Visceral Adiposity Is Associated With Shifts in the Gut Bacterial and Phage Microbiome in Postmenopausal Women

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Objectives: More than 40% of U.S. adults are obese. Obesity, and in particular abdominal obesity, is associated with increased risk for developing a variety of chronic diseases. Obesity, aging, and menopause are each associated with differential shifts in the gut microbiome. We examined the association of visceral adiposity tissue (VAT) and the gut bacterial and phage microbiome.

Methods: We selected postmenopausal women (mean age 78 yrs) from the extremes of VAT (n = 25 per group; low VAT area (45.6 ± 12.5 cm^2) and high VAT area (179.6 ± 30.4 cm^2)) using data from dual x-ray absorptiometry (DXA) scans and performed shotgun metagenomic sequencing on fecal DNA collected at the time of DXA scan. Women with history of hypertension, diabetes, hormone therapy use, or antibiotic use within 90 days from sample collection were excluded. DNA libraries were prepared using the Illumina Nextera XT library preparation kit and libraries were sequenced on an Illumina HiSeq platform to generate 150-bp paired-ends reads. We examined the α-diversity (Shannon or Chao1), principal coordinate analysis β-diversity distances, and prevalence of microbiome taxa comparing the high vs. low VAT groups.

Results: There was no significant difference in α-diversity or β-diversity between VAT groups. At the phyla level, women with high VAT displayed elevated Bacteroidetes and Proteobacteria proportional abundance ($p < 0.05$). At the species level, women with low VAT displayed significantly elevated proportional abundance of *Alistipes shahii*, *Anaerostipes hadrus*, and *Blautia wexlerae*. Women with high VAT area displayed significantly elevated *Parabacteroides distasonis*, *Bacteroides uniformis*, and *Roseburia intestinalis*. Women with high VAT displayed elevated proportional abundance of Escherichia phage TL-2011b ($p < 0.05$).

Conclusions: Data suggest that postmenopausal women with high VAT display a differential bacterial microbiome and phage profile compared to postmenopausal women with low VAT, consistent with changes seen with age. Moreover, we identified an elevated proportional abundance of *Alistipes shahii*, *Anaerostipes hadrus*, and *Blautia wexlerae* in women with low VAT, suggesting potential for anti-obesity activity of these microbes in postmenopausal women.