



## PERMÉABILITÉ INTESTINALE, INFLAMMATION SYSTÉMIQUE ET AGING

*Geroscience*, 2018 Jun;40(3):257-268. doi: 10.1007/s11357-018-0026-y. Epub 2018 Jun 5.

### Composition and richness of the serum microbiome differ by age and link to systemic inflammation.

Buford TW<sup>1</sup>, Carter CS<sup>2</sup>, VanDerPol WJ<sup>3</sup>, Chen D<sup>3</sup>, Lefkowitz EJ<sup>3,4</sup>, Eipers P<sup>5</sup>, Morrow CD<sup>5</sup>, Bamman MM<sup>5</sup>.

#### Author information

- 1 Department of Medicine, University of Alabama at Birmingham, Birmingham, AL, 35294, USA. [twbuford@uabmc.edu](mailto:twbuford@uabmc.edu).
- 2 Department of Medicine, University of Alabama at Birmingham, Birmingham, AL, 35294, USA.
- 3 Biomedical Informatics, Center for Clinical and Translational Sciences, University of Alabama at Birmingham, Birmingham, AL, USA.
- 4 Department of Microbiology, University of Alabama at Birmingham, Birmingham, AL, USA.
- 5 Department of Cell, Developmental, and Integrative Biology, University of Alabama at Birmingham, Birmingham, AL, USA.

#### Abstract

Advanced age has been associated with alterations to the microbiome within the intestinal tract as well as intestinal permeability (i.e., "leaky gut"). Prior studies suggest that intestinal permeability may contribute to increases in systemic inflammation—an aging hallmark—possibly via microorganisms entering the circulation. Yet, no studies exist describing the state of the circulating microbiome among older persons. To compare microbiota profiles in serum between healthy young (20-35 years, n = 24) and older adults (60-75 years, n = 24) as well as associations between differential microbial populations and prominent indices of age-related inflammation. Unweighted Unifrac analysis, a measure of  $\beta$ -diversity, revealed that microbial communities clustered differently between young and older adults. Several measures of  $\alpha$ -diversity, including chao1 ( $p = 0.001$ ), observed species ( $p = 0.001$ ), and phylogenetic diversity ( $p = 0.002$ ) differed between young and older adults. After correction for false discovery rate (FDR), age groups differed (all  $p$  values  $\leq 0.016$ ) in the relative abundance of the phyla Bacteroidetes, SR1, Spirochaetes, Bacteria\_Other, TM7, and Tenericutes. Significant positive correlations ( $p$  values  $\leq 0.017$  after FDR correction) were observed between IGF1 and Bacteroidetes ( $p = 0.380$ ), Spirochaetes ( $p = 0.528$ ), SR1 ( $p = 0.410$ ), and TM7 ( $p = 0.399$ ). Significant inverse correlations were observed for IL6 with Bacteroidetes ( $p = -0.398$ ) and TM7 ( $p = -0.423$ ), as well as for TNF $\alpha$  with Bacteroidetes ( $p = -0.344$ ). Similar findings were observed at the class taxon. These data are the first to demonstrate that the richness and composition of the serum microbiome differ between young and older adults and that these factors are linked to indices of age-related inflammation.

**KEYWORDS:** Aging; Inflammation; Leaky gut; Microbiome; Microbiota

PMID: 29869736 PMCID: PMC6060185 DOI: 10.1007/s11357-018-0026-y

*"Un âge avancé a été associé à des altérations du microbiome du tractus intestinal ainsi qu'à une perméabilité intestinale (c'est-à-dire un "leaky gut"). Des études antérieures suggèrent que la perméabilité de l'intestin peut contribuer à augmenter l'inflammation systémique - une caractéristique emblématique du vieillissement - éventuellement via l'entrée de micro-organismes dans la circulation. Pourtant, il n'existe pas d'études décrivant l'existence d'un microbiome circulant chez les sujets âgés.*

*Comparons les profils du microbiote sérique entre des adultes jeunes en bonne santé (20-35 ans, n = 24) et des adultes plus âgés (60-75 ans, n = 24), ainsi que les associations entre les différentes populations microbiennes et les principaux marqueurs de l'inflammation liée à l'âge. Une analyse Unifrac non pondérée, soit une mesure de la  $\beta$ -diversité, a révélé que les communautés microbiennes se groupaient différemment selon qu'il s'agisse d'adultes jeunes ou âgés. (...) Ces données sont les premières à démontrer que la richesse et la composition du microbiome sérique diffèrent entre les adultes jeunes et âgés, et que ces différences correspondent aux marqueurs de l'inflammation liée à l'âge."*