Table 2: Number of (multi)resistant Y. enterocolitica strains and resistance profiles

<table>
<thead>
<tr>
<th></th>
<th>Slaughterhouse 1 (medium-size farms)</th>
<th>Slaughterhouse 2 (large farms)</th>
<th>Slaughterhouse 3 (medium-size farms)</th>
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</thead>
<tbody>
<tr>
<td>Tested strains</td>
<td>15</td>
<td>26</td>
<td>8</td>
</tr>
<tr>
<td>Resistant strains</td>
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<td>26</td>
<td>8</td>
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<tr>
<td>Multiresistant strains</td>
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<tr>
<td>Dominant resistance patterns</td>
<td>AMP-KF (n=10)</td>
<td>AMP-KF-NA-C-ST (n=11)</td>
<td>AMP-KF</td>
</tr>
<tr>
<td>Multiresistance patterns</td>
<td>AMP-KF-TET, AMP-KF-ET-C, AMP-KF-IA</td>
<td>AMP-KF-TET-CA-C-ST, AMP-KF-NA-C-ST, TET-NA-C-ST, AMP-KF-NA-C-ST</td>
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</table>

Results

Of the 174 isolates analysed in this study, 68.4% (n=119) were resistant to three or more classes of antibiotics and therefore categorised as MDR. The most frequent MDR combinations detected were SXT-TE-STR (n=15), AM-SXT-TE-S (n=10) and AM-SXT-STR-K (n=8) (Table 1). E. coli strains resistant to four and five antibiotics were the most prevalent (21.3% and 19.0%, respectively). Of 141 isolates with a nalidixic acid resistant phenotype, 96.6% (n=139) possessed at least one nucleotide mutation in the QRDR of gyrA. Thereof, 49.6% (n=70) showed a single amino acid substitution at codon Ser83, namely Ser83 to Leu (n=67), or Asp87 to Tyr (n=2), or Asp87 to Gly (n=1). Further, 48.9% (n=69) possessed double substitutions at Ser83 to Leu and Asp87 to Asn (n=68) or Tyr (n=1). Two isolates (isolates no. 65 and 106, respectively) tested negative for mutations in the QRDR of gyrA (Table 1).

A total of 38 strains possessed one or more PMQR genes, representing 21.8% of the 174 analysed strains (Table 1). Among the 19.5% (n=34) of the isolates with one PMQR gene, twenty (11.5%) possessed qnrA, thirteen (7.5%) qnrB, thirteen (7.5%) qnrS and one isolate (0.6%) possessed qepA (n=2), respectively (Table 1). Four isolates (2.3%) possessed a combination of qnrB and qnrS genes.

No isolates tested positive for qnrA, qnrC, qnrD or qepA. The occurrence of PMQR positive isolates was remarkably higher in strains exhibiting intermediate resistance to nalidixic acid (90.9%/n=30), than in nalidixic acid resistant strains (5.7%/n=8). Moreover, all qnrB/qnrB combinations were detected in intermediately resistant isolates (Table 1). Isolates possessing PMQR were found in 11 (22.9%) of the dust samples (28.6%) of the wipe samples, and 11 (15.7%) of the slurry samples. Of the 23 farms with reported use of fluoroquinolones, 12 (52.2%) yielded environmental samples containing PMQR genes. Thereof, the majority (7 farms/58.3%) were farrowing and rearing farms, three (25%) were fattening farms and two (16.7%) were mating and gestation farms (Table 1).

By contrast, of the 32 farms without a history of fluoroquinolone use during the study period, nine (28.1%) tested positive for E. coli harbouring PMQR genes. Thereof, five (56.6%) were fattening farms, four (12.5%) were mating and gestation farms, and none (0%) were farrowing and rearing farms. The majority of the isolates were assigned to phylogenetic groups A (48.3%/n=84) and group B1 (33.0%/n=58), followed by group D (10.2%/n=18), group B2 (4.6%/n=8), group B1 (4.6%/n=8), and group E (2.4%/n=4). Resistance to all other tested antibiotics was detected for at least one isolate, except to nitrofurantoin.

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PROCEEDINGS

(n=20), ST453 (n=10), ST88 (n=9), ST898 (n=8), ST93 (n=6), ST2197 (n=6), ST737 (n=5), and ST2509 (n=5).

Discussion and Conclusion

Quinolone non-susceptible E. coli are widespread in the environment of Swiss pig farms. In particular, isolates showing intermediate resistance to nalidixic acid frequently possess transmissible PMQR genes. This is worrisome, since the presence of qnr genes may increase the ability of bacteria to acquire point mutations in the gyrase and topoisomerase IV genes, resulting in high level resistance to (fluoro)quinolones. Furthermore, plasmids harbouring qnr genes may contribute to the horizontal spread of antibiotic resistance in livestock and in the environment. In pig farms which are part of sow pool systems, inter-farm measures that aim to reduce the risk of spreading resistant bacteria and resistance genes from one stage of production to the next need to be assessed and promoted. Our data further show that farm environments contain commensal MDR E. coli as well as E. coli with zoonotic potential. In particular, we demonstrate for the first time the presence of EPEC O80:H2 in an environmental sample from a pig farm.

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Temporal dynamics of enterobacteriaceae antimicrobial resistance at the human-pig interface in Peri-Urban Kampala

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Antimicrobial resistance (AMR) leads to increased mortality, morbidity and health expenditure. Globally, there is an increasing concern over AMR which is claiming 700,000 people every year and this is projected to 10,000,000 people by 2050. The recently documented AMR rates paint an increasingly alarming scenario for Uganda, and if strategic measures are not taken to halt and reverse the trends, treatment options for infectious diseases will always become more limited to many financially constrained Ugandans.

A longitudinal study of linked human-pig pairs in Kampala and Wakiso Peri Urban setting was carried out to determine antimicrobial sensitivity profile of Enterobacteriaceae at the human-pig interface within a six months period. Purposive sampling was done to select pig farmers to be included in the study based on type of pigs kept. I selected farmers who had breeding sows or boars that were to be kept for more than one year. Here, we visited 35 pairs (human and pigs) for every two months, and for six months, we collected approximately 220 fecal samples. In addition, metadata i.e. household demographics Nutrition, Pig management, disease occurrences and antibiotic use by using a mobile deployed questionnaire was collected.

I found a 72% mono resistance prevalence for all isolates recovered, predominated by resistance to trimethoprim/sulfur, tetracycline and amoxicillin. 45.1% of the isolates were resistant to more than one antibiotic (multidrug resistant), dominated by E.coli (60%) and Klebsiella (36%). We observe evidence of AMR phenotype exchange/sharing in one among six pig farmers in Kampala, which reaffirms the occupational risk they represent to the general population. These findings taken together indicate that a highly dynamics flux in resistance prevalence generally increased over the six months period at the human-pig interface. In the short term, further investigation using granular molecular methods are needed to understand the observed dynamics. In the medium and long term, we need to understand behavioral drivers of antibiotic usage in order to limit the irrational use that is driving the observed resistance profiles. From a public health point of view, farmers are likely to be the source of animal generated resistance for the general population, therefore, occupational health experts need to focus on identifying critical control for transmissions arising from this group.