

## SESSION 7640 (SYMPOSIUM)

### GUT MICROBIOME IN OLDER MEN: FINDINGS FROM THE OSTEOPOROTIC FRACTURES IN MEN STUDY

Chair: Michelle Shardell

Co-Chair: Lisa Langsetmo

Discussant: Ryan Demmer

There is great interest in identifying determinants and health consequences of the human gut microbiota, the dynamic population of microorganisms living in the human digestive tract. However, the role of gut microbiota in the health of older adults has received considerably less attention than that among younger or middle-aged adults. Findings among younger age groups are not necessarily generalizable to older adults due to differences in lifestyle, health conditions, and medication usage. Therefore, understanding the role of gut microbial communities in aging-related phenotypes is an emerging gerontology research priority. To fill this significant knowledge gap, the Osteoporotic Fractures in Men (MrOS) Study Microbiome Ancillary Study was conducted in 2014-2016, coinciding with the parent study's 4th clinic visit. A total of 912 men with mean aged 84.2 (standard deviation=4.0) years provided fecal samples, and 16S ribosomal RNA target gene sequencing was used to characterize the gut microbiota composition. In this symposium, we present findings on the first research projects completed with these data. Dr. Lisa Langsetmo will characterize the association between objectively measured physical activity and the composition of gut microbiota. Dr. James Shikany will present dietary patterns, another lifestyle determinant of gut microbiota. Dr. Deborah Kado will focus on a specific micronutrient, vitamin D, and its metabolites as another factor that may influence the gut microbiota in older men. Lastly, Dr. Michelle Shardell will overview the analytical challenges of microbiome research and illustrate an approach to quantify the potential role of gut microbiota composition and weight in older men.

### COMPARING ANALYTICAL METHODS FOR GUT MICROBIOME AND AGING: GUT MICROBIOTA AND BODY WEIGHT IN THE MROS

Michelle Shardell,<sup>1</sup> Neeta Parimi,<sup>2</sup> Lisa Langsetmo,<sup>3</sup> Eric Orwoll,<sup>4</sup> James Shikany,<sup>5</sup> Deborah Kado,<sup>6</sup> and Peggy Cawthon,<sup>2</sup> 1. *University of Maryland School of Medicine, Baltimore, Maryland, United States*, 2. *California Pacific Medical Center, San Francisco, California, United States*, 3. *University of Minnesota, Minneapolis, Minnesota, United States*, 4. *Oregon Health & Science University, Portland, Oregon, United States*, 5. *University of Alabama at Birmingham, Birmingham, Alabama, United States*, 6. *University of California, San Diego, La Jolla, California, United States*

Gut microbiome datasets comprise microbial taxa relative abundances that necessarily sum to 1; analysis ignoring this feature may produce misleading results. We assessed 163 genera from the first batch of Microbiome Ancillary Study (n=530) stool samples and examined associations between microbiota and body weight. We compared conventional Bayesian linear regression (BLR) and network analysis to their compositional counterparts, adjusting for past weight and other covariates. Conventional BLR

identified Roseburia and Dialister (positive association) and Coprococcus-1 (negative association) after multiple comparisons adjustment (P<.0125). No conventional network module was associated with weight. Using compositional BLR, men with higher Coprococcus-2 and Acidaminococcus had higher weight, whereas men with higher Coprococcus-1 and Ruminococcus-1 had lower weight (P<.05), but findings were non-significant after multiple comparisons adjustment. Two compositional network modules with respective hub taxa Blautia and Faecalibacterium were associated with weight (P<.01). Findings depended on analytical workflow; compositional analysis is advocated to appropriately handle the sum-to-1 constraint.

### THE ASSOCIATIONS BETWEEN PHYSICAL ACTIVITY AND GUT MICROBIOTA AMONG OLDER COMMUNITY-DWELLING MEN

Lisa Langsetmo,<sup>1</sup> Abigail Johnson,<sup>1</sup> Ryan Demmer,<sup>1</sup> Kristine Ensrud,<sup>1</sup> Eric Orwoll,<sup>2</sup> and James Shikany,<sup>3</sup> 1. *University of Minnesota, Minneapolis, Minnesota, United States*, 2. *Oregon Health & Science University, Portland, Oregon, United States*, 3. *University of Alabama at Birmingham, Birmingham, Alabama, United States*

We determined the relationship between objectively measured physical activity (PA) and the gut microbiome among community-dwelling older men from the Osteoporotic Fractures in Men (MrOS) cohort participants at Visit 4 (2014-16). Eligible men (n=373, mean age 84 y) included participants with 5-day activity assessment and stool samples analyzed for 16S marker genes. Armband data together with sex, height, and weight were used to estimate total steps and energy expenditure. We used linear regression analysis, principal coordinate analysis, zero-inflated Gaussian models to assess association between PA and  $\alpha$ -diversity,  $\beta$ -diversity, and specific taxa, respectively, with adjustments for age, race, BMI, clinical center, library size, and number of chronic conditions. There was a slight association between PA and  $\beta$ -diversity but no association with  $\alpha$ -diversity. After multivariate adjustment, those who had higher step counts vs lower step counts had higher relative abundance of Cetobacterium and lower relative abundance of Coprobacillus, Adlercreutzia, Erysipelotrichaceae CC-115.

### ASSOCIATIONS OF DIETARY PATTERNS WITH THE GUT MICROBIOTA IN OLDER, COMMUNITY-DWELLING MEN

James Shikany,<sup>1</sup> Ryan Demmer,<sup>2</sup> Abigail Johnson,<sup>2</sup> Katie Meyer,<sup>3</sup> Kristine Ensrud,<sup>2</sup> Eric Orwoll,<sup>4</sup> Deborah Kado,<sup>5</sup> and Lisa Langsetmo,<sup>2</sup> 1. *University of Alabama at Birmingham, Birmingham, Alabama, United States*, 2. *University of Minnesota, Minneapolis, Minnesota, United States*, 3. *University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, United States*, 4. *Oregon Health & Science University, Portland, Oregon, United States*, 5. *University of California, San Diego, La Jolla, California, United States*

We investigated associations of dietary patterns with composition and diversity of the gut bacterial microbiota in 517 community-dwelling older men (mean age 84.3 y) who were participants in the Osteoporotic Fractures in Men