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Unsettling antibiosis: how might interdisciplinary researchers generate a feeling for the microbiome and to what effect?

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ABSTRACT Decades of active public health messaging about the dangers of pathogenic microbes has led to a Western society dominated by an antibiotic worldview; however recent scientific and social interest in the microbiome suggests an emerging counter-current of more probiotic sentiments. Such stirrings are supported by cultural curiosity around the ‘hygiene hypothesis’, or the idea it is possible to be ‘too clean’ and a certain amount of microbial exposure is essential for health. These trends resonate with the ways in which scientists too have adopted a more ‘ecological’ perspective on the microbiome. Advances in sequencing technologies and decreasing costs have allowed researchers to more rapidly explore the abundance and diversity of microbial life. This paper seeks to expand on such probiotic tendencies by proposing an interdisciplinary methodology researchers might use to generate more-than-antibiotic relations between lay participants and their domestic microbiome. The paper draws on findings from an ESRC-funded study, *Good Germs, Bad Germs: Mapping microbial life in the kitchen* (grant number ES/N006968/1), which sought to: (i) explore human-microbe relations in the domestic kitchen; and (ii) make scientific techniques for visualising the domestic microbiome available to non-expert publics through a form of ‘participatory metagenomics’. We examine how scientific knowledge and techniques are enroled into lay practices of making microbes sensible; how these intersect with, reinforce or disrupt previous feelings for microorganisms; and how new ways of relating with microbial others emerge. In reflecting on these findings we draw on work in animal geographies, environmental humanities and the social science of the microbiome. We examine how cultural, emotional and embodied responses to nonhuman others—their ability to affect ‘us’ humans—have implications for the ways in which public health authorities, researchers and ‘lay’ publics alike seek to engage with and govern nonhuman life. We argue that understanding and potentially generating different modes of relating to microbes—a feeling for the microbiome—offers opportunities for reconfiguring microbiopolitics and intervening into the ways in which publics respond to perceived microbial opportunities and threats.

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Introduction

Researchers [...] focus on interactions, communities and ecologies ... [P]opular (especially media) discourses about microbes are mainly framed by negative and fear-inducing metaphors, where microbes invade and contaminate bodies and where the public is exhorted to wage constant war against them in hospitals, homes and public spaces. (Nerlich and Hellsten, 2009, p. 21–22)

In a recent paper Nerlich and Hellsten (2009) suggest there is a significant divide between an emerging ecological perspective on microbes found in scientific research—one which focuses on ‘interactions, communities and ecologies’—and popular discourses which remain by and large antibiotic. While the threat represented by a few specific named species of microbes is genuine, these species are very much in the minority. Despite this, decades of active public health messaging about the dangers of pathogenic microbes has led to a Western society dominated by an antibiotic, antimicrobial worldview. The sanitation movement towards the end of the 19th century marked the start of a concerted effort across Western societies to be germ-free and hygienically clean, a movement whose traces can be found everywhere, from sewage and water treatment to the widespread prophylactic use of antibiotics. Over the course of the 20th century Western populations have been deliberately cultivated, Paxson (2008, p. 28, see also Nerlich and Hellsten, 2009) might say, to be ‘germophobic subjects who will make rational decisions to safeguard their health’. (Although it is important to note this antibiotic trend was neither uniform nor uncontested, see Sangodeyi, 2014). Recent concerns over emerging Anti-Microbial Resistance (AMR) have further muddied the waters. On the one hand the rise of the superbugs has led to an emphasis on keeping things hygienically clean and sterile; on the other hand critics point to the over use of antibiotics (antibiosis?)¹ as a key cause of AMR.

Alongside these sanitary concerns and the looming threat of AMR there is an enduring counter-current of more probiotic sentiments (Paxson, 2008; Paxson and Helmreich, 2014; Lorimer, 2017a). Within scientific communities microbes are differently apprehended, (as interesting as opposed to threatening) and comprehended (as communities as opposed to individual entities). Advances in sequencing technologies and the falling costs of sequencing have dramatically expanded the scope of scientific engagements with microbes, facilitating the development of a more ‘ecological’ perspective. As Paxson and Helmreich, (2014, p. 173) suggest, this is a form of scientific endeavour characterised more by ‘Darwinian exploration than industrial technoscience’ and driven (for the moment) by a curiosity about exactly who might be ‘out there’ rather than an imperative to capitalise on microbial resources. (Although rumours from the research community note an increasing interest expressed by venture capital in the emerging microbiome frontier). Researchers exploring the human microbiome characterise humans as superorganisms who are microbial ‘all the way down’ to paraphrase Haraway (2014), ‘accommodating, infected, and kept alive by diverse microbes in dynamic ecologies’ (Lorimer, 2016, p. 58). These perspectives have filtered down into popular science, encouraging non-expert readers to contemplate the life within us (see e.g., Yong, 2016). They also resonate with cultural curiosity around the ‘hygiene hypothesis’; the idea that it is possible to be ‘too clean’ and that a certain amount of microbial exposure is essential for health.

Probiotic cultures (in the sense of particular human-nonhuman collectives) can be enduring, reflecting long histories of human-microbe collaboration. Such collaborations include the tea-based mushrooms fermenting in jars on the shelves of

Bosnian kitchens (Jasaveric, 2015), the *Botrytis cinerea* in wine-making tanks in South Australia’s Barossa Valley (Brice, 2014), or the *Geotrichum candidum* moulding on the rinds of North American artisanal cheeses (Paxson, 2008). There are also new probiotic cultures emerging in the form of the experimental fermented pork product *butabushi* found in test kitchen of celebrity chef David Chang (Paxson and Helmreich, 2014), *kombucha*, a fermented, fizzy tea-based drink with purported health benefits (Spackman, 2018), the use of Fecal Microbial Transplants to address chronic health problems (Wolf-Meyer, 2017), or the helminths (or hookworms) reintroduced into affluent Western human bodies ‘to tackle allergies and inflammatory and auto-immune conditions’ (Lorimer, 2016, p. 59). We might describe the humans involved in co-producing cheese, wine and alternative therapies as engaging in forms of ‘lay microbiology’ (Enticott, 2003). Drawing on a hybrid and eclectic combination of scientific language and techniques, traditional knowledge and experimentation, lay microbiologists reacquaint themselves with old microbial friends (Lorimer, 2016) and develop tastes and applications for new ones (Paxson, 2008). This is not to decry the very real benefits that come from clean water and effective treatments for bacterial infections. Paxson (2018, p. 18) describes these lay-microbiological practices as being post (as opposed to anti) Pasteurian². In her words, ‘post-Pasteurianism takes after Pasteurianism in taking hygiene seriously. It differs in being more discriminating’. Furthermore, as Paxson and Helmreich (2014, p. 183) caution, ‘this optimistic vision of microbes has been enabled precisely by the fact that the Pasteurian project has been so successful; microbes can be promising for those people who no longer have to worry about smallpox, polio, cholera, and other agents of infectious disease.’ This point also reminds us that the possibilities of being post-Pasteurian are often, like many scientific innovations, a luxury enjoyed by the more affluent in society with access to resources and healthcare provision if things go awry (see Lorimer, 2017b).

