The Domestic Student Kitchen: A Microbiological Hazard?

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The domestic kitchen is increasingly being recognized as the most important area in relation to the incidence of foodborne disease. Literature relating to bacterial contamination and hygiene practices in shared kitchens is limited. This study aimed to investigate the microbiological quality of a shared student kitchen with 2 main objectives: to determine the level of bacterial contamination in three wet sites, and to identify the predominant isolates. Samples from the kitchen sponge, draining rack and sink drain were cultured on agar plates of varying selectivity. Gram-staining and biochemical tests were used to identify predominant colonies. The kitchen sponge showed the highest levels of bacterial contamination, followed by the draining rack and then the sink drain. *Staphylococcus* spp., *Micrococcus* spp., *Pseudomonas* spp., *Bacillus* spp. and Enterobacteriaceae were identified.

Keywords: Food borne diseases, domestic kitchen, *shared kitchens*, *Staphylococcus* spp., *Micrococcus* spp., *Pseudomonas* spp., *Bacillus* spp. and Enterobacteriaceae.

Foodborne disease is associated with significant morbidity and mortality globally[1] and is therefore a serious public health issue[2]. It has been previously estimated by the World Health Organization that the number of unreported cases could be as high as 90% with only serious incidents requiring medical attention presumably being reported.

The domestic kitchen is increasingly being recognized as the most important area relating to the cross contamination of foodborne pathogens in the home, in addition to the harboring and transferring of infection[3, 4]. This is despite estimations of the proportion of food poisoning cases originating in the household ranging from 12-17% to 50-80%[5]. Contamination of various foods, especially raw foods, consumed in the domestic kitchen with naturally occurring pathogenic microorganisms is inevitable[2, 6]. As a result, cross contamination of foodborne pathogens has been identified as the main hazard in the household, and can be either direct or indirect[7]. Direct cross contamination involves the transfer of microorganisms directly from raw food while the indirect route utilizes a vehicle such as kitchen cloths and sponges, hands, utensils and surfaces as an intermediate. A lot of studies show that the type and density of bacterial contamination is dependent on the physical nature of the site sampled and that wet to moist areas are more likely to be contaminated due to the preferential survival and proliferation of microorganisms in these conditions[2]. The present study was carried out to determine the level of bacterial contamination in three wet sites, and to identify the predominant isolates.

MATERIALS AND METHODS

Bacterial cultures and maintenance

Selective media used were xylose lysine deoxycholate (XLD) Agar, Pseudomonas

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agar base with added rehydrated Pseudomonas CFC Supplement (SR0103), mannitol salt agar (MSA), and MacConkey agar no.2. Non-selective media used were R2A agar and nutrient agar. All morphologically distinct colonies were sub-cultured onto nutrient agar and aerobically incubated for 24 hours at 37°C. This was repeated once a week for maintenance purposes.

Identification of bacteria

Isolates were identified by colony morphology, gram staining reaction, oxidase test, catalase test, and coagulase test as per standard procedures [8].

RESULTS

Investigation of microbiological quality of examined sites

The microbiological quality of samples taken from the sink drain, kitchen sponge and draining rack are summarized in Table 1. The kitchen sponge yielded the highest level of total bacterial contamination (represented in Table 1 as total viable count (TVC)) relative to the sink drain and draining rack. Furthermore, it harbored the highest number of heterotrophs, pseudomonads, enteric species, staphylococci and micrococci. The draining rack was found to be more heavily contaminated than the sink drain, harboring higher numbers of all the microorganisms mentioned above. Table 2 shows that more bacterial growth was observed on the relatively less selective agar types, nutrient and R2A agars, when compared with pseudomonas agar base, xylose lysine deoxycholate (XLD), MacConkey no.2 and mannitol salt (MSA) agars.

Bacterial identification

The results from microscopic examination and biochemical tests, together with knowledge of the type of agar from which the bacteria were isolated (i.e. selective or non-selective) and their appearance on the plate (descriptions not shown), were used to identify the predominant isolates. These are summarized in Table 3.

