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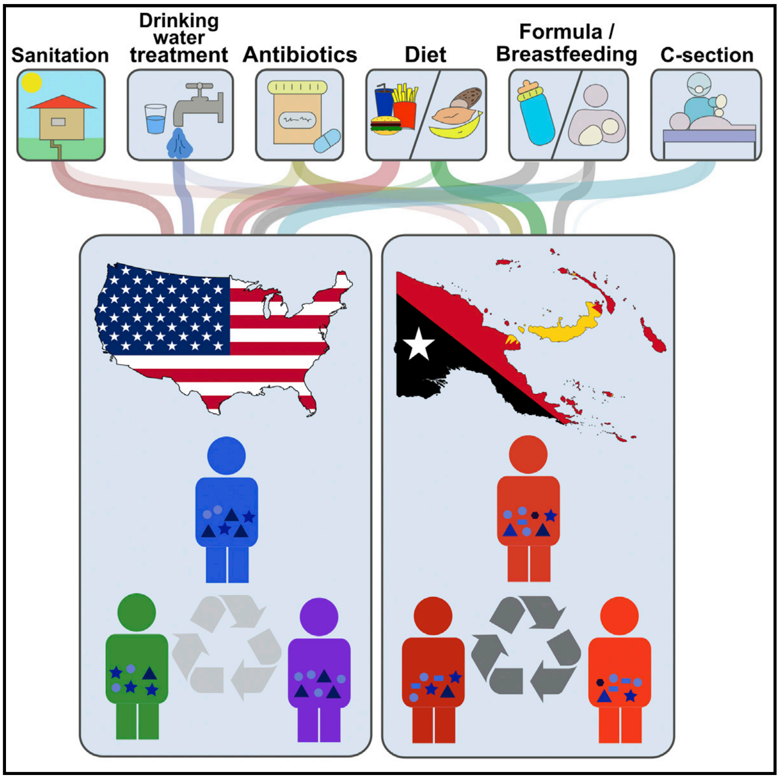
The Gut Microbiota of Rural Papua New Guineans: Composition, Diversity Patterns, and Ecological Processes

Graphical Abstract



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In Brief

The gut microbiome differs substantially between westernized and non-industrialized societies. Martínez et al. characterize the fecal microbiome structure, diversity patterns, and assembly processes in rural Papua New Guineans and United States residents and propose a model by which reduced bacterial dispersal due to modern lifestyle practices causes microbiome alterations associated with westernization.

Highlights

- The fecal microbiota in PNG is more diverse but less individualized than in the US
- Most bacterial species are shared among PNG and the US, but abundance profiles differ
- Impact of lifestyle on ecological assembly processes might explain these patterns
- Westernization may decrease bacterial dispersal rates, altering microbiota structure

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The Gut Microbiota of Rural Papua New Guineans: Composition, Diversity Patterns, and Ecological Processes

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SUMMARY

Although recent research revealed an impact of westernization on diversity and composition of the human gut microbiota, the exact consequences on metacommunity characteristics are insufficiently understood, and the underlying ecological mechanisms have not been elucidated. Here, we have compared the fecal microbiota of adults from two non-industrialized regions in Papua New Guinea (PNG) with that of United States (US) residents. Papua New Guineans harbor communities with greater bacterial diversity, lower inter-individual variation, vastly different abundance profiles, and bacterial lineages undetectable in US residents. A quantification of the ecological processes that govern community assembly identified bacterial dispersal as the dominant process that shapes the microbiome in PNG but not in the US. These findings suggest that the microbiome alterations detected in industrialized societies might arise from modern lifestyle factors limiting bacterial dispersal, which has implications for human health and the development of strategies aimed to redress the impact of westernization.

INTRODUCTION

The human gastrointestinal tract is colonized by an abundant and diverse microbial consortium (the gut microbiota) that impacts host physiology and health. Recent research in animal models has demonstrated an essential contribution of the gut microbiota in non-communicable diseases that have higher prevalence in westernized societies (western diseases), such as inflammatory bowel disease, autoimmune diseases (i.e., multiple sclerosis, type 1 diabetes, and rheumatoid arthritis), obesity-associated metabolic aberrancies, allergies, and colon cancer (Berer et al., 2011; Devkota et al., 2012; Koeth et al., 2013; Noval Rivas et al., 2013; Ochoa-Repáraz et al., 2010; Trompette et al., 2014; Wen et al., 2008). Epidemiological data further support that lifestyle practices (caesarian sections, antibiotic use, and formula feeding of infants) that affect the assembly of the microbiota are associated with an increased risk of disease (Conradi et al., 2013; Marra et al., 2009; Risnes et al., 2011; Tenconi et al., 2007). These observations have led scientists to hypothesize that aberrant (dysbiotic) microbiomes (Noverr and Huffnagle, 2005) and/or the loss of specific symbionts (Blaser and Falkow, 2009) predispose westerners to non-communicable diseases. On the other hand, non-industrialized societies are burdened with a high incidence of infectious diseases, including life-threatening diarrhea (Pop et al., 2014). The importance of the gut microbiome for non-communicable diseases in westernized societies and the prevalence of infectious diseases in non-industrialized communities warrant studies that compare the microbiome in both settings.

To determine how lifestyle, and especially westernization, resonates in the structure of the human gut microbiome, scientists have begun to systematically compare the fecal microbiota of humans from non-industrialized societies to those with a westernized lifestyle (De Filippo et al., 2010; Schnorr et al., 2014; Yatsunenko et al., 2012). Studies to date have compared the gut microbiome of Europeans and Americans to that of children in Burkina Faso (De Filippo et al., 2010), children and adults in Malawi and Amazonian Amerindians (Yatsunenko et al., 2012), and adult Hadza hunter-gatherers in Tanzania (Schnorr et al., 2014). Collectively, these studies have revealed higher fecal bacteria α diversity (within individuals) and lower β diversity (between individuals) in non-industrialized societies. These diversity patterns were accompanied by major compositional differences, likely reflecting distinct dietary habits, such as higher proportions of fiber-utilizing bacteria and lower abundances of bacterial lineages associated with intake of animal-derived products. Although these studies have begun to unravel the biogeographic