Title: Prevalence of antimicrobial resistance genes and integrons in commensal Gram-negative bacteria in a college community

Running title: Antimicrobial resistance genes in a college community

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Abstract

Although the human intestinal microbiome has been shown to harbor antimicrobial drug-resistance genes (ARG), the prevalence of such genes in a healthy population and their impact on extraintestinal infections that occur in that community are not well established. This study sought to identify ARG prevalence and their mobile elements in the intestines of a healthy community population at a California university, and compared these genes to those found in uropathogenic *Escherichia coli* isolated from patients with community-acquired urinary tract infection (CA-UTI). We isolated Gram-negative bacteria (GNB) from fecal samples of healthy volunteers and screened them by polymerase chain reaction (PCR) for ARG encoding resistance against ampicillin (AMP), trimethoprim-sulfamethoxazole (TMP-SMX), gentamicin (GENT), and colistin (COL). We found antimicrobial resistant GNB from 85 (83%) of 102 non-redundant rectal swab samples. Sixty-seven (66%) of these samples contained β -lactamase genes (*bla*_{TEM}, *bla*_{SHV}, *bla*_{CTX-M}, *bla*_{OXA}, *bla*_{OXY}), dihydrofolate reductase (DHFR) genes (*dhfr-A17*, *dhfr-A7*, *dhfr-A5*, *dhfr-A21*, *dhfr-A1*, *dhfr-A15*, and *dhfr-B3*), and aminoglycoside resistance genes (*aadA5*, *aadA1*, and *aadB*). Integron sequences were found in 37 fecal samples. These genes were found in 11 different GNB species isolated from the fecal samples. The same ARG were found in *E. coli* strains isolated from patients with CA-UTI examined at the college outpatient health clinic. The high prevalence of clinically-common ARG and integrons harbored by GNB in the intestine of a healthy population suggest that human intestines may serve as a major reservoir of these mobile ARG that appear in *E. coli* strains causing extraintestinal infections in the same community.

Importance

Increasing frequency of antimicrobial resistance (AMR) in human pathogenic bacteria has compromised our ability to treat infections. Since mobile antibiotic resistance genes (ARG) are readily exchanged between different species of bacteria through horizontal gene transfer, there is interest in investigating sources of these genes. The normal intestinal flora has been shown to contain a wide variety of ARG, which may have been introduced via food-containing AMR bacteria. We sought to assess the prevalence of ARG carriage in the intestines of a healthy population and determine if these ARG are found in *E. coli* strains that cause community-acquired urinary tract infection (CA-UTI) in the same community. Our findings indicate that the human intestine may serve as an important reservoir as well as a site in which ARG are

transferred into *E. coli* that cause UTI. Further research is needed to reduce ARG carriage and devise new strategies to prevent AMR infections.

Introduction

The emergence of antibiotic resistant bacteria and antibiotic resistance genes (ARG) has become a growing public-health concern worldwide. Gram-negative bacteria (GNB) including *Enterobacteriaceae* and glucose non-fermenter species are implicated in a large number of community and healthcare-associated infections. They are also common residents of the human intestinal microbiota as well as of the environment (1–10). Human and veterinary medicines rely on the use of antibiotics to treat infections caused by bacterial pathogens. Antibiotics are also used in food animal production as growth promoters. Extensive use of antibiotics over the last several decades has led to the rapid emergence and spread of resistant microbes, especially among enteric bacteria (11, 12). Due to the nature and complexity of the microbial communities harbored in our intestinal environment, the human gut has been recognized as a potential reservoir of ARG (3, 13, 14). However, ARG are also found in food animal intestines as well as in a variety of produce items humans eat (12, 13, 15–17, 21–34). Thus, food may serve as sources of ARGs that enter the human intestine. The prevalence of ARG in healthy human intestine and their impact on human infections is not well characterized.

The ability of bacteria to disseminate mobile ARG via horizontal gene transfer (HGT) has resulted in the rapid acquisition of resistance by enteric bacterial pathogens. ARG mobile elements include integrons, transposons, and plasmids. Integrons, which permit the simultaneous integration of multiple exogenous gene cassettes, represent an important vehicle for the rapid horizontal transfer of resistance across bacterial populations and thus could contribute to the sudden increase in prevalence of multidrug-resistant infections in a community (19, 20). In particular, class 1 integrons are the most ubiquitous class of integrons in enteric bacteria and have been found in all common pathogens including *Escherichia*, *Klebsiella*, *Salmonella*, *Shigella*, and other disease-causing *Enterobacteriaceae*. More than 70 different gene cassettes conferring resistance to most of the known β -lactam drugs, aminoglycosides, trimethoprim, rifampicin, chloramphenicol, and erythromycin have been reported in class I integrons (11). This is of further concern due to the increasing prevalence of extended spectrum beta lactamase (ESBL)-producing GNB, which are difficult to treat and often resistant to other families of antibiotics, in particular trimethoprim-sulfamethoxazole

and fluoroquinolones (7). Furthermore, the recent global spread of GNB containing plasmid-mediated colistin resistance has greatly challenged clinical management of infections caused by them (21). For example, colistin remains an important therapeutic agent for infections caused by carbapenem-resistant Enterobacteriaceae (CRE), in which there are limited alternative treatment options (22).

Previous studies have shown food and the environment to contain ARG found in pathogenic bacteria (12, 23, 24). Environmental reservoirs of ARG-containing pathogens include lakes and rivers (18), wastewater treatment plants (25, 26), houseflies (27), livestock (12, 28, 29), soil and manure (29, 30), retail meat products (12, 31–33), companion animals (5, 6, 8, 28, 34), alfalfa sprouts (35), retail spinach (15), and other vegetables (36). The findings from these studies indicate that human health may be impacted by uptake of pathogens from the environment, many of which harbor ARG on mobile genetic elements. Thus, humans may be acquiring pathogens as well as transmissible ARG through food and other environmental hosts.

A recent study by Yamaji et. al compared ARG and genotypes of *E. coli* isolates from patients with urinary tract infection (UTI) in a California university community to those of *E. coli* isolated from meat (pork, chicken, beef, and turkey) obtained from retail stores in the surrounding area (31). They found that despite 12 shared genotypes (sequence types) between humans and retail meat *E. coli* isolates, human isolates contained more ARG than did meat isolates (31). These findings led us to speculate that people may acquire uropathogenic *E. coli* from external sources (food or environment) but that these *E. coli* strains then may acquire ARG from commensal bacteria already in the gut. Therefore, we sought to understand the diversity and abundance of mobile ARG in the gut of healthy humans, and to elucidate potential links between ARG harbored in commensal gut bacteria and the acquisition of those ARG by pathogenic GNB.

Materials and methods

Sample collection

We prospectively cultured fecal samples from 113 healthy volunteers at a university campus in northern California between June and October 2017. Eligible participants included those between 18 and 65 years of age, with no medical history of urinary tract corrective surgery or abnormality, or bladder catheterization or hospitalization within the 6 months prior to sample collection.

At recruitment, participants were provided a pre-addressed collection kit containing a Cary-Blair transport media rectal swab (Becton Dickinson BBL™), two biosafety bags, and detailed collection instructions. Each kit also included a questionnaire regarding antibiotic use, history of UTI, and diet and lifestyle characteristics. Participants were instructed to send the rectal swab back to the laboratory via USPS mail immediately after collection. Once delivered, the study coordinator analyzed samples within 48 hours.

Fecal sample analysis

Fecal swab tips were placed in a 1.5-ml Eppendorf tube containing 1mL of Luria-Bertani broth and vortexed for 60 seconds. A 10µl aliquot of fresh fecal material was dilution streaked onto MacConkey agar plates and incubated overnight at 37°C. All samples were screened for resistance against four antimicrobial agents: ampicillin (AMP) (32µg/ml), gentamicin (GENT) (16µg/ml), trimethoprim-sulfamethoxazole (TMP-SMX) (4-76 µg/ml), and colistin (COL) (2µg/ml), as well as on one MacConkey agar plate containing no drug. All antimicrobial agents were dissolved in nuclease free water and filter sterilized. Dimethyl sulfoxide (DMSO) was used to prepare TMP-SMX solution (final concentration <5% DMSO). Dihydrofolate reductase (DHFR) mediates trimethoprim resistance. We tested trimethoprim-sulfamethoxazole in this study as this combination drug is commonly used to treat UTI and other bacterial infections. Interpretive criteria from the Clinical Laboratory Standard Institute (37) or from literature recommendations (38) were used to determine resistance. *E. coli* 25922 (ATCC) was used as a reference strain.

DNA extraction and ARG identification

Five bacterial colonies were randomly selected from each plate. If multiple colony morphologies were noted, all colonies with unique morphologies were sampled. If less than five colonies were present, all colonies were selected for analysis. Single colonies were selected and inoculated into 3 ml tryptic soy broth and incubated in a shaking incubator for 20 hours at 37°C. Basic procedures for DNA extraction by a freeze-thaw method were performed as previously described (15, 19). The 2ml aliquots of the cultures were centrifuged, and the pellets were re-suspended in a test tube with 350µl of distilled water, boiled for 10 min in a water bath, and then cooled on ice for 2 min. The samples were centrifuged for 2 min at 13,000 rpm, and the supernatants were stored at 20°C before they were subjected to PCR tests.

