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The Microbiomisation of race: postgenomic determinism at the nexus between bioprospecting biodiversity and bioinequalities in microbial science

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Abstract

The human microbiome challenges the tenet of a fixed and self-contained human nature by recognising the role of microbes along with environmental and lifestyle factors in the shaping of the immune function. Does this mean that the material-semiotic paradigm of the immune self, or immunity-as-defence (Cohen, 2009), is obsolete? This article draws on ethnographic fieldwork of the human microbiome project 'Microbiomes of Homes across Cultures' (MHC) conducted between 2013 and 2017. MHC's experimental core is based on the bioprospection of microbes from biodiversity-rich locales and peoples of the Peruvian Amazon. Among the principal aims of MHC was the search for 'ancient microbes' as potential solutions for restoring the microbiome of Western and westernised societies. Through the development of the notion of the 'microbiomisation of race', the article demonstrates that, contrary some perspectives in 'more-than-human' (Braun & Whatmore, 2010) literature (including 'multispecies' approaches) (Hird, 2009; Kirksey & Helmreich, 2010; Lorimer, 2016), postgenomic microbial science re-enacts an immunity model of inclusion and exclusion, self and other. I substantiate this by evidencing that the microbiomisation of race is constituted within a nexus between bioprospection (i.e. population genomic research) and bioinequalities (personalised medicine projects).

Keywords: microbiome science, race, microbiomisation, postgenomics, bioprospection, bioinequalities

Introduction

Echoing feminist technoscientist Donna Haraway's 'naturecultures' (1991) and anthropologist of science Paul Rabinow's 'biosocialities' (1996b), contemporary sociological and anthropological literature has conceptualised the nature-culture or social-biological interplay that inhabits postgenomic fields such as epigenetic, circadian biology or microbial science with the adjective 'biosocial' (Ingold & Palsson, 2013; Meloni, 2014a, 2014b, 2014c, 2015; Lock, 2012, 2013a, 2013b). Maurizio Meloni (2014a), refers to a "social turn" in the life-sciences in which 'the new social biology' (pp. 594–595, 603) 'has become porous to social and even cultural signals to an unprecedented extent' (Meloni, 2014a, p. 594). While the divisions between the social and biological, nature and nurture, and so forth have been a recurrent concern for scholarship in the social sciences and humanities, the existing body of literature on the biosocial conceals a vital and elucidatory precursor: feminist writer and poet Denise Riley's notion of 'socialised biology', which refers to how biology is 'lived within particular lives', demonstrates that 'the opposition of the biological to the social' can be undone by acknowledging that "most of what is understood as biology is *lived out* by the individual in a social form" (1983, pp. 31, 40). Riley's notion provides a situated account of embodied biological experience in everyday life. 'Socialised biology' serves as a heuristic device to complement the 'biosocial' literature. The article tackles the existing lacunae of multispecies studies/ethnographies and biosocial literature on the historical, philosophical, and cultural dimensions at the intersections of the biopolitics of immunity and human microbiome science. In doing so, I examine how and to which extent scientific research on the human microbiome is shaping and reconfiguring biomedical practice and experimentation and older scientific and popular ideas associated with the immune self. Is microbiome science qualifying alternative modes of scientific knowledge production that include more-than-humans (i.e. microbes, environment)? Are there vestiges of the immunological past (i.e. biological essentialism, environmental determinism) percolating the epistemic, ontological, and empirical values of microbiome research?

Results from my ethnographic fieldwork on human microbiome science research and historical, science policy and popular science literature analysis on the topic show that microbial science takes social groups and socio-cultural practices as pre-existing 'natural' phenomena and biologises them by creating and attributing microbes and microbial profiles to them. By correlating certain microbial species and diversity and hunter-gatherers, ideas of race, nation, and ethnicity become 'microbiomised', a neologism originally coined as 'microbiomisation' by anthropologist of science Stefan Helmreich (2016). In this article, I argue that, unlike other biological-social interplays—such as the personification of cells, by which biomedicine writes and speaks about cells as if they were interchangeable with persons (Martin, 2006)—in the process of the 'microbiomisation of race', the 'social' (i.e. lifestyle, cultural habits, ritual, traditions, local milieus) is the main element that animates scientific research on microbes.

The concept of race emerged as early as the thirteenth and fourteenth centuries in Europe to refer to 'lineage, breed, or stock in animals and humans' (Wade et al., 2014, p. 3). Represented by 'naturalists' Carl Linnaeus (1707–1778) and Comte de Buffon (1707–1788), among others, taxonomy developed as part of the Enlightenment project during the eighteenth and nineteenth centuries. It was a way of ordering and classifying plants and human and non-human animals according to their physiological characteristics (Wade et al., 2014, p. 4). The hierarchical taxonomic systems developed at that time, part of what we might call 'race science' or 'raciological science' (TallBear, 2013) have made their way to our time (El-Haj, 2007). As several social scientists have demonstrated (El-Haj, 2007; Wade et al., 2014), race as a biological concept was not fully abandoned, even after the emblematic UNESCO Statements on Race (1950), a series of documents produced by the United Nations (UN) in the aftermath of the Second World War. As El-Haj argues, the 'documents did not deny the reality of race as a biological concept' (2007, p. 286) as an ´absent presence´ (M´charek, Schramm & Skinner, 2014). Instead, the concept of race was gradually substituted with the concept of 'populations' (El-Haj, 2007;

TallBear, 2013; Wade et al., 2014). In an idiom of 'percentages and allelic frequencies', physical traits, the phenotype, were gradually replaced by genetic information, the genotype (Wade et al., 2014, p. 227). El-Haj refers to the embeddedness of race in population genomics as the 'molecularisation of race' (2007) in reference to sociologist Nikolas Rose's influential notion of 'molecularisation' (of the life sciences) (2007).

With the emergence of population genomics in the second half of the twentieth century, the fact that all humans share 99.9 per cent of their genome reached an iconic status. This, in turn, gave rise to several genomic projects aimed at the understanding the 0.1 per cent difference among different human populations (via the data mining of their genomes). For example, in 1991 the Human Genome Diversity Project (HGDP) began in Stanford University (US), directed by the influential geneticist Luigi Cavalli-Sforza. The HGDP has established a landmark in population genomic research in terms of biological research on human evolution and migration. The database of the HGDP is in use today (Wade et al., 2014, p. 5). In an epoch of unprecedented environmental damage and extinctions, the HGDP—along with other genomic initiatives such as the International Hapmap Project (2002–2009) or the more recent Human Microbiome Project (2007) and the 1000 Genomes Project (2008–2015)[1]—aims at studying and generating DNA databases of populations of humans and non-humans (especially plants and microbes) before it is too late; before they disappear (Dominguez-Bello, 2013).

As scientists exploring the co-evolution of humans and microbes, the practices of population genomics are also present in the research of the team of microbial ecologists I follow and analyse. For example, in an influential article on the use of the bacterium *Helicobacter pylori* as a marker of ancestry and migrations, Dominguez-Bello and Blaser (2011) argue that 'these microbes [*H. pylori*, ANC] are mostly vertically transmitted, they have evolved within each human group and provide a view of human ancestry' (Dominguez-Bello & Blaser, 2011, p. 451) Furthermore, they suggest that because 'human mixing affects microbial phylogeographic signals, and lifestyles impact the human microbiome population structure', this approach can be useful as a way to gain 'insights into the population structure of the human microbiome' (p. 451).
Ancestry genomics is in fact one of the biomedical areas that better reflects the contemporary imbrication between race and the life sciences. In the book *Native American DNA* (2013), feminist indigenous studies scholar Kim TallBear shows how 'the DNA profile helps to reconfigure the concept of tribe' (p. 4). Linking population genomics with colonialism, TallBear argues that 'without "settlers", we could not have "Indians" or "Native Americans"—a panracial group' (p. 5). This is because

> scientists who trace human migrations do not tell a story from the standpoint of those peoples who were encountered; they tell a story from the standpoint of those who did the encountering—those who named and ordered many thousands of peoples into undifferentiated masses of 'Native Americans', 'Africans', 'Asians', and 'Indo-Europeans' (p. 5).

