The human gut microbiome of Latin America populations: a landscape to be discovered

Fabien Magne[a], *Miguel L. O'Ryan*[a], *Roberto Vidal*[a], *and Mauricio Farfan*[b]

Purpose of review
The gut microbiome is critical for human health, and its alteration is associated with intestinal, autoimmune and metabolic diseases. Numerous studies have focused on prevention or treatment of dysbiotic microbiome to reduce the risk or effect of these diseases. A key issue is to define the microbiome associated with the state of good health. The purpose of this review is to describe factors influencing the gut microbiome with special emphasis on contributions from Latin America. In addition, we will highlight opportunities for future studies on gut microbiome in Latin America.

Recent findings
A relevant factor influencing gut microbiome composition is geographical location associated with specific genetic, dietary and lifestyle factors. Geographical specificities suggest that a universal 'healthy microbiome' is unlikely.

Summary
Several research programs, mostly from Europe and North America, are extensively sequencing gut microbiome of healthy people, whereas data from Latin America remain scarce yet slowly increasing. Few studies have shown difference in the composition of gut microbiome between their local populations with that of other industrialized countries (North American populations). Latin America is composed of countries with a myriad of lifestyles, traditions, genetic backgrounds and socioeconomic conditions, which may determine differences in gut microbiome of individuals from different countries. This represents an opportunity to better understand the relationship between these factors and gut microbiome.

Keywords
dysbiosis, geographic populations, gut microbiome, Latin America, lifestyle

INTRODUCTION

The human gut is colonized by trillions of commensal bacteria known as microbiota or microbiome, playing a role in human physiology and health. Although the definition of terms 'microbiota' (microbial taxa inhabiting the human gut) and 'microbiome' (catalog of microbes and their genes) are in fact slightly different, both are often used interchangeably in the literature [1]. In our review, we shall use preferentially the term 'microbiome'. The gut microbiome is considered symbiont to the human body and has been classified as a 'superorganism' [2]. This microbiome is important to extract, synthetize and for the absorption of many nutrients and metabolites (such as bile acids, lipids, amino acids, vitamins and short-chain fatty acids), prevents colonization by potential pathogenic microorganisms, educates and contributes to the development of the immune system [2]. In addition, recent studies highlight a role of the gut microbiome in the development of the nervous system and its regulation [3–5]. Despite the fact that various roles are recognized for the gut microbiome, a profound understanding of the influence of this bacterial community on host physiology remains far from complete. It is quite clear that alterations or instability of the gut microbiome composition can be responsible for host physiology disorders leading to specific diseases [6]. The development of more advanced low-cost generation sequencing techniques has allowed a significant increase in the number and quality of studies on gut microbiome

[a]Microbiology and Mycology Program, ICBM and [b]Department of Pediatrics, Center of Molecular Studies, Faculty of Medicine, University of Chile, Santiago, Chile

Correspondence to Miguel L. O'Ryan, MD, Microbiology and Mycology Program, ICBM, Faculty of Medicine, University of Chile. Av. Independencia 1027, Independencia, Santiago, Chile. Tel: +56 2 2978 6642; e-mail: moryan@med.uchile.cl

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KEY POINTS

- The state of 'dysbiosis' characterized by an alteration of the gut microbiome composition has been observed not only in gastrointestinal diseases but also in autoimmune diseases, metabolic disease and neurologic disorders.
- It is difficult to conceptualize the existence of a 'universal microbiome' common to all individuals, a concept that has to consider the geographical localization of the population.
- Lifestyles, particularly the diet and host genetic factors, impact the composition of gut microbiome. Latin America includes genetically diverse populations with various lifestyles and different socioeconomic situations.
- The rapid development status of several Latin American countries may provide an interesting scenario to better understand transformations of the gut microbiome and its role in physiopathology of specific diseases associated with 'development' (chronic and metabolic diseases).

