

What is the Microbiome of the Human Home?

Dancer SJ^{1,2}, McNally L¹, McLaren J¹, McGill G³, Fletcher L⁴, Noakes C⁴ and Sharpe T³

¹ Dept. of Microbiology, Hairmyres Hospital, NHS Lanarkshire, Scotland

² School of Applied Sciences, Edinburgh Napier University, Edinburgh, Scotland

³ Mackintosh School of Architecture, Glasgow School of Art, Scotland

⁴ Water Public Health and Environmental Engineering Group, School of Civil Engineering, University of Leeds, England

Background

There is currently little known about the range and diversity of microorganisms in the indoor home,¹ particularly in the context of modern airtight homes. People spend a great deal of time in their homes, especially those at the extremes of age, and it is possible that the indoor microbiome could impact upon human health in ways not yet understood.²

Aims

This project aimed to systematically screen sites in 100 houses in the Lanarkshire community in order to determine the amount and type of cultivable aerobic bacteria and fungi in the home. It was hoped to be able to characterise the microbiome of the 'normal' home.

Methods

Chosen sites were: indoor bathroom handle; telephone; kettle handle; bedside table; top of bedroom door; TV remote; toilet handle; and bedroom window sill (Table 1). These sites were screened using double-sided dipslides coated with nutrient and staphylococcal selective agars (Figure 1). Bacteria and fungi were quantified for each site and staphylococci and Gram-negative bacilli identified if possible.

Results

Each site furnished specific microbiological characteristics which reflected room function and touch frequency. Most sites yielded a mixture of coagulase-negative staphylococci, *Bacillus* spp., and micrococci (Figures 2a and b). Two or more sites were positive for *Staphylococcus aureus* and Gram-negative bacilli in 23% and 63% homes, respectively; these were mostly found on TV remote and kettle handle (Figure 3a & b; Figure 4). Gram-negative bacteria included *Pantoea* spp., *Acinetobacter* spp., *Serratia* spp. and pseudomonads (Table 2). Coliforms such as *Klebsiella pneumoniae* and *Enterobacter cloacae* were recovered from less than 1 in 10 homes. No *Escherichia coli* were isolated. Fungi including *Aspergillus* spp. and *Candida* were found on door top, window sill and bedside table, and these sites were also the most heavily contaminated. Surprisingly, the sites most likely to yield 'no growth' were toilet and bathroom door handles (Figure 3c & 5). None of the bacterial pathogens identified were multiply resistant to antibiotics.

Table 1:

Sites chosen for microbiological sampling
Bathroom (inside) Door Handle
Telephone
Kettle Handle
Bedside Table
Top of Door
TV Remote
Toilet Handle
Bedroom Window Sill

Table 2:

Cultivable Gram-negative bacteria identified
Most isolates were <i>Pantoea</i> spp. or <i>Pantoea</i> agglomerans
Also found:
<i>Acinetobacter baumannii</i> (also <i>lwoffii</i> ; <i>radioresistens</i> ; <i>ursingii</i> ; <i>haemolyticus</i>)
<i>Sphingomonas paucimobilis</i> ; <i>Pseudomonas putida</i> (also <i>fluorescens</i>)
<i>Lerclercia adecarboxylata</i>
<i>Paracoccus yeei</i>
<i>Klebsiella pneumoniae</i>
<i>Enterobacter cloacae</i>
<i>Roseomonas gilardii</i>
<i>Aeromonas sobria</i>
<i>Serratia liquefaciens</i>
<i>Brevundimonas</i> spp.
<i>Cronobacter sakazakii</i>
<i>Moraxella</i> spp.