Similarly, in *Mestizo genomics* (2014), Peter Wade and colleagues theorise 'mestizaje as an ideology of national identity' (p. 211). Analysing the several laboratories of ancestry genomics in three Latin American countries (Brazil, Mexico, and Colombia), *Mestizo genomics* provides an insightful account of local differences in the scientific knowledge production of genomic lineages. Emphasising 'local biologies' (Lock & Nguyen, 2010), the authors show how, for example, in Mexico, harvesting population DNA is a question of national sovereignty. In Brazil, by contrast, national population genomics programmes rest on a narrative of mixture, which, in turn, finds itself justified in ancestry genomic data (see also Kent et al., 2015). Both TallBear's (2013) and Wade et al.'s (2014) studies show how biological knowledge connects to several forms of citizenship(s) and identities, a process sociologist Adriana Petryna coined 'biological citizenship' (2002; see also Novas & Rose, 2005; Rose, 2007) and sociologist Nicholas Rose refers to as 'vital politics' (2001) (El-Haj, 2007). Crucially,

[1] The Hapmap Project (2002–2009) was a multinational organisation created to develop a haplotype map (i.e. HapMap) of the human genome, to describe the common patterns of human genetic variation. The 1000 Genomes Project has developed a catalogue of human genetic variation.

'Native American DNA' (TallBear, 2013) and 'mestizo genomics' (Wade et al., 2014) 'how new versions of race are being assemblaged globally through local practices' (Wade et al., 2014, p. 238). This is to say that, mainly through population genomics projects, postgenomics reauthorises and reifies race (El-Haj, 2007; TallBear, 2013; Wade et al., 2014). Likewise, I will show that human microbiome science, as an area of postgenomics, also involves the reinscription of race in biological experimentation and knowledge about human–microbe entanglements. By conceptualising these processes as the 'microbiomisation of race', I demonstrate that human microbiome science does not only operate at the level of populations, contradicting what Hinterberger (2012a, 2012b) and other authors (see Fox-Keller, 2010) have argued in relation to genomics and postgenomics medicine. Instead, I argue that the individual dimension of human microbiome science, although sustained by microbial DNA data from human populations through bioprospecting practices, gains meaning through informal, online networks of pseudoscientific microbial-related evidence. The importance of this argument is paramount as it shows how and to what extent medicalisation, optimisation, and inequalities inhabit newer genomic articulations of difference in microbial science.

In the first part of the article, I provide an ethnographic examination of a landmark human microbiome research, the Microbiomes of Homes across Cultures (MHC), which assumes the "isolation" of a contemporary Achuar community of the Peruvian Amazon as proxy of a common ancestral human evolutionary past (Sommer, 2015). This part intercalates a critical analysis of the MHC with the main three research stages of the study: hypothesis, data gathering, and results. Using conceptual frameworks from STS, feminist theory and anthropology of science, the critical analysis of each of the phases shows different degrees of environmental determinism in microbial science structured around (1) the essencialisation of race and a humoral understanding of the body, (2) operationalisation and datafication of environmental and human microbiomes, (3) biologisation social values and cultural traditions associated to lifestyles. Bringing the framework of microbiomisation together with an analysis of personalised microbiome online platforms, the last part of the article goes on to argue that, while the human microbiome is displacing older ideas of immunity as a guarantor of biological identity and individuality, it instantiates new forms of difference, particularly immunitary privilege based on a higher microbial diversity, and reproduces old ones in terms of neocolonial practices of expropriating nature (microbes in this case) and structural differences in (Western) societies.

Hypothesis: Essentialising a common 'ancestral' past and the re-emergence of humoralism

> *Dearest Father Luigi,*
>
> *We returned from our trip at the end of August and every week I thought about writing to you! How are you? I hope you are as well as when we left. I'm sending you pictures of you and us. This is a long letter because I have a lot to tell you as well as to ask about. So, I divide it into sections.*
>
> *I'm sending you paper and pens, a notebook, and a book about New York (where I am living now), which contrasts so much with the pristine environment where you live … these are the contrasts that take away my sleep, what is between Checherta and New York, and what is the significance of those differences.*
>
> Personal correspondence of Maria Gloria Dominguez-Bello with Father Luigi Bola, 6 October 2012, my translation

The above excerpt is from a letter sent by a professor of microbial ecology from the University of New York to Father Luigi Bola, known as 'Yankuam Jintia' in Achuar, a Catholic missionary from the

Salesian Congregation who lived in the Achuar community of Checherta (Peru), where he spent forty years before he died in Spring 2015. In the letter, the scientist enclosed a twenty-six-questions questionnaire touching on issues of child mortality, breastfeeding, fertility, longevity, and diet in Checherta. Two months earlier, they both met for the first time in Checherta.

Between 2013 and 2017, I conducted ethnographic fieldwork of a microbial ecology study, entitled "Microbiomes of Homes across Cultures" (MHC), looking at changes in microbial patterns and changes across an evolution of lifestyle, from less to more "westernised" modes of living attending to urbanisation, diet and medicalisation among other sociocultural elements and characteristics of lifestyles. The scientific team I followed consisted of microbial ecologists and other scientist coming from diverse fields including architecture, environmental engineering, and anthropology. They conducted two main expeditions (2012 – 2014) structured around four locations at the same latitude of the Peruvian and Brazilian Amazon (see Figure 1) and sampled microbial DNA from the environment (air, surfaces of objects), human and non-human animal bodies.

Fig 1. Google Earth still images showing the four locations at the same latitude of the Peruvian and Brazilian Amazon where the MHC team sampled microbial DNA. From West to East (in a gradient of transculturation—less to more westernised): huts of isolated Achuar villages (Checherta); rural settlement of an Amerindian-mestizo town (Puerto Almendros), mestizo cities (Iquitos), and mestizo modern buildings (Manaus).

The objective of the MHC study was to investigate whether the built environments (i.e. open-air huts) of Checherta—along with their inhabitants' diet (non-processed food) and lack of exposure to antibiotics—correlate with a more diverse composition of their human microbiome as well as their environmental microbes. The contention of the principal investigator of the project was that 'modern lifestyle has led to changes in microbial patterns in humans and their environments, with reduced microbial diversity … [producing] profound changes transmitted by descent, and perpetuated in future generations' (personal correspondence, 2012). Besides Western lifestyle practices and trends associated with diet, modes of delivery at birth (Dominguez-Bello et al., 2010a), or antibiotic usage (Bisgaard et al., 2011), the MHC project explored changes in the pattern and composition of microbiota associated with the quantity of time spent indoors and the lack of 'natural' ventilation of modern architectural designs (Dominguez-Bello, 2012, p. 3). In indoor environments, 'humans are exposed to surfaces with a bacterial content that reflects the space and object uses' and they 'also shed microbes to the environment, and ventilation greatly affects microbial transmission by aerosol, which is of special

interest in hospital design' (p. 3) The study was part of an emerging interdisciplinary area in the of human–microbe entanglements in human constructed environments known as 'microbiology (also "microbiomes") of the built environment'. The field encompasses studies of microorganisms and various types of built environment, including houses, vehicles, hospitals, water systems, and clothing. Biologists collaborate with architects, designers, and doctors. More recently, particularly in relation to AMR and the built environment (mainly hospitals and operating theatres), humanities and social sciences scholars are collaborating with scientists, designers, and architects to reimagine ways in which building design, technologies, processes, and behaviours lessen the dependency on antibiotics. Since (western) humans spend most of their time in indoor environments—especially in Western (and I would add Northern) societies—and building design determines microbiological communities (see Brown et al., 2019). Hence, microbiome initiatives studying indoor and built environments bridging architecture, design, sociology, ecology, and microbiology, for instance, can potentially mitigate nosocomial diseases and bacterial infections, as well as improve the air quality of homes and public transport systems, for example.

