




The microbiome and its publics

A participatory approach for engaging publics with the microbiome and its implications for health and hygiene

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The past 20 years have seen a significant drop in the cost of DNA sequencing, which along with high-throughput (or next-generation) sequencing has helped to analyse the microbial diversity from environmental samples. Most of this research has focused on microbiomes of the human body and, although there is still much uncertainty about what constitutes a “normal” or “healthy” human microbiome, microbial “dysbiosis” has already been implicated in a range of non-communicable diseases.

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This research is also challenging the common understandings of pathogens and the beneficial role of bacteria for human health [1], and increases awareness of how hygiene and antibiotics impact early-life microbial colonisation and exposure, and their effects on human health and development [2]. There is both public health and commercial interest in translating this research that might lead to probiotic applications to improve human and animal health, domestic hygiene, waste management and agricultural productivity, amongst other potential benefits.

As with the human genome, interest in the microbiome and its effect on health has begun to move beyond the laboratory. The growing affordability of DNA sequencing

has facilitated a range of citizen science, crowd-funded and DIY microbiome projects (<http://robdunnlab.com/projects/wild-life-of-our-homes/>; <http://americangut.org/>; www.ubiome.com; <https://mapmygut.com/>). Various publics have become involved by providing samples, through personalised sequencing and by designing their own experiments in personal microbiome management. Such health-focused projects often reflect a growing anxiety about the “hygiene” or “microbiome depletion” hypotheses [3]: that the increase in the prevalence of autoimmune and inflammatory disease might be linked to dysbiosis caused by “missing microbes” [2], whose absence is caused by modern hygiene, diet and other lifestyle practices.

Affordable sequencing offers new challenges and has great potential for new science. It could lead to the development of new therapies and diagnostics along with new tools for engaging publics with microbiology to address questions of health and environment stewardship. It also enables a more radical democratisation of scientific technology, allowing publics—including some who are gravely ill—to ask questions, develop hypotheses, and to run their own experiments to understand what the microbiome means for their everyday lives.

“Upstream” methods for making the microbiome public

In this article, we describe a recently completed project to explore these challenges and opportunities. We developed a participatory methodology for using next-generation sequencing to engage publics

with the microbiome in relation to questions of health and hygiene. Our project focused on domestic kitchens and the hygiene practices of a small group of households in a community in Oxford, UK. We wanted to explore what people knew about the bacteria that live in their kitchen, how they would investigate them if they were given the tools to find out more, and how their perceptions and practices would change if we made their kitchen microbiomes more visible.

“... we were interested in the participants’ questions about microbial life in their kitchens and how these changed as they gained more familiarity with the technology.”

Social scientists have long argued that not all forms of public participation with science are equal. Less substantive approaches largely confine participants to the role of data gatherers with scientists retaining control over research questions, experimental design and communication, whereas more substantive approaches give participants greater control in all these areas. Often, the metaphors of upstream and downstream engagement are used to indicate the extent of participation: upstream giving more control at an earlier stage. In this project, we used an innovative, upstream engagement process known as the “apprentice model” [4], in which small community groups learn to use scientific tools to address specific concerns. Rather than merely educating these publics,

the aim is to develop new approaches to solving problems with scientists and “apprentices” working in partnership.

Our project took the method further upstream, in that we were not trying to develop a solution to an existing problem. Through apprenticing a community group in the tools of next-gen 16S sequencing, we were interested in the participants’ questions about microbial life in their kitchens and how these changed as they gained more familiarity with the technology. We wanted to explore how they understand and engage with the domestic microbiome through practices such as cleaning and what, if any, implications this holds for research. Our community group was a self-selecting sample assembled initially by curiosity, and through the shared use of sequencing technology. It was not assembled to be representative of “the public” at large.

“Participants’ understanding of risk, in this context, was strongly informed by the germ theory of diseases...”

Researchers in Science and Technology Studies (STS) have combined the theories of public participation with a more nuanced understanding of publics. The latter term is pluralised to represent the idea that there is not a single, homogenous general public as sometimes suggested in media accounts. Instead, publics are diverse and are made up of people with different experiences, knowledge, values and habits [5]. Much research in this vein is concerned with how such publics cohere—what draws them together in the first place and what keeps them together?