Two microliters of the resulting supernatant were used as template DNA in 25µl of PCR mixture. Bacterial isolates that grew in the presence of AMP were examined for β -lactamase

gene families by multiplex PCR as described previously (39). These β -lactamase gene families included: TEM variants (*bla*_{TEM-1} and *bla*_{TEM-2}), an SHV variant (*bla*_{SHV-1}), CTX-M (all variants), OXA variants (*bla*_{OXA-1}, *bla*_{OXA-4}, and *bla*_{OXA-30}), and KPC variants (*bla*_{KPC-1} to *bla*_{KPC-5}). Samples that showed bands corresponding to CTX-M universal variants were further examined for CTX-M group variants: CTX-M group 1 (*bla*_{CTX-M-1}, *bla*_{CTX-M-3}, and *bla*_{CTX-M-15}), CTX-M group 2 (*bla*_{CTX-M-2}), CTX-M group 9 (*bla*_{CTX-M-9} and *bla*_{CTX-M-14}), CTX-M group 8/25 (*bla*_{CTX-M-8}, *bla*_{CTX-M-25}, *bla*_{CTX-M-26}, and *bla*_{CTX-M-39} to *bla*_{CTX-M-41}). Bacteria that grew on plates containing GENT or TMP-SMX were examined for 5' and 3' conserved sequences flanking the class I integron gene cassettes. Thus, the entire cassette sequences harbored in the integron were analyzed. If present, these gene cassettes were sequenced to detect the presence of *aad* and *dhfr* gene types for GENT and TMP-SMX, respectively. Bacterial colonies isolated from colistin-containing plates were examined for *mcr-1* and *mcr-2* genes as previously described (40). All isolates were speciated by 16S ribosomal RNA sequencing. Species diversity was calculated by the Shannon diversity index:

$$H = -\sum_{i=1}^s (P_i * \ln P_i)$$

where:

H = the Shannon diversity index

P_i = fraction of the entire population made up of species i

S = numbers of species encountered

Σ = sum from species 1 to species S

Primers used in these procedures are noted in Table S1. PCR products were visualized on a 1.5% agarose gel stained with SYBRsafe DNA gel stain (Invitrogen) and visualized under UV transillumination.

Sequencing Analysis

To identify gene or gene variants, we sequenced each PCR product that showed an electrophoretic band of an expected molecular weight. For amplicons over 1000 base pairs in length, bidirectional sequencing was performed. Each sequence was then compared against sequences in GenBank by BLAST (National Center for Biotechnology Information). Species were determined by the criteria of >98% sequence identity and genus by >95% sequence identity.

Results

Between June 2017 and February 2018, we obtained 113 unique rectal swab samples.

Of these, 11 exhibited no growth on a MacConkey control plate, and were not further analyzed.

Of the 102 remaining samples, 76 (75%) contained GNB that exhibited resistance to AMP, 14

(14%) to GENT, 47 (46%) to TMP-SMX, and 10 (10%) to COL. Eighteen (18%) samples

contained isolates that were sensitive to all drugs tested (Figure 1).

Bacterial growth on at least one drug-containing plate was observed in 85 (83%) of 102

samples. Resistance to only 1 antimicrobial agent was observed in 33 (32%) of samples; 39

(38%) were resistant to two antimicrobial agents, and 13 (13%) were resistant to 3 or more

agents (Table 1).

Detection of β -lactamase genes

Three hundred sixty-seven colonies obtained from 76 fecal samples containing AMP-

resistant isolates were analyzed for the presence of β -lactamase genes. Of the 76 fecal samples,

68 (89%) contained at least one β -lactamase gene. Among the 102 total fecal samples, TEM

variants (*bla*_{TEM-1}, *bla*_{TEM-116}) were detected in 57 (55%); 19 (18%) contained a SHV variant, 1

(1%) contained an OXA variant (*bla*_{OXA-1}), and 15 (15%) contained at least one CTX-M variant.

Upon further analysis of CTX-M subgroups, 6 (6%) had CTX-M group 1 (i.e. *bla*_{CTX-M-15}), 2 (2%)

had CTX-M group 2, and 4 (4%) contained CTX-M group 9 variants (i.e. *bla*_{CTX-M-14}, *bla*_{CTX-M-27}).

Two (2%) contained more than one CTX-M group variant. Six samples contained a CTX-M gene

that did not belong to any of the four CTX-M family members tested. Sequence analysis of these

PCR products detected an OXY variant sequence in 4 of these samples (41, 42). Twenty-five

isolates from 9 fecal samples contained confirmed CTX-M variants. No KPC or CTX-M group

8/25 gene types were detected in this study (Table S2).

Detection of dihydrofolate reductase genes contained in class 1 integron gene cassettes

Two hundred twenty TMP-SMX-resistant colonies were recovered from 45 fecal

samples; they were analyzed for the presence of a class 1 integron gene cassette to detect *dhfr*

gene types. Gene cassettes were detected in 30 (67%) of 45 samples and ranged from 1-2.2

kilobases in size. We detected *dhfr* genes in 21 samples, consisting of the following gene

variants: *dhfr-A17*, *dhfr-A7*, *dhfr-A5*, *dhfr-A21*, *dhfr-A1*, *dhfr-A15*, and *dhfr-B3*. *Dhfr-A17* was the

most prevalent gene of this type, present in 10 (22%) of 45 samples (Table 3). Nine (30%) of

the 30 samples that contained gene cassettes from phenotypically TMP-SMX resistant isolates

did not contain any *dhfr* genes (Table S3).

Detection of aminoglycoside adenylyltransferase genes contained in class 1 integron gene cassettes

One of the 14 samples that initially showed resistance to GENT was unable to be cultured in growth media and thus was not further analyzed. Fifty-nine GENT-resistant colonies were isolated from 13 samples; they were analyzed for class 1 integron gene cassettes. Seven (54%) of the 13 samples contained the gene cassette; 6 (46%) of these contained at least 1 *aad* gene type. The following *aad* genes were detected: *aadA5*, *aadA1*, and *aadB*. Of the samples containing *aad* genes, *aadA5* was detected in 5 of the 6 samples, while 1 sample contained both *aadA1* and *aadB* (Table S4).

Detection of mobile colistin resistance genes

Thirty-eight COL-resistant colonies were isolated from 10 samples and analyzed for *mcr-1* and *mcr-2* genes. No *mcr-1* or *mcr-2* was detected by PCR in these samples (Table S4).

Detection of integron cassette sequences:

We used PCR to amplify cassette sequences integrated in class 1 integrons in GNB strains that were resistant to GENT and TMP-SMX. Of 58 strains, 37 (64%) had integron sequences. In addition to the *dhfr* sequences described above, sequences from TMP-SMX-resistant bacteria were annotated in the NCBI BLAST database as *bla_{OXA}* (-1, -2, -10, -48), *bla_{DHA}*, *bla_{KPC}*, *bla_{CTX-M}* (-2, -3, -15), *bla_{NDM}*, *bla_{CMY}*, *bla_{IMP}*, *bla_{GES}*, *bla_{VIM}*, *aadA1*, *aadA2*, *aadA5*, *aadA6*, *aacA4*, *aacA6*, *aacA7*, *aacA8*, *sul1*, and *mcr-1* (Table 2). In addition to the *aad* sequences described above, integron gene cassettes sequenced from GENT-resistant bacteria were annotated in the NCBI BLAST database as *bla_{OXA-1}*, *bla_{CTX-M}* (-3, -15), *bla_{NDM}* (-5, -9), *bla_{CMY}*, *bla_{IMP}*, *dhfr-A17*, and a *mcr* variant (Table 2, S3, S4).

Characterization of bacterial communities by 16S rRNA sequencing

Of the 696 resistant bacterial isolates, 79 (11%) were unable to be speciated by 16S ribosomal RNA sequencing. From the remaining 617 resistant GNB isolates recovered from 102 samples, 11 unique genera were identified; AMP-resistant bacteria consisted of 6 distinct genera, TMP-SMX-resistant bacteria consisted of 7 distinct genera, GENT-resistant bacteria consisted of 2 genera, and COL-resistant bacteria consisted of 7 genera. The relative abundance of each bacterial genus is shown in

Table 2.

Based on Shannon diversity index, COL-resistant colonies had the highest species diversity ($H=1.9$), followed by those resistant to AMP ($H=1.2$), TMP-SMX ($H=0.8$), and GENT ($H=0.3$) (Figure 2).

Species identified in these samples included: *Escherichia* spp (*E. fergusonii*, *E. coli*, *Shigella flexneri*, *Shigella sonnei*, *Shigella dysenteriae*, *Shigella boydii*), *Klebsiella* spp (*K. pneumoniae* or *quasipneumoniae*, *K. oxytoca*, *K. aerogenes*, *K. variicola*), *Raoultella ornithinolytica* or *planticola*, *Enterobacter* spp (*E. ludwigii*, *E. bugandensis*, *E. xiangfangensis*, *E. aerogenes*), *Pseudomonas aeruginosa*, *Morganella morganelli*, *Comamonas jiangduensis* or *terrigena*, *Kluyvera cryocrescens*, *Fusobacterium varium*, *Hafnia paralvei*, and *Obesumbacterium proteus*.

Although *Escherichia* sp. and *Klebsiella* sp. represented the majority of our fecal samples (79%), there were 21 samples that contained other types of bacteria (i.e. *Enterobacter* sp., *Pseudomonas* sp., *Shigella* sp., *Morganella* sp., *Raoultella* sp., and *Kluyvera* sp.). Among these 21 samples, 13 (62%) harbored the antibiotic resistance genes described above.

Discussion

Our results demonstrate that there is an abundance of ARG (β -lactamase, *dhfr*, *aad*) carried by commensal GNB in healthy human intestine. Only 18% of rectal swab samples contained GNB that exhibited no phenotypic resistance to any of the four classes of drugs used to treat extraintestinal infections caused by enteric bacterial pathogens.