association with several disease states. The state of 'dysbiosis' characterized by an alteration of the gut microbiome composition has been observed not only in gastrointestinal diseases but also in autoimmune diseases, metabolic disease and neurologic disorders (Table 1) [6]. Various bacterial groups have been associated with these diseases, although for the same disease, results can be conflicting. Table 2 depicts two diseases intensively studied during the last decades: obesity and inflammatory bowel disease. A common finding among studies is the decrease of bacterial diversity observed during dysbiosis of the gut microbiome associated with disease states [18]. The microbiome is thought to be playing a role in the development in these disorders, disrupting intestinal homeostasis. For some, this role has been confirmed by inducing the disease phenotype after transplanting the altered human microbial community to germ-free animals. For example, transplantation of the microbiome from obese human to genetically 'normal' axenic mouse alters metabolism parameters implicated in the development of obesity [19]. Consequently, the gut microbiome is seen as a potential therapeutic target to improve health. In the future, dietary interventions, fecal transplantation, use of prebiotic and probiotic strains as 'natural methods' to 'normalize' the gut microbiome composition and thus for intestinal homeostasis can be envisioned. But first it seems necessary to define the composition of a 'healthy gut microbiome', an aim that has been approached largely by two consortiums: the Human Microbiome Project in the United States and Metagenomics of the Human Intestinal Tract Project in Europe [2,20].

Table 1. Diseases associated with gut microbiome [6]

Diseases associated with gut microbiome	
Gastrointestinal diseases	Autoimmune diseases
Diarrhea	Asthma
Irritable bowel syndrome	Allergies
Inflammatory bowel diseases	Diabetes type 1
Metabolic disease	MS
Obesity	Neurologic disorders
Diabetes type 1	MS
Diabetes type 2	Autism
Atherosclerosis	Parkinson's disease

MS, multiple sclerosis.

Table 2. Bacterial groups involved in obesity and inflammatory bowel diseases

Diseases	Bacterial groups	Increased	Decreased
Obesity			
	Bacteroidetes/Firmicutes ratio	[7,8]	[9–11]
	Lactobacillus	[11]	
	Methanobacteriales		[7,8,12]
Inflammatory bowel disease			
	Bacteroidetes	IBD [13]	IBD [14]
			CD [15]
	Bifidobacteria	IBD [16]	
		CD [14]	CD [13]
		UC [13]	
	Proteobacteria	IBD [13,14]	
		CD [16]	
	Clostridium leptum group (or *Faecalibacterium prasnitzii*)		IBD [13]
			CD [17]
	Clostridium coccoides		IBD [13]

CD, Crohn's disease; IBD, inflammatory bowel disease; UC, ulcerative colitis.

THE HUMAN GUT MICROBIOME

Based mostly on studies from North American and European populations, the adult human gut microbiome is dominated by the phyla *Firmicutes* and *Bacteroidetes* that can compromise 90% of the total gut microbiome, followed in lower proportions by the phyla *Actinobacteria*, *Proteobacteria*, *Verrucomicrobia* and *Fusobacteria* [21]. Within this phyla predominance, the gut microbiome is estimated to be

composed of more than 1000 bacterial species, most of which are obligate anaerobes belonging to the genera *Bacteroides*, *Eubacterium*, *Clostridium*, *Ruminococcus*, *Peptococcus*, *Peptostreptococcus*, *Bifidobacterium* and *Fusobacterium*. The facultative anaerobes are less predominant and are represented by *Escherichia*, *Enterobacter*, *Enterococcus*, *Klebsiella*, *Lactobacillus* and *Proteus* [22,23].

For years, researchers have aimed to identify a core microbiome, at the species level, associated with a state of good health. Metagenomic analysis of the gut microbiome performed in 142 Europeans described at least 160 phylotypes (likely bacterial species) shared among all individuals, in addition to 57 phylotypes identified in more than 90% of individuals [2]. Nevertheless, other analysis of 154 individuals revealed that no phylotype was present at more than about 0.5% abundance in all samples of this study [10]. Thus, the concept of a core microbiome represented by bacterial species common to all individuals seems improbable [24], more likely, the composition at the level of bacterial species seems to be proper to each person [24,25].