In our case, it was geography and curiosity. Our public lived close to the community centre that was hosting our project and were interested in exploring microbial ecologies in their kitchens. There are obvious implications of this experimental design as our “results” cannot be universalised, but they are nonetheless informative in their ability to open up novel questions for microbiome research. And while our findings are not intended to be generalised, our methods are.

Metagenomics in the community

Our project was called *Good Germs, Bad Germs: mapping microbial life in the kitchen* (www.goodgerms.org). The binary moral in

this title was deliberate, as we wanted to recruit participants who were open to understanding bacteria as more than just pathogens. Funding came from the UK Economic and Social Research Council, and the UK Food Standards Agency (a government body) was an official project partner. We used a series of posters, flyers (Fig 1) and community newsletters to recruit 14 households. We screened all applicants through a questionnaire, to make sure they were willing to commit for the duration of the project, to rule out anyone with a health condition that could be exacerbated through taking part and to identify prior levels of expertise. Each household received a retail voucher worth £150 at the end of the project as recompense for their time.

We began with detailed semi-structured 45-min interviews with each household in the participants’ homes. We asked them about their ideas of “bacteria”, “microbes” and “germs”, how they used their kitchens—as places to cook and eat, to work and socialise—where their pets lived and what areas of the kitchen those animals could access. We also asked about cleaning routines—why they used certain products rather than others, which areas they cleaned more often and how their cleaning schedules related to their ideas about health and well-being.

We then gave each household a freezer bag with sampling instructions, sterile swabs and container tubes, and non-latex gloves (Fig 2), and asked them to conduct a “kitchen safari”. Each household took samples from the sink, chopping boards, a kitchen surface, a cupboard handle and the kitchen floor. Here, we followed a landmark study by Gilberto Flores and colleagues of the diverse microbial communities found in different parts of domestic kitchens [6]. A sixth swab was used to sample a place of their choosing—six swabs was the limit of our financial budget—and participants could swab anything except people or animals, for which we did not have ethical approval.

The aims of this initial safari were twofold: to introduce our participants to next-gen 16S sequencing, and to start their “apprenticeship” as experiment designers rather than simply as data gatherers. Using the sixth swab, the participants selected a series of sites that demonstrated some of the issues important to them. Several participants swabbed their pet’s bedding, to see whether they had distinct microbial communities. Others chose to see whether the

kitchen rubbish bin stood out as hosting particular kinds of bacterial communities. Both examples suggest an underlying similarity—our participants were concerned about lurking pathogens. As we learned through the project, and as evidenced elsewhere [7], they were strongly attached to the idea of “bad” germs.

“Participants also showed a background anxiety about being too clean and a familiarity with the “hygiene” hypothesis.”

We had five group meetings in a local community centre over an 18-month period to discuss the results of the previous experiment and plan the next one in small discussion groups. Attendance at group meetings fluctuated between 50 and 90%. At each group meeting, the participants were given a printout of their results, and a fresh swab kit for the next round. The results were distributed at the meeting and sent by email to those who were unable to come. At the first meeting, the scientists suggested some experiments to spark conversation and to demonstrate the possibilities of the technology, but as the project progressed, the participants increasingly took ownership of the experimental design.

Towards the end of each meeting, the groups would present their ideas to the whole room. The scientists would answer questions about feasibility, and the whole group would vote on their preferred choice—usually the day afterwards, through an online poll. During the first four rounds, we required that the group all conduct the same experiment, to generate data that could be compared across households and discussed in the subsequent meetings. In the final experiment, the participants were individually given free rein to sample whatever sites they liked. Households were asked to conduct the next experiment within 2 weeks of the meeting, and research staff collected the samples, so as to reduce the effort required on the part of the participants and to ensure that the swabs were kept at a stable temperature on their way to the laboratory.

The 3-month cycle—group meeting, sampling and another group meeting, was designed to facilitate a form of “cyclical learning”. Originally developed in the 1960s

Good Germs, Bad Germs

Mapping microbial life in the kitchen

Invitation to participate in a research project



What is the research about?

