Age and sex-associated variation in the microbiome of a rhesus macaque social group

Mareike Cora Janiak
Michael Montague
Catalina Villamil
Michala Stock
Amber Trujillo
Allegra DePasquale
Joseph Orkin
Samuel Bauman Surratt
Olga Gonzalez
Michael Platt
Melween Martinez
Susan Antón
Gloria Dominguez-Bello
Amanda Melin
James Higham

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Abstract

Our bodies are home to millions of microscopic organisms – our microbiome. While these microbes have many important functions that maintain our health and well-being, our microbiome changes as we age, which can cause infection or inflammation. Understanding these changes in humans is difficult due to our long lifespan and confounding factors such as healthcare and diet. A recent study used an animal model – free-ranging rhesus macaques – to better understand the changes that occur in our microbiomes with age, using a cross-sectional dataset of oral, rectal, and genital swabs collected from 105 macaques belonging to one social group. In contrast to adult macaques, researchers found that infant gut microbial communities had higher abundances of *Bifidobacterium* and *Bacteroides*, consistent with a milk-rich diet. The genital microbiome varied substantially between males and females, and while penile microbiomes changed with age, vaginal microbiomes did not. Oral microbiome composition changed with age, with infants exhibiting the most distinct microbiome. While longitudinal studies are needed to confirm these changes in the same animals throughout their lives, this study highlights the age-related microbial changes that occur in primates and identifies rhesus macaques as an ideal model to help prevent age-related diseases in humans.