The data showed that the predominant isolates largely consisted of oxidase positive Gram-negative rods, presumably *Pseudomonas* spp., being isolated from all three sites investigated. Enterobacteriaceae were the second most common taxa identified, also isolated from all three sites.

Gram-positive cocci were relatively less common and were identified as *Staphylococcus* spp. or *Micrococcus* spp. in the sink drain sample and *Staphylococcus aureus* in the kitchen sponge sample. Overall, it appears that similar bacterial species were observed regardless of location of isolation except in the case of *Bacillus* spp. (isolate R4 in Table 3) which was only isolated from the kitchen draining rack.

MacConkey agar no.2 (MAC2) was highly selective for enteric species. Pseudomonas agar base (PAB) was highly selective for *Pseudomonas* spp., with no enteric colonies formed. However, XLD and MSA agars were less selective, with *Pseudomonas* spp. frequently isolated from XLD plates and enteric species being isolated from MSA plates in addition to staphylococci and micrococci.

Table 3 shows the presumptive identifications of predominant isolates based on microscopic and biochemical investigations

DISCUSSION

The kitchen examined in this study was shared by 5 male final year university students and, due to limitations in time and resources available to complete the study, the focus of the investigation was mainly on biofilms in predominantly wet areas of the kitchen. Specifically, the microbial content of an 'in use' sponge, the sink drain and the draining rack were examined and the predominant isolates identified.

The total contamination levels at each of the 3 sites investigated in this study were determined by means of total viable counts (TVC). Out of these 3 sites, the sponge exhibited the highest level of microbial contamination as shown in Table 1. The sponge also showed the highest levels of heterotrophic bacteria, pseudomonads, coliforms/Eneterobacteriaceae, staphylococci and micrococci. A series of morphological and biochemical tests were conducted in an attempt to identify the predominant isolates (Table 3). These tests indicate that *Pseudomonas* spp., Enterobacteriaceae and *Staphylococcus aureus* predominated in the sponge sample. These findings are consistent with those of Speirs *et al*[9], Josephson *et al*[10], and Rusin *et al*[3].

Speirs *et al*[9] found that cloths used for wiping surfaces and/or drying equipment, such

as dish washing cloths and sponges and tea towels, were associated with the highest microbial loads. The authors note the predominance of *Enterobacter* spp. among other enterobacteria such as *Klebsiella pneumoniae* and *Escherichia coli* and identified *Pseudomonas aeurginosa* as the most common pseudomonad isolated which supports the prevalence of *Pseudomonas* spp. and Enterobacteriaceae observed in the sponge sample in this study. Furthermore, their investigation revealed that *Staphylococcus* spp. and *Micrococcus* spp. were found in all 46 domestic kitchens examined in many of the sites sampled, including the kitchen sponge, which is not surprising as these organisms are normally found in the skin microflora. This suggests that cross-contamination from the hands to the sponge during washing up or wiping down of surfaces most probably explains

Table 1. Microbiological quality of samples obtained from the sink drain, kitchen sponge and draining rack after growth on a variety of non-selective and selective agar types

Organism	No.[a]		
	Sink drain	Sponge	Draining Rack
Total viable count[b]	4.24 ± 0.08	75.52 ± 0.33	6.75 ± 0.00
Heterotrophs[c]	4.25 ± 0.08	75.61 ± 0.20	6.54 ± 0.31
Pseudomonads[d]	3.59 ± 0.08	70.29 ± 0.13	6.05 ± 0.02
Enteric species[e]	2.90 ± 0.00	74.25 ± 0.26	5.52 ± 0.01
Staphylococci/Micrococci[f]	2.83 ± 0.07	66.51 ± 0.13	5.52 ± 0.09

[a] Data are mean $\log_{10}$ CFU/ml for samples isolated from the sink drain and draining rack and mean $\log_{10}$ CFU/g for the kitchen sponge from duplicate experiments ± standard deviation.
[b] Total viable count based on sum of all colonies cultured on nutrient agar.
[c] Total culturable heterotrophs based on sum of all colonies cultured on R2A agar.
[d] Total culturable pseudomonads based on sum of all colonies cultured on pseudomonas agar base.
[e] Total culturable enteric species based on sum of all colonies cultured on MacConkey no.2 agar.
[f] Total culturable staphylococci and micrococci based on sum of all colonies cultured on mannitol salt agar.