Microbial life is everywhere and not all of it is harmful. There are good germs and bad germs.

This project will allow you to see the microbial life in your kitchen and to explore how this 'microbiome' changes when you carry out normal cooking and cleaning practices.

We want to examine what happens to how we think about cooking and cleaning when we can see their effects on life in the kitchen.

What's in it for me?

The project is designed as a collaboration that will be driven by the interests of those who participate. We hope it will be both fun and informative. We are especially interested in households with children and hope to involve them in the research.

The project aims to pioneer new approaches to kitchen hygiene and to engaging people in making government policy. You will get to meet experts and policy-makers, as well as become part of a community group

As a token of our appreciation each household that takes part in this study will receive **£150 in high street vouchers**. Read more at www.goodgerms.org, or email goodgerms@ouce.ox.ac.uk



Figure 1. Recruitment flyer.

by the cognitive psychologist Jerome Bruner [8], this approach is based on the idea that revisiting the same topic in cycles of increasing conceptual sophistication can facilitate particularly effective forms of learning. Thus, with each experiment, we sought to re-visit our participants' understandings of microbes and their intersection with hygiene practices. The project biologist increased the conceptual sophistication of his explanations as the participants gained more experience with the technologies and terminologies.

This was not always a smooth process, but our project was not merely an attempt to educate our public as per the "deficit model"—in which scientists have a pre-established set of knowledge that they wish to impart to an audience—which is assumed to be homogenous and ignorant [9]. Instead, we were facilitating a form of apprenticeship in which the participants set the questions and direction of research. There is an inescapable overlap between these approaches, most notably around the education required to

utilise complex research tools such as sequencing. The difference might be understood as a matter of emphasis, but the emphasis is important and has consequences.

The second noteworthy pedagogical design feature of this participatory approach is the reliance on collective forms of learning. The meetings were structured around group discussions—large groups, small breakout groups and back to large groups. One reason for working as a group is the commonplace pedagogical understanding that collective approaches are particularly effective ways to facilitate discovery-based forms of learning—which clearly applies to our apprentice model. Another is that collective forms of learning are very useful from a social science perspective, because they require participants to externalise their thoughts, understandings, uncertainties, opinions and attitudes—all of which are of interest in a research project of this type. Thus, each meeting was attended by three social scientists, in addition to the project biologist. Two had facilitative roles, welcoming participants, running the meeting schedule, moderating discussions and responding to questions. The third was an ethnographic observer, producing a detailed record of the meeting in addition to audio recordings. The project concluded with another round of in-depth, semi-structured qualitative interviews, conducted in a similar manner to those at the beginning.

The experiments

In all, our participants conducted five "participatory experiments" on the microbial life in their kitchens (Table 1).

The first experiment, the "kitchen safari", was designed by the project team and based on the work of Flores *et al* [6]. For the group meeting, we created a "kitchen GIS" to map the microbial diversity in the sampled surfaces. Before disclosing the results to the group, we gave participants a blank map and asked them to colour in the patterns they expected to find. A comparison of these two images (Fig 3) generated a fertile subject for subsequent discussion.

The next three experiments were designed and selected by the participants themselves, with technical assistance from the project team. The second explored the effects of different cleaning products on domestic microbial abundance and diversity. Each household tested two cleaning products of their own choice from a list that



Figure 2. The Good Germs sampling kit.

Table 1. A summary of the experiments.

Experiment	Research question	Sites sampled
Kitchen safari	What lives in your kitchen?	Work surface, sink, chopping board, cupboard door handles, floor, and one other
Cleaning products	What difference do cleaning products make?	Cloth and work surface before and after using two different products
Chopping board	How is a new chopping board colonised?	Chopping board on day 0, 1, 2, 4, 7, 14
Fridge ecology	What is microbiome of the fridge?	Composite of fridge surfaces, and four food items in fridge
Personal choice	Where do my pet's microbes show up? (n = 6)	Animal or animal bed, various domestic surfaces
	What is the effect of the Christmas tree on the domestic microbiome?	The tree, and a picture rail before delivery, and in days 1, 2, 7 and 14.
	What is the difference between organic and conventional vegetables?	The surface of an organic and a non-organic carrot, kiwi, and leek
	Does the microbiome differ between term time and the holidays?	Door handles, cupboard handles, and light switches before and during the holiday

included common detergents, bleach, anti-bacterial cleaners, vinegar, warm water, special “e-cloths” and (at the research team’s suggestion) a probiotic cleaner. They each swabbed their kitchen surfaces before cleaning, swabbed the cloths they usually used to clean with and swabbed the surfaces again after cleaning.