From transculturation to urbanisation

In several earlier and unpublished versions of the MHC research, the word 'transculturation was an analytical tool to describe the degree of westernisation, from 'unimpacted peoples' to communities adopting a Western lifestyle (Dominguez-Bello, 2013). I traced the genealogy of the word 'transculturation' back to the work of anthropologist Fernando Ortiz in his 1947 book *Cuban counterpoint: Tobacco and sugar.* In the aftermath of Spanish colonialism in Cuba, Ortiz suggests the term 'transculturation' to refer to the converging of two cultures and the creation of a new one (neo-culturation), in contrast to the unidirectional acquisition of another culture (acculturation). At this first contact with Dominguez-Bello's human microbiome research, I speculated on the reformulation of the concept within a scientific emancipatory process: a female scientist bringing a Latin American concept (i.e. transculturation) to the forefront of international microbiome research. Progressively, transculturation, westernisation, and urbanisation became interchangeable concepts in the MHC research, as the following quote reads:

> While the world is converging toward Western lifestyles (a process known as transculturation/Westernization), there is a need to characterize the changes that occur during this convergence, and to provide insights into which factors may contribute to specific immunologic and metabolic diseases … We observed important dietary changes across the villages in the transculturation/urbanization gradient. From plant-rich natural product diet in the jungle village, void of dairy products, to a more diverse, high-caloric, high sugar processed diet consumed less frequently but in bigger meals (Ruiz-Calderon, 2015, pp. 19, 29).

Figure 2. The four different types of housing architecture across the 'westernisation gradient'. Courtesy of Jean Ruiz-Calderon.

In the journal article versions, however, transculturation no longer appears. Here, the experimental design and rationale of the MHC research is framed in terms of urbanisation, understood as an outcome of westernisation:

> Westernization has propelled changes in urbanization and architecture, altering our exposure to the outdoor environment from that experienced during most of human evolution. These changes might affect the developmental exposure of infants to bacteria, immune development, and human microbiome diversity … This study addresses the associations between architectural design and the microbial biogeography of households across a gradient of urbanization in South America (Ruiz-Calderon et al., 2016, p. 1).

The progressive substitution of transculturation with the concepts of urbanisation and westernisation, I argue, elicits the socio-cultural and anthropological dimension of the MHC research, moving towards an architectural context under the framework of microbiology of the built environment. Talking about 'urbanisation', I suggest, sounds more technical and is less problematic in terms of research ethics (access to indigenous communities, sampling DNA, etc.). In other words, talking about buildings and design (i.e. urbanisation) instead of race, nation, and ethnicity (i.e. transculturation, westernisation) is a way to 'sanitise' scientific discourse, avoiding controversies and criticism. Importantly, I suggest that the evolution of the concept of transculturation in the main hypothesis of the MHC study—how it travels, transforms, and 'normalises' itself as part of more common and accepted concepts in contemporary scientific discourse (i.e. 'westernisation', 'urbanisation')—is important because it links microbiome science and race from the very inception of the study but also because it links postgenomic microbiology with an humoral understanding of the body.

Humoralism in postgenomics

As part of a new generation of biologists concerned with relational and ecological ontologies of life, this team of life and environmental scientists are dealing with the outcomes of the 'biology of history' (Landecker, 2016) in microbial life, specifically in relation to the disappearance of microbes and the resulting disrupted balance of the 'holobiont'. For the PI of the project, 'the microbiome and environmental microbes need to be viewed as an entity integrated in their physical and biological dimension to fully assess the impact of modernisation on human biology' (Dominguez-Bello, 2013). She alludes to the differences in the (pre-modern) cultural characteristics and, generally, the 'ancestral' lifestyles of the Achuar community of Checherta as holding key answers for contemporary microbial ecology questions on enhancing and maintaining 'microbial balance', nowadays understood as prerequisite of health and wellbeing. 'The lifestyle and habits of the Checherta are very different from those in Western or westernised towns or cities', she tells me passionately. They live in open huts (twenty-one) made of natural materials (wood and reed) (see Figure 2). The huts are single open-plan spaces, with two functional areas: a dormitory (for all the family) and a fire area for cooking and socialising. Apart from vaginal birth, breastfeeding until the babies are 2 years old, and a plant-rich diet, the Checherta community has natural light and ventilation, and close contact with animals. From when they are around 10 or 11 years old, members of the community practice a ritual known as 'wayusear', in which they consume a leaf-infused tea (Wayusa tea) that induces vomiting. The community 'wayusea' every morning as a body-cleaning ritual. In addition, they consume masato, a pre-Columbian traditional beverage prepared with yucca and served in different degrees of fermentation. Masato is consumed daily by men and less frequently by women and children from seven months of age. The ritual of 'wayusear', together with the consumption of masato, scientists suspects, might play a key role on increasing microbial diversity and maintaining microbial balance.

Although dietary habits were one among the many parameters constituting the MHC samples, nutrition was a key factor for the scientists, since the easier way to alter the microbial composition is through food. The research results of the study correlated processed foods with a lack of microbial diversity which, in turn, is associated with a higher susceptibility to metabolic, autoimmune, and inflammatory diseases. On the contrary, an unprocessed plant-based diet rich in wholegrains, seasonal fresh fruits

and vegetables, nuts, and seeds and probiotics bestow a higher microbial diversity, microbiome scientists hypothesise, leading to a higher microbial diversity and therefore to healthier outcomes. Here, indigenous' bodies are not only conceived as embedded in and porous to the environment but also as having an inherent performative quality. That is, the microbial composition of the human microbiome is understood by science as enacted (i.e., done) daily by cultural practices such tea rituals and consumption of pre- and probiotics-rich foods as well as by specific historical conditions and socioeconomic circumstances. Bodies are figured as deeply present, in constant flux, in exchanged with their immediate environment and thus malleable through foods and ventilation, for instance. This understanding not only departs from late nineteenth and twenty century biological determinism, but surprisingly concurs with the current biomedical epistemologies, particularly in the fields of microbial science, epigenetics, and chronobiology. However, although I lack of the space in this paper to further elaborate this point is worth noting that this epistemic shift towards plasticity in biomedicine (Sanabria, 2016, Pitts-Taylor, 2009) involves forms of the biomedicalization and commodification of non-biomedical understandings of health and illness as in indigenous health cultures, Ayurveda, Traditional Chinese Medicine, for example (Mathpati et al., 2020), as I will discuss later in relation to personalised microbiome initiatives.

