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

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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

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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 α -diversity, β-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 β -diversity but no association with α -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

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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

(MrOS) study. Eligible participants provided a stool sample and completed a food frequency questionnaire at the MrOS Visit 4 in 2014-2016. Dietary patterns were derived by factor analysis. 16S rRNA target gene sequencing was performed. Linear regression and PERMANOVA considered variation in alpha and beta-diversity by dietary pattern, and metagenomeSeq assessed taxonomic variation by dietary pattern. In multivariable-adjusted models, greater adherence to the Western pattern was positively associated certain taxa, including Alistipes, Desulfovibrio, Dorea, Eubacterium, and Ruminococcus, while greater adherence to the prudent pattern was positively associated with certain taxa, including Faecalibacterium, Lachnospira, and Paraprevotella. Dietary patterns were not associated with measures of alpha diversity; beta diversity measures were significantly associated with both Western and prudent patterns.

VITAMIN D METABOLITES AND THE GUT MICROBIOME IN OLDER MEN

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We examined the bidirectional impact of vitamin D on the composition and diversity of the gut microbiome in 567 MrOS men. Vitamin D metabolites were measured using LC-MSMS and stool sub-operational taxonomic units defined from 16S ribosomal RNA sequencing data using Deblur and Greengenes 13.8. Men's mean serum level of 25(OH)D was in the sufficient range. Faith's Phylogenetic Diversity and non-redundant covariate analyses revealed that 1,25(OH)2D explained 5% of variance in α -diversity; the other non-redundant covariates of site, race, recent antibiotic and antidepressant use explained another 6%. In β-diversity analyses using unweighted UniFrac, 1,25(OH)2D was the strongest factor assessed, explaining 2%. Random forest plot analyses identified 12 taxa, 6 in the phylum Firmicutes, positively associated with either 1,25(OH)2D and/or [1,25(OH)2D/25(OH)D] activation ratio. Higher levels of the active 1,25(OH)2D, but not 25(OH)D, were associated with butyrate producing bacteria. Men with favorable vitamin D activation profiles also had greater gut microbial diversity.

SESSION 7645 (SYMPOSIUM)

MULTIDIMENSIONAL BENEFITS OF WEIGHT MANAGEMENT IN OLD AGE: THE MOBILITY AND VITALITY LIFESTYLE PROGRAM

Chair: Steven Albert Co-Chair: Elizabeth Venditti Discussant: Barbara Nicklas

The high prevalence of overweight or obesity in older adults is a public health concern because obesity is associated with risk of mobility disability. The benefits of brief community-based lifestyle interventions that promote modest weight loss and increased physical activity are

unclear. We assessed the impact of a 13-month lifestyle intervention, the Mobility and Vitality Lifestyle Program (MOVE UP), delivered by community health workers (CHW), on a variety of outcomes, including weight loss, performancebased lower extremity function (Short Physical Performance Battery, SPPB), activity, diet, and health-related quality of life (CDC U48 DP005001). The 32-session behavioral weight management intervention enrolled 303 community-dwelling adults (90.4% of those eligible), who were followed for 12 months (2015-19). Participants completed the program at 26 sites led by 22 CHWs. Participants were age (sd) 67.7 (4.1) and were mostly female (87%). 22.7% were racial minorities. The mean (sd) BMI at baseline was 34.7 (4.7). Median weight loss in the sample was 5% of baseline body weight. SPPB total scores improved by +0.31 units (p < .006), gait speed by +0.04 m/sec (p < .0001), and time to complete chair stands by -0.95 sec (p < .0001). Presenters will assess the effect of MOVE UP on activity, diet, fatigue, and healthrelated quality of life. A final paper examines implementation of MOVE UP and how site and CHW factors affected outcomes. Findings suggest that promoting healthier eating, weight loss, and physical activity in a community setting is an effective strategy for reducing risk of disability in older adults.

WEIGHT LOSS IMPROVES HRQOL PHYSICAL FUNCTION AND VITALITY MORE IN BLACKS THAN WHITES

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Participant-reported outcomes are important. Prior MOVE UP reports show ≥5% weight loss was not significantly associated with depressive symptoms but was associated with positive SPPB physical function and the Physical Component Score of the SF-36 HRQOL scale. We examined the SF-36 subscales that showed, a priori, clinically meaningful +5.0-point increases over 13 months, the change in subscales per 5% weight loss, and variability by race. Among all participants (n =240) several subscales show significant pre-post changes [mean (SD)] but only Vitality [+5.6 (15.4)] and Physical Function [+5.0 (16.7)] meet the criterion. Blacks (n = 60) compared to Whites (n = 172) had higher baseline scores on these subscales, were less likely to lose $\geq 5\%$ (31.7% vs. 59.9%), but mixed regression models indicate that those who did demonstrated a larger change on Vitality (+5.2; p<0.048) than Whites (+3.1; p<0.0003). Studying weight loss and HRQOL associations in larger minority samples is needed.

PERCEIVED PHYSICAL FATIGABILITY IMPROVES AFTER A WEIGHT MANAGEMENT INTERVENTION

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The effects of a weight loss and physical activity (PA) intervention on improving perceived physical fatigability are unknown. We examined this question in a subset (n=79) of