The interpretation of these data was challenging as the sampling technique cannot differentiate between DNA from live or dead organisms, though only bleach and the anti-bacterial cleaners are supposed to kill microbes. The results were interesting: the bacterial communities found on kitchen surfaces after cleaning looked more like

those found on the cleaning cloths than they did before cleaning (Fig 4). This might be unsurprising to a microbiologist, but it was news to many in the group and led to a discussion about what people should do in their kitchens in order to be “clean” or “hygienic” (e.g. using paper towel rather than cleaning cloths).

The third experiment explored how a new chopping board was colonised by bacteria during a 2-week period. Half of the group received a new plastic board, and the other half a new wooden board. Each household kept a record of what they chopped on the board each day and swabbed the board after it had been cleaned on days 0, 1, 2, 4, 7 and 14. There was not much discernible difference between the types of board, but it appears that the communities across all boards were becoming a little more similar over time (Fig 5). This was not a statistically significant finding, but it did generate interesting discussions about likely sources, and the possible existence of a common local microbiome.

The fourth experiment was partly inspired by the guest speaker at the previous meeting, a scientist from the Food Standards Agency, who had helped the group make sense of the results from the cleaning products experiment. He had commented that, in the agency’s experience, domestic fridges were often kept at the wrong temperature and could harbour pathogenic bacteria if not used and cleaned appropriately. The participants swabbed the insides of their fridges, and four pieces of food (or packaging) before placing them into the fridge for the first time. At the end of the week, they swabbed the fridge again. This time, the results were inconclusive, partly owing to low content mass in the samples. Nevertheless, from a social science perspective, the choice and justification for the experiment remained interesting.

Finally, the participants were allowed to design a personal swab experiment (Table 1). Several households opted to track the microbial communities associated with their pets, by swabbing the animals’ bedding and other sites around the kitchen. Others examined the differences between conventional and organic vegetables or the effect of their Christmas tree on the wider microbiome of their kitchen. A household with two school-age children tried to test the effect of the school holidays on their kitchen microbiome. Interestingly, nearly all of the experiments operated through a logic of “source” and “effect”. The

