbiome of recurrent BV patients is distinct from that of asymptomatic controls; recurrent BV patients exhibit different β diversity, less *Lactobacillus* and more *Gardnerella* and *Prevotella*. Asymptomatic *Gardnerella vaginalis*-colonized controls demonstrate similar microbiome profiles to those of recurrent BV patients. These findings suggest that individual factors may influence whether or not a patient with a BV microbiomic profile experiences symptoms. Further investigation into these mechanisms could yield insights into the treatment of recurrent BV.

Recurrent Bacterial Vaginosis Patients Cluster Separately from Control Patients



(A) Alpha diversity is not significantly different between recurrent BV and control groups (p = 0.076). (B) Beta diversity significantly differs between recurrent bacterial vaginosis and control groups (p=0.045).

Control Patients Colonized with *Gardnerella Vaginalis* Have Similar Microbiomic Profiles (alpha and beta diversity) to Recurrent Bacterial Vaginosis Patients



Neither (A) Alpha diversity (p=0.31) nor (B) Beta diversity differ significantly between recurrent BV patients and control patients colonized with *Gardnerella vaginalis* (p = 0.096).

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

2577. Periodontal Disease and the Oral Microbiome in Alcohol-Dependent Individuals

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Background: Periodontal disease results from a polymicrobial infection composed of pathogenic bacteria that colonize the oral cavity, resulting in loss of periodontal attachment and alveolar bone. Periodontitis can increase the risk or exacerbate other comorbidities. Alcohol use increases the risk of periodontitis, but there is little knowledge about periodontitis among people who misuse alcohol.

Methods: As part of a larger oral and gut microbiome study, this analysis examines the oral microbiome in the occurrence and severity of periodontitis among alcohol-dependent (AD) subjects undergoing a 28-day inpatient alcohol treatment program. Tongue brushings were collected from 22 subjects within the first week of admission, and 16S rDNA sequencing was performed. All subjects had a dental examination during the inpatient stay. This analysis divided periodontal disease status into three major groups–no disease, mild or moderate disease, and severe disease. One-way ANOVA was used to compare microbial genera across the 3 groups.

Results: Nineteen (86%) of the subjects had periodontitis: 16 had mild or moderate disease, and 3 had severe disease. Statistically different microbial genera in at least one of the three groups (P ≤ 0.05 corresponding to FDR ≤ 0.25) that had a relative abundance of at least 0.5% include: *Bifidobacterium, Lactobacillus, Parvimonas, Peptostreptococcus, Porphyromonas*, and *Treponema*. Surprisingly, the subjects with no periodontitis had increased abundances of genera that are often pathogens, *Porphyromonas* and *Peptostreptococcus*. Subjects with severe periodontitis had increased abundances of known pathogens *Treponema* and *Parvimonas*, as well as *Lactobacillus*, which has been associated with dental caries.

Conclusion: We observed that periodontitis accompanies chronic AD, given that 86% of our subjects had the disease. While some microbiome differences for individuals with and without periodontitis were not consistent with the existing literature, this