A previous study conducted at the same college community between 2016-2017 found that among 233 *E.coli* isolates cultured from human UTI cases, 97 (42%) were resistant to AMP, and 76 (78%) of these contained at least one β -lactamase gene. β -lactamase gene types from these isolates included *bla*_{TEM}, *bla*_{CTX-M} group1, *bla*_{CTX-M} group9, *bla*_{SHV}, and *bla*_{OXA} (43) (Table 3). Forty (17%) of the 233 *E. coli* isolates were resistant to TMP-SMX (43).

Another study of gene cassettes in human UTI *E. coli* isolates collected from the same college community from 1999-2001 found similar ARG harbored within the gene cassettes of these uropathogenic *E. coli*. *dhfr-A17* and *aadA5* were the most common cassette genes among these UTI isolates, which are the same ARG found in GNB in fecal samples in the current study. The findings of this study are summarized in Table 3.

A 2013 study by Adams-Sapper et al. found that *E. coli* isolates from patients with blood stream infection (BSI) at a San Francisco hospital contained β -lactamase genes similar to those of fecal GNB in our healthy volunteers (9); these included *bla*_{CTX-M} (CTX-M-15, CTX-M-14), *bla*_{TEM}, and *bla*_{OXA}. There was no significant difference between number of isolates containing CTX-M variants, or resistance to TMP-SMX in clinical BSI isolates compared to those in commensal bacteria in the present study (9). These observations demonstrate the potential for acquisition by extraintestinal pathogenic *E. coli* (ExPEC) of ARG via HGT from intestinal reservoirs.

Recent literature suggests geographic differences in gut ARG distribution. A 2008 study of fecal carriage of AMR in *E. coli* isolated from the gut of healthy adults in Paris found that only 2 (0.6%) of 332 fecal *E. coli* isolates contained ESBL CTX-M-15 gene (13). The present study identified at least 8 *Escherichia* spp isolates containing CTX-M-15, and 9 (9%) of 103 samples contained bacteria harboring CTX-M variants. These findings indicate a varying geographical distribution of the prevalence of AMR genes in healthy individuals, or a change in the prevalence of ARG over time, or both, which may be affected by differences or change in ingested food products containing AMR bacteria. Indeed, a 2018 study analyzed the resistome of 1,267 human gut samples from various countries. The findings indicated country-specific gut microbial signatures and significant differences in the gut resistome among different nationalities (44, 45). These studies, however, did not examine which gut GNB species carried the ARG.

In the present study, isolates from a given fecal sample usually contained the same set of ARG, even when the sample contained multiple species of bacteria. Forty-one (62%) of 76 AMP-resistant samples contained isolates in which all isolates of a given sample had the same composition of β -lactamase genes. These isolates belong to 8 different GNB species (*E. fergusonii*, *E. coli*, *E. marmotae*, *Shigella flexneri*, *Shigella sonnei*, *K. oxytoca*, *K. pneumoniae*, *K. dysenteriae*). Our findings also suggest that *Klebsiella* species were more likely than non-*Klebsiella* species to possess SHV variants ($P < .001$), while *Escherichia* species were more likely than non-*Escherichia* species to harbor TEM variants ($P < .001$). This observation suggests high frequency of HGT of ARG among a host's intestinal GNB microbiota when ARG enter the intestine.

Within integrons in both TMP/SMX- and GENT-resistant strains, all isolates within a given fecal sample contained the same ARG. This further supports the claim that genes are readily horizontally transferred to one another within the human gut, with integrons playing a particularly important role in this process (20). Gene cassettes present in the commensal

bacteria analyzed in this study possessed sequences that were annotated to belong to carbapenemase and metallo-carbapenemase genes (*bla_{KPC}*, *bla_{NDM}*, *bla_{IMP}*, *bla_{VIM}*) as well as *mcr*-variant genes (Table 2). Interestingly, strains carrying cassette sequences annotated as *mcr*-variant were not phenotypically resistant to COL. Similarly, not all strains carrying cassette sequences annotated as beta-lactamase genes were resistant to AMP.

In the study of *E. coli* isolates by Ajiboye et al., pathogenic strains from food animal origins and human UTI isolates shared many of the same gene cassette sequences (19), as well as those found in commensal bacteria in the current study (Table 3). Such mobile elements carrying ARG may be introduced into the human intestine by food contaminated with pathogenic as well commensal bacteria harboring these ARG, creating an abundant intestinal reservoir for ARG that then may get transferred into GNB strains that cause extraintestinal infections.

The scope of this study was limited to analysis of aerobic or microaerophilic GNB species. This design was intentional as most mobile ARG found in GNB pathogens are restricted to these species. However, it must be noted that the majority of gut microbial organisms are anaerobic, and thus the findings of our study may underestimate the frequency of HGT of ARG that may originate in anaerobes. In addition, our analysis of integron sequences was limited to class 1 integrons and to strains resistant to GENT or TMP-SMX, which would underestimate the prevalence of ARGs in integrons in fecal samples from this healthy college study population. Many of the ARG in this study's AMP-resistant strains may be harbored by integrons, together with other ARG cassettes. Further studies that investigate HGT between a broader range of microbial species must be conducted to wholly reveal the reservoir of ARG among intestinal bacterial organisms, and the implications for human health.

This study also utilized a screening method to identify ARG based on the patterns of phenotypic resistance. It is possible that the GNB isolates harbored ARG that conferred resistance to antimicrobial agents we did not use for screening. Further investigations into the resistome separated by GNB species in commensal bacteria will illuminate the implications of HGT between bacterial species.

Our study showed abundance and diversity of resistance genes among healthy adults in a particular college community. While these results may not be generalizable to other communities, it highlights the need for community-based comparisons between commensal and pathogenic bacteria. These observations made in a non-healthcare environment raise questions about how these ARG were introduced into the intestines of people residing in this community, including food and environment as sources. It calls for further investigation into

possible risk factors for acquisition of ARG other than just exposures to antibiotics, as they clearly pose a risk to public health. The findings in this study illuminate the relationship between gut microbial ARG content and infections such as UTI caused by Gram-negative pathogens. These observations may have global implications for the spread of antibiotic resistance through mobile genetic elements, as infections become increasingly difficult to treat with current antibiotic therapies.

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Tables

Table 1: Colony growth was observed in 82 fecal samples on MacConkey plates containing distinct types of antimicrobial agents. The number of types of antimicrobial agents to which a sample contained bacterial isolates that displayed resistance. AMP=ampicillin-resistant, TMP/SMX= trimethoprim-sulfamethoxazole-resistant, COL=colistin-resistant, GENT=gentamicin-resistant.

Resistance to (number of) antimicrobial agents	
Number, name of Antimicrobial agents	Number (%) of samples exhibiting phenotypic resistance
0	19 (19%)
1	31 (30%)
AMP	27 (26%)
TMP/SMX	2 (2%)
COL	2 (2%)
2	39 (38%)
AMP, TMP/SMX	32 (31%)
AMP, COL	3 (3%)
GENT, TMP/SMX	1 (1%)
AMP, GENT	3 (3%)
3 or more	13 (13%)
AMP, GENT, TMP/SMX	8 (8%)
AMP, TMP/SMX, COL	4 (4%)
AMP, GENT, TMP/SMX, COL	1 (1%)
TOTAL	102 (100%)

Table 2: Number of fecal samples containing bacterial colonies from each genus. Colonies were isolated from bacteria resistant to indicated antimicrobial agent. Colony growth from fecal culture may represent multiple species. Class 1 integron cassette sequences were analyzed only for TMP-SMZ and GENT-resistant isolates.

Genus	AMP-resistant (# of samples)	β -lactamase gene	TMP-SMX-resistant (# of samples)	<i>dhfr</i> gene in integron	Other ARG in integron in TMP-SMX-resistant strains	Growth on GENT (# of samples)	<i>aad</i> gene in integron	Other ARG in integron in GENT-resistant strains
Escherichia or Shigella sp.	38	<i>bla</i> _{TEM} , <i>bla</i> _{CTX-M} , <i>bla</i> _{SHV} , <i>bla</i> _{OXA}	34	<i>dhfr</i> -A7, <i>dhfr</i> -A17, <i>dhfr</i> -B3, <i>dhfr</i> -A5	<i>bla</i> _{OXA} (-1, -2, -10, -48), <i>bla</i> _{CTXM} (-3, -15), <i>bla</i> _{NDM} -5, <i>bla</i> _{CMY} , <i>bla</i> _{GES} -11, <i>bla</i> _{DHA} -1, <i>bla</i> _{IMP} , <i>bla</i> _{SIM} , <i>bla</i> _{VIM} , <i>aacA6</i> , <i>aacA4</i> , <i>aacA7</i> , <i>aacA8</i> , <i>aadA5</i> , <i>aadA6</i> , <i>sul1</i> , <i>mcr</i> -1	11	<i>aadA5</i> , <i>aadB</i> , <i>aadA1</i> , <i>aadA5</i>	<i>bla</i> _{NDM} (-5, 9), <i>bla</i> _{OXA} -1, <i>bla</i> _{CTXM} (-3, -15), <i>bla</i> _{IMP} , <i>bla</i> _{CMY} , <i>dhfr</i> -17, <i>mcr</i>
Klebsiella sp.	18	<i>bla</i> _{TEM} , <i>bla</i> _{SHV} , <i>bla</i> _{OXY}	4	<i>dhfr</i> -A1	<i>bla</i> _{CTXM} -2, <i>bla</i> _{NDM} , <i>aadA1</i> , <i>aadA2</i> , <i>sul1</i>	0	n/a	n/a
Raoultella sp.	3	none	1	<i>dhfr</i> -A15	<i>bla</i> _{NDM} , <i>bla</i> _{VIM} , <i>aadA2</i> , <i>aacA7</i> , <i>sul1</i>	0	n/a	n/a
Enterobacter sp.	2	<i>bla</i> _{TEM} , <i>bla</i> _{SHV}	1	none	none	0	n/a	n/a
Pseudomonas sp.	6	<i>bla</i> _{TEM} , <i>bla</i> _{CTX-M}	1	<i>dhfr</i> -B3	<i>bla</i> _{OXA} -2, <i>bla</i> _{VIM} -4, <i>bla</i> _{NDM} -1, <i>bla</i> _{CMY} , <i>aadA6</i> , <i>aacA8</i> , <i>aacA7</i> , <i>sul1</i>	0	n/a	n/a
Morganella sp.	1	<i>bla</i> _{TEM}	0	n/a	n/a	0	n/a	n/a
Brenneria sp.	4	<i>bla</i> _{TEM} , <i>bla</i> _{CTX-M} , <i>bla</i> _{SHV}	0	n/a	n/a	0	n/a	n/a
Comamonas sp.	0	n/a	1	none	none	0	n/a	n/a
Kluyvera sp.	0	n/a	1	<i>dhfr</i> -A21	<i>bla</i> _{KPC}	0	n/a	n/a
Fusobacterium sp.	0	n/a	0	n/a	n/a	1	<i>aadA5</i>	n/a

Table 3: Comparison of ARGs found in fecal samples (current study) compared to UTI samples obtained from the same population in 2016-2017 (Yamaji, 2018) and 2009 (Ajiboye, 2009). *P-value > .05 indicates a significant difference in genetic component between fecal samples and UPEC isolates.