The contradicting and complex ways in which microbial science understands bodily boundaries is an aspect that, paradoxically, connects both public health and microbiology, rooted in the germ theory of diseases, with a humoral understanding of health (see Meloni, 2019). Such understanding around the differences between indigenous and European bodies by colonists was an important element of subjugation during the European invasion and violent occupation of the Americas. As Rebecca Earle has cogently showed in *The Body of the Conquistador* (2012), diet was a crucial element 'in the construction and maintenance of the colonial body' (p. 11). Spaniards believed that by keeping their food cultures and diet based on wheat flour, almonds, sugar, meat, and wine, they would be protected from ¨malign¨ warm and damp climate and other drastic environmental differences between the Iberian Peninsula and the New World. This is a far-reaching aspect considering that the health and wellbeing of Europeans in the Americas and, therefore, the success of the imperial expansion, depended on the ability to cultivate those foods in the colonies (ibid: 16), an aspect that Haraway and colleagues connect to the 'Plantationocene' (2015) (Author, forthcoming). The pre-modern focus on the theory of the four humours and the influence of climate and foods on phenotypical characteristic of human bodies "only emphasises that race is a historical, rather than strictly physical, category" (Müller-Wille, 2014, p. 603).

Sampling: Bioprospecting biodiversity and the techno-environmental determinism of microbial science

During the MHC project, scientists first collected the microbial DNA samples from humans, non-humans (including pets and objects), and homes. They collected skin, nose, mouth, and anal swabs from ninety-four humans (thirty-seven men and fifty-three females) (Ruiz-Calderon, 2015, p. 37). They took microbial samples from the floors and walls of the living rooms, kitchens, bedrooms, and bathrooms of each household (forty in total, ten per location). Immediately after the collection, they stored the swabs in liquid nitrogen (−80°C). The team brought with them a questionnaire to collect additional information or 'metadata', including anthropometric and dietary information, surface material, sample height (walls), cleaning frequency, and the presence of pets in the home.

Unlike classical microbiology, in which microbes were cultured in Petri dishes and so the work was purely done at the benches, the study of microbiomes is conducted in the natural environment in which microbes reside (which is literally everywhere). This approach is known as 'metagenomics', that is, 'the study of genetic material directly extracted from an environmental sample' (Rhodes et al., 2013, pp. 35–36). Culture-independent analysis of microbiomes using a metagenomics approach has revealed an overwhelming microbial diversity in natural environments such as lakes, as well as in and on the bodies of humans and non-human animals. The metagenomics approach is about identifying

'communities' of microbes (i.e. populations of bacteria) through the DNA, rather than individual bacterial 'colonies'. Once they extract the DNA from the microbial sample, they follow, what in microbiome science is known as the '16S-based approach'. The 16S rRNA gene is an essential, highly conserved, and universal component of bacterial ribosome (prokaryotic). The 16S rRNA sequences 'serve as a proxy for the entire genome' (Rhodes et al., 2013, p. 37). This is because by looking at 'the diversity and distribution of 16S rRNA sequences in an environment, researchers can quickly and easily ascertain the diversity and distribution of microorganisms in that environment' (ibid).

Sequencing the entire DNA of a microbial community taken directly from the environment to identify species present in the human body or in a body of water, for instance, is technically possible through methods of DNA sequencing or high-throughput sequencing (HTS) technologies, also known as 'second -generation' or 'next-generation' sequencing (NGS). At the laboratory, the scientists amplify and sequence the 16S rRNA gene using HTS. HTS methods are technologies that 'parallelize the sequencing process, producing thousands or millions of sequences concurrently' (Church, 2006). These sequencing technologies became available at the onset of the 21st century and they are continually improved to become faster, more efficient and cheaper' (Barba, Czosnek, & Hadidi, 2014, p. 106). More than two decades after the classic *Making PCR* (1996) by anthropologists of science Paul Rabinow, HTS is the prominent postgenomic technology to decipher genetic material. Yet, this new way of accounting for microbial communities has important limitations, and so it is the subject of controversies in microbiome science. The scientific literature highlights that these limitations mostly have to do with the complex management of large datasets or 'big data' produced, the insufficient scope of visualisation software, and the strong demand for bioinformaticians specialised in HTS and able to develop new methods for retrieving biological data and conducting data analysis (H. Saadeh, personal communication, April 15, 2013). In addition, HTS lacks accuracy across the genome (Ross et al., 2013) and the technology cannot be integrated into the clinic (i.e. translational research) because of the 'cost and the timescales associated with storage and interpretation of genome data' (Reuter et al., 2015, p. 594). This is an important drawback, because data-driven microbiome science is cataloguing microbial variation in humans with the main goal of rapid translational outcomes in the form, for example, of probiotics, prebiotics, and synbiotics (i.e. a combination of probiotics and prebiotics) (Benezra, 2016). Importantly, beyond these documented limitations of HTS, some scientists argue that the current methods of microbiome analysis miss a great number of microbial species, jeopardising the reliability of microbiota data and data analysis. In an interview, Graham Rook, Emeritus Professor of Medical Microbiology at University College London (UCL), summarised the methods of study of the microbiome as follows:

> They used methods normally used for soil organisms, which means to say they took DNA swabs and they beat it up with mechanical means, and they boiled it and then they beat it up again, then they put in enzymes and they boiled it and they beat it. I mean, they really bashed it around (G. Rook, personal communication, April 21, 2017).

According to Rook, the mechanical and technical means used in metagenomics wipe out a huge amount of relevant microbial data. For example, the stomach lumen of mammals is very rich in spore-forming environmental microbes. However, as Rook notes, HTS methods do not pick up spore-forming microorganisms. This is an important limitation for microbiome research, especially for studies that, like the Microbiomes of Homes across Cultures (MHC) I examined, focus on the interplay between the human and environmental microbiomes. Rook's point is very remarkable, because there is hardly any criticism with regard to microbiome methods of analysis among the human microbiome scientific community, as he repeatedly complained.

Clearly, in microbiome studies like the MHC, 'biomedical and environmental research are converging on genome sequence data as the main data type' (McNally & Mackenzie, 2012, p. 83). The data-driven environmental determinism in microbial science, that is, the 'datafication' of environmental and human

microbiomes, inaugurates a new regime of visibility of microbes (Latour, 1988). This goes together with a new microbiology research culture relying on comparative population genomics and which connects microbiome data to human cultural traditions and social values, as I discuss in what follows.

Results: The microbiomisation of race

Unsurprisingly, the scientists found major changes in microbial diversity and composition between the two extremes of the urbanisation gradient (i.e., Checherta, hunter-gatherer village, and Manaus, urban city). The results emphasise on the importance of the human skin microbiome since it 'reflects environmental microbes that the subjects are exposed to (…) [and] skin microbes are one of the main sources of bacteria in the indoor environment in urban societies (Klepeis et al., 2001, as cited in Ruiz-Calderon, 2015, p. 53). In fact, the characterisation of 'the skin microbial community structure is vital to reduce exposure of harmful bacteria indoors' (ibid). As the authors note, MHC is the first human microbiome study to compare and to observe loss in microbial diversity in the skin microbiome. The study showed that 'urbanized spaces uniquely increase the content of human-associated microbes—which could increase transmission of potential pathogens—and decrease exposure to the environmental microbes with which humans have coevolved' (Ruiz-Calderon et al., 2016, p. 1).The microbial changes documented in the MHC research might translate 'into differences in microbial exposure that might have developmental health implications for humans', more likely 'immune and metabolic disorders that have become the new disease paradigm in the industrialised world' (Ruiz-Calderon et al., 2016, p. 5).