Most awarded 'poor discrimination' by VITEK

Figure 1: Dipslides for quantitating cfu's from surfaces

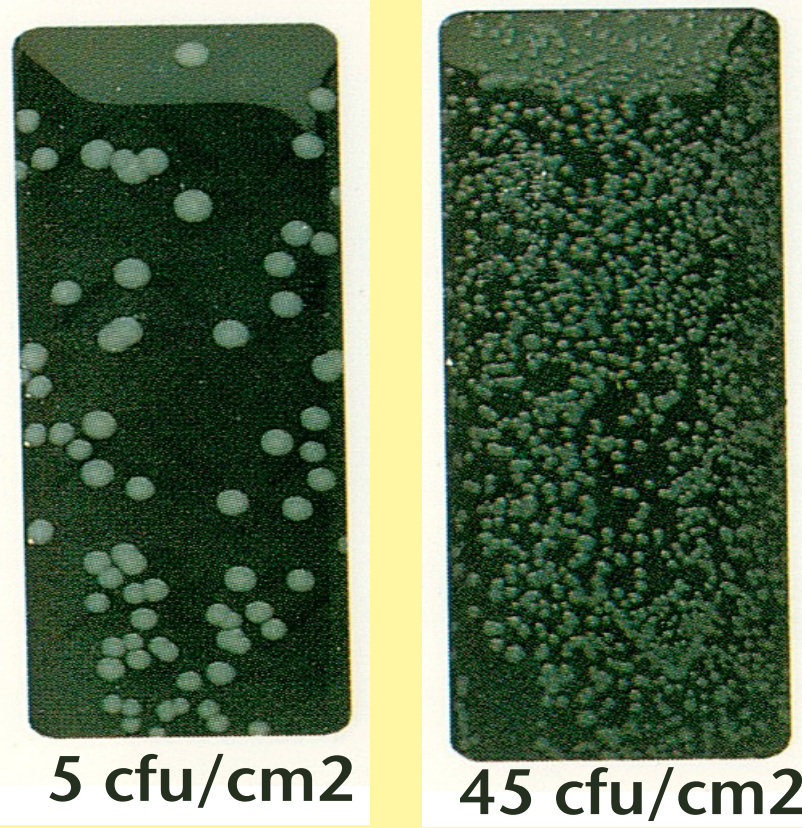


Figure 2a: Environmental flora on blood agar;



Arrows show fungal colonies

Figure 2b: Most common findings on nutrient agar;