Genes found in current study vs. clinical UPEC samples in same study population (Yamaji, 2018 and Ajiboye, 2009)			
ARG	No. (%) fecal isolates (current study)	UPEC (Yamaji, 2018; Ajiboye, 2009)	P value
<i>bla</i> TEM	57 (74)	72 (74)	1.000
<i>bla</i> CTX-M	11 (14)	6 (6)	0.1209
group 1	6 (8)	4 (4)	0.3409
group 2	2 (3)	0 (0)	0.1944
group 8/25	0 (0)	0 (0)	1.000
group 9	3 (4)	2 (2)	0.656
<i>bla</i> SHV	19 (25)	1 (1)	.0001*
<i>bla</i> OXA	1 (1)	7 (7)	0.0784
<i>dhfr</i> -A17	10 (21)	38 (56)	.0005*
<i>dhfr</i> -A7	5 (11)	3 (4)	0.2621
<i>dhfr</i> -A5	1 (2)	3 (4)	0.6438
<i>dhfr</i> -A21	1 (2)	0 (0)	0.3982
<i>dhfr</i> -A1	2 (4)	2 (3)	1.000
<i>dhfr</i> -A15	1 (2)	2 (3)	1.000
<i>dhfr</i> -B3	1 (2)	0 (0)	0.3982
<i>dhfr</i> -A12	0 (0)	0 (0)	1.000
<i>aad</i> A1	1 (8)	17 (25)	0.2783
<i>aad</i> A5	5 (38)	38 (56)	0.3642
<i>aad</i> A2	0 (0)	5 (7)	0.5868
<i>aad</i> B	1 (8)	1 (1)	0.2969

Figures

Figure 1: Bacterial growth (%) on MacConkey plates containing antimicrobial agents. Pansusceptible isolates were defined as those that exhibited growth on MacConkey control plate, but no growth in the presence of each of four antimicrobial agents tested.

Figure 2A

Figure 2B

Figure 2C

Figure 2D

Figure 2: Relative frequency of genera represented by bacterial colonies exhibiting resistance to A) ampicillin, B) trimethoprim-sulfamethoxazole, C) gentamicin, and D) colistin.

539
540 **Supplemental Material**
541
542 **Table S1:** Polymerase chain reaction (PCR) primers and conditions

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Target, primers	Sequence 5'—3'	PCR protocol	Amplicon size (bp)	Reference
16S rRNA		94°C 2 min + 33X (94°C 15s + 48°C 30s + 68°C 1.5min)	1465	Frank et. al., 2008
27F	AGAGTTTGATCMTGGCTCAG*			
1492R	TACCTTGTTACGACTT			
Class 1 gene cassette		94°C 5 min + 33X (94°C 45s + 64°C 30s + 72°C 1.5min)	variable	Ajiboye et.al., 2009
RB317	GAACCTTGACCGAACGCAG			
RB320	AGCTTAGTAAAGCCCTCGCTAG			
MCR-1 and MCR-2 (duplex)		94°C 15 min + 25X (94°C 30s + 58°C 1.5min + 72°C 1min) + 72°C 10min		Cavaco et. al., 2016
MCR1-F	CGGTCAGTCCGTTTGTTC		309	
MCR1-R	CTTGGTCGGTCTGTAGGG			
MCR2-IF	TGTTGCTTGTGCCGATTGGA		567	
MCR2-IR	AGATGGTATTGTTGGTTGCTG			
CTX-M		94°C 2min + 39X (94°C 30s + 60°C 30s + 72°C 1 min) 72°C 5min		
CTX-M Univ F	TTTGCGATGTGCAGTACCAGTAA		500	Adams-Sapper et al., 2013
CTX-M Univ R	CTCCGCTGCCGGTTTTATC			
CTXMGp1_F	TTAGGAARTGTGCCGCTGYA*		688	Dallenne et al., 2010
CTXMGp1_R	CGATATCGTTGGTGGTRCCAT*			
CTXMGp2_F	CGTTAACGGCACGATGAC		404	Dallenne et al., 2010
CTXMGp2_R	CGATATCGTTGGTGGTRCCAT*			
CTXMGp9_F	TCAAGCCTGCCGATCTGGT		561	Dallenne et al., 2010
CTXMGp9_R	TGATTCTCGCCGCTGAAG			
CTXMGp8/25_F	AACRCRCAGACGCTCTAC*		326	Dallenne et al., 2010
CTXMGp8/25_R	TCGAGCCGGAASGTGTYAT*			

TEM, SHV, OXA (multiplex)		94°C 2min + 30X (94°C 30s + 60°C 30s + 72°C 1min) 72°C 5min		Dallenne et al., 2010
TEM_F	CATTTCCTGTGTCGCCCTTATTC		800	
TEM_R	CGTTCATCCATAGTTGCCTGAC			
SHV_F	AGCCGCTTGAGCAAATTAAAC		713	
SHV_R	ATCCCGCAGATAAATCACCAC			
OXA1_4_30_F	GGCACCAGATTCAACTTTCAAG		564	
OXA1_4_30_R	GACCCCAAGTTTCCTGTAAGTG			
KPC		94°C 5min + 30X (94°C 5min + 94°C 40s + 60°C 40s + 72°C 1min) 72°C 7min	538	Dallenne et al., 2010
KPC_F	CATTCAAGGGCTTTCTTGCTGC			
KPC_R	ACGACGGCATAGTCATTTGC			
*M=A or C; Y=T or C; R=A or G; S=G or C; D=A or G or T				

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546 **Table S2: ARG and species associated with AMP-resistant colonies**

SAMPLE#	Univ	CTX-M	CTX-M Gp1	CTX-M Gp2	CTX-M Gp8/25	CTX-M Gp9	TEM	SHV	OXA	KPC	Species
3-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
3-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
3-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
3-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
4-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
4-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
4-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
4-4_	-		n/a	n/a	n/a	n/a	-	-	-	-	Escherichia fergusonii
4-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
6-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
6-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
6-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
6-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
6-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
7-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Enterobacter xiangfangensis
7-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
7-3_	-		n/a	n/a	n/a	n/a	-	-	-	-	Enterobacter aerogenes
7-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
7-5_	-		n/a	n/a	n/a	n/a	-	-	-	-	Escherichia fergusonii
8-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
8-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
9-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
9-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
9-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
9-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
9-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
10-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
11-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
11-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
11-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
11-4_	-		n/a	n/a	n/a	n/a	-	-	-	-	
11-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
12-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
12-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
12-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
12-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
12-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
13-1_	-		n/a	n/a	n/a	n/a	-	-	-	-	Escherichia fergusonii
13-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
13-3_	-		n/a	n/a	n/a	n/a	-	-	-	-	Escherichia fergusonii
13-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
13-5_	-		n/a	n/a	n/a	n/a	-	-	-	-	Escherichia fergusonii
15-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella dysenteriae
15-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella dysenteriae
15-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella dysenteriae
15-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella dysenteriae
15-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella dysenteriae
16-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
16-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
16-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
16-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
16-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
17-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri or Shigella sonnei
17-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
17-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri or Shigella sonnei
17-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri or Shigella sonnei
17-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
18-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
18-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
18-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri or Shigella sonnei
18-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri or Shigella sonnei
18-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella sonnei or Escherichia fergusonii
20-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
20-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri or Shigella sonnei
20-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
22-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-27 or blaSHV-110	-	-	Klebsiella pneumoniae
22-2_	-		n/a	n/a	n/a	n/a	-	blaSHV-27	-	-	Klebsiella pneumoniae
22-3_	1	CTXM-15	-	-	-	-	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
22-4_	1	CTXM-15	-	-	-	-	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
22-5_	1	CTXM-15	-	-	-	-	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
28-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri
28-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
28-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
29-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
29-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
29-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
29-4_	-		n/a	n/a	n/a	n/a	-	-	-	-	Escherichia fergusonii or Shigella flexneri
29-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
35-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
35-2_	-		n/a	n/a	n/a	n/a	-	-	-	-	Escherichia fergusonii or Shigella flexneri
35-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
35-4_	-		n/a	n/a	n/a	n/a	-	-	-	-	Escherichia fergusonii or Shigella flexneri
35-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
38-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Morganella morganii
38-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Morganella morganii
38-3_	1	CTXM-15	-	-	-	-	blaTEM-1	-	-	-	Shigella boydii
38-4_	1	CTXM-15	-	-	-	-	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
38-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
39-1_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
39-2_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
39-3_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
39-4_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
39-5_	-		n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
40-1_	-		n/a	n/a	n/a	n/a	-	-	-	-	Enterobacter ludwigii
40-2_	-		n/a	n/a	n/a	n/a	-	-	-	-	Enterobacter bugandensis