In the process of microbiomisation, socio-cultural practices such as cleaning frequency, architecture, family size, along with assessments of age, diet, and kinship are reduced and essentialised to racial categories when microbial species are used as markers of population differences. For example, in 2012, Dominguez-Bello took part in a landmark cross-cultural and cross-geographical human microbiome study entitled 'Human gut microbiota viewed across age and geography'. The aim of the study was to establish the foundations of human genetic and metabolic variation through the characterisation of the human microbiota. The study used faecal samples from three different populations: 'Amerindians from the Amazonas of Venezuela, residents of rural Malawian communities, and inhabitants of US metropolitan areas' (Yatsunenko et al., 2012, p. 222). The authors note that:

> Pronounced differences in bacterial species assemblages and functional gene repertoires were noted between individuals residing in the USA compared to the other two countries … In addition, the similarity of fecal microbiomes among family members extends across cultures. These findings underscore the need to consider the microbiome when evaluating human development, nutritional needs, physiological variations, and the impact of Westernization (p. 222).

Here, the authors groups human populations into two different categories: one based on race/ethnicity (i.e. 'Amerindian') and the other based on nationality/country of residence (residents of the US and residents of Malawi).

As I have previously argued, in the MHC research, the biologisation of the social and cultural is exemplified through the words transculturation, westernisation, and urbanisation. However, published versions of the research avoid invoking social and cultural explanations as well as categorisation into racial/ethnic groups by focusing on differences in the built environments:

> Urbanized spaces uniquely increase the content of human-associated microbes—which could increase transmission of potential pathogens—and decrease exposure to the environmental microbes with which humans have coevolved (Ruiz-Calderon et al., 2016, p. 1).

By contrast, drawing on results from the MHC research, several other journal articles co-authored by Dominguez-Bello deliberately focus on nationality and race of the human samples. In an article entitled

'The microbiome of uncontacted Amerindians' (Clemente et al., 2015), the authors state that the 'Yanomani[s] harbor a microbiome with the highest diversity of bacteria and genetic functions ever reported in a human group' (p. 1). As a result, the article insists on 'the need for extensive characterisation of the function of the microbiome and resistome in remote non-westernized populations before globalization of modern practices affects potentially beneficial bacteria harbored in the human body' (p. 6). The microbiome of 'uncontacted peoples', such as the high Oricono Yanomamis of Venezuela or the Peruvian Amerindians of Checherta, is a reservoir for microbiome science. Put differently, microbiome science relies on comparative studies of genetic (microbial) variation in human populations. Harvesting the microbiome of non-Western peoples and territories is not a side project or a specific 'approach' within the field. Rather, it is the key element which constitutes this new area of scientific knowledge production.

The microbiomisation of race is indeed a result of the 'inclusive' science policy framework that Epstein documents and analyses in *Inclusion* (2007). Human microbiome research comparing citizens or residents in different countries (i.e. 'biological citizenship') (Petryna, 2002; Novas & Rose, 2005), is clearly designed using the lens of an inclusionary practice of difference (see for instance De Filippo et al., 2010; Yatsunenko et al., 2012). However, in human microbiome science, not all differences and populations belong to a framework of inclusion. This is evident in the MHC study. Here, the Achuar population of the Peruvian village of Checherta were not selected as participants following an inclusionary practice. The Checherta peoples do not get any medical benefit out of the MHC research, simply because their microbiome is the gold standard for the microbiomes of other populations. Studying their microbiome then is not about inclusion and cannot be explained under that framework. It is rather a question of bioprospection. This is not to say that these microbial scientists are not well intentioned. The point is that, although they do provide an ethical framework in which to situate their practice (i.e. bioprospecting biodiversity) (see Dominguez-Bello et al., 2016), the ultimate outcome of the latter is to address a medical problem (i.e. a lack of diversity of microbiomes leading to metabolic, inflammatory, and autoimmune diseases) that affects a specific segment of populations/countries (high-income, fundamentally Western countries). This objective in postgenomic biomedicine is deeply rooted in geneticist Cavalli-Sforza's "liberal discourse of unity in diversity" and the new force of the human population tree in the 1960s "once it began to be based on the novel genetic, molecular and information technologies" (Sommer, 2015, p. 115). In this sense, knowledge about the microbiome of indigenous communities 'is evaluated in terms of how well it correlates to orthodox scientific and technological thought, rather than in terms of the belief system that supports it' (Last & Chavunduka, 1986, p. 217). Clearly, this type of studies only benefit "western science and economy" (Sommer, 2015, p. 133).

The comparative study of the human microbiome in non-Western versus Western populations is indeed the principal research line of the microbial scientists I followed. In the research article 'Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania' (Smits, et al., 2017), the authors demonstrate how the Hadza's human microbiota shifts according to seasonal changes. The study compared the Hadza microbiome profile of 350 stools collected (by Leach) longitudinally over more than a year, with 'data collected from 18 populations in 16 countries with varied lifestyles' (p. 802). The results clearly correlate the racial/ethnic category of the Hadza with the Prevotellaceae (bacteria) family and 'industrialised populations' (read Western) with the Bacteroidaceae family:

> During the cyclic disappearance of taxa, the Hadza microbiota shifts to a state with increased similarity to those of industrialized microbiotas (fig. S1). Conversely, some OTUs within microbial families common to both traditional and industrialized populations are less seasonally volatile (…). Second, the Prevotellaceae, a member of the Bacteroidetes phylum, is a common family in the Hadza microbiota, leading us to wonder about its relationship to the Bacteroidaceae, a dominant family in industrialized populations, which is also a member of the Bacteroidetes phylum (Smits, et al., 2017, p. 804).

It is interesting to note how the designation of social categories of difference varies among different human microbiome studies. While the Tanzania study uses the racial category of the 'Hadza' and the socio-economic category of 'industrialised', or the study by Yatsunenko et al. (2012) combines racial/ethnic categories (i.e. 'Amerindians') with nationality (i.e. US, Malawi), other studies use political categories to signify race/ethnicity. For instance, De Filippo et al. (2010) is a highly cited study on the impact of diet on the gut microbiome that compares 'European' children and Burkina Faso children:

> BF [Burkina Faso, ANC] children showed a significant enrichment in Bacteroidetes and depletion in Firmicutes ($P < 0.001$), with a unique abundance of bacteria from the genus Prevotella and Xylanibacter, known to contain a set of bacterial genes for cellulose and xylan hydrolysis, completely lacking in the EU children. In addition, we found significantly more short-chain fatty acids ($P < 0.001$) in BF than in EU children (2010, p. 14691).

Clearly, comparing populations within a political and economic 'consortium' of nation states (i.e. Europe) with a single nation state (i.e. Burkina Faso) is an unequal and problematic comparison. This is accentuated by the fact that neither this study nor the previously mentioned ones provided any explanation about the criteria followed for the categorisation of populations (see also Wade et al., 2014). There is also microbiome literature that uses the term 'Caucasian'. In 'The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites' (Ursell et al., 2012), co-authored by some of the team I followed, the authors outline the inter- and intrapersonal microbial variation of five body sites across several populations: gut, skin, vagina, mouth, and nose. Summarising the results of the vaginal microbiome, they write:

> The vaginal communities of Asian and Caucasian women were most often dominated by lactic-acid producing Lactobacillus than Hispanic and African American women, possibly causing the lower vaginal pH levels found in Asian and Caucasian women (Ursell et al., 2012, p. 1204).

While the terms 'Asian' and 'Hispanic' are blurry racial/ethnic categories, denoting geographic provenance and colonial history respectively, the word 'caucasian', as the paediatrician Dennis Fortenberry (2013) points out, 'is a peculiar—but commonly used—racial term because it originates in 18th-century European assumptions of beauty, intelligence, and natural superiority' (p. 166). In fact, Fortenberry continues, 'a word steeped in such assumptions amplifies the stigma of sexuality and sexually transmitted infections often associated with racial and ethnic minorities' (p. 166). Similarly, Wade et al. (2014) argue that mestizaje 'is a sexualised and gendered practice and ideology' (p. 19). Genomic research 'often finds evidence in today's populations that reflects early colonial matings between European men and indigenous or African women' (p. 19). The indissociability and intersectionality of race from other social categories of difference, as Fortenberry and Wade et al. demonstrate, is a remarkable point I have elaborated in relation to class and gender elsewhere (Author, 2018, 2019, 2021).