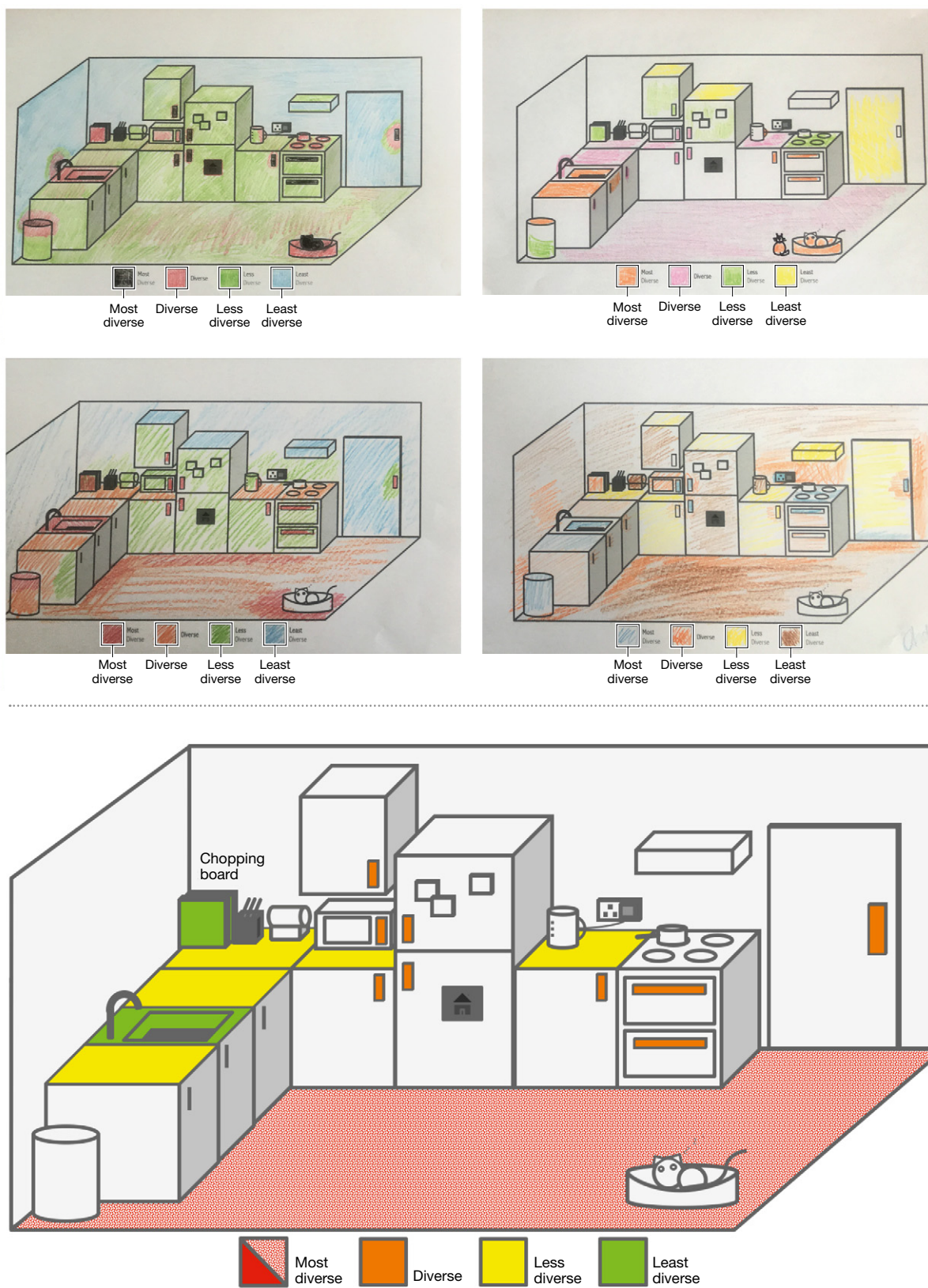


Figure 3. Maps of expected (above) and actual microbial diversity on kitchen surfaces.