40-3	-	n/a	n/a	n/a	n/a	-	-	-	-	Enterobacter bugandensis
40-4	-	n/a	n/a	n/a	n/a	-	-	-	-	Enterobacter ludwigii
40-5	-	n/a	n/a	n/a	n/a	-	-	blaSHV-157 or blaSHV-62 or blaSHV-85	-	Enterobacter bugandensis
43-1	1	CTXM-15	-	-	-	-	-	-	-	Escherichia fergusonii or Shigella flexneri
43-2	1	CTXM-15	-	-	-	blaTEM-1	-	-	-	Shigella flexneri
43-3	1	CTXM-15	-	-	-	-	-	-	-	Escherichia fergusonii or Shigella flexneri
43-4	1	1	-	-	-	-	-	-	-	Shigella flexneri
43-5	1	1	-	-	-	-	-	-	-	Escherichia fergusonii or Shigella flexneri
47-1	1	1	-	-	-	1	1	-	-	Escherichia fergusonii
47-2	1	1	-	-	-	1	-	-	-	Escherichia fergusonii
47-3	1	1	-	-	-	1	-	-	-	Escherichia fergusonii
47-4	1	1	-	-	-	1	-	-	-	Escherichia fergusonii
47-5	1	1	-	-	-	1	1	-	-	Escherichia fergusonii
48-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
48-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
48-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia marmotae
48-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia marmotae
49-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia coli
49-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia coli
49-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia coli
49-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia coli
49-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia coli
50-1	blaOXY-2	-	-	-	-	-	-	-	-	Klebsiella oxytoca
50-2	blaOXY-2	-	-	-	-	blaTEM-1	-	-	-	Klebsiella oxytoca
50-3	blaOXY-2	-	-	-	-	-	-	-	-	Klebsiella oxytoca
50-4	blaOXY-2	-	-	-	-	-	-	-	-	Klebsiella oxytoca
50-5	blaOXY-2	-	-	-	-	-	-	-	-	Klebsiella oxytoca
51-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
51-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
51-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri
51-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri
51-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri
52-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
52-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
52-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
52-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri
52-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri
54-1	1	1	1	-	CTXM-27	-	-	-	-	Escherichia coli
54-2	1	1	1	-	CTXM-27	-	-	-	-	Escherichia coli
54-3	1	1	1	-	CTXM-27	-	-	-	-	Escherichia coli
54-4	1	1	1	-	CTXM-27	-	-	-	-	Escherichia coli
54-5	1	1	1	-	CTXM-27	-	-	-	-	Escherichia coli
55-1	-	-	-	-	-	-	-	-	-	Pseudomonas aeruginosa
55-2	-	-	-	-	-	-	-	-	-	Pseudomonas aeruginosa
55-3	-	-	-	-	-	-	-	-	-	Pseudomonas aeruginosa
55-5	-	-	-	-	-	-	-	-	-	Pseudomonas aeruginosa
56-1	-	-	-	-	-	-	-	-	-	Pseudomonas aeruginosa
56-2	-	-	-	-	-	-	-	-	-	Pseudomonas aeruginosa
56-3	-	-	-	-	-	-	-	-	-	Pseudomonas aeruginosa
56-4	-	-	-	-	-	-	-	-	-	Pseudomonas aeruginosa
56-5	-	-	-	-	-	-	-	-	-	Pseudomonas aeruginosa
57-1	-	n/a	n/a	n/a	n/a	-	blaSHV-190	-	-	Pseudomonas aeruginosa
57-2	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-190	-	-	Klebsiella pneumoniae
57-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Klebsiella pneumoniae
57-4	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-190	-	-	Escherichia coli
57-5	-	n/a	n/a	n/a	n/a	-	blaSHV-190	-	-	Klebsiella pneumoniae
59-1	blaOXY-1	-	-	-	-	-	-	-	-	Klebsiella pneumoniae
59-2	blaOXY-1	-	-	-	-	-	-	-	-	Klebsiella oxytoca
59-3	blaOXY-1	-	-	-	-	-	-	-	-	Klebsiella oxytoca
59-4	blaOXY-1	-	-	-	-	-	-	-	-	Klebsiella oxytoca
59-5	blaOXY-1	-	-	-	-	-	-	-	-	Klebsiella oxytoca
60-1	blaOXY-6	-	-	-	-	-	-	-	-	Klebsiella oxytoca
60-2	blaOXY-6	-	-	-	-	-	-	-	-	Klebsiella oxytoca
60-3	blaOXY-6	-	-	-	-	-	-	-	-	Klebsiella oxytoca
60-4	blaOXY-6	-	-	-	-	-	-	-	-	Klebsiella oxytoca
60-5	blaOXY-6	-	-	-	-	-	-	-	-	Klebsiella oxytoca
61-1	blaOXY-1	-	-	-	-	-	-	-	-	Klebsiella oxytoca
61-2	blaOXY-1	-	-	-	-	-	-	-	-	Klebsiella oxytoca
61-3	blaOXY-1	-	-	-	-	-	-	-	-	Klebsiella oxytoca
61-4	blaOXY-1	-	-	-	-	-	-	-	-	Klebsiella oxytoca
61-5	1	-	-	-	-	-	-	-	-	Klebsiella oxytoca
62-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Klebsiella oxytoca
62-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia marmotae
62-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia marmotae
62-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia marmotae
62-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia marmotae
63-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
63-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
63-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
63-4	1	1	-	-	-	blaTEM-1	-	-	-	Escherichia fergusonii
63-5	1	1	-	-	-	blaTEM-1	-	-	-	Escherichia fergusonii
64-1	-	-	-	-	-	-	-	-	-	Escherichia fergusonii
64-2	-	-	-	-	-	-	-	-	-	Klebsiella quasipneumoniae
64-3	-	-	-	-	-	-	-	-	-	Klebsiella quasipneumoniae
64-4	-	-	-	-	-	-	-	-	-	Klebsiella quasipneumoniae
64-5	-	-	-	-	-	-	-	-	-	Klebsiella quasipneumoniae
65-1	-	-	-	-	-	-	-	-	-	Klebsiella oxytoca
65-2	-	-	-	-	-	-	-	-	-	Klebsiella oxytoca
65-3	-	-	-	-	-	-	-	-	-	Klebsiella oxytoca
65-4	-	-	-	-	-	-	-	-	-	Klebsiella oxytoca
66-1	-	-	-	-	-	-	-	-	-	Klebsiella oxytoca
66-2	-	-	-	-	-	-	-	-	-	Raoultella planticola
66-3	-	-	-	-	-	-	-	-	-	Raoultella planticola
66-4	-	-	-	-	-	-	-	-	-	Raoultella planticola
66-5	-	-	-	-	-	-	-	-	-	Raoultella planticola
67-1	-	-	-	-	-	-	-	-	-	Raoultella planticola
67-2	-	-	-	-	-	-	-	-	-	Raoultella planticola
67-3	-	-	-	-	-	-	-	-	-	Klebsiella pneumoniae
67-4	-	-	-	-	-	-	-	-	-	Klebsiella pneumoniae

