

Editorial

Rural and Urban Schism: It is more than Economical... It is Ecological

Senan S*

Department of Dairy Science, South Dakota State University, USA

***Corresponding author:** Suja Senan, PhD,
Department of Dairy Science, South Dakota State University, Brookings, SD 57007, USA**Received:** May 30, 2016; **Accepted:** June 06, 2016;**Published:** June 07, 2016

Editorial

When was the last time you stood on the weighing balance and felt satisfied with the figures looking up to you? Well, after you conveniently subtract the few pounds that your attire may attribute, let me tell you to confidently subtract three pounds off from your total weight. This big chunk is contributed by the miniscule invisible inhabitants (microbes) that outnumber the quantum of cells in your body by a factor of ten. Human beings thus carry a second genome of millions of microbial genes located in the various body cavities especially the gastrointestinal tract, termed as the microbiome [1]. The relationship between man and microbe has evolved in close association with each other for millions of years. The human host provides a nutrient-rich environment while the microbiota performs functions including digestion, and modulation of the immune system. Humans were rightly termed as “holobionts,” because their state of wellness and disease are a result of the intricate balance between human and microbial cells [2]. Recent advances in high-throughput sequencing technologies or metagenomic sequencing, have helped to demystify the relationship between constituents of the healthy human microbiome and the functional capacity of microbiome in particular diseased states like irritable bowel syndrome, obesity, diabetes, allergy, rheumatoid arthritis as well as mental health to name a few [3]. Microbiome studies have been employed to study ancestry and migrations [4].

Similar to human genes, the microbial genes are unique to each individual but unlike human genes, the microbiome exhibits greater plasticity. The primary source of the microbiome for humans is through the maternal transmission with distinctions between caesarian-section and vaginal births [5]. Second major influence on inter individual microbiome diversity is the long term dietary intake as well the short-term consumption of specific diets. The external factors that cause variations in human microbiome include human population size, mobility, mixing, lifestyle, and technologic advances affect the characteristics of the carried microbes [4]. Assemblages of microbes on a variety of the inanimate objects with which specific organisms come into contact like cleaning sponge, shower curtain, kitchen and bathroom surface, cell phone, and computer microbiomes have all been described in an effort to better understand the microbial populations with which humans interact [6,7].

Considering the external factors affecting human microbiome, we can build the hypothesis that there would be a contrast in the microbiome of urban populations in highly industrialized countries and rural populations. The driving factors coupled to geography could be diet, sanitation, use of antibiotics, parasitism, and host genetics. It has been proposed that the decreased exposure to microorganisms as well as the loss of the ancestral indigenous organisms has resulted in the prevalence of modern allergic and metabolic diseases [8]. A study by De Filippo and team in 2010 [9] compared the human intestinal microbiota from children up to 6 years old from rural Burkina Faso, whose diet was primarily composed of locally grown cereals, legumes and vegetables and children following a modern western diet. Children from rural community showed a significant abundance of bacteria known to contain a set of bacterial genes for cellulose and xylan hydrolysis that were completely lacking in the western diet following children. Also, *Enterobacteriaceae* (*Shigella* and *Escherichia*), the indicators of sanitation and hygiene were significantly underrepresented in rural than in urban children. Remarkably, the abundance of Short Chain Fatty Acid producing bacteria that were abundant in the rural children’s gut possibly helped to prevent the establishment of some potentially pathogenic intestinal microbes causing diarrhea, like *Enterobacteriaceae*, such as *Shigella* and *Escherichia*. Increased gut microbial diversity and reduced quantities of potentially pathogenic strains in rural children reinstate the “hygiene hypothesis”, indicating a role of microbiota in protecting children from pathogens as well as from gastrointestinal diseases. Lin and team in 2013 [10] compared the diversity, composition, and temporal stability of the fecal microbiota of healthy children living in an urban slum in Bangladesh with that of children of the same age range in an upper-middle class suburban community in the United States. The diet of the Bangladeshi children was carbohydrate-rich and heavily dependent on rice, bread, and lentils with rarely any meat. Their U.S. counterparts consumed typical Western diets including animal fat and protein in addition to carbohydrates and vegetables. Bangladeshi and U.S. children had distinct fecal bacteria community membership and structure. The microbiota of Bangladeshi children was enriched in *Prevotella*, *Butyrivibrio*, and *Oscillospira* and depleted in *Bacteroides* relative to U.S. children. Similarly a community of human hunter-gatherers, the Hadza of Tanzania, had higher levels of microbial richness and biodiversity than Italian urban controls with a peculiar arrangement of *Clostridiales* taxa that may have enhanced the Hadza’s ability to digest and extract valuable nutrition from fibrous plant foods [11]. Recently Obregon-Tito and team in 2015 [12] attempted to establish a relationship between lifestyle and gut microbiota through metagenomic characterization of fecal samples from hunter-gatherer and traditional agriculturalist communities in Peru and an urban-industrialized community from the USA. They found that in addition to taxonomic and metabolic differences between urban and traditional lifestyles, hunter-gatherers formed a

distinct sub-group among traditional people like the gut *Treponema* were found in non-human primates and all traditional peoples studied to date, suggesting they were the symbionts lost in urban-industrialized societies.

Hunter-gatherer communities harbor novel microbiome profiles that depart from those previously described in urban and semi-urban settings, and that may be tailored to the specific dietary sources within each population.

Recently, at Anand Agricultural University, India, we conducted a double blind placebo controlled crossover trial comprising of feeding periods and intermittent washout periods of 4 weeks with 72 elderly community dwellers aged 65-75 years from rural and urban centers of the city. There was no clear separation between the urban and rural metagenomes detected based on their taxonomic compositions, but it was observed that the rural population could be earmarked as having a higher abundance of *Clostridium*, *Shigella* and *Listeria*. That was indicative of their hygiene status and sanitation standards. Probiotic consumption brought down the level of *Shigella*, *Clostridium* and *Listeria* in rural and urban population. The members of the rural community did not respond better than the urban members to probiotic therapy which could be due to an over representation of *Shigella* and *Clostridium* in the gut microbiome [13].

The diverse findings from the metagenomics analysis of the gut microbiome from various parts of the world emphasize that biomarkers identified for a particular nationality or geographic location cannot be extrapolated to other human populations. This calls for a whole-community genetic analysis of geographically diverse human microbiota studies to explicitly understand the interaction between geographic factors and the gut microbiota.

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