Table 2. Bacterial enumeration of samples obtained from the sink drain, kitchen sponge and draining rack after growth on a variety of non-selective and selective agar types

Agar type	No.[a]		
	Sink drain	Sponge	Draining Rack
NA[b]	4.24 ± 0.08	75.52 ± 0.33	6.75 ± 0.00
R2A[c]	4.25 ± 0.08	75.61 ± 0.20	6.54 ± 0.31
PAB[d]	3.59 ± 0.08	70.29 ± 0.13	6.05 ± 0.02
XLD[e]	2.91 ± 0.04	65.43 ± 0.06	5.64 ± 0.02
MAC2[f]	2.90 ± 0.00	74.25 ± 0.26	5.52 ± 0.01
MSA[g]	2.83 ± 0.07	66.51 ± 0.13	5.52 ± 0.09

[a] Data are mean $\log_{10}$ CFU/ml for samples isolated from the sink drain and draining rack and mean $\log_{10}$ CFU/g for the kitchen sponge from duplicate experiments ± standard deviation.
[b] Nutrient agar; non-selective medium.
[c] R2A agar; selective for heterotrophic bacteria.
[d] Pseudomonas agar base; selective for pseudomonads.
[e] Xylose lysine deoxycholate agar; selective for salmonellae and shigellae.
[f] MacConkey agar no.2; selective for enteric species.
[g] Mannitol salt agar; selective for staphylococci and micrococci.

the presence of *S. aureus* in the sponge sample. Hilton and Austin[11] also reported the recovery of *S. aureus* from sponge-type dishcloths, while Finch *et al*[12] reported the isolation of *S. aureus* from 47% of domestic towels and teacloths sampled thus further corroborating this finding.

Josephson *et al*[10] found particularly high counts of heterotrophic bacteria associated with the kitchen sink and sponge and noted 'surprisingly high' total and faecal coliform counts across all sites examined in the kitchen (sink basin, faucet handle, table, counter top, refrigerator door, oven control, cutting board and sponge). The authors found *Staphylococcus* and *Pseudomonas* isolates to be present in the lowest concentrations pointing out that only the sink and sponge samples exhibited significant populations of pseudomonads which is in agreement with the findings of this study. Indeed, three out of the five predominant isolates from the sponge sample were identified as *Pseudomonas* spp. This is most probably reflective of the high level of moisture in kitchen sponges; a specific requirement of pseudomonads[10]. To further support this finding, a bacteriological investigation looking at used cellulose sponges and cotton dishcloths in domestic kitchens identified *Pseudomonas* spp. as the most common species isolated from cleaning materials[13]. In their two-year study of 10 domestic kitchens, Josephson *et al*[10] found that the two most consistently contaminated sites were the sink and the sponge and attributed this to the fact that these areas are constantly moist under normal use.

Rusin *et al*[3] investigated different sites in household kitchens and bathrooms of 15 homes to determine which of these sites exhibited the highest levels of faecal coliform, coliform and heterotrophic plate count (HPC) bacteria. Of all the examined sites, the sponge/dishcloth showed the highest microbial load across all three categories of bacteria being investigated and thus further corroborates the findings of this study. It is interesting to note that both Finch *et al*[12] and Rusin *et al*[3] found the domestic kitchen to be more heavily contaminated with coliforms and faecal coliforms than the household bathroom, thus highlighting the importance of adequate hygiene measures in the kitchen.