There is a characteristic of microbiomisation that is easy to go unnoticed. This has to do with the fact that Western categories of difference are often broader than non-Western ones. Take for example, comparing Burkina Faso children with European children (De Filippo, et al., 2010). Or 'industrialised' populations versus 'traditional' 'Hadza' hunter-gatherers (Smits et al., 2017). The Western category is not only broader, but is also blurrier. Following a universal and colonial logic, I argue, the Western (microbiome scientists, in this case) defines others ('hunter-gatherers', 'Hispanic', 'Amerindians', and so forth), but does not need to define itself.

Microbiomisation of race as a nexus between bioprospection and bioinequalities

Beginning with non-scientific assumptions about cultural and social differences associated with certain populations and geographies (i.e. diet, sanitation, family size, architecture, antibiotic use, child-rearing), microbiome science turns these differences into a heuristic device based on microbial taxonomy. It is then that Tanzanian 'hunter-gatherers', 'Burkina Faso' children, or simply 'Hispanics' have more Lactobacillus or Bacteroidetes than 'industrialised populations' or 'EU children'. This process involving the biologisation of social groups as pre-existing 'natural' phenomena is what I call 'microbiomisation'. In this sense, microbiomisation entails what philosopher Alfred North Whitehead calls 'the fallacy of misplaced concreteness' (1997), also known as the 'fallacy of reification', that is 'the tendency to assume that categories of thought coincide with the obdurate character of the empirical world' (Duster, 2005, p. 1050).

By encapsulating my findings under the framework of 'microbiomisation', I want to tell a story about 'how social structures get under the skin' (Meloni, 2015, p. 136). Microbiomisation is similar to what environmental scientist Becky Mansfield calls 'epigenetics biopolitics', which involves shifting 'the responsibility of exposure to chemicals towards the "abnormal" diets of women of color instead of blaming contamination itself' (2012, p. 352). However, in contrast to Mansfield's 'epigenetics biopolitics', the specificity of the process of the microbiomisation of race (and microbiomisation more broadly) involves two interlocking elements articulated at population and individual levels.

1) Bioprospection refers to neocolonial practices of data mining and expropriation of microbial biodiversity from non-Western peoples and territories (i.e. populations) (see Section 3.3.1).

2) Bioinequalities is a reformulation of the Foucauldian concepts of biopolitics and biopower by medical anthropologist Didier Fassin (2009). Going beyond 'a politics of population', it is about 'life and more specifically about inequalities in life' (Fassin, 2009, p. 57, see also Povinelli, 2011). I associate the individualisation of microbial profiles with the production and reproduction of 'bioinequalities' in microbiome science.

I discuss these two elements of the process of microbiomisation of race. Social studies of science tend to associate postgenomics with the individualisation of medicine (El-Haj, 2007; Wade et al., 2014). Some discordant voices, however, have recently suggested that postgenomics is still very much about populations (Fox-Keller, 2010; Hinterberger, 2012a, 2012b). My argument is that microbiome science, as an area of postgenomic science, is about individuals as much as it is about populations. This is because, through bioprospecting practices, microbiome science relies on comparative studies of genetic (microbial) variation in human populations. These studies are then used, as I will show, to create individual microbial profiles via online personalised medicine projects. Yet, those who can access to their 'microbial profile' belong to privileged strata of (predominantly Western) societies. In other words, this means that bioprospecting populations is indissociable from the bioinequalities that the individualisation of microbiome data produces and reproduces.

Bioinequalities: the case of the American Gut Project

The 'population imagination has not faced in the post-genomic era' (Hinterberger, 2012a, p. 76). I concur with Hinterberger that 'we [as social scientists and humanities scholars, ANC] should opt for an approach that interrogates what is at stake in population constructions' rather than transcend them (pp. 76–77). Following Hinterberger's suggestion on critically examining contemporary population genomics research, I will argue in the section that follows that human microbiome science does not only operate at the level of populations, contradicting what Hinterberger (2012a, 2012b) and other authors (see Fox-Keller, 2010) have argued in relation to genomics and postgenomics medicine. Instead, I argue that the individual dimension of human microbiome science, although sustained by microbial DNA data from human populations through bioprospecting practices, gains meaning through informal, online networks of pseudoscientific microbial-related evidence.

MHC has several online and offline ramifications. In the following section of the article, I follow those networks and examine the para-ethnographic evidence (non-scientific) of the microbiome online community associated with the American Gut Project (AGP) mostly, but also with AGP's affiliated initiatives: the British Gut (BG).

The American Gut Project (AGP) is a not-for-profit microbiome initiative co-founded by anthropology-trained entrepreneur Jeff Leach and scientist Rob Knight in 2012. The AGP, as its website claims, has 'many more samples representing more groups of people than other studies, such as the Human Microbiome Project, Global Gut, or Personal Genome Project' (AGP, 2018). During the four years that the initiative has been running, over ten thousand contributors have participated and over $1.5 million was raised. The AGP has processed and sequenced around eight thousand samples from different ages, diets, and BMIs (body mass indexes). Participants receive a kit for providing samples from the body site(s) of their preference and send the kit back along with a personal survey, detailing their diet and whether they are taking any medication. Once the samples are analysed, they are provided with the results—together with information on how their sample correlates to other profiles, what this data means, and the latest articles and scientific research that relates to their profile. AGP's strategy uses a technical lexicon and develops an open-data model, through which all the sequenced data is made public and accessible to anyone. Interestingly, this so-called 'Science 2.0' project uses the popular term 'citizen science' for describing their ethos and procedures, despite charging between $69 and $99 for their most basic service. The AGP's purpose is to build a large data set of microbial profiles as well as provide a personalised medicine-like platform in which individual participants (North American) can explore their microbial profile by comparing it with the microbiome of different populations.

Meta-analysis is a key element of the AGP. A 'meta-analysis' means that Dominguez-Bello's data of the MHC project, for example, can be used for the AGP to 'contextualise' and 'interpret' results from individual profiles. This is made possible through microbial databases. The microbial genomic data obtained from population genomic studies such as MHC, as well as from AGP's participants, is anonymised and added to the database of the Earth Microbiome Project (EMP). The EMP is a massive, open-source and open-access global microbiome study founded by Rob Knight, whose aim is to catalogue the microbial profiles of the Earth's ecosystems. This nexus between population genomics data of the human microbiome and an individual microbial profiling acquires meaning through the visualisation of the results participants receive in a PDF file after the samples are processed and sequenced at Knight's Lab (see Figure 3).