Based on grouping microbial species, 'enterotypes' have been defined according to the predominance of the genera *Bacteroides*, *Prevotella* or *Ruminococcus* [26,27]; a classification which is currently in discussion [28]. Importantly, the composition of the adult gut microbiome is relatively stable throughout the adult life, although various factors influence its composition such as diet, lifestyle and the host genetic profile. In effect, in animals, gut microbiome diversity decreases from herbivore to omnivore to carnivore [29]. In humans, some have proposed that the long-term diet may determine the 'Enterotype' of an individual [27]. A diet rich in carbohydrate is associated with the '*Prevotella* Enterotype', whereas a diet rich in protein and fat animal with the '*Bacteroides* Enterotype' [27]. Clearly, diet is a major factor determining the composition of the gut microbiome.

Furthermore, similarities in the gut microbiome have been observed among individuals belonging to the same family suggesting a role for genetic similarities. The analysis of 416 twins pairs revealed a higher similarity of the gut microbiome between monozygotic compared with dizygotic twins [30]. Although the diet can be similar in a family, this study showed that the host genetic profile shapes the gut microbiome composition, although remaining unclear how genetic variations would influence the composition of the gut microbiome. Several host genes such as *MEFV* (MEditerranean FeVer), *APOA1* (Apolipoprotein A1), *NOD2* (Nucleotide-binding Oligomerization Domain-containing protein 2) and *FUT2* (Fucosyltransferase 2) influence the composition of the gut microbiome [31–35]. In 645 mice, the analysis of DNA site variations associated with phenotype variations [denominated host quantitative trait loci (QTL)] showed that 18 host QTLs were associated with abundance of specific bacterial groups [36]. Collectively, these data demonstrate that host genetic factors influence the gut microbiome and that some host genes may be of particular relevance, an issue that nevertheless requires more in-depth studies.

Studies in populations from different geographic localizations have provided important insights. For example, significant differences of gut microbiome composition were observed between European compared with Burkina Faso children. The latter presented an enrichment in *Bacteroidetes* and depletion in *Firmicutes* compared with European children, which may be the result of differences in lifestyle and/or genetic factors [37]. Other studies have also observed differences in gut microbiome composition of populations living in different continents (USA, Europe, Asia and Africa) [37–40]. Based on these results, it is difficult to conceptualize the existence of a 'universal microbiome' common to all individuals, which could be considered as 'normal' or 'healthy'. It seems quite clear that the identification of a 'normal microbiome' will have to take into account the geographical localization of the population considered.

THE HUMAN GUT MICROBIOME IN LATIN AMERICA POPULATIONS

As discussed previously, geographic localization seems to play an important role in the composition of the gut microbiome of individuals. The large majority of studies on human gut microbiome have been performed in Europe and North America, with only a few studies from others continents including Latin America.

In Latin America, studies have focused on gut microbiome characterization in healthy adults as well as adults with diverse disease processes and on the initial bacterial colonization of the neonatal gut including the impact of factors altering its composition. As depicted in Table 3, information is available from nine countries, including 12 studies in adult populations and 12 studies in children. In most, the gut microbiome has been studied using culture, qPCR (quantitative polymerase chain replication) and/or FISH (fluorescence in-situ hybridization) methods, which do not provide a complete assessment of all bacterial groups composing the gut microbiome. Briefly, culture methods only permit one to detect cultivatable bacterial species (known species), and qPCR/FISH are dependent on probe sequences. Altogether, these

Table 3. Published studies on gut microbiome in Latin America (last reviewed in March 2016)