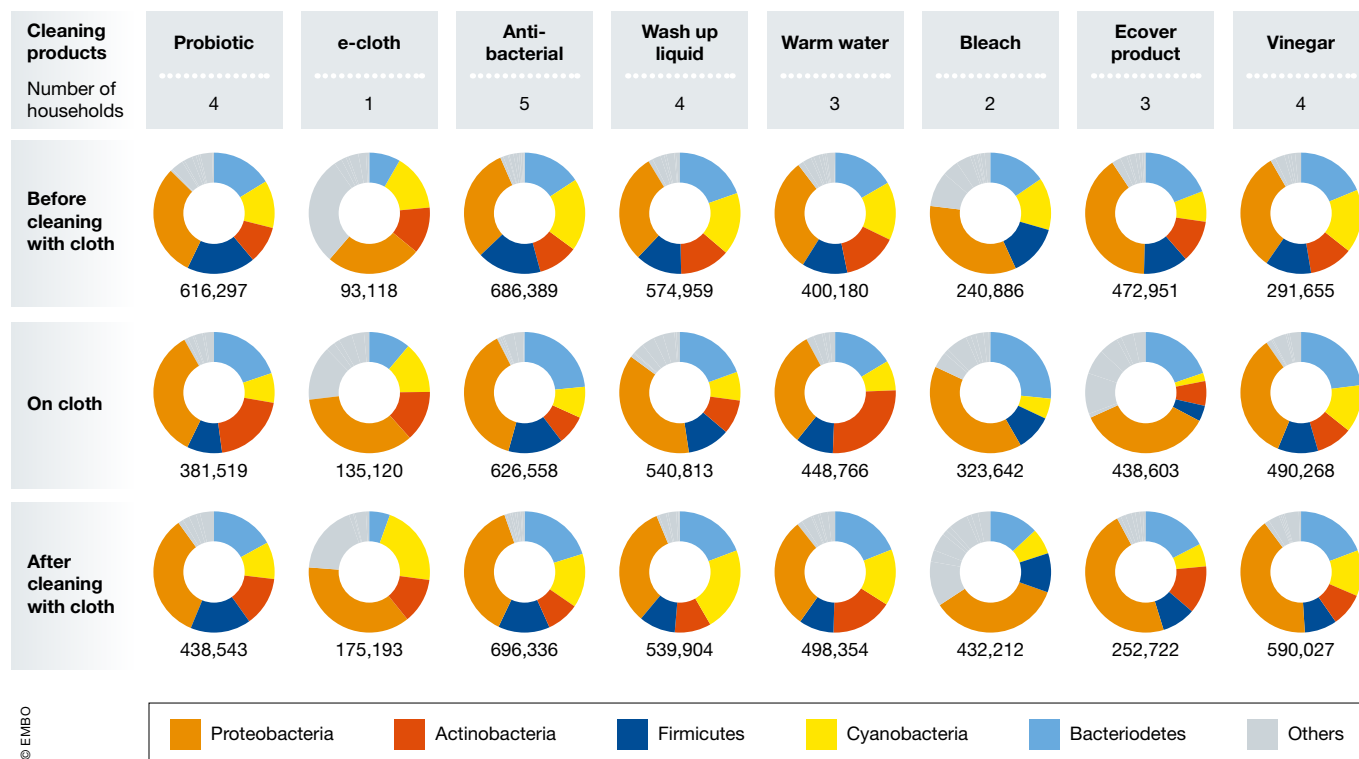


Figure 4. Type and abundance of bacteria on kitchen cloths and before and after cleaning with different products.

participants asked about the microbial effects of things they brought into their kitchens (pets, yeasts, trees and children). In part, this focus on source-tracking was an artefact of the strengths of 16S sequencing as a technology.

Suggesting priorities for public microbiome research

Analysis of the data gathered in these experiments is ongoing, but two themes became increasingly evident as the project progressed. Throughout the series of group meetings, our participants sought advice about how to manage microbes to reduce their risks of illness. They wanted to know how to properly clean, to store food and to cook. This was evident in the choice and design of the various experiments, the justifications for doing these and the comments made during group discussions. Participants' understanding of risk, in this context, was strongly informed by the germ theory of diseases, and they continued to focus on the presence of specific pathogens, despite the ability of the sequencing and sampling technique to examine the wider microbial community.

Nevertheless, the same people also retained other opinions and attitudes that were less beholden to a hygiene agenda and reflect more practical knowledge—a common refrain was that certain cleaning or eating practices “had not made them sick”, and by implication were deemed to be safe. Others considered probiotic approaches to domestic hygiene by tolerating or nurturing commensal bacteria. Participants also showed a background anxiety about being too clean and a familiarity with the “hygiene” hypothesis. There was an evident tension between these two notions, often within rather than between individuals, and about which inclination to trust in order to stay healthy. Sometimes this played out geographically with participants suggesting that it was more important to keep some sites (kitchens, bathrooms, surfaces) cleaner than others.

Social scientists have more experience of using participatory methods in decision-making for controversial issues than the type of open-ended agenda-setting processes described here. Often, participatory approaches invoke the precautionary principle: advocating restraint or refraining from

certain actions if the effects are hard to predict given the current level of knowledge. Yet, when it comes to hygiene in the kitchen, it is not clear how this principle could be applied. One answer would be to use antibacterial cleaners and to take no chances. Yet, as noted above, emerging research into the microbiome suggests that we actually may need more microbial exposure rather than less [2]. In fact, the Royal Society for Public Health now promotes a “targeted hygiene” approach, in which antibacterial action is focussed on key sites (taps, door handles, sinks, etc.) rather than the unachievable goal of totally eradicating all microbes [10].