Within geography scholars exploring the complex relationships between microbes and human and animal health have noted distinctive antimicrobial geographical imaginations; put simply the conviction that fewer microbes equals better places (Lorimer, 2017b). Challenging this reading scholars have argued that the problem is not the presence of dangerous microbes per se, but rather a sense that human-microbial relations are out of balance or in ‘dysbiosis’ (see Lorimer, 2017a, p. 33). They propose that disease is the ‘emergent outcome of complex, spatio-temporal interactions between the host immune system and the internal and external microbial environment’ (Lorimer, 2017b, p. 544; see also Hinchliffe et al., 2016). This in turn has implications for the governance of human-microbe relations. For example, Hinchliffe et al. (2013, p. 531) argue for a shift from a focus on being germ-free and ‘walling off’ valued spaces, human and animals ‘against an ‘outside’ world of infection’, to an approach which recognises that ‘being healthy does not necessarily mean being free of pathogens’. Rather than seeking to create barriers between infected/contaminated and uninfected/uncontaminated life, they advocate critically interrogating the conditions under which diseased and healthy forms of life emerge and exploring how they might be reconfigured towards making better and healthier lives possible. Here we suggest that a post-Pasteurian perspective might also offer a model for re-thinking microbiopolitics (Paxson, 2008).

The term microbiopolitics is an extension of Foucault’s (1978) analysis of how 19th century Western populations were made visible through emerging statistical techniques, which in turn rendered them governable as biological objects. Biopolitics describes how nation states seek to maintain the health of their

population through policies which foster some forms of life—through for example programmes for sanitation, vaccination and public hygiene—while letting others die. Paxson (2008) finds a parallel for this in Latour's (1988) account of the work of Louis Pasteur, whose experiments served to both make microbial agencies visible and to develop a means (Pasteurisation) through which they could be seemingly controlled. For Paxson (2008, p. 17), therefore, the process of Pasteurisation marks the point where biopolitics 'is joined by microbiopolitics', namely 'the recognition and management, governmental and grassroots, of human encounters with the vital organismic agencies of bacteria, viruses, and fungi' (Paxson, 2008, p. 23). However, given the rather indiscriminate ways in which processes of pasteurisation operate—the focus seems to be more on killing as many bacteria as possible, as opposed to just letting them die—it might be more accurate to term such practices micronecropolitics (after Mbembe, 2003).

Within the UK the Food Standards Agency (FSA), which regulates food production, distribution and consumption, might be framed as a key biopolitical authority. Their work spans a number of sites, ranging from the production lines of meat-processing plants to the stainless steel worktops of restaurant kitchens. Of particular interest to this paper is the space of the domestic kitchen, as it is within this space that Pasteurian microbiopolitics is combined with the production of biological citizens. According to Rose and Novas (2004) biological citizens draw on biological knowledge to understand their bodies, seeking to conform to the norm of a 'healthy' citizen and differentiate themselves from (unhealthy) others. We suggest that the FSA's kitchen-check campaign engages in microbiopolitics by seeking to govern human-microbe relations, offering advice on cleaning, chilling and cooking food in order to minimise the spread and proliferation of harmful bacteria. Simultaneously the campaign also works towards the production of microbiopolitical citizens by inviting members of the public to 'find out if your kitchen habits are putting you, or your family and friends, at risk of food poisoning' (FSA, 2012). The implication is that good microbiopolitical citizens are those whose hygiene practices do not put themselves or their families at risk. Collectively the practices of domestic microbiopolitics and the construction of microbiopolitical citizens begin to set out what distinguishes valued subjects and spaces from unwanted, microbially-contaminated, unhygienic, unclean others (compare Craddock, 2004).

The emerging probiotic movement sits in contrast to practices of microbiopolitics and microbiopolitical citizenship that largely distinguish themselves through the exclusion of unwanted microbial others and their hosts (see also Spackman, 2018). For example, new 'probiotic' cleaning products claim to reseed your kitchen surfaces with 'friendly' bacteria to hopefully outcompete more harmful kinds³. Rather than seeking to create a germ-free environment, such products—in Paxson's (2008) terms—discriminate between 'beneficial' and other kinds of microorganisms. Such moves suggest there may be alternative approaches to managing domestic human-microbe relations. Less well known are the implications of such shifting human-microbe cultures for microbiopolitical citizenship, and the implications of changing human-microbial relations for understandings of self, other, health and hygiene. Taking the possibility of more probiotic, post-Pasteurian approaches to domestic hygiene as our starting point, we explore how scientific methods of making microbes visible might enable a group of Oxford households to relate differently to the microbes in their kitchens, reconfiguring their status as microbiopolitical citizens. The next section outlines our interdisciplinary methodology for 'participatory metagenomics'. Two subsequent sections then explore how far the project facilitated our participants in learning to be differently affected by

the domestic microbiome, and how their responses complement and extend existing readings of human-microbe relations. The first section asks 'How did the ability to survey, visualise and potentially intervene in their domestic microbial ecologies change the ways in which our participants made sense of the microbes who shared their homes?' Subsequent sections explore *how the encounters with microbes facilitated by our project reinforce or disrupt previous feelings for microorganisms, perhaps even allowing new ways of relating with microbial others to emerge*. In concluding, we consider the implications of participatory metagenomics as a means of reconfiguring both lay microbiologies and the microbiopolitics (Paxson, 2008) of the domestic kitchen.

Participatory metagenomics: developing an interdisciplinary approach

This paper draws on the findings from a recent ESRC-funded study, *Good Germs, Bad Germs: Mapping microbial life in the kitchen* (grant number ES/N006968/1), which sought to make scientific techniques for visualising the domestic microbiome available to non-expert publics through a form of 'participatory metagenomics' (see Hodgetts et al., 2018 for further details on the project methodology). Metagenomics represents a significant advance in scientific approaches to studying microbial biodiversity. Previously, the main method for understanding the composition (organism types and abundance) of a microbial community was to culture its members, allowing them to reproduce under controlled laboratory conditions. Metagenomics, in contrast, involves 'a series of experimental and computational approaches that allow a microbial community's composition to be defined by DNA sequencing without having to culture its members' (Benezra, DeStefano and Gorden, 2012, p. 6378). Such techniques have been credited with revolutionising microbiology, revealing the hidden diversity of microbial life, allowing a better understanding of microbial ecosystem functions and services, and enabling the search for new therapeutic and diagnostic tools for human health. However, currently barriers of cost and expertise arguably make metagenomic methods inaccessible to those outside of specialist research institutes or commercial research facilities.

