Lactobacillus iners (predominant in 21%), and L. crispatus (predominant in 14%). 90% of LTNP and 45% of EC samples were Lactobacillus-dominant vs. 28% of HIV- and 30% of HIV+ATs. L. crispatus and L. iners in ECs/LTNPs had significantly different gene content and greater gene richness vs. controls. G. vaginalis -predominant communities were found in 66% of HIV- and 68% of HIV+ATs, compared to 46% of EC and 0% of LTNP. The G. vaginalis strains present in EC/LTNP also showed significantly lower gene richness and different gene content vs. controls. DISCUSSION/SIGNIFICANCE OF IMPACT: These results suggest unique VM communities among EC/LTNP, and led us to hypothesize that differential regulation of vaginal immunity drives the observed differences. The similarity between VMs of HIV- and HIV+ATs warrants further study. Larger longitudinal VM studies are needed to assess associated functional pathways and understand the etiology of VM association with HIV progression. CONFLICT OF INTEREST DESCRIPTION: The authors have no conflicts of interest to disclose.

Unraveling the role of the interaction between enteric virus and commensal bacteria in a physiological relevant model of human intestinal epithelium

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OBJECTIVES/GOALS: In the crowded environment of the intestine, selected commensal bacteria and enteric viruses interact. The biological significance of this interaction, in either normal or pathological condition is not known. To study this interaction, we are developing a physiologically relevant model of an human intestinal epithelium. METHODS/STUDY POPULATION: Intestinal biopsies (ileum region) and fecal samples of 6 healthy and 6 active Crohn’s patients are being collected to derive human intestinal enteroid (HIE) lines. 2D-polarized HIE will be first characterized with studies of epithelial permeability, tight junctions and cell type composition, and co-cultured with matching fecal samples. The (co-)cultures will be then infected with human norovirus (HNoV), our model enteric virus, and infection will be quantified by RT-qPCR. In addition, the interaction of HNoV with bacteria derived from healthy or Crohn’s will be determined quantitatively by flow cytometry (viral tagging) and qualitatively by 16S sequencing of the total versus HNoV-bound bacterial species. RESULTS/ANTICIPATED RESULTS: Crohn’s patients are characterized by a microbiome dysbiosis and, in particular, by a high abundance of Enterobacteriaceae. HNoV interacts with Enterobacter cloacae, and interestingly, HNoV infection is associated with exacerbation and reactivation of Crohn’s disease. By re-creating the intestinal milieu of healthy and Crohn’s patients, we expect that the kinetics of infection by HNoV will be higher in Crohn’s as compared to healthy volunteers. In addition, by studying the composition of the HNoV-bound bacterial component of Crohn’s versus healthy volunteers, we will be able to identify the contribution of selected bacteria to the expected increase of infection. DISCUSSION/ SIGNIFICANCE OF IMPACT: With this study, we will fill the gap of knowledge on the importance of commensal bacteria and enteric virus interactions in healthy and diseased condition. This new knowledge will be paramount for the identification of novel strategies to combat highly prevalent virus infections.
Association between Brain Volumes and Posttraumatic Stress Disorder in Intensive Care Unit Survivors

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OBJECTIVES/GOALS: To explore the severity of posttraumatic stress disorder (PTSD) symptoms in association with hippocampal and amygdala volumes in ICU survivors. We hypothesize that the severity of posttraumatic stress symptoms in ICU survivors is associated with lower volumes of both the hippocampus and amygdala.

METHODS/STUDY POPULATION: Secondary analysis of the VISIONS study, a prospective sub-study of the BRAIN-ICU cohort, which included survivors of critical illness. Patients were screened for preexisting PTSD before discharge. The PTSD Checklist Specific (PCL-S) was used at 3 and 12 months to evaluate the ICU as a traumatic experience. A score of >30, indicated significant symptoms of PTSD. A Philips Achieva 3T MRI scanner was used to scan patients at both discharge and 3-month follow-up. To compare median brain volumes at discharge and 3 months for those with and without significant PTSD symptomatology (PCL-S ≥30) at 3 and 12 months, we used a Kruskal-Wallis (KW) equality-of-populations rank test.

RESULTS/ANTICIPATED RESULTS: The median age for our sample was 58.5 (52.6, 63.7). One-third of the sample was female, and 90% were Caucasian. Fifty-seven percent of individuals (N = 12) had at least one prior mental health diagnosis, with two having a prior history of PTSD. One third of individuals experienced delirium during their critical illness. At 3-month follow up, there were three patients with PTSD symptomatology and one at 12-month follow up.

Median brain volumes (hippocampus or amygdala) did not differ between individuals with or without PTSD symptomatology at either 3 or 12 months (p-values for all tests >0.05). DISCUSSION/SIGNIFICANCE OF IMPACT: Although our study did not reveal significant differences in brain volumes between PTSD patients and non-PTSD patients, sample size is a major limitation and larger scale studies should be undertaken to elucidate possible neurobiological markers of PTSD in ICU survivors. CONFLICT OF INTEREST DESCRIPTION: Dr. Wilson would like to acknowledge salary support from the Vanderbilt Faculty Research Scholars Program (1KL2TR002245), HL111111 and GM120484. Drs. Ely and Jackson as well as Mrs. Kiehl all receive funding for their time working on this investigation from AG035117 and HL111111. Dr. Ely would additionally like to acknowledge salary support from the Tennessee Valley Healthcare System Geriatric Research Education and Clinical Center (GRECC). Dr. Ely will also disclose additional funding for his time from AG027472 and having received honoraria from Orion and Hospira for CMEE activity; he does not hold stock or consultative relationships with those companies. The authors would like to acknowledge the following: this work was conducted in part using the resources of the Center for Computational Imaging at Vanderbilt University Institute of Imaging Science and the Advanced Computing Center for Research and Education at Vanderbilt University, Nashville, TN, and study data were collected and managed using REDCap electronic data capture tools hosted at Vanderbilt University.