Molecular types, virulence profiles and antimicrobial resistance of *Escherichia coli* causing bovine mastitis

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**ABSTRACT**

**Background** *Escherichia coli* is an important aetiological agent of bovine mastitis worldwide.

**Methods** In this study, 82 *E. coli* from bovine mastitis milk samples from 49 farms were analysed for their genetic diversity using phylogenetic grouping and multilocus sequence typing. The isolates were examined by PCR for a selection of virulence factors (VFs). Antimicrobial susceptibility profiles were assessed using the disk diffusion method.

**Results** The most prevalent phylogroups were group B1 (41.5 per cent of the isolates) and group A (30.5 per cent). A variety of 35 different sequence types (STs) were identified, including ST1125 (11 per cent), ST58 (9.8 per cent), ST10 (8.5 per cent) and ST88 (7.3 per cent). Aggregate VF scores (the number of unique VFs detected for each isolate) ranged from 1 to 7 for 8 per cent of the isolates and were at least 4 for 12.2 per cent. For 24.4 per cent of the isolates, the score was 0. The three most frequent VFs were *traT*, *fyuA* and *iutA*. The majority (72 per cent) of the isolates harboured *traT*. The majority (68.3 per cent) of the isolates were fully susceptible to all antimicrobials tested, with 22 per cent resistant to ampicillin and 14.6 per cent to tetracycline. Resistance rates were low for gentamicin (3.7 per cent), amoxicillin/clavulanic acid (2.4 per cent) and cefotirax (1.2 per cent), respectively.

**Conclusion** Among the study’s sample population, *E. coli* strains were genotypically diverse, even in cows from the same farm, although some STs occurred more frequently than others. Susceptibility to clinically relevant compounds remained high.

**INTRODUCTION**

*Escherichia coli* occurs in the digestive tract of human beings and animals as a non-pathogenic, commensal part of the normal gut flora; however, some *E. coli* types may cause gastrointestinal disease and a range of extraintestinal infections.

Many pathogenic *E. coli* are distinguished from commensal strains due to specific virulence features that increase their ability to cause disease in otherwise healthy individuals. Among the pathogenic features, certain virulence factors (VFs) are characteristic of intestinal pathogenic *E. coli* (IPEC), which comprise well-described and important categories such as enteropathogenic *E. coli* (EPEC), Shiga toxin-producing *E. coli* (STEC), and its subgroup enterohaemorrhagic *E. coli* (EHEC), enteraggregative *E. coli* (EAEC) or enterotoxigenic *E. coli* (ETEC).

Other virulence attributes are associated with extraintestinal pathogenic *E. coli* (ExPEC), which encompass uropathogenic *E. coli*, newborn meningitis *E. coli* and avian pathogenic *E. coli* (APEC), which causes respiratory tract infections and septicaemia in poultry.

In cattle, *E. coli* is an important aetiological agent of mastitis, which is one of the most common and economically significant diseases in the dairy industry worldwide. Bovine mastitis *E. coli*—unlike many other pathogenic *E. coli*—appears to lack consistent genotypes and specific defining virulence profiles, making a differentiation from commensal *E. coli* challenging. Previous studies show that virulence traits typically identified in IPEC or ExPEC are not accountable for invasion and survival of *E. coli* inside mammary epithelial cells in vitro, nor do they appear to contribute to clinical severity of the disease. Bovine mastitis *E. coli* is generally thought to bear the same pathogenic potential as commensal or environmental *E. coli*. Nevertheless, some studies suggest that certain genotypes may be more prevalent among mastitis-associated *E. coli* compared with environmental strains. Therefore, further assessment of the genotypes of *E. coli* causing bovine mastitis is needed to fill current knowledge gaps.

Bovine mastitis is the most frequent reason for use of antimicrobials in dairy cattle. To promote the efficient and appropriate use of antimicrobials in veterinary medicine, the Swiss Veterinary Society (SVS), which is the official representing body of veterinarians, together with the Federal Food Safety and...
Veterinary Office have issued guidelines that provide practical recommendations for the prescription and application of antimicrobials for treating livestock. The recommendations are in accordance with the Swiss law on pharmaceutical and medicinal products and with international Good Clinical Practice standards.13

For mastitis cases requiring treatment, the SVS guidelines recommend gentamicin as first-line antimicrobial agent for intramammary treatment in cases of bovine mastitis caused by E. coli, and fourth-generation cephalosporins as second-line therapy.13 However, third-generation and fourth-generation cephalosporins belong to the highest priority critically important antimicrobials (HPCIA) for the use in human beings, and the emergence and global dissemination of antimicrobial resistance in general, and extended-spectrum β-lactamase (ESBL) producing Enterobacteriaceae in particular, represent a threat to public health.14 ESBL producers have been described infrequently in E. coli isolated from bovine mastitis in Germany, France, Switzerland and the UK.15–18

Further, a study from Germany found a prevalence of 9.5 per cent ESBL-producing E. coli in bulk tank milk.19 Therefore, current data on the antimicrobial susceptibility profiles of bovine mastitis isolates are warranted.