There is already considerable evidence of increased citizen interest and involvement in the microbiome. An active community of 'expert publics'—many of whom suffer from immune-related conditions which have been increasingly linked to microbial dysbiosis (Blaser, 2014; Velasquez-Manof, 2013)—run their own private experiments with pro and prebiotic diets and worm therapies (Lorimer, 2016). Concerned publics are also lining up to provide samples for microbiome research⁴, sometimes in exchange for personalised microbiome profiles⁶. However such forms of participation are relatively 'downstream'. Participants may be granted partial access to the results of analyses conducted using the environmental samples they supplied, but they have little say in determining the kinds of scientific questions asked. Against this background we took inspiration from Whatmore and Landström's (2011) 'apprentice model', in which scientists and social scientists work with small community groups learning how to use scientific tools to address their specific concerns⁷. Interdisciplinarity in this context therefore reflects the divergent expertise of firstly the research team, who combine expertise in evolutionary biology, molecular biology, bioinformatics, animal and health geographies, and secondly the diverse knowledges and backgrounds of our 14 recruited households. While we deliberately excluded anyone with expertise in the field of microbiome science, our participants did include alternative forms of expertise ranging from microbiology and environmental science to cleaning and catering. This form of interdisciplinarity

also reflects the ongoing process of mutual apprenticeship shared by researchers and participants as we learnt to be affected by both the domestic microbiome and by each other's divergent experiences. Our interdisciplinary knowledges were further supplemented by a series of stakeholder interviews the team conducted with microbiologists, regulators and cleaning product manufacturers, and by contributions from the Food Standards Agency who participated in one of the group meetings.

In Whatmore and Landström's (2011) model participants were identified through a pre-existing shared interest in a specific project (in their case local flood damage prevention). Like Whatmore and Landström, we sought to assemble a group of participants that was not the assumed and undifferentiated 'public' of the so-called deficit model of public engagement (Irwin, 1995), defined only by their assumed lack of knowledge about (in this case) microbial science. Yet in seeking to explore 'What questions might a public ask if given the opportunity to conduct their own investigations into their domestic microbiome?', we could not rely on a shared or pre-existing 'concern for the microbiome' as our selection criteria. Instead, we sought out a local community group who were both interested in learning more about the microbes in their kitchen and who might be interesting in terms of their domestic microbiome. Those who might be *interested* were defined both pragmatically—resource constraints making it prudent to use households in our local Oxford community who lived close enough to make the collection of samples and hosting of group meetings feasible—and in the sense that our recruitment strategy (of leafleting and snowballing through community contacts) meant there was a degree of self-selection in terms of who we recruited. The local community group were *interesting* in the sense that, in the absence of any pre-existing evidence as to what might be empirically relevant about the lay engagements with the domestic microbiome, we sought out multigenerational, multispecies households whose domestic arrangements we speculated might promote microbial biodiversity.

In total the project recruited 14 Oxford households. We began our experiment in April 2016 with an 'entry' interview which explored people's thoughts on and attitudes towards their kitchen microbiome. At the end of this interview we gave participants an initial sampling kit and instructions to swab five key sites in their kitchens, as well as a sixth site of their own choosing. We then arranged to collect the swabs and extracted, amplified and analysed the samples in order to try to identify the kinds of bacteria present. To do this we employed a technique called 16S rRNA sequencing. The technique works by isolating all the examples of a specific gene (16S rRNA) from a sample of nucleic material. All bacteria have this gene, but some of the sections within it vary significantly between bacterial types, allowing types to be identified by comparing variations in 16S rRNA to a known library. 16S is a form of next generation sequencing, so-called because it facilitates the analysis of the entire microbial community within a sample without the need to culture each individual strain. (For more details on the method and the challenges of its application see Hodgetts et al., 2018). This technique had significant advantages, being both accessible and affordable (to social science researchers if not (yet) to the majority of the public), but it was not without its limitations. For example, we were unable to identify the specific species of bacteria our participants were interested in.

The results of this first experiment became the focus for the first of six group meetings. At each meeting we would share and discuss the results of the DNA analysis and work with participants to design the next experiment. Following their initial kitchen 'safari' participants developed and analysed the results of four further experiments: (i) exploring the impact of cleaning

products; (ii) tracking the microbial colonisation of chopping boards; (iii) and of fridges; (iv) and a final 'free choice' experiment where participants could sequence sites of most interest to them. An 'exit' interview in July 2017 re-examined participant's understandings of microbes, health and hygiene in light of the experiments conducted, as well as providing space for reflecting on their experience of being 'microbiome apprentices'.

Our project had four key aims. Firstly, we sought to sample the microbiome of specific components of the built environment, focusing on domestic kitchens but allowing the sampling strategy to be determined deliberately, through a collaboratively derived set of questions participants would like to ask about microbial life in their kitchens. Secondly, through interviews and group meetings, we sought to explore *lay microbiologies*, popular understandings of and means of interacting with these microbes, although given the range of expertise outlined above we might better term these *interdisciplinary microbiologies*. Thirdly, we sought to develop methods for visualising the microbiome for deliberation with these publics and to track the effect of such visualisations on perceptions and practices. Hird (2009, p. 36) suggests much of the contemporary work on human-nonhuman relations is characterised by a 'profoundly myopic humanism', consequently researchers working in multispecies studies and animal geographies tend to focus on those nonhumans most easily sensed and seen by bipedal, diurnal mammals who are 'big like us' (see also Lorimer, 2006, O'Malley and Dupre, 2007, Paxson, 2008). Hence a key challenge for this project lay in finding ways to 'make the microbiome visible' which were distinctive from the more familiar visceral/embodied encounters through which microbes make their presence felt; the coughing and sneezing experiences of catching cold (Greenhough, 2012) or the digestive discomfort of microbial dysbiosis (Lorimer, 2016). Fourthly, we sought to understand the character and implications of prevalent ways in which the microbiome of the built environment is governed; what Paxson (2008) might term *domestic microbiopolitics*, giving our participants the opportunity of asking 'who lives well and who dies well under current arrangements, and how they might be better arranged' (Ginn et al., 2014, p. 115)?

We might describe our study, therefore, as tentatively probiotic; concerned with working with and modulating 'the emergent properties of interspecies interaction webs to reconfigure the basic conditions in which life persists' (Lorimer, 2017a, p. 36). For example, one experiment (experiment 2) explored the impact of different cleaning products on the bacterial communities living on kitchen work surfaces, testing what kinds of microbial life were removed by different cleaning regimes and what grew back after cleaning. Another (experiment 3) examined the ways in which new chopping boards (either wooden or plastic) were colonised by bacteria over a period of 14 days. Focus group discussions and exit interviews provided a space within which participants reflected on what they had (and hadn't) learned, and how it effected the ways in which they went about (and in particular cleaned) their kitchen spaces. Discussions were loosely framed around the hygiene hypothesis (see for an overview Bloomfield et al., 2016), or the theory that excessive sterilisation and sanitation and a corresponding lack of exposure to microbial life was directly linked to the significant rise in autoimmune and inflammatory diseases in the global North. However participants often brought in a much wider range of theories, ideas and experiences through which to make sense of these new forms of microbial encounter. Drawing on these discussions below, we explore firstly the extent to which participatory metagenomics opened up new spaces through which participants learned to be differently affected by the domestic microbiome. Secondly, we examine the extent to which this process allowed new kinds of

interdisciplinary microbiologies and domestic microbiopolitics to emerge.