Country	Year	Population	Samples	Aim of the study	Method	Main conclusions	Ref.
Argentina	2016	Adult	Palatine tonsils, saliva, buccal mucosa, throat, nares and fecal	Characterize the microbiota of healthy individuals living in a metropolitan area in Argentina	*16S rRNA* gene pyrosequencing	Abundance of *Bacteroidaceae* family was higher in the US gut microbiome, whereas *Ruminococcaceae*, *Lachnospiraceae*, *Rikenellaceae* and *Prevotellaceae* were more abundant in the Argentine gut microbiome	[41]
Brazil	2012	Neonates	Fecal	Characterization of fecal microbiota from exclusively breastfed neonates living in low socioeconomic conditions during the first month of life	*16S rRNA* gene cloning sequencing qPCR	In Brazilian neonates, predominance of *Escherichia* and reduced *Staphylococcus* colonization were observed in contrast with patterns observed in neonates from developed countries	[42]
Brazil	2014	Children	Fecal	Analyze the effect of surgical palate repair on gut microbiota of infants with cleft palate before and 24 h after treatment (cefazolin)	Culture	Reduction of *Bifidobacterium* spp., *Lactobacillus* spp. and *Bacteroides* spp. 24 h after treatment	[43]
Brazil	2005	Adult	Fecal	Effect of respiratory tract infection and amoxicillin treatment on intestinal microbiota	Culture	Respiratory tract infections decreased significantly the number of *Bacteroides* spp. and *Lactobacillus* spp. Amoxicillin also decreased the number of *Bifidobacterium* spp. and *Lactobacillus*	[44]
Brazil	2012	Adult	Fecal	Effect of a prebiotic inulin/partially hydrolyzed guar gum mixture for treatment of constipated women, on gut microbiota and production of short-chain FAs	qPCR	Total *Clostridium* spp. was significantly decreased in the prebiotic group, and no changes were observed in fecal short-chain FA profiles	[45]
Brazil	2007	Adult	Mouth, esophagus, stomach, duodenum, jejunum, ileum, colon and rectum	Determine microbiota in healthy volunteers from Brazil	Culture	Oral cavity was predominantly colonized by Gram-positive aerobic and anaerobic cocci; stomach and duodenum microbiome were composed of *Veillonella* spp., *Lactobacillus* spp. and *Clostridium* spp.; jejunum and upper ileum were composed of *Bacteroides* spp., *Proteus* spp., *Staphylococcus* spp. and *Veillonella* spp.	[46]
Chile	2006	Children	Fecal	Evaluate supplementation of milk formulas with prebiotic fructooligosaccharides or a probiotic, *Lactobacillus johnsonii* La1 on composition of fecal microbiota of formula-fed compared with breastfed infants	FISH culture	No major differences for *Clostridium*, *Bacteroides* or *Enterococcus* were observed between the groups or during follow-up	[47]

Table 3 (*Continued*)