“Allowing publics to think and experiment with microbes will shift how people understand themselves, their relationships with others, and their wider environments.”

For future interdisciplinary microbiome research, this suggests new directions for

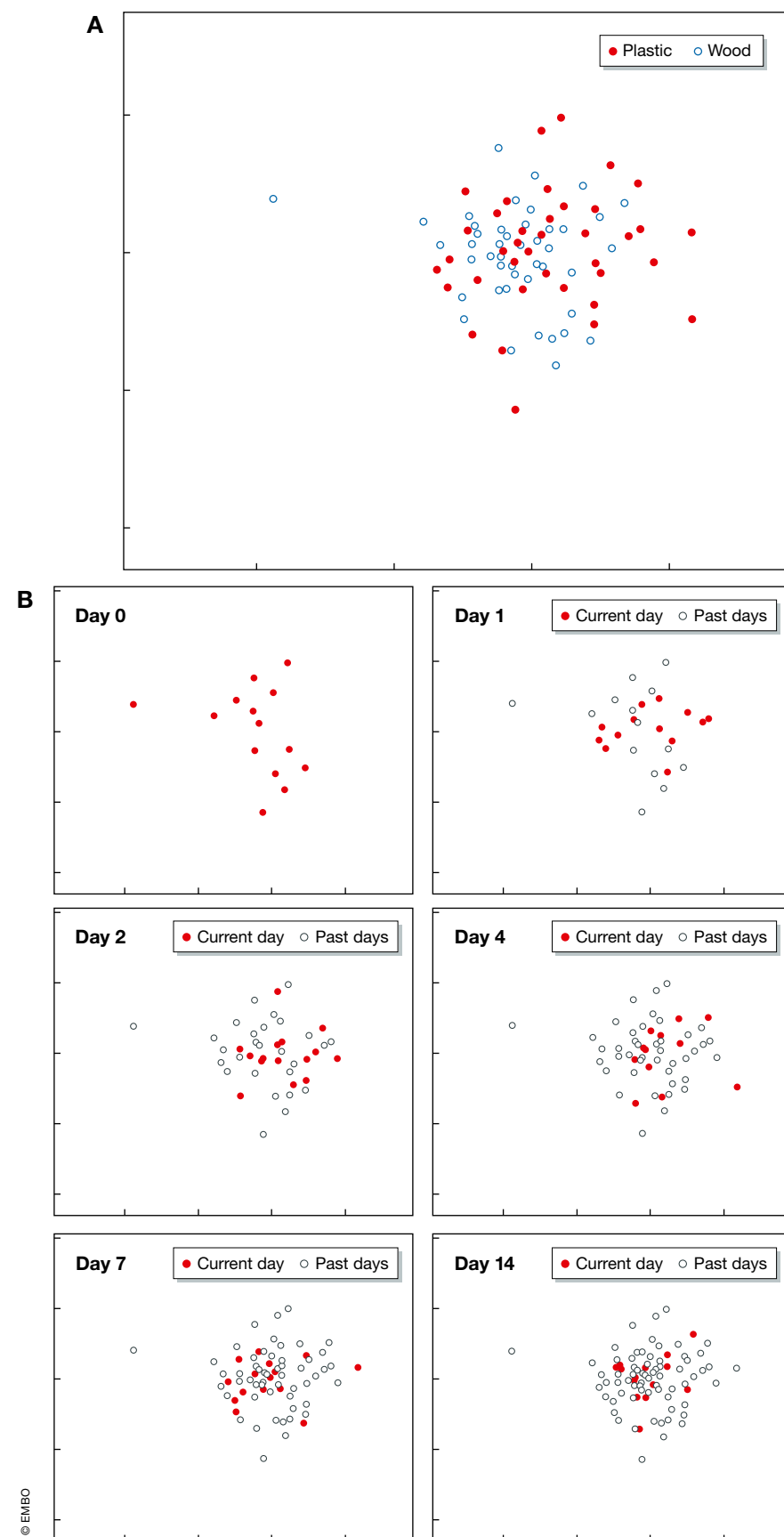


Figure 5. The difference in composition of plastic and wooden chopping boards (A) and how these changed over 14 days (B).

research to establish what a healthy domestic microbiome might look like and how it might be perceived as such; and how to maintain such a microbiome through domestic practices. The first objective would address microbial ecology, and how the presence of particular species, or community properties might protect against pathogenic strains. The second would focus on people's domestic behaviours—how to clean, what products to use, how to store and prepare food—to facilitate microbial communities that benefit, rather than harm, human health.