Interdisciplinary microbiologies: learning to be affected

One of the key issues we were keen to explore through this research was how the scientific knowledge and techniques we shared with our participants were enroled into lay practices of sensing and responding to the domestic microbiome: *How did the ability to survey, visualise and potentially intervene in their domestic microbial ecologies change the ways in which our participants viewed the microbes who shared their homes?* The question of how we learn to be affected by (Bingham, 2006; Lorimer, 2007), attuned, attentive or responsive to (Despret, 2004; Haraway, 2008; Greenhough and Roe, 2010; Van Dooren et al., 2016; Druglito, 2016) or even notice (Tsing, 2015) nonhuman agencies is one which has preoccupied scholars in environmental humanities, animal studies and animal geographies for some time now. In particular, the recognition of the ways in which our human bodily capacities limit our engagements with the nonhuman world (Lorimer, 2006; Hodgetts and Lorimer, 2014) and more specifically those critters who are not ‘big-like-us, leading towards a bias in our investigations towards creatures that ‘easily bear ocular scrutiny—creatures we can see unaided by the technology of microscopes’ (Hird, 2009, p. 21).

This has led to calls for researchers to ‘supplement the familiar repertoire of human geography methods that rely on generating talk and text with experimental practices that amplify other sensory, bodily and affective registers and extend the company and modality of what constitutes a research subject’ (Whatmore, 2004, p. 1362). For example Hinchliffe and colleagues (2005, p. 647) describe how they needed to develop new skills to understand how water voles inhabited a brownfield urban site, in particular developing ‘noses’ to sense the difference between rat and vole faeces or that ‘omnivores produce far more pungent faeces than the rush-eating water voles’. It is at this point that the role and significance of lay and amateur microbiologies becomes interesting. Lay microbiologies, we might say, are replete with such methods. As lay microbiologists we smell and taste when wine goes bad (or at least when *Botrytis cinerea* makes it unpalatable, Brice, 2014) and the gastronomic transformations wrought by bacteria on artisan cheese (Paxson, 2008). We observe the biofilms stretching over jams and marvel at the bubbles and smells emanating from a sourdough starter or ‘that thing in a jar’ (Jasarevic, 2015). We experience ‘through an invisible corporeal interface’ (Lorimer, 2016, p. 72) the ‘assorted seeping, dribbling, spraying of excessive bodily fluid’ of an infection by the common cold virus (Clark, 2004, see also Greenhough, 2012). In short, for lay microbiologists, embodied, affective, multisensual methods are the norm, not the innovation (compare Enticott, 2003 on lay immunologies). Consider, for example how, when these participants describe how they know when something is hygienically ‘clean’ or pathogen free, a particular mode of sensing (smell) is combined with technically informed knowledge of the capacities of bleach and dominant antibiotic biopolitical norms:

FS1: You use your sense of smell a lot, don’t you?

MS1: If something smells bad, then that’s usually a sign that something’s not right.

Q: Yes, and in reverse, if there was a strong smell of bleach or,

MS1: Yeah, you’d realise that somebody had cleaned, yeah.

(Exit interview 114, July 2017)

What then, might an interdisciplinary project drawing on scientific methods bring to the table? From a critical Science and Technology Studies perspective we could speculate that our methods might actually more readily lead to participants becoming ‘unaffected’ by microbial agencies, setting them at a technologically-mediated distance. Not unlike the drone technologies described by Derek Gregory (2014), our technologies and techniques gave primacy to visual forms of representation whilst simultaneously failing to engage other sensory registers—notably taste and smell—that are often central to the practices of lay microbiology. In this way our scientific methodologies seem almost counterintuitive to posthumanist dispositions, carrying with them the risk of veering ‘toward universalizing metaphysical claims about the nature of ‘matter’ as such’ and also at times taking ‘scientific truth claims about the world at face value’ (Paxson and Helmreich, 2014, p. 169, see also Landecker, 2016). Our methods also at times resonated uncomfortably with colonial imaginations, such as those explored by Willis (2018, p. 327), which contrast a ‘sensorially neutral or blank’ White and hygienic space with a smelly—and by implication dirty and less-valued—black Brazilian other. Building on her work, we might pay attention to how microbes (and the sensory responses they generate) become bound-up in a ‘politics of felt [and sensed] difference’, which—as described above—all too often becomes means of discriminating between good microbiopolitical citizens and unwanted others.

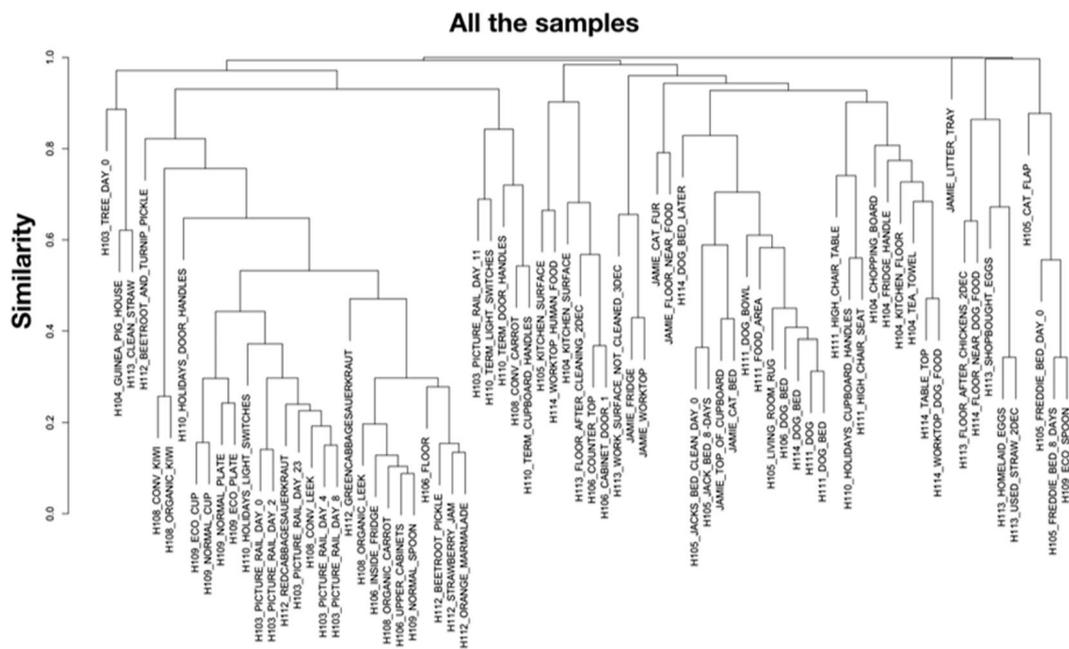
It is here that the value of our upstream participatory approach really begins to make itself felt, as our participants constantly questioned and challenged our attempts to translate and ‘visualise’ the sequencing data our experiments generated. For example, here a participant tries to combine the ‘blob’ and tree diagrams we produced (see Fig. 1) with their own ‘lay’ microbiologies in ways which made simple truth claims hard, if not impossible, to derive.