67-5	-						-	-	-	Klebsiella pneumoniae
68-1	1	-	-	-	-	blaTEM-1	-	-	-	Klebsiella pneumoniae
68-2	-						-	-	-	Klebsiella quasipneumoniae
68-3	-						-	-	-	Pseudomonas aeruginosa
68-4	-						-	-	-	Pseudomonas aeruginosa
68-5	-						-	-	-	Pseudomonas aeruginosa
69-1	-						-	-	-	Escherichia fergusonii or Shigella flexneri
69-2	-						-	-	-	Raoultella ornithinolytica
69-3	-						-	-	-	Raoultella planticola
70-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Raoultella ornithinolytica
70-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Raoultella planticola
70-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
70-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
70-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
71-1	-						-	-	-	Escherichia sp.
71-2	-						-	-	-	Escherichia sp.
71-3	-						-	-	-	Pseudomonas aeruginosa
71-4	-						-	-	-	Pseudomonas aeruginosa
71-5	1				1		-	-	-	Pseudomonas aeruginosa
72-1	1	-	1	-	CTXM-27	-	blaSHV-11	-	-	Pseudomonas aeruginosa
72-2	-	n/a	n/a	n/a	n/a	-	blaSHV-11	-	-	Pseudomonas aeruginosa
72-3	1	-	1	-	CTXM-27	-	1	-	-	Escherichia fergusonii
72-4	1	-	1	-	CTXM-27	-	-	-	-	Escherichia sp.
72-5	1	-	1	-	CTXM-27	-	blaSHV-11	-	-	Escherichia sp.
73-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
73-2	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-11	-	-	Escherichia fergusonii or shigella sp. or brenneria alni
73-3	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-11	-	-	Escherichia mamotae
73-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Brenneria alni or Escherichia fergusonii or Shigella flexneri
73-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Brenneria alni or Escherichia fergusonii or Shigella (flexneri or dysenteriae)
74-1	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Escherichia sp.
74-2	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Escherichia sp.
74-3	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
74-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Klebsiella pneumoniae
74-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Klebsiella pneumoniae
75-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or shigella flexneri
75-2	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
75-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella sonnei or Brenneria alni or Escherichia sp.
75-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Klebsiella pneumoniae
75-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Brenneria alni or Escherichia sp.
77-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Klebsiella varicola
77-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or shigella flexneri
77-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or shigella flexneri
77-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
77-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp. or Shigella sonnei or Shigella flexneri
78-1	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-121 or blaSHV-25 or SHV-136	blaOXA-1	-	Escherichia sp.
78-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
78-3	-	-	-	-	-	blaTEM-1	-	-	-	
78-4	-	-	-	-	-	blaTEM-1	-	-	-	
78-5	-	-	-	-	-	blaTEM-1	-	-	-	
79-1	-						-	-	-	
79-2	-						-	-	-	Escherichia fergusonii or shigella flexneri
79-3	-						-	-	-	Pseudomonas aeruginosa
79-4	-						-	-	-	Pseudomonas aeruginosa
79-5	-						-	-	-	Pseudomonas aeruginosa
80-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Pseudomonas aeruginosa
80-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or shigella flexneri
80-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
80-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
80-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella sonnei or Brenneria alni or Escherichia sp.
81-1	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Escherichia sp.
81-2	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
81-3	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
81-4	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
81-5	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
82-1	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
82-2	-	n/a	n/a	n/a	n/a	-	blaSHV-1 or blaSHV-196 or blaSHV-187	-	-	Klebsiella pneumoniae
82-3	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or SHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
82-4	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or SHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
82-5	-	n/a	n/a	n/a	n/a	-	blaSHV-226 or blaSHV-211 or blaSHV-1	-	-	Klebsiella pneumoniae
83-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Klebsiella pneumoniae
83-2	-	n/a	n/a	n/a	n/a	-	-	-	-	Escherichia fergusonii or shigella flexneri
83-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
83-4	-	n/a	n/a	n/a	n/a	-	-	-	-	Escherichia sp.
83-5	-	n/a	n/a	n/a	n/a	-	-	-	-	Escherichia sp.
84-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia sp.
84-2	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-28 or blaSHV-1 or blaSHV-75	-	-	Escherichia sp.
84-3	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-28 or blaSHV-1 or blaSHV-75	-	-	Klebsiella pneumoniae
84-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	
84-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or shigella flexneri
85-1	-						-	-	-	
85-2	-						-	-	-	Pseudomonas aeruginosa
85-3	-						-	-	-	Pseudomonas aeruginosa
85-4	-						-	-	-	Pseudomonas aeruginosa
85-5	-						-	-	-	Pseudomonas aeruginosa
86-1	-	n/a	n/a	n/a	n/a	blaTEM-116	blaSHV-11	-	-	Pseudomonas aeruginosa
86-2	-	n/a	n/a	n/a	n/a	blaTEM-116	blaSHV-11	-	-	Klebsiella pneumoniae
86-3	-	n/a	n/a	n/a	n/a	blaTEM-116	blaSHV-11	-	-	Klebsiella pneumoniae
86-4	-	n/a	n/a	n/a	n/a	blaTEM-116	blaSHV-11	-	-	Klebsiella pneumoniae
87-1	-	n/a	n/a	n/a	n/a	blaTEM-116	blaSHV-27	-	-	
87-2	-	n/a	n/a	n/a	n/a	blaTEM-116	blaSHV-27	-	-	Klebsiella pneumoniae
87-3	-	n/a	n/a	n/a	n/a	blaTEM-116	blaSHV-27	-	-	Klebsiella pneumoniae
87-4	-	n/a	n/a	n/a	n/a	blaTEM-116	blaSHV-1	-	-	Klebsiella pneumoniae

87-5	-	n/a	n/a	n/a	n/a	blaTEM-116	blaSHV-27	-	-	Klebsiella pneumoniae
89-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Klebsiella pneumoniae
89-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
89-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
89-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
89-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
90-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
90-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
90-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
90-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
90-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
92-1	1	-	-	-	CTX-M-14	-	-	-	-	Escherichia fergusonii
92-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	-
92-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
92-4	1	-	-	-	CTX-M-14	-	-	-	-	Escherichia fergusonii or Shigella flexneri
92-5	1	-	-	-	CTX-M-14	-	-	-	-	-
93-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	-
93-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
93-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
93-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
93-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
95-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
95-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	-
95-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	-
95-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
95-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
96-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
96-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
97-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
97-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
97-3	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-288 or blaSHV-11	-	-	Escherichia fergusonii
97-4	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-211 or SHV-11 or SHV-1	-	-	-
97-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	-
98-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
98-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia coli or fergusonii or Shigella flexneri
98-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia coli or fergusonii or Shigella flexneri
98-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia coli or fergusonii or Shigella flexneri
98-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	-
100-1	-	n/a	n/a	n/a	n/a	-	blaSHV-211 or SHV-11 or blaSHV-11	-	-	Shigella flexneri
100-2	-	n/a	n/a	n/a	n/a	-	blaSHV-211 or blaSHV-11 or SHV-1	-	-	Klebsiella pneumoniae
100-3	-	n/a	n/a	n/a	n/a	blaTEM-1	blaSHV-211 or SHV-11 or blaSHV-11 or SHV-1	-	-	Klebsiella pneumoniae
100-4	-	n/a	n/a	n/a	n/a	-	blaSHV-211 or blaSHV-11 or SHV-1	-	-	Escherichia fergusonii or Shigella flexneri
100-5	-	n/a	n/a	n/a	n/a	-	-	-	-	-
100-6	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	-
101-1	-	n/a	n/a	n/a	n/a	-	blaSHV-190	-	-	-
101-2	-	n/a	n/a	n/a	n/a	-	blaSHV-190	-	-	Klebsiella pneumoniae
101-3	-	n/a	n/a	n/a	n/a	-	blaSHV-190	-	-	Klebsiella pneumoniae
101-4	-	n/a	n/a	n/a	n/a	-	blaSHV-190	-	-	-
101-5	-	n/a	n/a	n/a	n/a	-	blaSHV-190	-	-	Klebsiella pneumoniae
102-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
102-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
102-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
102-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	-
102-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii
105-1	-	n/a	n/a	n/a	n/a	-	blaSHV-228 or blaSHV-11	-	-	Klebsiella pneumoniae
105-2	-	n/a	n/a	n/a	n/a	-	blaSHV-228 or blaSHV-11	-	-	Klebsiella pneumoniae
105-3	-	n/a	n/a	n/a	n/a	-	blaSHV-228 or blaSHV-11	-	-	Klebsiella pneumoniae
105-4	-	n/a	n/a	n/a	n/a	-	blaSHV-228 or blaSHV-11	-	-	Klebsiella pneumoniae
105-5	-	n/a	n/a	n/a	n/a	-	1	-	-	Klebsiella pneumoniae
106-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri
106-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri or Shigella sonnei
106-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri or Shigella sonnei
106-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
106-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri
107-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
107-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	-
107-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
107-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
107-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
108-1	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
108-2	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
108-3	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
108-4	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
108-5	-	n/a	n/a	n/a	n/a	blaTEM-1	-	-	-	Shigella flexneri
113-1	-	1	-	-	-	-	-	-	-	Shigella dysenteriae
113-2	blaOXY	-	-	-	-	-	-	-	-	Shigella dysenteriae
113-3	-	1	-	-	-	-	-	-	-	Shigella dysenteriae
113-4	blaOXY	-	-	-	-	blaTEM-1	-	-	-	Escherichia fergusonii or Shigella flexneri
113-5	-	1	-	-	-	blaTEM-1	-	-	-	Shigella dysenteriae