Country	Year	Population	Samples	Aim of the study	Method	Main conclusions	Ref.
Chile	2006	Children	Fecal	Effects on the intestinal microbiota of a prebiotic-supplemented milk formula after an antibiotic treatment	FISH combined with flow cytometry	Amoxicillin decreased total fecal bacteria and increased *Escherichia coli*. The prebiotic significantly increased *Bifidobacteria*	[48]
Chile	2010	Children	Fecal	Impact on fecal *Bifidobacterium* species of a 7-day amoxicillin treatment	PCR-TTGE qPCR	*Bifidobacteria* concentration was not significantly altered by amoxicillin. Amoxicillin treatment decreased the number of *Bifidobacterium* spp., induced a complete disappearance of *B. adolescentis* species, a significant decrease in *B. bifidum*; *B. longum* and *B. ultranationalistess/B. catenulatum* remained unchanged	[49]
Chile	2005	Adult	Fecal	Impact of *Lactobacillus johnsonii* La1 ingestion on predominant bacterial populations of the fecal microbiota	FISH combined with flow cytometry	La1 intake marginally increased populations of *Clostridium histolyticum*, *Lactobacillus* and *Bifidobacterium*, and decreased *Faecalibacterium prausnitzii* while it did not affect *Bacteroides*, *Eubacterium rectale* and *Atopobium* populations	[50]
Chile	2010	Adult	Fecal	Evaluate gut permeability in asymptomatic obese individuals and associate with plasma and fecal markers of inflammation and microbiota alterations	G+C profiling	Alteration of the fecal microbiota among obese individuals with predominance of bacterial populations having a lower G+C content and a decreased concentration of high G+C populations compared with control	[51]
Chile	2016	Adult	Fecal	Determine whether higher amounts of dietary fat reaching the colon (through orlistat administration) affect the colonic ecosystem and the effect of prebiotic in healthy volunteers	*16S rRNA* gene pyrosequencing	Only slight changes were observed in the composition of the fecal microbiota between different groups. Orlistat induced a significant reduction in the *Cyanobacteria* phylum and the *Erysipelotrichaceae* family. Prebiotic stimulated the *Actinobacteria* phylum and the *Bifidobacteriaceae* family while it decreased the phylum *Synergistetes* and the *Enterobacteriaceae*, *Synergistaceae*, *Erysipelotrichaceae* and *Tissierellaceae* families. In presence of the prebiotic, Orlistat stimulated the *Barnesiellaceae* family and reduced the *Verrucomicrobiaceae*, *Lactobacillaceae*, and *Mogibacteriaceae*	[52▪▪]

Table 3 (*Continued*)

Country	Year	Population	Samples	Aim of the study	Method	Main conclusions	Ref.
Colombia	2013	Children	Fecal	Compare fecal microbiota of healthy children with that of children with diarrhea attended in two different locations	qPCR	The abundance of *Bifidobacterium* spp. was significantly reduced in children with clinical diarrhea from both locations, whereas certain *Lactobacillus* spp. were reduced in children from both locations. In children with diarrhea, different fecal microbiota were observed between the both locations	[53]
Colombia	2014	Adult	Fecal	Characterization of gut microbiota in Colombian adults, comparing with Americans, Europeans, Japanese and South Korean populations	*16S rRNA* gene pyrosequencing	Composition of gut microbiota of Colombians was significantly different from that of Americans, Europeans and Asians. In Colombians, *Firmicutes* tend to decrease with increasing BMI, whereas no change was observed in *Bacteroidetes*	[54▪]
Ecuador	2008	Children	Fecal	Comparison of gut microbial composition of feces from infants that were weaned to regular family food, formula with probiotics (*B. lactis BL* and *Streptococcus thermophilus*) or formula without probiotics	PCR-DGGE	Microbiota of children supplemented with formula with probiotics or without probiotics was different than those supplemented with regular food	[55]
Ecuador	2013	Children	Fecal	Effects of *Trichuris trichiura* infestation on fecal microbiota compared with noninfested controls and evaluation of anthelmintic treatment on composition of intestinal microbiome	*16S rRNA* gene pyrosequencing	Comparisons of microbiome at different taxonomic levels showed no statistically significant differences in composition between uninfested children and those with *T. trichiura* infestation. Anthelmintic treatment of children with *T. trichiura* did not alter fecal microbiota composition	[56]
French Guyana	2015	Adult	Fecal	Assess in an isolated Amerindian Guianese community whether intestinal carriage of Enterobacteria producing extended spectrum beta-lactamases was associated with specificities in gut microbiome	Metagenomic Metatranscriptomic	*Desulfovibrio, Oscillospira, Parabacteroides* and *Coprococcus* generas were significantly more abundant in the active microbiome of noncarriers than in carriers	[57]
Peru	2015	Children and adult	Fecal	Characterization of gut microbiome from a population living ancestral lifestyles and a rural population compared with US population	*16S rRNA* gene pyrosequencing Metagenomic	Taxonomic and metabolic differences were observed between urban population from United States and traditional lifestyles population from Peru. *Treponema* are characteristic of traditional gut microbiomes	[58▪]

Table 3 (*Continued*)