The aims of the present study were to determine the genotypes and the virulence profiles of E. coli strains isolated from bovine mastitis, and to obtain data on their antimicrobial susceptibility profiles.

**MATERIALS AND METHODS**

**Bacterial isolation and species identification**

In this study, a total of 82 non-duplicate E. coli strains were collected from 82 dairy cows with clinical mastitis on 49 different farms during 2017. The farms were customers of the ambulatory veterinary hospital of the University of Zürich that services the canton of Zürich and the surrounding region. The client population consists of approximately 124 cattle farms, whereof 60 per cent are dairy farms. The average dairy herd size in the study region is 20–30 cows, and the most common dairy cow is the Brown Swiss. Clinical mastitis diagnosis was performed during farm calls by the veterinarian in charge according to a standardised procedure which included physical examination of the udder and the estimation of the somatic cells in the milk using the California mastitis test. Milk samples were taken from the affected quarter of each cow and were submitted to the diagnostic laboratory of the Institute for Food Safety and Hygiene in Zürich. Overall, during the study period, a total of 1281 milk samples from the farms in the client population were submitted for culture to the diagnostic laboratory. From samples yielding microbial growth, the range of pathogens identified as the cause of mastitis included staphylococci (16.6 per cent), Staphylococcus aureus (7 per cent), Streptococcus uberis (12.6 per cent), Streptococcus dysgalactiae (3 per cent), E. coli (11.9 per cent) and other pathogens (10 per cent).

Samples were cultured according to standard procedures.20 Briefly, using a sterile loop, the samples were streaked onto sheep blood agar base (Becton Dickinson, Allschwil, Switzerland), supplemented with 5 per cent sheep blood (Oxoid, Pratteln, Switzerland) and incubated at 37°C overnight. The strains were confirmed by colony morphology, Gram stain, and biochemical tests such as the mannitol fermentation test, O-nitrophenyl-beta-D-galactopyranoside (ONPG) test, tests for urease, indole and hydrogen sulfide (H₂S) production, and the lysine decarboxylase test. The strains were stored at –80°C.

**Phylogenetic and multilocus sequence typing**

DNA from E. coli isolates was subjected to quadruplex PCR targeting arpA, chuA, yjaA and an unspecified DNA fragment termed TspE4.C2, as described previously.21 The isolates were classified as belonging to one of the eight phylogenetic groups A, B1, B2, C, D, E, F (E. coli sensu stricto), or Escherichia clade I.

For multilocus sequence typing (MLST), internal fragments of the seven housekeeping genes (adk, fumC, gyrB, ica, mdh, purA and recA) were amplified by PCR as described by Wirth and colleagues.22 Sequencing of the amplification products was performed by Microsynth (Balgach). Sequences were imported into the E. coli MLST database website (https://pubmlst.org/escherichia/) to determine MLST types. Alleles and sequence types (STs) that had not been previously described were designated ‘new ST’, but not assigned numerical designations, since whole-genome sequencing was not performed. Data were visualised using the platform independent JAVA software Phylodust 2.0 and the goeBURST algorithm.23

**Virulence factor determination**

All 82 isolates were screened for genetic markers of virulence associated with ExPEC by conventional PCR using primers and conditions described previously for targeting sfa, papAH, papC, papEF, sfaS, yjaA, hlyA, rtuA, KpsMII, PAI and traT,24 vat and yfcV.25 The aggregate VF score was defined as the number of unique VF detected for each isolate, counting the PAI marker as one.

Strains were further screened by PCR for genetic markers characterising IPEC. Screening for stx1 and stx2 genes in STEC was performed by real-time PCR (LightCycler 2.0 Instrument, Roche Diagnostics Corporation, Indianapolis, Indiana, USA) using the QuantitFast Multiplex PCR Kit (Qiagen, Hombrechtikon, Switzerland) according to the guidelines of the European Union Reference Laboratory (EURL).26 The determination of stx1 subtypes was performed by conventional PCR amplification.27

The presence of subAB encoding subtilase cytotoxin SubAB was tested by conventional PCR using primers described previously.28

Screening for the intimin gene eae in EPEC, and for the heat-labile and heat-stable enterotoxins LT, STp and STh in ETEC, was performed by real-time PCR according
to the guidelines of the EURL.29 30 Screening for 
aggR, which encodes a transcriptional regulator of EAEC, 
was performed by conventional PCR using primers and 
conditions described previously.31

For all PCR assays, DNA from previously characterised 
isolates from the authors’ strain collection was used as 
positive or negative controls for strains harbouring VFs 
associated with ExPEC32 33 and VFs characteristic of 
IPEC.32 34 35

Antimicrobial susceptibility testing

The strains were subjected to antimicrobial susceptibility 
testing (AST) using the standard disk diffusion method 
according to the protocols recommended by the Clinical 
and Laboratory Standards Institute (CLSI),36 which 
is currently the only committee offering interpretive 
criteria for veterinary AST.37 The isolates were classified 
as susceptible, intermediate or resistant using the break-
points listed by the VETO1S of the CLSI.38 Multidrug 
resistance (MDR) was defined as resistance to three or 
more classes of antimicrobials, counting ß-lactams as one.