552 **Table S3: ARG and species associated with TMP/SMX-resistant colonies.**

SAMPLE#	Class I gene cassette (size in kb)	ARG found in gene cassette	Species
3-1	-		Escherichia fergusonii or shigella flexneri
3-2	-		Escherichia fergusonii or shigella flexneri
3-3	-		Escherichia sp.
3-4	-		Escherichia sp.
3-5	-		Escherichia sp.
4-1	2.2	mcr-1, NDM, CMY	Escherichia fergusonii or shigella flexneri
4-2	2.2	mcr-1, NDM, CMY	Escherichia sp.
4-3	2.2	mcr-1, NDM, CMY	Escherichia sp.
4-4	2.2	mcr-1, NDM, CMY	Escherichia sp.
4-5	2.2	mcr, NDM, CMY	Escherichia sp.
6-1	2.2	mcr, NDM, CMY	Escherichia fergusonii or shigella flexneri
6-2	2.2	NDM, CMY	Escherichia sp.
6-3	2.2	NDM, CMY, mcr	Escherichia sp.
6-4	2.2	mcr, NDM, CMY	Escherichia sp.
6-5	2.2	mcr, NDM, CMY	Escherichia sp.
7-1	1	dfrA7, sul1, blaGES-11, aac(6)-Ib (aacA4)	Escherichia fergusonii or shigella flexneri
7-2	1	dfrA7, sul1, blaGES-11, aac(6)-Ib (aacA4)	Escherichia sp.
7-3	2.2	mcr, NDM, CMY, IMP	Escherichia sp.
7-4	1	dfrA7, sul1, blaGES-11, aac(6)-Ib (aacA4)	Escherichia sp.
7-5	1	dfrA7, sul1, blaGES-11, aac(6)-Ib (aacA4)	Escherichia sp.
8-1	-		Shigella flexneri
8-2	-		Escherichia fergusonii or shigella flexneri
8-3	-		Escherichia sp.
8-4	-		Escherichia sp.
8-5	-		Escherichia sp.
9-1	-		Escherichia fergusonii or shigella flexneri
9-2	-		
9-3	-		
9-4	2.2	mcr, NDM, CMY	Escherichia sp.
9-5	2.2	mcr, NDM, CMY	Escherichia sp.
10-1	-		Escherichia fergusonii or shigella flexneri
10-2	-		Escherichia sp.
10-3	-		Escherichia sp.
10-4	-		Escherichia sp.
10-5	-		Escherichia sp.
12-1	-		Escherichia fergusonii or shigella flexneri
12-2	-		Escherichia sp.
12-3	-		Escherichia sp.
12-4	-		Escherichia sp.
12-5	-		Escherichia sp.
13-1	1	dfrA7	escherichia fergusonii or shigella flexneri
13-2	1	dfrA7	Escherichia sp.
13-3	1	dfrA7	Escherichia sp.
13-4	1	dfrA7, sul1	Escherichia sp.
13-5	1	dfrA7, sul1	Escherichia sp.
15-1	1	dfrA5, NDM, OXA-48	Shigella dysenteriae
15-2	1	dfrA5, NDM, OXA-48	Shigella dysenteriae
15-3	1	dfrA5, NDM, OXA-48	Shigella dysenteriae
15-4	1	dfrA5	Shigella dysenteriae
15-5	1	dfrA5, NDM, OXA-48	Shigella dysenteriae
16-1	1	mcr, NDM, CMY	Escherichia fergusonii
16-2	1	mcr, NDM	Escherichia fergusonii
16-3	1	mcr, NDM, CMY	
16-4	1	mcr, NDM, CMY, IMP	escherichia coli or fergusonii
16-5	1	mcr, NDM, CMY, IMP	escherichia coli or fergusonii
19-1	2	dfrA17, aadA5, NDM, OXA-1, DHA-1	Escherichia fergusonii or shigella flexneri
19-2	2	dfrA17, aadA5, NDM, OXA-1, DHA-1	Escherichia sp.
19-3	2	dfrA17, aadA5, NDM, OXA-1, DHA-1	Escherichia sp.
19-4	2	dfrA17, aadA5, NDM, OXA-1, DHA-1	Escherichia sp.
19-5	2	dfrA17, aadA5, NDM, OXA-1, DHA-1	Escherichia sp.
20-1	2	dfrA17, NDM-5, OXA-1, CTXM-15, CTXM-3, aadA5, DHA-1	Escherichia fergusonii or shigella flexneri
20-2	2	dfrA17	Escherichia sp.
20-3	2	dfrA17	Escherichia sp.
20-4	2	dfrA17	Escherichia sp.
20-5	2	dfrA17	Escherichia sp.
29-1	2.2	mcr-1, IMP, NDM, dfr	Escherichia fergusonii or shigella flexneri
29-2	2	mcr-1	Escherichia sp.
29-3	2.2	-	Escherichia sp.
29-4	2.2	-	Escherichia sp.
29-5	2.2	-	Escherichia sp.
38-1	2	dfrA17, OXA-1, CTXM-3, CTXM-15, DHA-1, aadA5, NDM	Escherichia fergusonii or shigella flexneri
38-2	2	dfrA17, NDM, OXA-1, CTXM-15, CTXM-3, aadA5, DHA-1	Escherichia sp.
38-3	2	dfrA17, NDM, OXA-1, CTXM-15, CTXM-3, aadA5, DHA-1	Escherichia sp.
38-4	2	dfrA17	Escherichia sp.
38-5	2	dfrA17	Escherichia sp.
39-1	-		Shigella flexneri
39-2	-		Escherichia fergusonii or shigella flexneri
39-3	-		Escherichia sp.
39-4	-		Escherichia sp.
39-5	-		Escherichia sp.
40-1	-		Escherichia sp.
40-2	-		Shigella flexneri
40-3	-		Shigella flexneri

40-4	-		<i>Escherichia fergusonii</i> or <i>Shigella flexneri</i>
40-5	-		<i>Shigella flexneri</i>
47-1	-		<i>Escherichia fergusonii</i>
47-2	-		
47-3	-		<i>Escherichia fergusonii</i>
47-4	-		
47-5	-		
49-1	-		<i>Klebsiella pneumoniae</i>
49-2	-		<i>Klebsiella pneumoniae</i>
49-3	-		<i>Klebsiella pneumoniae</i>
49-4	-		<i>Klebsiella pneumoniae</i>
49-5	-		<i>Klebsiella pneumoniae</i>
52-1	1-1.2	dfrA7	<i>Escherichia</i> sp.
52-2	1-1.2	dfrA7	<i>Escherichia</i> sp.
52-3	1-1.2	dfrA7, sul1	<i>Escherichia</i> sp.
52-4	1-1.2	dfrA7, sul1	<i>Shigella flexneri</i>
52-5	1-1.2	dfrA7	<i>Escherichia</i> sp.
54-1	-		<i>Escherichia</i> sp.
54-2	1.5-2	dfrA17, OXA-1, CTXM-3, CTXM-15, aadA5, NDM	<i>Escherichia</i> sp.
54-3	1.5-2	dfrA17	<i>Escherichia</i> sp.
54-4	-		<i>Escherichia</i> sp.
54-5	-		<i>Escherichia</i> sp.
59-1	1	dfrA21, KPC	
59-2	1	dfrA21, KPC	<i>Kluyvera cryocrescens</i>
59-3	1	dfrA21	<i>Kluyvera cryocrescens</i>
59-4	1	dfrA21	<i>Kluyvera cryocrescens</i>
59-5	1	dfrA21	<i>Kluyvera cryocrescens</i>
63-1	-		<i>Kluyvera cryocrescens</i>
63-2	-		<i>Shigella flexneri</i>
64-1	-		<i>Shigella flexneri</i> or <i>Shigella sonnei</i>
64-2	-		<i>Klebsiella pneumoniae</i>
64-3	-		<i>Klebsiella pneumoniae</i>
64-4	1.5-2	dfrA1, aadA1, NDM, aadA2, sul1, CTXM-2	<i>Klebsiella pneumoniae</i>
64-5	1.5-2	dfrA1	<i>Klebsiella pneumoniae</i>
68-1	-		<i>Klebsiella pneumoniae</i>
68-2	-		<i>Escherichia</i> sp.
68-3	-		<i>Escherichia</i> sp.
68-4	-		<i>Escherichia</i> sp.
68-5	-		<i>Escherichia</i> sp.
69-1	1.5-2	dfrA15, aadA1, dfrA1, blaVIM, OXA-10, aacA4, NDM, blaSIM, aacA7	<i>Escherichia</i> sp.
69-2	1.5-2	dfrA15	<i>Raoultella planticola</i>
69-3	1.5-2	dfrA15, aadA1	<i>Raoultella planticola</i>
69-4	1.5-2	dfrA15, dfrA1, aadA1, aadA2, NDM, blaVIM-1, aacA7, sul1	<i>Raoultella planticola</i> or <i>Raoultella ornithinolytica</i>
69-5	1.5-2	dfrA15	<i>Raoultella planticola</i>
71-1	-		<i>Raoultella planticola</i>
71-2	1.2-1.5(weak); 2	dfrA17, OXA-1, NDM-5, CTXM-15, CTXM-3	<i>Escherichia</i> sp.
71-3	-		<i>Escherichia</i> sp.
71-4	1.5-2	dfrA17	
71-5	1.5-2	dfrA17	<i>Escherichia</i> sp.
75-1	1.5-2	dfrA17, OXA-1, NDM-5, CTXM-15, AADA5	<i>Escherichia</i> sp.
75-2	1.5-2	dfrA17, OXA-1, NDM-5, CTXM-15, AADA5	<i>Shigella flexneri</i>
75-3	-		<i>Escherichia</i> sp.
75-4	-		<i>Escherichia</i> sp.
75-5	-		<i>Escherichia</i> sp.
77-1	-		<i>Escherichia</i> sp.
77-2	2; 1.5-2	dfrA17, OXA-1, NDM-5, CTXM-15, AADA5	<i>Escherichia</i> sp. or <i>Shigella flexneri</i>
77-3	2	dfrA17, OXA-1, NDM-5, CTXM-3, CTXM-15, AADA5, DHA-1	<i>Escherichia</i> sp. or <i>Shigella flexneri</i>
77-4	2	dfrA17, OXA-1, CTXM-15, CTXM-3, aadA5, NDM-5	<i>Escherichia</i> sp. or <i>Shigella flexneri</i>
77-5	2	dfrA17, OXA-1, NDM-5, CTXM-15, CTXM-3	<i>Escherichia</i> sp. or <i>Shigella flexneri</i>
80-1	3	bad seq	<i>Shigella flexneri</i>
80-2	3	bad seq	<i>Escherichia</i> sp. or <i>Shigella flexneri</i>
80-3	2	bad seq	<i>Escherichia</i> sp. or <i>Shigella flexneri</i>
80-4	2	dfrA17	
80-5	-		<i>Escherichia</i> sp. or <i>Shigella flexneri</i>
82-1	2	dfrA1, aadA1, sul1	<i>Escherichia</i> sp. or <i>Shigella flexneri</i>
82-2	2	dfrA, aadA1, aadA2, sul1, ctxm-2	<i>Klebsiella pneumoniae</i>
82-3	-		<i>Klebsiella pneumoniae</i>
82-4	2	dfrA1	
82-5	2	dfrA1	<i>Klebsiella pneumoniae</i>
83-1	-		<i>Klebsiella pneumoniae</i>
83-2	-		<i>Shigella flexneri</i>
83-3	-		<i>Escherichia fergusonii</i> or <i>Shigella flexneri</i>
83-4	-		<i>Escherichia fergusonii</i> or <i>Shigella flexneri</i>
83-5	-		<i>Shigella flexneri</i>
84-1	2-3	-	<i>Escherichia fergusonii</i> or <i>Shigella flexneri</i>
84-2	2-3; 2	-	<i>Escherichia fergusonii</i> or <i>Shigella flexneri</i>
84-3	-		<i>Escherichia fergusonii</i> or <i>Shigella flexneri</i>
86-1	1.5	dfrB3, aadA6, sul1, aacA6, blaOXA-2, aacA7, aacA8, bla VIM-4	<i>Escherichia fergusonii</i> or <i>Shigella flexneri</i>
86-2	1.5	dfrB3	
86-3	1.5	dfrB3, aadA6, aacA8, OXA-2, aacA7	<i>Pseudomonas aeruginosa</i>
86-4	1.5	dfrB3, blaVIM-4, aacA7, aadA6, blaNDM1, sul1	<i>Pseudomonas aeruginosa</i>
86-5	1.5	dfrB3	<i>Escherichia fergusonii</i>
90-1	1	mcr-1, NDM, CMY	<i>Pseudomonas aeruginosa</i>
90-2	1	mcr-1, NDM	<i>Escherichia fergusonii</i>