Table 3. Presumptive identifications of predominant isolates based on microscopic and biochemical investigations

Isolate	Agar Type	Gram Stain	Appearance	Oxidase	Catalase	Coagulase	Presumptive Identification
D1	MSA[a]	+	Cocci	…	+	-	*Staphylococcus spp./Micrococcus* spp.
D2	R2A[b]	-	Rods	-	…	…	Enterobacteriaceae
D3	R2A	-	Rods	+	…	…	*Pseudomonas aeruginosa*
D4	XLD[c]	-	Rods	+	…	…	*Pseudomonas* spp.
D5	NA[d]	-	Rods	-	…	…	Enterobacteriaceae
S1	NA	-	Rods	+	…	…	*Pseudomonas* spp.
S2	XLD	-	Rods	+	…	…	*Pseudomonas* spp.
S3	MSA	-	Rods	-	…	…	Enterobacteriaceae
S4	R2A	+	Cocci	…	+	-	*Staphylococcus aureus*
S5	MAC2[e]	-	Rods	+	…	…	*Pseudomonas* spp.
R1	NA	-	Rods	+	…	…	*Pseudomonas* spp.
R2	MAC2	-	Rods	-	…	…	Enterobacteriaceae
R3	XLD	-	Rods	+	…	…	*Pseudomonas* spp.
R4	MSA	+	Rods	…	+	-	*Bacillus* spp.
R5	PAB	-	Rods	+	…	…	*Pseudomonas* spp.

Legend: Sink drain (D); Sponge (S); Draining Rack (R); Positive (+); Negative (-); Not Tested (...).
[a] Mannitotal salt agar (MSA): selective for staphylococci and micrococci.
[b] R2A agar (R2A): selective for heterotrophs.
[c] Xylose lysine deoxycholate agar (XLD): selective for salmonellae and shigellae.
[d] Nutrient agar (NA): non-selective medium.
[e] MacConkey agar no.2 (MAC2): selective for enteric species

The kitchen sponge has been described as an especially conductive environment enabling the growth and survival of microorganisms[2]. This is due to the adherence of food residues/organic matter to the sponge during washing up and wiping down of surfaces together with moisture retention creating an ideal environment for microorganisms to flourish once contamination occurs[2, 14]. This explains why the sponge was the most heavily contaminated of the three sites investigated. This is concerning as this suggests that sponges may act as reservoirs and disseminators of foodborne pathogens in the domestic kitchen thus potentially causing illness[4]. Indeed, the ability of sponges to disseminate significant numbers of microorganisms onto food preparation surfaces has been demonstrated[11].

Perhaps the most interesting finding in this study was that the kitchen draining rack sample was found to exhibit heavier bacterial contamination than the sample taken from the sink drain. Indeed, the draining rack exhibited higher levels of heterotrophic bacteria, pseudomonads, coliforms/Enterobacteriaceae, staphylococci and micrococci. This is surprising as the kitchen sink drain area has been reported in several studies to display one of the highest levels of microbial contamination, including coliforms and faecal coliforms, when several different sites in domestic kitchens were compared[3, 7, 10, 12]. Morphological and biochemical tests revealed that the predominant isolates obtained from the draining rack were most probably *Pseudomonas* spp., Enterobacteriaceae, and *Bacillus* spp. while those from the sink drain sample were most likely *Staphylococcus* spp. or *Micrococcus* spp., Enterobacteriaceae, *Pseudomonas aerugionosa* and *Pseudomonas* spp. (shown in Table 3).