New metaphors needed

The other theme that emerged from the project was the need for new metaphors to develop public understandings of microbial life. Our participants were particularly attached to two, related perceptions of microbiomes. First, they tended to think in terms of “species”. In our efforts to visualise the 16S data, we encountered much incomprehension and even resistance to a conceptual model of microbial ecology that is based on communities characterised at higher taxonomic levels or on physiological functions. Second, they tended to think in terms of “pathogenic species” in particular. More than a century of public health messages about the dangers of “germs” has created a deeply embedded perception. “Probiotic” approaches may be gaining traction when it comes to bodily health—probiotic drinks, for example, that claim to benefit the gut flora—but our project showed the limits of such metaphors when it comes to domestic hygiene. This might not be a bad thing, given the importance of hygienic practices in the household, but if research on the microbiome suggests a more nuanced approach towards domestic microbial management, it may prove a tough sell to wider publics. In particular, the concept of characterising communities by functional or (phylo)genetic diversity is less likely to be assimilated than those based around particular species or strains.

Thus, we need new metaphors, and new stories, to replace the dominant tropes of species and pathogens, or “bad germs”.

A comparison can be made with macro-ecology and ideas about the “balance of nature”, despite the fact that ecological science has long since rejected such models and moved towards a dynamic understanding of ecological processes. Not only are ideas about the “balance of nature” still prevalent in wider society, they even continue to be held amongst many ecologists despite their formal training to the contrary [5]. A similar problem awaits micro-ecology. Indeed, we found that metaphors taken from macro-ecology had some traction—such as describing microbial ecologies as “deserts”, “rainforests” or “fields”; and metaphorically linking cleaning to gardening and keeping pathogenic bacterial “weeds” at bay through cultivating bacterial “lawns”. The social sciences and humanities can help to map public understandings of microbes and to enable the collaborative development of new ways of seeing the microbial world.

Future developments for upstream research and engagement with the microbiome

This type of upstream participatory microbiology is challenging. It can be a delicate task to teach people how to use highly complex technologies without slipping into a “deficit” mode of science communication. While working with small groups may generate rich discussions and group learning, such groups are not necessarily “representative” of broader society and cultural and economic differences within societies. Nevertheless, we suggest that the themes that became important in our project—a desire for more guidance on how to live healthily with microbes in the light of emerging understandings of the microbiome, and a need for new metaphors through which to understand microbial ecologies—may be important for broader society. This would require a different

form of project, one that could work with larger groups of people across a range of locations.

Ongoing developments will make sequencing technology cheaper and easier to use outside of the laboratory. Devices such as the Oxford Nanopore MinIon® and its even smaller successor, the SmidgIon®, have the potential to move bacterial metagenomics into workplaces, schools and the home. They will also provide a means to explore the microbiome in near real time; or certainly much faster than the turnaround time of several weeks we had to deal with. In addition, social media are making larger-scale participatory methodologies increasingly possible—see, for example, the rise of personalised microbiome sequencing companies such as uBiome. These approaches may lose some of the nuance of a fine-scale study, but they have the potential to empower a larger and more diverse set of publics. The possible advent of a consumer-friendly sequencing device, accessible analytical platforms and online groups to interpret their data would have important social consequences. Allowing publics to think and experiment with microbes will shift how people understand themselves, their relationships with others and their wider environments. The type of upstream participatory methodology outlined in this paper may help molecular biologists to democratise this exciting new field of microbiological science and to navigate new and emerging social and political contexts.

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Conflict of interest

The authors declare that they have no conflict of interest.

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