I found the blobs harder to understand to make sense of, so I’m not sure to what extent I fully understood them especially because then it was just, you know, say a group which within itself could be all sorts of different [...] so there wasn’t like green blobs of lots of good things and red blobs of lots of bad [all laugh]. (Exit interview 107, July 2017)

The answer perhaps lies in the ways in which our knowledge of the microbiome is already in many senses inherently interdisciplinary. This became evident in the division of the project labours of surveying, visualising and potentially intervening in the domestic microbiome. As noted above, the work of turning the data into visualisations rested largely with the research team, whose diagrams, charts and maps often diverged significantly from participant’s imagined microbial geographies. At times participants (and at some stages - when we outsourced part of the sequencing work - the research team also) were relatively excluded from the lab-based work of 16S sequencing. In contrast, the research team was absent at the point of data collection, and increasingly took a back seat in the process of designing interventions. Key for this project, therefore, is not prioritising one form of expertise and experience above another, but remaining attentive to the ways in which knowledges and practices—as well as microbes (see Landecker, 2016)—can communicate and hybridise horizontally as well as vertically, and recombine in ways which have interesting implications for domestic microbiopolitics. At times in the course of the project our mode of knowledge exchange felt uncomfortably similar to the deficit model, whereby the scientific expert educates the novice public, a top-down vertical transmission of knowledge. For example, the moments we stood in front of the group ‘explaining’ the scientific



‘Blob’ or Phinch bubble diagram showing the combined group results of our initial ‘kitchen safari’. Each circle or ‘bubble’ in the diagram represents a different phylum. The size of the bubble represents the abundance of that phylum in the dataset. Larger bubbles are more abundant, smaller bubbles less abundant.



‘Tree’ diagram showing the collective results from the final ‘free choice’ experiment. Hxxx refers to the participating household, alongside a description of the site sampled. On a tree diagram, two samples form a pair of leaves if they are more similar to each other than to any other samples. The same is true of any group of branches – they form a group on the tree diagram because their samples are closer to all the other samples in the group than to those in a different group.

Fig. 1 Examples of some of the visualisations we used to present the sequencing data to participants. This figure is covered by the Creative Commons Attribution 4.0 International License. Reproduced with permission of Beth Greenhough, Jamie Lorimer, Richard Grenyer, Timothy Hodgetts, Carmen McLeod and Andrew Dwyer; copyright © Beth Greenhough, Jamie Lorimer, Richard Grenyer, Timothy Hodgetts, Carmen McLeod and Andrew Dwyer; all rights reserved

process or how to interpret the results. At other times we found ourselves challenged (from the bottom-up) by participants' ambitions for what we could potentially discover. Equally though, discussions amongst research team, amongst the participants, and between us all, reflected more 'horizontal' exchanges, where everyone speaks from a position of both knowledge and ignorance. In such exchanges, the expertise of one party in industrial cleaning protocols and another in metagenomic sequencing place them on a similar plane, albeit coming at it from different trajectories. The 'ways of knowing' generated over the course of 18 months of working together did not replace previous ways of knowing, but added to them. As one participant observed, 'we don't really have a common language for thinking about the microbiome' and therefore the project offered 'new perspectives' and 'ways of visualising thinking' (exit interview 108, July 2017). The impacts of our participatory metagenomic experiment are consequently more complex than a simple reassertion of a scientific truth about how, why and where the domestic microbiome matters. This in turn leads to the formation of what Das and Das (2006) might call local 'ecologies' or 'cultures' for knowing the domestic microbiome.

Unsettling antibiotic

Germ seems very old fashioned to me now as a way of thinking about microbes. (Exit interview 108, July 2017)

While small and exploratory in scale the evidence from our research suggests it is possible to begin to shift and unsettle dominant antimicrobial feelings by facilitating new modes of engaging nonexperts with their domestic microbiome. These new sensibilities resonate with themes found elsewhere within environmental humanities and by those working on the social science of the microbiome. In this section we draw on participants' reflections on their participation in the project to explore how *the encounters with microbes facilitated by our project reinforced or disrupted previous feelings for microorganisms, and perhaps even allowed new ways of relating with microbial others to emerge.*

We might instinctively allocate germs to a similar realm as other 'unwanted' or 'monstrous critters' which evoke disgust, horror and killing (Davies, 2013, Ginn et al., 2014), but such

relations seemed strikingly absent amongst our participants. Perhaps in part because both the lives and deaths of microbes remain—even through the course of our experiments—largely invisible; our 16S sequencing technology was unable to distinguish between 'living' and 'dead' DNA. Ginn (2014) describes how killing a slug is a deliberate and often visible act. Even the gardeners he interviewed who did not like slugs were made uncomfortable when the slugs died a horrible death. In contrast the act of bleaching microbes, (one of the few methods widely accepted as being effective in 'killing' bacteria), seems curiously benign, and the scent of a freshly bleached bathroom even evokes pleasurable connotations, a form of micronecropolitics perhaps (Mbembe, 2003)? Nonetheless there was a degree to which our participants remained 'willing to recognise and be open to the vulnerability of non-human others and, perhaps, to be transformed by that recognition' (Ginn, 2014, p. 541). Many expressed the conviction that bleach was not a good thing:

Some people I know bleach everything, so they're sort of like wiping everything out. It actually doesn't necessarily make you healthier because we live together in harmony with them most of the time, and we haven't been ill from what we live with, so it shows that it's, you know, it's fine really. We should keep them there. (Exit interview 104, July 2017)

There are, we would suggest, several things going on here. Technically our sequencing data—and in particular our method's inability to distinguish between living and dead bacteria—was perhaps not highly effective in making microbial death sensible. However, the practice of swabbing surfaces before and after cleaning made participants notice (Tsing, 2015) or become attuned and attentive to (Despret, 2004; Dooren et al., 2016; Druglito, 2016) the presence (and absence) of a domestic microbiome. As members of a relatively affluent, sanitised Western society, where good microbiopolitical citizens are those who keep themselves and their kitchens 'germ-free', we might expect out participants to be particularly sensitive to microbial presence and absence at particular sites. Indeed, such assumptions are reflected in the colour-coded maps of their kitchens produced by participants to indicate where they thought might be the sites of highest microbial diversity (Fig. 2). We might define the sites they

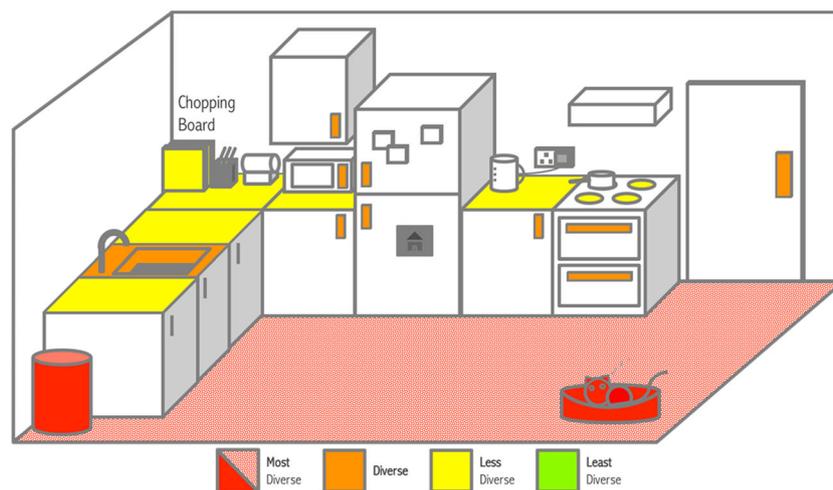


Fig. 2 Combined image, created from the individual kitchen maps coloured by participants (based on Flores et al., 2013), showing the sites where they expected to find the most microbial diversity. This figure is covered by the Creative Commons Attribution 4.0 International License. Reproduced with permission of Beth Greenhough, Jamie Lorimer, Richard Grenyer, Timothy Hodgetts, Carmen McLeod and Andrew Dwyer; copyright © Beth Greenhough, Jamie Lorimer, Richard Grenyer, Timothy Hodgetts, Carmen McLeod and Andrew Dwyer; all rights reserved

highlighted, drawing on a combination of their existing microbial knowledges and imaginations, as spaces of microbial intensity (after Hinchliffe et al., 2013). These sites included those associated with the production of food and disposal of waste—kitchen bins, door handles, floors—and those targeted by public health messaging, and by some of our participants with bleach: ‘toilet, put it down the sink, you know, that kind of thing.’ (Exit interview 111, July 2017)