90-3	1	-	Escherichia sp.
90-4	1	-	Escherichia fergusonii
90-5	1	-	Escherichia sp.
92-1	-		Escherichia sp.
92-2	-		
92-3	-		
92-4	1	dfrA17	
92-5	1	dfrA17	Escherichia marmotae or escherichia coli or salmonella sp
93-1	-		Escherichia marmotae or fergusonii
93-2	1	dfrVII	
93-3	-		
93-4	-		Escherichia fergusonii or Shigella flexneri
93-5	-		Shigella sonnei or brenneria alni or escherichia fergusonii
94-1	-		Escherichia fergusonii or Shigella flexneri
94-2	-		Comamonas sp.
94-3	-		Comamonas sp.
94-4	-		Comamonas sp.
94-5	-		Comamonas sp.
97-1	1	dfrA17	Comamonas sp.
97-2	1	dfrA17	
97-3	1	dfrA17	Escherichia fergusonii or Shigella flexneri
97-4	1	dfrA17	Shigella sonnei or escherichia fergusonii
97-5	1	dfrA17	Escherichia fergusonii or Escherichia coli or Shigella flexneri
100-1	-		Escherichia sp.
100-2	-		Escherichia fergusonii or Shigella flexneri
100-3	-		Escherichia fergusonii or Shigella flexneri
100-4	-		Shigella flexneri
100-5	-		Escherichia fergusonii or Shigella flexneri
101-1	1	mcr, NDM, IMP	Escherichia fergusonii or Shigella flexneri
101-2	1	-	Escherichia fergusonii or escherichia coli or Shigella flexneri
101-3	1	-	Escherichia fergusonii or shigella flexneri
101-4	1	-	Escherichia sp.
101-5	1	-	Escherichia sp.
102-1	1	dfrVII	Escherichia sp.
102-2	1	dfrVII	escherichia fergusonii or shigella flexneri
102-3	1	dfrVII	Escherichia sp.
102-4	1	dfrVII	Escherichia fergusonii or Shigella flexneri
108-1	-		Escherichia sp.
108-2	-		Escherichia sp. or shigella sp.
108-3	-		Escherichia fergusonii or Shigella flexneri
108-4	-		Escherichia fergusonii or Shigella flexneri
108-5	-		Escherichia sp.
112-1	1 (1.2)	-	Escherichia sp.
112-2	1 (1.2)	-	Escherichia fergusonii or Shigella flexneri
112-3	1 (1.2)	-	Escherichia fergusonii or Shigella flexneri
112-4	1 (1.2)	-	Escherichia fergusonii or Shigella flexneri
112-5	1 (1.2)	-	Escherichia fergusonii or Shigella flexneri
113-1	-		Escherichia fergusonii or Shigella flexneri
113-2	-		Escherichia fergusonii or Shigella flexneri
113-3	-		Escherichia fergusonii or Shigella flexneri
113-4	-		Escherichia fergusonii or Shigella flexneri
113-5	-		Klebsiella aerogenes or Enterobacter aerogenes

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557 **Table S4: ARG and species associated with GENT-resistant colonies**

SAMPLE#	Class I gene cassette	ARG found in gene cassette	Species
19-1	1	aadA5, NDM-5, OXA-1, CTXM-15	Escherichia fergusonii or shigella flexneri
19-2	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
20-1	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
20-2	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
20-3	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
20-4	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
20-5	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
38-1	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
38-2	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
38-3	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
38-4	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
38-5	1	aadA5, OXA-1, CTXM-15, CTXM-3, NDM-9, NDM-5	Escherichia fergusonii or shigella flexneri
47-1	-		escherichia fergusonii
47-2	-		escherichia fergusonii
47-3	-		escherichia fergusonii
47-4	-		escherichia fergusonii
47-5	-		escherichia fergusonii
57-1	-		escherichia fergusonii
57-2	-		escherichia fergusonii
57-3	-		escherichia fergusonii
57-4	-		escherichia fergusonii
57-5	-		escherichia fergusonii
68-1	-		Escherichia coli
68-2	-		Escherichia coli
68-3	-		Escherichia coli
68-4	-		Escherichia fergusonii or shigella flexneri
68-5	-		Escherichia sp. or Shigella sonnei or shigella flexneri
70-1	1	aadA5	Shigella flexneri
70-2	1	aadA5	Shigella flexneri
70-4	1	aadA5	Shigella flexneri
70-5	1	aadA5	Shigella flexneri
73-1	1	NDM, IMP, MCR, CMY	Escherichia fergusonii or shigella flexneri
73-2	1	NDM, IMP	Escherichia marmotae
73-3	1	NDM, IMP, CMY	Escherichia fergusonii or shigella flexneri or Escherichia marmotae
73-4	1	AADA2, NDM, CMY, IMP	Escherichia marmotae
73-5	1	NDM, IMP, CMY	Escherichia fergusonii or shigella flexneri or Escherichia marmotae
74-1	-		Shigella sonnei or Escherichia fergusonii or shigella flexneri
74-2	-		Shigella sonnei or Escherichia fergusonii or shigella flexneri
74-3	-		Shigella sonnei or Escherichia fergusonii or shigella flexneri
74-4	-		Shigella sonnei or Escherichia fergusonii or shigella flexneri
74-5	-		Escherichia fergusonii or shigella flexneri
75-1	1	aadB, aadA1	Escherichia fergusonii or shigella flexneri or shigella sonnei or brenneria alni
75-2	1	aadB, aadA1	Shigella flexneri
75-3	1	aadB, aadA1	shigella flexneri
75-4	1	aadB, aadA1	Escherichia fergusonii or shigella flexneri
75-5	1	aadB, aadA1	Escherichia fergusonii or shigella flexneri
86-1	-		Escherichia fergusonii or shigella flexneri
86-2	-		Escherichia fergusonii or shigella flexneri
86-3	-		Escherichia fergusonii or shigella flexneri
86-4	-		Escherichia fergusonii or shigella flexneri
86-5	-		Escherichia fergusonii or shigella flexneri
106-1	1	aadA5	Fusobacterium varium
106-2	1	aadA5	
106-3	1	aadA5	Escherichia fergusonii or shigella flexneri or shigella dysenteriae
113-1	-		
113-2	-		
113-3	-		
113-4	-		
113-5	-		

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560 **Table S5: ARG and species associated with COL-resistant colonies**

SAMPLE#	mcr-1	mcr-2	Species
16-1	-	-	<i>Escherichia fergusonii</i>
17-1	-	-	<i>Enterobacter</i> sp.
18-1	-	-	<i>Escherichia</i> sp.
18-2	-	-	<i>Escherichia</i> sp.
26-1	-	-	<i>Klebsiella pneumoniae</i>
26-2	-	-	<i>Klebsiella pneumoniae</i>
26-3	-	-	<i>Klebsiella pneumoniae</i>
26-4	-	-	<i>Klebsiella pneumoniae</i>
26-5	-	-	<i>Klebsiella pneumoniae</i>
40-1	-	-	<i>Hafnia paralvei</i>
40-2	-	-	<i>Hafnia paralvei</i>
40-3	-	-	<i>Hafnia paralvei</i>
40-4	-	-	<i>Hafnia paralvei</i>
40-5	-	-	<i>Hafnia paralvei</i>
42-1	-	-	<i>Escherichia coli</i> or <i>fergusonii</i>
42-2	-	-	<i>Escherichia coli</i> or <i>fergusonii</i>
42-3	-	-	<i>Escherichia coli</i>
42-4	-	-	<i>Escherichia fergusonii</i> or <i>coli</i>
42-5	-	-	<i>Escherichia coli</i>
47-1	-	-	<i>Klebsiella pneumoniae</i>
47-2	-	-	<i>Klebsiella pneumoniae</i>
47-3	-	-	<i>Klebsiella pneumoniae</i>
47-4	-	-	
47-5	-	-	<i>Klebsiella pneumoniae</i>
100-1	-	-	<i>Morganella morganii</i>
100-2	-	-	<i>Morganella morganii</i>
100-3	-	-	<i>Morganella morganii</i>
100-4	-	-	<i>Morganella morganii</i>
100-5	-	-	<i>Pseudomonas aeruginosa</i>
105-1	-	-	<i>Obesumbacterium proteus</i> strain
105-2	-	-	<i>Obesumbacterium proteus</i> strain
105-3	-	-	<i>Obesumbacterium proteus</i> strain
105-4	-	-	<i>Obesumbacterium proteus</i> strain
105-5	-	-	<i>Obesumbacterium proteus</i> strain
113-1	-	-	<i>Morganella morganii</i>
113-2	-	-	<i>Morganella morganii</i>
113-3	-	-	<i>Morganella morganii</i>
113-4	-	-	<i>Morganella morganii</i>
113-5	-	-	<i>Morganella morganii</i>

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