While a few studies have investigated the microbiological quality of draining boards[12, 15], there is no data to our knowledge relating to the microbial content of kitchen draining or drying racks. Finch et al[12] reported *Escherichia coli* as the predominant microorganism isolated from draining boards (13 out of the 21 draining boards sampled were positive for *E. coli*). Other microorganisms isolated from the draining boards included coagulase negative Micrococcaceae, *Klebsiella pneumonia*, *Citrobacter* and *Enterobacter* spp.; the latter three being isolated from a fifth of the 21 domestic

homes investigated in the study. *Bacillus spp.* was isolated from 17 of the 21 draining boards examined while *P. aeruginosa* was isolated from only two. Scott et al[15] report *E. coli*, *Citrobacter freundii*, *K. pneumonia* and *Enterobacter cloacae* as the most frequently isolated microorganisms from draining boards among other wet sites in the kitchen such as U-tubes and the kitchen sink. The authors expressed concern regarding the prevalence of enteric organisms associated with these sites suggesting that, although food is most likely the continual source of contamination in the domestic kitchen, wet sites such as the sink, U-tubes and surrounding areas, including draining boards and possibly draining racks, serve as reservoirs harboring Enterobacteriaceae and enabling their proliferation[15].

It would not be unreasonable to assume that the microbiological content of kitchen draining racks closely mirrors that of draining boards due to their very close proximity in most domestic kitchens together with the close similarities between the results reported here and those reported by Finch et al. [12] and Scott et al[15]. If this assumption is taken to be true then these studies help support the findings reported here. Furthermore, the higher counts obtained from the draining rack sample relative to the sink drain may be explained by the fact that although food residues are constantly passing through the sink drain, so are dishwashing detergents and water which may cause a reduction in the microbial load; this is not the case with the draining rack where plates and cutlery that have been washed, usually using a contaminated sponge, are left to dry and potentially cross-contaminate the rack. An alternate explanation maybe that the sink was recently cleaned using a disinfectant cleaner such as household bleach thus reducing the microbial load.

Although in this study the kitchen drain was found to be the least heavily contaminated of the three sites investigated, it should not be disregarded as a source of potential pathogens. Indeed, the solid surfaces provided by the pipe work are suitable for the purpose of biofilm formation while the open nature of drains means they are constantly challenged by a variety of different microorganisms including high risk infectious materials from uncooked meat and vegetable

waste[16]. The predominant isolates identified from the sink drain sample concur with the findings of Finch et al[12] who reported the isolation of E. coli from 13 out of 20 sink drains among other Enterobacteriaceae, and Scott et al[15] who also found enterobacteria in addition to pseudomonads and S. aureus, albeit in relatively smaller numbers. The prevalence of E. coli in kitchen sink drains presents a public health threat as some strains have been implicated in enteritis in young children, adult diarrhea, travelers' diarrhea and food poisoning[12].

It is important to note that Salmonella spp. were not detected in this study despite being present in a significant proportion of retail chickens in the UK[17]. Possible explanations for this include that the sample size, in this case one kitchen, was too small[15] and/or the fact that there are relatively low numbers of Salmonella on chicken carcasses compared to Campylobacter[6].

No attempt was made to isolate obligate anaerobes in this study. Finch et al[12] failed to isolate any obligate anaerobes despite extensively examining several sites in the kitchens, bathrooms and toilets of three homes for this group of organisms. Therefore, it is highly unlikely that these organisms would have been isolated in this study had they been searched for.

Little research has been conducted relating to communal kitchens despite the fact that several individuals sharing a confined space is likely to exacerbate the risk of cross-contamination and thus compromise food safety[7]. The findings in this study have revealed high levels of bacterial contamination in the sites investigated and indicate that more adequate hygiene measures are required in order to reduce the risk of cross-contamination and, consequently, foodborne illness. However, this is opposed by the lack of feelings of responsibility, lack of motivation and the varying knowledge and hygiene standards among the individuals sharing the kitchen as the actions of just one user could potentially compromise food safety[7]. For example, Sharp and Walker[7] found that at least one person in each of the six communal student kitchens investigated would move mess to one side when preparing food instead of cleaning the work surface.

The authors also point out the ineffectiveness of the occasional official clean by students and attributed this to the lack of regular cleaning arrangements.

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