Other sites, such as the human gut or the compost heap, carried more positive associations; ‘I was doing some gardening last night knowing you were coming today I was thinking, oh, I wonder what’s in there, what’s in this garden’ (exit interview 110, July 2017). Significantly, the sites of human-microbial ‘flourishing’ were also drawn on as examples of alternative modes of relating to and ‘living with’ microbes that might be generalised towards other sites. Even the initial proposal to participants that they could survey their domestic spaces for microbial diversity opened up new ways of thinking about the home as a microbial habitat: ‘before doing this I don’t think I would have thought about kitchen surfaces, and house biome [...] chopping board biome and fridge biome’ (exit interview 108, July 2017). Such multiple senses and sensings of microbiogeographies suggest previous assumptions about what microbes are and where they do (and don’t) belong are being replaced. Instead what emerged was more ‘a topological landscape of embeddings and disembeddings’, where human-microbiome relations are made present through ‘the density’ of their ‘intra-actions’ informed by the working of ‘different rhythms and logics’ (Hinchliffe et al., 2013, p. 538), combining kitchen safaris and imagined compost communities.

This in turn led to our participants questioning and to some extent reimagining microbial others. When asked how they saw microbes many participants acknowledged the ways in which popular representations of microbes, such as those featured in cleaning commercials or the fluffy viruses which populate museum shops, have shaped the ways in which they envision microbes. We can recall, for example, how engaging participants found the cuddly MRSA virus we brought along to the first workshop. There were also tensions between the taxonomic levels used to describe and think about types of bacteria used by our participants—usually the genus level (e.g., *Salmonella* or *Campylobacter*)—and the levels we used in our visualisations. The vast majority of our samples had significant levels of bacterial diversity. To present this diversity through a manageable number of categories we often chose to focus on the higher taxonomic levels, such as phyla. Participants sometimes struggled with an inability to relate the data on bacterial phyla with the taxonomic categories with which they were more familiar, or the fact that a single ‘blob’ ‘could be all sorts of different’ (exit interview 107, July 2017). Yet the ways in which the study allowed them to visualise microbial abundance and diversity generated what Lorimer (2007) might refer to as a kind of ‘feral charisma’ or what Kirksey (2017) terms compersion, a kind of voyeuristic appreciation that others are absorbed in ‘their own bubbles of pleasure and affection’. Or as one of our participants terms it, a fascination with something ‘like a festival going on on the worktops’ (exit interview 114, July 2017):

I think it was surprising to know the breadth and the, of the microbial life. I think you kind of think they’re, it’s hard to kind of fathom how many, and the numbers that we talked of, that they’re so huge that you can’t really imagine a number that big. You know, and how plentiful they really are. (Exit interview 111, July 2017)

Yet at the same time the microbiome retained a sense of radical alterity; beyond a moment of passing fascination, the default participant response is one of struggling to relate:

I’m sure on their level there’s this massive community of little microbes running round and doing stuff, but it’s not on a level that I can interact with, so I don’t think about them. (Exit interview 103, July 2017, emphasis added)

The ability to interact—to sense and respond to, to touch and be touched by the other—seemingly remains central to more-than-human relating. In this study often the microbiome was seen as a facilitator of relations rather than their object. In other words, our participants were interested in the microbiome because of what it might reveal to them about their relationship with animals who are ‘big like us’, and with whom humans can more easily interact. Benezra et al. (2012, p. 6378) observe, ‘our microbial communities provide snapshots of those with whom we have lived, the diversity of our daily habits, as well as the impact of our changing lifestyles.’ Haraway describes her fascination with the traces left by her dog Cayenne’s ‘quick and lithe tongue’ as it ‘swabbed the tissues of my tonsils’ (Haraway, 2008, p. 16). Like Haraway, many of our participants seemed most fascinated by the possibilities of metagenomics for allowing them to know and relate to other more familiar animals, in particular their pets. In the final ‘free choice’ experiment six participants chose to sample animals or animal beds alongside domestic surfaces in order to address the question, ‘Where do my pet’s microbes show up?’ Fig. 1 above includes a tree diagram which indicates how proximate (in terms of shared numbers of microbes-in-common) different sites sampled around participants’ homes are. Discussions in the exit interview often revealed a fascination with the ways in which the ‘microbial signatures’ (see Paxson and Helmreich, 2014) of shared spaces serve as markers of close human-pet domestic relations.

Domestic microbiopolitics

I suppose before, I was, it was called ‘good germs and bad germs’ and I suppose that’s my concept that there were good germs and bad germs. I suppose what I think, I suppose one of the things it’s done is made me realise there’s a lot more, sort of, fluidity, is that the right word? (Exit interview 110)

So, how does this specific configuration of the domestic microbiome as a site of (un)mourned death, feral charisma, indifference and multispecies conviviality shape the ways in which we might think with and relate to the domestic microbiome in the future? To what extent—if at all—can participatory metagenomics change ‘who lives well and who dies’ (Ginn et al., 2014, p. 115) in the contemporary Oxford kitchen? In the manner of other forms of participatory experiments, participants noted how our project posed far more questions than it provided answers. It unsettled previous modes of relating without providing a clear agenda for future relations:

I think the surprise for me was how uncertain and complex it is and how I just thought we knew more than we did and that we would kind of come along and find out what was good, what was bad and then know [laughs] how to, what was the best way to do x, y, z. (Exit interview 107, July 2017)

Data from our initial ‘entry’ interviews in many ways reflected dominant concerns over the potential presence of ‘bad germs’ or pathogenic microbes, with one participant expressing his disappointment that we were unable to track down, in the manner of the hit US TV series *Crime Scene Investigation*, the ‘bad germs’. At times though, it seemed a tentative gesture towards more positive modes of relating emerged, redolent of the kind of post-Pasteurian microbiopolitics envisioned by Paxson (2008), or the

more probiotic approaches which emphasise symbiosis, ‘inter-species communication and diplomacy’ described by Lorimer (2016, p. 67). In contrast to the micronecropolitical rationales of commercial cleaning products, often sold on their ability to kill 99.9% of *all* germs, harmful, beneficial or neither, participants spoke of the need for more careful approaches to domestic hygiene. Rather than clean with the objective of eradicating all microbes, they instead sought to engineer a more ‘balanced’ ecology:

I suppose when you interviewed me before I suppose I may have expressed more anxiety about bad germs I suspect. Now I think I’m more prepared to see, I would have said the inter-play between them, maybe. Whereas before I might have automatically grabbed antibac and now I think [...] absolutely fine. (Exit interview 110, July 2017)

The hesitancy this participant describes, the moment they pause to ‘think’ before grabbing the antibacterial spray might be constructed as a microbiopolitical gesture. Microbiopolitical both in the sense of the microbial objects of its concern (Paxson, 2008); but also in terms of the specific micropolitical gesture it makes, encapsulated in a willingness to abandon previous established positions and fixed categories and to pay attention to what might be ‘found in the interval between feeling and doing’ (after Jellis and Gerlach, 2017, p. 564). The need to ‘slow things down’ has been a common theme in recent work on science-policy relations around environmental issues, seen as a means of ‘redistributing expertise’ and ‘stating more and different opportunities for new knowledge politics to emerge’ (Whatmore and Landstrom, 2011, p. 606; see also Bingham, 2006). Might such a slowing-down also facilitate a renegotiation of domestic microbiopolitics? Could the hesitancy, uncertainty and unwillingness to act expressed by our participants be seen as a small move towards more diplomatic forms of human-microbe relations? This then opens up further questions. Who and what did our participants conceive themselves to be relating with?

Participants’ responses reflected an implicit sense that microbes were non-self. Absent is a sense of questioning notions of identity, self and kin. While Benezra et al. (2012, p. 6378) suggest that humans may be learning to see themselves as a ‘supraorganism’, and Nerlich and Hellsten (2009) suggest metaphorically at least, society seems open to the notion human-microbe hybridity, for our participants microbes remained distinct and distinguishable from selves: Microbes may live around, on and in you, but they are not you. In part this could be seen as a product of our deliberate decision to focus on kitchens and cleaning as opposed to human microbiomes. However, even when participants spoke of their gut microbiome, they did so in ways which envisioned a community living in or on them—‘all the flora that lives in your gut’ (exit interview 104, July 2017)—as opposed to one which is part of them.

Accounts did however suggest participants had begun to think of the microbiome in terms of ecologies as opposed to individuals. Landecker (2016, p. 41) notes antibiotic resistance is an ecology, one which ‘our commensals, our pathogens, our parasites, our domestic animals and fish and their commensals, the pathogens of our parasites, the avian scavengers of our cities and the wildlife—are all now participating in’. Could the domestic microbiome model a more probiotic ecology? Our participants drew comparisons between their more open and convivial approach to microbial life and that of other non-participants:

One of the ladies at work said, ‘Oh, my God, they can’t come to my flat ‘cause I use every product going. Everything.’ ... I would call her flat hygienically clean as

in, you know, nothing lives in there apart from her. (Exit interview 106)

In contrast, participants seemed more probiotic in their approaches to domestic hygiene. They tolerated and sometimes even nurtured commensal bacteria. They supplemented inconclusive (at least in terms of good germs/bad germs) scientific evidence from our collective experiments with more practical knowledges of living with microbes; a common refrain was that certain cleaning or eating practices ‘hadn’t made them sick’, so by implication they deemed them to be safe. This in turn led them to question other sources of microbial knowledge, such as that gleaned from cleaning product commercials or parents:

So I guess, you know, I too really like this idea of sparkling whites, bath and sink and so I am tempted by that but I feel like I’m more aware of that being a marketing thing and less about actually cleaning it effectively in a way that improves safety and allows for a good diversity of microbes and sort of actually healthy living environment for us as well.’ (Exit interview 107, July 2017)

‘...whereas my mum is completely different. She comes into my kitchen and thinks it’s unclean. She starts bleaching stuff or, you know, it’s the first thing she does when she walks in the back door, she starts bleaching things [both laugh]. And I think, what? But that’s her idea of clean.... Yeah, she’s of the...’ generation where she wants to walk into a kitchen for example and be able to smell bleach or that kind of thing. (Exit interview 106, July 2017)

Similarly, if our experimental ‘kitchen safaris’ led our participants to question their imagined microbiome geographies, might they also begin ‘to think again about the spatial assumptions that underpin the geometry of disease outbreaks, where pathogens are thought to cross over into healthy lives as if a pure space can somehow exist in contrast to an impure, diseased space’ (Hinchliffe et al. 2013, p. 531)? To draw on Hinchliffe et al.’s (2013) terminology, if the fronts or borderlines previously envisioned for domestic microbiopolitics were found in toilet bowls, sinks and dustbins, a more ecological perspective encourages more careful forms of engagement across much more broadly conceived sites of human-microbe encounter, echoing the hygiene hypothesis in the conviction it is possible to be ‘too clean’:

I always knew you couldn’t eliminate all germs but I’ve always considered some germs to be healthy germs and children who aren’t exposed to a decent amount of germs tend to be very sickly, in my opinion, quite frequently. (Exit interview 114)

There is a sense of encountering the domestic microbiome as a work in progress, whereby participants sought-out some kinds of entanglements as a means of immunising themselves against others:

For example, with a baby’s high chair, I’ll give that a good clean after the baby’s been in it but I don’t, before baby gets in it again, I don’t anti-bacterial the whole thing down, which I have seen some mums and grandparents do, because I think baby needs to be able to touch germs, microbes, erm, and put them in his mouth so that he develops his own immunity system and isn’t constantly ill with whatever little bug’s flying around. (Exit interview 114)

While tolerant of microbial diversity, such accounts fall short of drawing on the languages of companionship (Haraway, 2003),

friendship (Bingham, 2006) and corporeal generosity (Diprose, 2002), or speaking of microbes as ‘gut buddies’ (Lorimer, 2017a, 2017b) or ‘old friends’ (see also Nerlich and Hellsten, 2009). Instead what is sought is linked to more normative and familiar ecological values. Where probiotic ecologies might be distinguished by their non-equilibrium dynamics (Lorimer, 2017a), there is still a sense that a good domestic microbiome is one which is in ‘balance’, ‘You have a healthy balance of good and bad.’ (Exit interview 104, July 2017). Furthermore this idea of a healthy balance is one defined as being good for the humans involved. In this version of microbiopolitics there remains an understandable concern with letting humans live at the cost of at least some forms of microbial life. In the manner of other forms of probiotic intervention, experimenting with the domestic microbiome is always tempered by a focus on ‘securing valued versions of human life’, albeit ones recognised to be ‘fundamentally entangled with the nonhuman world in all its biological, geological and technological diversity’ (Lorimer, 2017a, p. 34).

