

## Assessing the Microbiome

### Take Home Message

The *microbiome*, the set of microorganisms that live in and on us, is known to play an important role in many diseases and conditions. We investigated whether there might be a link between the gut microbiome and overall health in a cohort of 47 individuals between the ages of 65 and 97, with varying degrees of frailty. We found several groups of bacteria that associated positively and negatively with frailty, age, and time of residence at Northwood; although more work needs to be done, these results suggest that microorganisms are important indicators and potential drivers of health.

Why was this research done?	How was the research done?
<p>Research into the human microbiome has exploded over the last fifteen years, with many studies aiming to show a “baseline” in healthy adults, track the progression of bacteria in the earliest years of life, and show associations between diet and gut bacteria. Another important line of investigation has been the relationships between the microbiome and disease; although its role in infectious disease is obvious, there appear to be links with chronic conditions such as inflammatory bowel disease and diabetes. These observations raise the question of possible linkages between the microbiome and the health of older subjects, especially as pertains to increasing frailty.</p> <p>Although research is still in early stages and applications of microbiome research are only starting to emerge, assessing potential linkages between aging, frailty, and the microbiome can point to microbes as complementary indicators of frailty, and potentially drivers of frailty (especially if potentially harmful bacteria identified in previous studies can be found here). Although the present study cannot show causality, it may suggest ways in which the microbiome might be manipulated (for example, through probiotics) to promote overall patient health.</p>	<p>A total of forty-seven residents at Northwood participated in the study to its completion. Fecal samples, surrogates for the gut microbiome, were collected approximately weekly for a maximum of five weeks, subject to sample collection and availability. Frailty was assessed via a Comprehensive Geriatric Assessment and expressed as a score from 0 (no indicators of frailty) to a theoretical maximum of 1 (all checked indicators of frailty identified). Comprehensive data about diet, medication, and specific health conditions were also collected.</p> <p>No patient interventions were carried out.</p> <p>Since culturing of all microorganisms present in a fecal sample is not feasible, we used the commonplace procedure of DNA sequencing to identify members of each individual’s microbial community. All of the 205 samples collected were assessed for species composition using the sequencing procedure, and one sample from each study subject was also sequenced in greater depth to identify possible roles of microbes in each subject. Examples of functions include antimicrobial resistance and virulence factors, but also potentially indicators of metabolic pathways of benefit to the human host.</p>

<p>The research question is “can we find associations between overall health and their microbiome in older subjects?”</p>	
<p><b>What were the findings?</b></p>	<p><b>What can be done next?</b></p>
<p>Provide a brief, plain language summary of the results (e.g. stats, key themes) and what they mean.</p> <ul style="list-style-type: none"> <li>- Different groups of bacteria were found to associate with age, frailty, and residence time at Northwood; some of these were consistent with groups identified previously in the literature. Surprisingly, the strongest associations were found with age rather than frailty.</li> <li>- Although previous studies have detected associations between health and biodiversity, we found no strong relationships to this effect.</li> <li>- The majority of individuals had a very stable microbiome over the month of sampling. There were, however, exceptions where individuals showed substantial changes over the month. One intriguing example was an individual that exhibited <i>Pseudomonas</i> and other potential pathogens in week 1, but switched to a microbiome dominated by the candidate probiotic genus <i>Akkermansia</i></li> <li>- Potential pathogenic organisms were identified. The majority of individuals showed little evidence of antimicrobial resistance, apart from some resistance to beta-lactam and tetracycline antibiotics. However, three outlier individuals showed evidence of resistance to cephalosporins, polymyxin, and elevated resistance to beta-lactams.</li> </ul>	<p>The most salient outcome of the research is the identification of potential pathogens, especially those carrying genes that confer resistance to specific antibiotics.</p> <p>We are currently carrying a study that examines the question of antimicrobial resistance in greater depth, with the specific objective of developing computational tools to rapidly identify these genes in samples collected from patients. In combination with the emergence of rapid, on-site DNA sequencing devices, these approaches will yield rapid diagnostic tools within the next few years.</p> <p>Given the absence of easy-to-interpret correlations between age, frailty and the microbiome, specific diagnostics are not suggested at this time. However, one interesting area of further investigation would be the triggers for microbiome instability that were observed in some subjects.</p>