Figure 3: a. Kettle; b. TV remote; c. Toilet flush

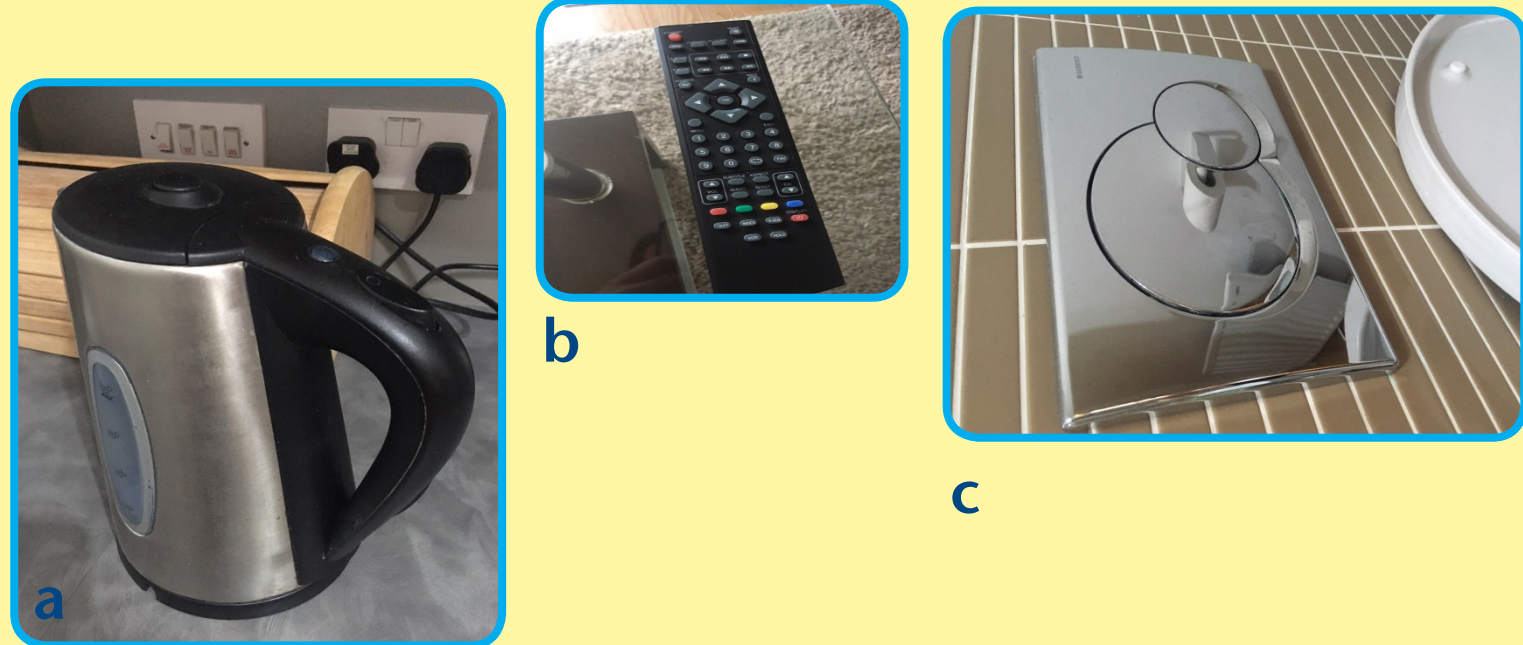
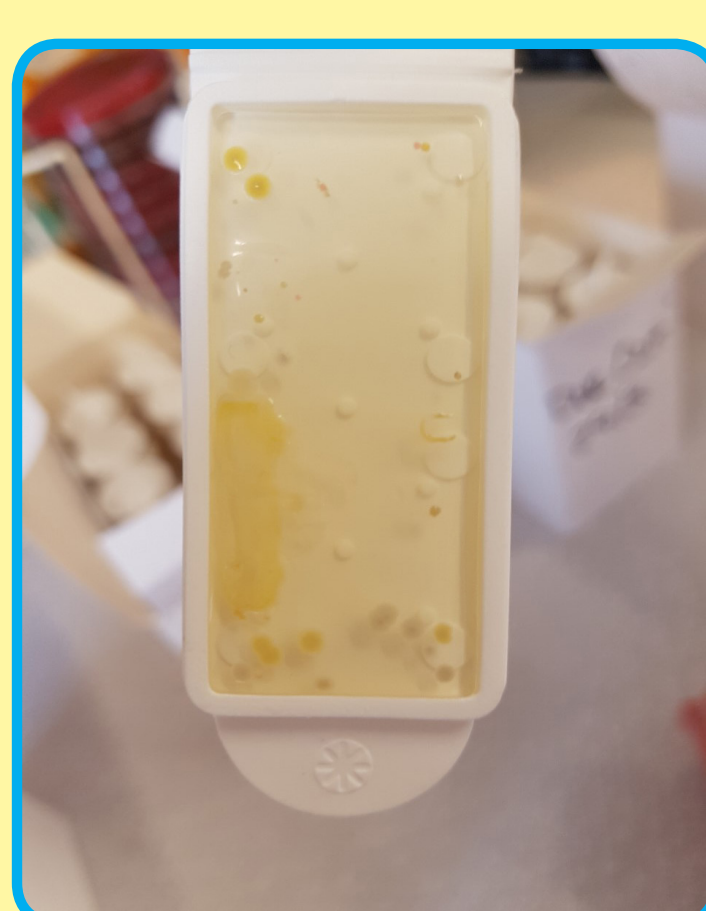


Figure 4: Staphylococci on Baird Parker agar from kettle handle



Figure 5: Dipslide from bathroom handle showing Gram-negative smear



Conclusion

Each of the eight sampled sites revealed its own distinct microbiological character, both in the type and amount of cultivable microbes. Human pathogens, particularly *S.aureus*, were more likely to be associated with commonly touched sites such as TV remote, kettle handle and telephone.³ Whole houses also demonstrated unique microbiological characteristics, with morphologically similar and identifiable microbes observed at multiple sites within the same home.⁴ Each home thus displayed its own unique microbiome but with identifiable similarities between other homes according to site.



References

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