While participants were keen to preserve the ‘good germs’, they were at best ambivalent towards concerns with preserving broader microbial biodiversity, especially in the absence of any direct links to their health and wellbeing. As Lorimer (2016, p. 72, see also Lorimer 2017a) notes in his analysis of helminth (hookworm) therapy: ‘there is little concern for the independent welfare of the individual worm, as some express for their mammalian pets, or for the wider flourishing of free-ranging helminth species, as some express for wolves or tigers’. In contrast to the more positive connotations of ‘living together’ or ‘flourishing’, there is a sense that living well with microbes is more a case of letting them do their thing while you do yours:

We’ve just kind of seen them as like, they’ve always been there. They’ve never really done any harm to me, and they just kind of exist alongside us, and that’s always how I’ve thought about them, and I still do because I don’t really see any, I mean, they’re not deadly so I’m not going to try and avoid them. (Exit interview 104, July 2017)

Such tolerance, bordering on indifference, suggests there are limits to the willingness of our participants to care both for and about the domestic microbiome. For example, one participant described a probiotic cleaner, a means by which they could positively cultivate (care for) the microbes on their kitchen worksurface, as ‘a mental leap too far for me’ (exit Interview 108, July 2017). It is one thing to hold back on the bleach, to let microbes live as opposed to actively making them die (necrobiopolitics). Another frame of mind is required in order to actively cultivate microbial presence. Others professed their indifference to, or inability to care about, the threat of microbial extinction: ‘I don’t think I’m particularly concerned about it’ (exit interview 111, July 2017). This was tied to a conviction that the vitality of microbial life makes it resilient in the face of anthropogenic change and a sense of the limitations of human capacities to influence microbial liveliness: ‘I don’t think we’re probably as good as we think we are at destroying things in our homes [all laugh] or outside where you have little control over that kind of thing’ (exit interview 111, July 2017).

Conclusion

In concluding we wish to consider the potential of participatory metagenomics as a means of reconfiguring relations between professional and lay microbiologies, with implications for the microbiopolitics of the domestic kitchen. What might microbiology learn from the questions posed by an interdisciplinary perspective? Is there scope for rethinking who is let live and who is killed on work surfaces, floors, bins, door handles and pet beds?

What promise of resistance to antibiosis might be found in the moments of hesitation before the bleach is brought to bear?

Firstly we would argue that a ‘feeling for the microbiome’ constitutes both a methodological strategy and an outcome of the research. Feeling captures the way in which participatory metagenomics combines scientific techniques with the more multi-sensual, interdisciplinary knowledges of participatory research, characterised by hesitancy and tentative, sometimes fumbling, experimental practices of ‘feeling for’ or ‘grasping for’. Feeling too captures the affectual possibilities generated by collaboratively designed experiments. If—as Haraway tells us—it matters which stories we use to tell stories (2015), it matters also which cultures we use to culture microbial relations. Significantly, while one of the virtues of metagenomic sequencing is the absence of a need to culture (in the sense of allowing microbes to multiply under controlled laboratory conditions) environmental samples, there is still a space—and we might argue a need—to culture (in the sense of generating forms of social interaction, research design and knowledge exchange) new ways of determining which kinds of expertise are brought to bear in deciding what is sampled and how the resulting sequence data is interpreted. This is especially important in light of the limited sensory capacities and representational scope of 16S sequencing.

Secondly, understanding and potentially generating different modes of relating to microbes offers important resources for those seeking to manage human-microbe relations, and opportunities for intervening into the ways in which publics respond to perceived microbial opportunities and threats. Paxson and Helmreich (2014, p. 183) suggest that in ‘both artisanal cheesemaking and astrobiology, practitioners of microbial ecology (in cheesemaking, these are both scientific and lay practitioners) appeal to microbes to anchor their cultural projects, whether these are to valorize and stabilise local and artisanal foodmaking or to extend the possible reach of biological speculation about life elsewhere.’ We might similarly ask what we might learn about the cultural projects of our participants, although tempered by a recognition of the limitations to experimental design imposed by both the framing technologies of this specific project and the methodologies in use (see Hodgetts et al., 2018, for a fuller account of the methods and their limitations). Given free reign to sample any site they chose, participants drew on the tools of 16S sequencing to question relations with pets and foodstuffs, amongst others. Microbes here are understood as an important component of other kinds of multispecies relations. Whilst our participants did not feel for the microbes *per se*, there remained a curiosity about others brought into yet closer proximity through visualising shared microbial entanglements, not unlike Haraway’s (2003) fascination with the microbes shared in a canine kiss. If, as Rose and Novas (2004) have argued, biological citizenship paves the way for the formation of biosocial communities, brought together by shared experiences of having or being at risk of disease, might we also see the formation of multispecies micro-biosocial communities, brought together by shared microbial cultures?

Thirdly, we have argued for a form of post-Pasteurian microbiopolitics which combines with Paxson’s (2008, p. 17) concern for ‘the creation of categories of microscopic biological agents; the anthropocentric evaluation of such agents; and the elaboration of appropriate human behaviours vis-à-vis microorganisms engaged in infection, inoculation, and digestion’; with Jellis and Gerlach’s (2017) attention to particular forms of micropolitical gesture that holds our participants—momentarily—in the space between thinking and doing. A way of ‘slowing things down’ (Bingham, 2006), perhaps just long enough to allow other kinds of human-microbe relations to be contemplated. The project offered a means by which participants could take on a different

position in relation to their domestic microbiome, distinctive from that inscribed in them through the performance of ‘good’—i.e., hygienic—microbiopolitical citizenship. Such moves are politically important if we are to move away from discourses which discriminate a valued (usually White Western) citizen from a microbially-contaminated other. Our participants remained wary of pathogens, and perhaps largely indifferent to questions and concerns over microbial extinction and diversity, but nonetheless they showed evidence of being open to the possibilities of relating to microbes otherwise, modulating cleaning practices to make kitchen surfaces hospitable to more diverse and abundant microbial ecologies.

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Notes

- 1 Throughout this paper the terms antibiotic/antibiosis and probiotic/probiosis are used to describe different human dispositions towards the microbiome. In its narrowest sense, the term antibiotic is used to refer to medicines that destroy or inhibit the growth of microorganisms. Antibiosis is an expansion of this term to encompass the intention behind the use of antibiotics, namely the desire to destroy, kill or inhibit the growth (usually indiscriminately) of microorganisms. Similarly, ‘probiotic’ is more commonly used to describe a group of foods and supplements that either contain microorganisms or that promote the growth of microorganisms seen to be good for human health. In this paper the term is used to also reflect the desire to promote colonisation by and growth of microorganisms, in particular those microorganisms seen as being ‘friendly’ or good for human health.
- 2 Here we follow Paxson’s (2018) use of the term Pasteurian to describe an approach towards microbes orientated towards the elimination of germs. The term is derived from the name of Louis Pasteur, a French microbiologist and chemist known for both identifying bacteria as the cause of spoilage in beer, wine and milk and for inventing a process—which became known as pasteurisation—for sterilising contaminated beverages.
- 3 See for example <http://www.mylivingwateruk.com>
- 4 ^{bl} See for example citizen science projects led by Rob Dunn <http://robdunnlab.com/projects/wild-life-of-our-homes/>, The American Gut Project <http://americangut.org/>, and crowd-funded initiatives like uBiome www.ubiome.com, or MapMyGut <https://mapmygut.com/>
- 5 See, e.g., ubiome.com
- 6 For a more detailed account and evaluation of the project’s methodology see Hodgetts et al. (2018)

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Data availability

The qualitative datasets generated during and/or analysed during the current study are publicly available in the UK Data Service Archive (UKDA ReShare Record No. 853055). Material from the genomic sequencing will shortly be publically available and is currently available from the authors by reasonable request.

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Additional information

Competing interests: The authors declare no competing interests.

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