

Urbanization is linked to a shift in gut microbiota among the Maasai pastoralists in Kenya

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Background: Urbanization is marked by significant shifts in lifestyle and dietary practices, particularly in low- and middle-income countries. Understanding how these lifestyle changes affect the gut microbiome, can provide insights into how to curb the increasing prevalence of non-communicable diseases. Most research on gut microbiome has focused on the high-income urban areas, leaving a substantial knowledge gap in remote and transitioning environments along the urbanization gradient.

Objective: This study identifies the differences in gut microbiome between rural and urban Maasai populations in Kajiado County, Kenya.

Methods: This comparative cross-sectional study was conducted among 33 randomly selected respondents, 19 from urban and 14 from rural populations. Anthropometric data were collected, and body mass index was computed. Additionally, stool samples from a single bowel movement were collected, placed in Cary-Blair transport media, and transported in cold boxes to a metagenomic laboratory in Nairobi. DNA was extracted, 16S rRNA gene sequencing was performed to characterize the gut microbiome, and the data were compared with BMI.

Results: There was no statistical difference in BMI between the urban ($22.5 \text{ kg/m}^2 \pm 5.2$) and the rural ($20.9 \text{ kg/m}^2 \pm 4.1$) respondents ($p=0.333$). The gut microbiome of the urban respondents exhibited a higher *Firmicutes* to *Bacteroidetes* (F/B) ratio [$t(18)=1.6$, $p=0.07$] compared to the rural respondents. At the same time, the gut microbiota of the rural respondents showed a higher abundance of *Prevotella* [$t(31)=-1.9$, $p=0.035$]. A higher F/B ratio is potentially associated with increased risks of obesity, inflammation, and other metabolic conditions, while a high abundance of *Prevotella* suggests a diet rich in complex carbohydrates.

Conclusion: The study findings suggest that urbanization, even among the pastoralist communities, can impact the gut microbiome, potentially contributing to adverse metabolic health outcomes.