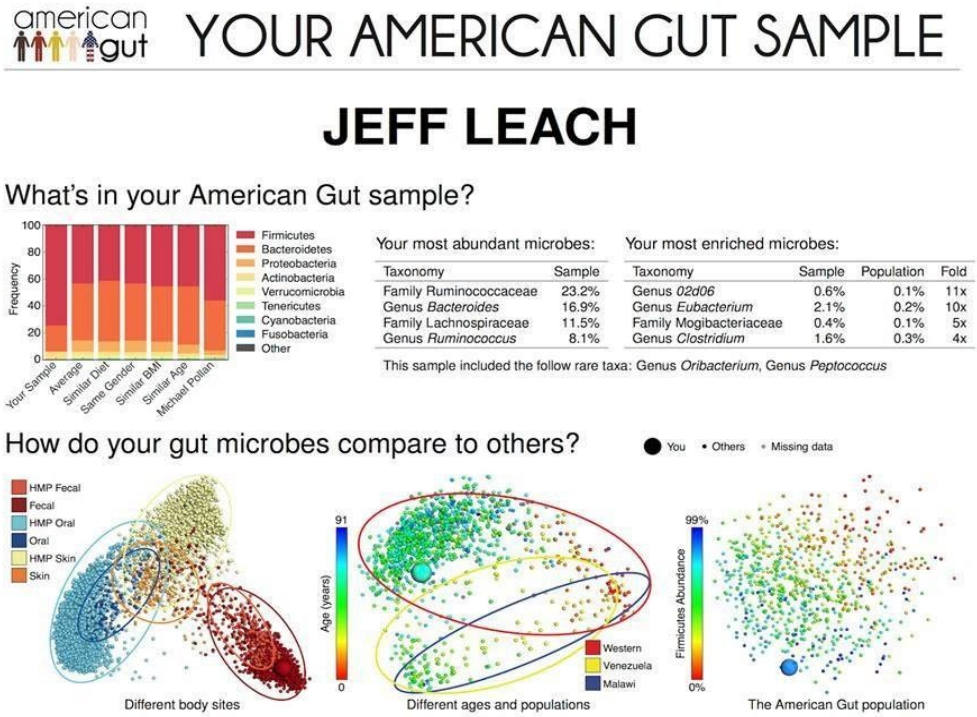

Figure 3. Jeff Leach's results from his participation in the AGP.

These results are from Jeff Leach, founder of the Human Foood Project (HFP) and co-founder of the AGP. They were part of the course material of 'Gut Check'. Results are divided into two (microbial) perspectives: the first, above in the PDF file, deals with the bacteria taxa of the faecal sample. This includes percentages of the most abundant and most enriched microbes, as well as less common or 'rare' taxa. The second perspective, on the bottom of the figure, includes three graphs representing how the (individual) gut sample compares to other populations: Venezuelan, Malawi, and Western. The first graph on the left situates these three populations in relation to the microbial composition of different body sites. The biggest red dot represents Leach's samples, which fall in the 'Western' category (red circle). The graph in the centre situates the individual sample in relation to different ages and populations (Leach's sample is represented by the biggest turquoise dot). Lastly, the right graph situates the AGP participants in relation to the abundance of *Firmicutes*, a bacteria phylum which constitutes a large portion of the human gut microbiome. Leach's sample (represented by the biggest blue dot) has a low abundance of the bacteria.

As I have previously argued in relation to the MHC research, the population categories (i.e. Western, Venezuelan, Malawi) deployed to compare individual samples of the AGP participants are extremely confusing: to what extent is the Venezuelan or the Malawi population 'traditional'? Does the 'Western' category include North American residents or just North American citizens? Many different populations with different lifestyles (that do not fit under the 'Western' label) live in the US; how do these categorisations reflect the heterogeneous social (and economic) reality of the US? The AGP does not address any of these questions, nor does it provide any criteria detailing how these categories were established. A closer look at the data and the AGP website reveals that these three (racial) categories of difference based on nationality/residency—'Venezuelans', 'Malawians', and 'Westerners'—are taken from a single human microbiome study conducted by Yatsunenko et al. (in which Dominguez-Bello and Rob Knight are co-authors) in 2012. This cross-cultural and cross-national study is a model for microbiome studies because of the diversity of the variables studied (Fortenberry, 2013). It included

mono- and dizygotic twins, children and adults, assessments of residency, kinship, diet, and cultural and social practices and habits. Regarding sample collection, the authors only mention that '(s)ubjects were recruited for the present study using procedures approved by Human Studies Committees' of each of the participating institutions (Yatsunenko et al., 2012, p. 9).

Furthermore, there clearly is a remarkable difference between the AGP and the MHC research regarding how the embodied form of the microbial samples is produced in the scientific discourse of microbiome science: the participants of the AGP are 'citizen scientists', while the Malawians, Amerindians Venezuelans, and the blurry category of 'Westerners' are 'research subjects'. Clearly, the former have a proactive role: they hold a 'biological citizenship' (Petryna, 2002), while the latter are purely passive, devoid of citizenship, 'illegal', as it were. While the AGP is an open-access scientific project exploring population-level patterns and trends, and therefore does not provide any clinical or commercial information, those who can relate to the sequenced microbial DNA are predominantly, if not all, Western (white) individuals. From a conceptual perspective, this is because biomedicine's general assumption is that bodies are the same and they can be normalised through biomedical technologies, a thought that has its roots in the European colonial empires (Lock & Nguyen, 2010). But the fact that knowledge of the microbiome is articulated using biomedical propositions about health and disease is not the main reason that microbiome science is reinstating the old immunological precept of inclusion and exclusion (through the inclusion of certain bodies [Western] and the exclusion of others [non-Western]). This is since human microbiome research is focused on 'modern diseases' or 'lifestyle diseases' such as diabetes, asthma, and obesity; diseases that affect those populations living in the West or adopting a 'Western' lifestyle.

Despite the initiative having been publicised as 'open to all' (North Americans), filling the gap of the NIH HMP (Knight, 2014), I suggest that participants of the AGP belong to a very selective population within the US, with substantial socio-economic and cultural capital. Not everyone has $100 to spend on this kind of personalised medicine initiative, and not everyone has the educational and cultural conditions to access information on personalised medicine initiatives such as the AGP.-The point is that the human microbiome of different populations provides context to individual samples. In that way, 'you will know which ancient lineages you have'. Invoking the ancestral and, in turn, racialising human populations is, I argue, a central element of these initiatives (AGP, HFP) (AGP, 2018). For medical anthropologist Alex Nading, moving beyond the passivity of 'cultural interpretation and social documentation of scientific practice' requires 'taking seriously not only the technoscientific claims that experts make about microbes in scholarly papers but also the qualitative claims … that they make in blogs, popular writing, and public engagement' (2016, pp. 561, 562). These assertions about the higher microbial diversity of the Hadza in comparison with 'us "moderns"' plays a nostalgic and exclusionary role. As Nading points out, 'ecological nostalgia is selective; it engages with the bodies of colonized others while insisting that they occupy a space beyond "global" environmental or economic life' (West, 2006, as cited in Nading, 2016, p. 572). On the assumption of isolation together with using contemporary human and non-human communities and populations as proxy of an ancestral past, microbiologists Graham Rook suggested me that the extrapolation of DNA microbial data from African to American or European populations is problematic, because these studies overlook evolutionary adaptations to local biologies (Lock & Nguyen, 2010) and, importantly, epigenetic mechanisms. Humans, Rook argues, have developed enormous flexibility through epigenetics. He illustrates this abstract biological idea with a specific case in pregnancy. If a woman with helminths (intestinal parasitic worms) is treated (with an antiparasitic drug) during pregnancy, her baby has a considerably increased likelihood of having allergic disorders, even in communities and populations where allergic diseases are not prevalent. This mechanism is 'almost certainly epigenetic' (G. Rook, personal communication, April 21, 2017). This shows, Rooks explains, that helminths protect from developing non-communicable diseases (NCD). Yet, he emphasises that these epigenetic mechanisms also mean that 'after a few generations in the United States without helminths, helminths are no longer necessary' and their re-introduction in Western populations would not mean a decrease in NCD. Rook's argument