Country	Year	Population	Samples	Aim of the study	Method	Main conclusions	Ref.
Venezuela	2010	Neonates and mothers	*For mothers*: skin, oral mucosa and vagina *For neonates*: skin, oral mucosa, nasopharyngeal aspirate and meconium	Influence of delivery mode and on neonate's 'first' microbiota	*16S rRNA* gene pyrosequencing	Vaginally delivered infants acquired gut bacterial communities resembling their mother's vaginal microbiota, dominated by *Lactobacillus*, *Prevotella* or *Sneathia* spp. C-section infants harbored gut bacterial communities similar to those found on the skin surface of their mothers, dominated by *Staphylococcus*, *Corynebacterium* and *Propionibacterium* spp.	[59]
Venezuela	2015	Children and adult	Fecal	Characterization of fecal, oral and skin microbiome and resistome of members of an isolated Yanomami Amerindian village with no documented previous contact with western people	*16S rRNA* gene pyrosequencing Metagenomic	Yanomami population harbored a microbiome with the highest diversity of bacteria and genetic functions ever reported in a human group. Bacteria carrying functional antibiotic resistance genes, including those that confer resistance to synthetic antibiotics	[60▪]
Venezuela	2012	Children and adult	Fecal	Microbiome characterization of Amazon population from Venezuela, rural Malawi and US populations	*16S rRNA* gene pyrosequencing Metagenomic	Pronounced differences in bacterial species composition and functional gene repertoires were noted between US residents and those in the other two countries. These distinctive features were evident in early infancy as well as adulthood	[61]

DGGE, denaturing gradient gel electrophoresis; FAs, fatty acids; FISH, fluorescence in-situ hybridization; qPCR, quantitative polymerase chain replication; TTGE, temporal temperature gradient gel electrophoresis.

methods are unable to identify unknown bacterial species in contrast to *16S rRNA* gene sequencing and metagenomic methods. The main conclusions from these studies are summarized in Table 3. Published studies are currently lacking from such relevant countries as Uruguay, Paraguay, Bolivia and Suriname. The studies performed to date in Argentina, Brazil, Chile, Peru, Ecuador, Colombia, Venezuela and French Guyana are clearly insufficient to define microbiome profiles specific to Latin America. Interestingly, among these studies, few have compared the gut microbiome composition from their local population with that of other countries and particularly with North American populations [54▪,58▪,60▪,61]. Among these studies, authors have highlighted the impact of lifestyle, and especially westernization, on the composition of the human gut microbiome [58▪,60▪,61]. Globally, the gut microbiome of westernized societies from the North American populations showed lower diversity than those of nonindustrialized societies from Latin America (Venezuela and Peru) [58▪,60▪,61]. Further, the gut microbiome of nonindustrialized societies is enriched with the phyla *Proteobacteria*, *Spirochaetes* and *Bacteroidetes*, and industrialized populations have a gut microbiome enriched with the phylum *Firmicutes*. Within the phylum *Bacteroides*, *Prevotella* abundance was more significant in nonindustrialized societies, whereas the abundance of *Bacteroides* is more significant among industrialized societies [58▪,61]. Analogous findings have been shown in other nonwesternized populations from Africa and Papua New Guinea [37,38▪,39▪]. One possible explanation for this difference is that in nonindustrialized societies, people tend to eat more plant-derived carbohydrates and dietary fiber, known to have a higher bacterial diversity in their microbiome [62] and to favor the colonization of *Prevotella* [27,37,38▪] as compared with the western diet (including high fat and cholesterol, high protein, high sugar and excess salt intake). Furthermore, some hypothesize that populations of nonindustrialized societies are exposed to a large variety of environmental microbes that can favor the enrichment of their gut microbiome. In contrast, the reduction of bacterial diversity observed in industrialized societies can be the result of selective pressure exerted by the globalization effect of eating generic, nutrient-rich and uncontaminated foods, in association with increased hygiene practices [37].