contrasts with advocates of biome restoration, which refers to the controlled reintroduction of parasites or bacteria into the human body. DIY biome restoration through helminths and similar therapies such as faecal transplantation are popular among certain (online) communities, predominantly in the US. Contrary to Rook's argument, geographer Jamie Lorimer subscribes to the idea of helminth therapy as a potential solution to NCD (2016, p. 59). According to Lorimer, helminth therapy implies 'an ecological model of immunity as involving a multispecies community' (p. 69) and it offers 'new ways of thinking companionship and hospitality as more-than-human, but not posthuman, achievements' (p. 59). I concur with Lorimer in that, contrary to posthumanist hopes of decentring the human (see Hird, 2009; Esposito, 2008, 2011), the 'human' of the human microbiome remains the goal of multispecies ethics and therapies. However, I argue that biome restoration through helminths is not about an 'ecological model of immunity', as he suggests, but about a delocalised model of immunity based on qualitative, para-ethnographic data (pseudoscientific). Here, the (ancestral) role of helminths in traditional cultures and societies is the principal element (para-ethnographic data) sustaining DIY experiments with helminths in the West via an empowered online community. This model of immunity is, in fact, articulated in exclusion ('us', moderns, versus others, traditionals) and nostalgia for a (better and healthier) evolutionary past (see TallBear, 2013).

Similarly, despite the scientific epistemology of postgenomic microbiome science resting upon a discourse of 'ecological holism', co-evolution, and harmonious balance between microbes and humans, through the case of the Microbes of Homes across Culture (MHC) research, along with its online ramifications, the article has demonstrated that microbial science it is not about holism, but about a disembodied knowledge practice based on the expropriation (via bioprospection) of 'ancestral microorganisms'. This is, in fact, very much a neoliberal capitalist model of microbiome research, based on the individualisation and privatisation of biological knowledge production, therefore distant from the delivery of universal and public health (Author, 2019).

In conclusion, sociologist Amy Hinterberger (2012a) has pointed out that the 'question of population needs to be reactivated as human genome science is increasingly linked to promises of individualized and personalized medicine' (p. 87). As Hinterberger also argues, historian of science Evelyn Fox-Keller has elaborated on the contradictory use of individual and population categories in contemporary life sciences, a confusion, she argues, that is rooted in language, particularly in the terms heritable and heritability (2010, pp. 55–57):

> The difficulty in maintaining the essential distinction between individual and population persists, and it may even have been compounded. When authors write about sorting genetic from environmental contributions to the development of traits, it is not only the distinction between trait and trait difference that has been tacitly erased, but also the distinction between individual and population. … Our difficulty in maintaining this conceptual distinction is sustained, if not caused, by the words we use (Fox-Keller, 2010, p. 55).

In this light, coming from Foucault's idea of population as a question of power and politics, Hinterberger (2012a) argues that social and humanities studies of large-scale human genome science should tackle the concept of populations in all its ambiguity, as Fox-Keller shows. I concur with Hinterberger that, while Euro-American science policy discourse focuses on the construction of the 'responsible and self-policing individual', life science research is concerned with populations (Hinterberger, 2012a, p. 87), as the chapter has demonstrated. However, Hinterberger misses an important element of contemporary population genomics research. A closer analysis of human microbiome research through Dominguez-Bello's MHC project research have revealed that online initiatives such as the AGP or the BG use open-access population genomic data (particularly data from non-Western populations) to provide contextual information for certain (privileged) Western individuals. While the Foucauldian concept of population in relation to power and politics might be a useful framework through which to analyse large-scale postgenomic projects like human microbiome science, as Hinterberger suggests, I instead associate this trend of the process of microbiomisation—by

which microbiome science takes social groups as pre-existing, 'natural' phenomena and biologises them by attributing microbes and microbial profiles to them—with what medical anthropologist Didier Fassin (2009) calls 'bioinequalities'.

In sum, I maintain that the process of microbiomisation not only rests upon (1) the bioprospection of DNA from human and non-human populations (see Section 3.3), but also, and equally importantly, on (2) the economic, social, and cultural capital of consumers (mostly from Northern richer nations) of microbiome profiling online platforms such as the AGP, an aspect that I link with Fassin's concept of bioinequalities.

Conclusion

The article drew on ethnographic fieldwork of 'Microbiomes of Homes across Cultures' (MHC), a landmark microbiome study on the relationship between microbial diversity, disbalance and human health (2012 -2016) in San Juan (Puerto Rico) and New York (US), interviews with influential microbiome scientists, attendance of microbiome conferences, and an analysis of scientific publications and the microbiome online community. Weaving my research results with the concept of 'microbiomisation', the article showed that both environmental determinism and biological essentialism are being re-enacted in human microbiome research.

Only when genetic sequences are put together with non-genetic factors, such as lifestyle habits or environmental exposures, can genetic information be meaningful. Put differently, genes, and therefore genomes, do not say much in and of themselves (see Keller, as cited in Richardson & Stevens, 2015). Postgenomics might not necessarily imply a break with genomics, with biological determinism. It rather entails continuities and discontinuities of genomics (Richardson & Stevens, 2015) by figuring and refiguring the latter as embodied in the wider milieu of the organism. Likewise, by correlating certain microbial species and diversity and hunter-gatherers, ideas of race, nation, and ethnicity become microbiomised. Unlike other biological-social interplays—such as the personification of cells, by which biomedicine writes and speaks about cells as if they were interchangeable with persons (Martin, 2006)—in the process of microbiomisation, the 'social' (i.e. lifestyle, cultural habits, ritual, traditions, local milieus) is the main element that animates scientific research on microbes (see figure 3). Microbiomisation is similar to what environmental scientist Becky Mansfield (2012) calls 'epigenetics biopolitics', which involves shifting 'the responsibility of exposure to chemicals towards the 'abnormal' diets of women of colour instead of blaming contamination itself' (p. 352). I have demonstrated that the bioprospection of microbial 'populations' from human and non-human populations is a key element of the process of microbiomisation. Yet, human microbiome science, as part of postgenomics, does not only operate at the level of populations, as some authors have suggested (Fox-Keller, 2010; Hinterberger, 2012a), nor does it only operate on the individual via personalised medicine projects, as others have claimed (El-Haj, 2007; Wade et al., 2014). By contrast, I have contended that the individual dimension of human microbiome science is sustained by microbial DNA data from human populations and gains meaning through informal online networks of pseudoscientific microbial-related evidence.

The principal contribution of this article to the history, philosophy and social studies of the life sciences was to show that postgenomic interventions (including initiatives such as the AGP) aimed at defining a 'healthy' microbiome is 'a gendered and racialized demand' (Mansfield, 2012, p. 369) articulated upon a nexus between (1) bioprospecting the microbial genetic makeup of non-Western(ised) communities, societies, and locales (Hayden, 2003; Shiva, 1997; TallBear, 2013) and (2) individual economic, social, and cultural capital in neoliberal societies. Hence, while human microbiome science displaces older

ideas of immunity as a guarantor of biological identity and individuality, it instantiates new forms of difference, particularly 'immunitary privileges' based on a higher microbial diversity and reproduces old ones in terms of neocolonial practices of expropriating nature (microbes in this case) and structural differences in (Western) societies. Microbial science brings human agency together with environmental effects and socio-cultural habits and traits into processes of pathologisation, medicalisation, and optimisation. In postgenomic, bodies are 'semi-permeable' to their surroundings, including other humans and non-humans such as microbes and environments. Yet, environments are rarely neutral or 'just' environments. This means that 'surroundings', 'environments', and consequently, (leaky) bodies are sites of constraint, control, and subjugation as well as sites of contestation and resistance.

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