It is clear that lifestyles, particularly the diet, and host genetic factors impact the composition of the gut microbiome and that the geographical-associated factor plays a key role in composition of this microbiome.

OPPORTUNITIES TO REALIZE STUDIES ON GUT MICROBIOME IN LATIN AMERICAN POPULATION

Gut microbiome dysbiosis has been associated with various diseases, leading to the emergence of potential new therapeutic strategies targeting the microbiome with the aim of preventing or controlling these diseases. To achieve this objective, it is important to define the 'normal microbiome' for different geographic localization around the world, to study factors influencing gut microbiome composition and to characterize the origin of gut dysbiosis preceding diseases.

In Latin America, few studies have been conducted and they do not permit at the moment to determine the existence of a gut microbiome specific or not to Latin American populations. In addition, Latin American countries include different genetic backgrounds that may influence specific associations between gut microbiomes and host genetic profiles. In general, the genetic background of Latin American populations is influenced by native American and European ancestry and less so by African ancestry [63], and different proportions of origin can be observed between countries (Table 4). Interestingly, various native American populations remain in Latin America with lifestyles similar to those of our human ancestors, and these populations have low or no genetic admixture due to their confinement. In addition to providing information on the shaping between host genetic profiles and the gut microbiome, studying native populations can help to understand changes occurring during human evolution.

Furthermore, Latin American populations have diverse dietary habits according to their geographic localization and history, offering the opportunity to study the coevolution between the gut microbiome and the diet. In addition, rapid changes in socioeconomic conditions observed in some Latin American countries have led to changes in lifestyle of

Table 4. Estimation of ancestry proportions in five countries of Latin America (based on Ruiz-Linares *et al.* [63])

Countries	Native American ancestry	African ancestry	European ancestry
Brazil	0.09	0.09	0.82
Chile	0.48	0.05	0.49
Colombia	0.29	0.11	0.60
Mexico	0.56	0.05	0.37
Peru	0.64	0.00	0.29

populations and not uncommonly advantaged groups within countries have a diet comparable with developed societies. In parallel, the prevalence of chronic and metabolic diseases has increased, and although this increase can be attributed to lifestyle changes, most are also associated with gut microbiome alterations. Consequently, the study of the effects of this rapid socioeconomic transition on gut microbiome may improve our knowledge on the role of gut microbiome in the development of these diseases and particularly on the origin of dysbiosis states.

Importantly, infectious diseases and particularly gastrointestinal infections remain a public health problem in Latin America despite vaccination strategies and improved sanitary conditions that have reduced their prevalence during these last years [64]. In addition, the increasing flow of tourists and immigrants, who can be both affected by intestinal pathogens and import them to their countries, plays a role in sustained gastrointestinal infections [65]. Recent studies support the contribution of intestinal microbiota in the genesis of these infections [66,67]. Latin America can provide large cohorts to study the impact of gut microbiome on the origin and the development of gastrointestinal infections. Recent studies suggest that gut microbiome may act as a reservoir of antibiotic resistance [68], and resistant strains can persist in absence of selective pressure [69]. In Latin America, microorganisms acquired in the community are more resistant to antibiotics compared with Europe and the United States or industrialized countries [70]. In addition, some antibiotics can have an impact on the gut microbiome composition for periods as long as 10 months [71] and opportunistic pathogens such as *Clostridium difficile* can take advantage of the dysbiosis produced by antibiotics and enhance their growth [72]. Consequently, Latin America is a region where the relationship between intestinal pathogens, antimicrobial use and resistance, and gut microbiome can be actively investigated.

CONCLUSION

Latin America includes a genetically diverse population with various lifestyles, which can provide cohorts to study the impact of several factors on gut microbiome composition. In addition, the rapid development status of several Latin America countries provides an interesting scenario to better understand transformations of gut microbiome and its association with specific diseases associated with 'development'.

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Conflicts of interest

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Papers of particular interest, published within the annual period of review, have been highlighted as

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