Susceptibility disks containing ampicillin (AM), amoxi-
cillin/clavulanic acid (AMC), tetracycline (TE) and sulfu-
methoxazole/trimethoprim (SXT) were obtained from 
Becton Dickinson, and disks containing ceftiofur (EFT) 
and gentamicin (CN) were from Thermo Fisher Diagnos-
tics (Pratteln, Switzerland). E. coli ATCC 25922 was used 
as a control during AST.

The antibiotics were chosen on the basis of their recom-

dendations for intramammary application in Switzer-
land and of the panel included in the German national 
antibiotic resistance monitoring of veterinary pathogens 
fro m cattle (GermVet).13 19

To test for the presence of ESBL-producing E. coli, the 
isolates were cultured on Brilliance ESBL agar plates 
(Oxoid, Hampshire, UK) and incubated for 24 hours at 
37°C.

RESULTS

Bacterial isolates and herd data

For this study, a total of 82 E. coli strains originating 
from 82 different animals from 49 different herds were 
obtained. Twelve (24.5 per cent) of the herds were 
sampled more than once, whereby each sample derived 
from a case of mastitis diagnosed by the veterinarian in 
charge. The highest numbers of E. coli mastitis cases per 
farm were eight cases on farm F8 and F16, respectively, 
and seven cases on farm F14 (online supplementary table 
S1). Acute mastitis was diagnosed in 66 cases, subclinical 
in two cases and chronic mastitis in one case, respectively. 
For 13 cases, the type of mastitis was unspecified (online 
supplementary table S1).

Phylogenetic groups, STs and VF distribution

Of the 82 E. coli isolates, 34 (41.5 per cent) belonged to 
phylogenetic group B1, followed by group A (n=25; 30.5 
per cent), C (n=9; 11 per cent) and D (n=8; 9.8 per cent).

The remaining isolates (n=2; 2.4 per cent each) belonged 
to phylogenetic groups B2, E and F (table 1 and online 
supplementary table S1).

MLST identified 35 different STs, the four most 
common represented by ST1125 (n=9; 11 per cent of the 
isolates), ST38 (n=8; 9.8 per cent), ST10 (n=7; 8.5 per 
cent) and ST88 (n=6; 7.3 per cent). Twenty-one (26 per 
cent) of the isolates belonged to STs that occurred only 
one. Five (6 per cent) of the isolates belonged to human 
ExPEC lineages ST69 or ST117 (online supplementary 
table S1). Seven (8.5 per cent) of the isolates belonged 
to STs with a total of five new allelic profiles (online 
supplementary table S1). The new STs were not assigned 
umerical designations by the E. coli MLST database. 
Further, two isolates could not be typed due to failure to 
sequence the purA gene. The goeBURST analysis of the 
strains is shown in figure 1.

On farms with multiple cases of mastitis, various STs 
were observed. On farms F8 and F16 (eight individual 
cases of E. coli mastitis each), a total of seven STs and on 
farm F14 (seven cases of mastitis) four different STs were 
noted (online supplementary table S1).

Among the 82 isolates, the prevalence of individual 
ExPEC associated VFs ranged from 0 per cent (afa and 
yfa, respectively) to 72 per cent (traT).

The frequency of VFs among the phylogenetic groups 
is shown in table 1. Median aggregate VF scores were 
higher for isolates belonging to phylogenetic group B2 
(median VF score 5, range 2–8) and group F (median 
VF score 4, range 4–4); however, these two groups only 
included two isolates each. Median aggregate VF scores 
were lower for isolates belonging to phylogroup D 
(median VF score 0.5, range 0–3).

The distribution of VFs among the most frequently 
occurring STs is summarised in table 2. Median aggregate 
VF scores were highest for isolates belonging to ST58 
(median VF score 3, range 1–5) and ST88 (median 
VF score 3, range 0–5), and low for isolates belonging 
to ST1125 (median VF score 2, range 2–2) and ST10 
(median VF score 1, range 0–1). For all other STs, the 
median VF score was 1, with a range of 0–8 (table 2).

Among these, one isolate with a new ST scored a VF 
factor of 8 (online supplementary table S1). The diversity 
of VF scores among all the isolates analysed in this study 
is illustrated in figure 1.

IPEC-associated VFs stx1a and subAB were detected in 
two (2.4 per cent) and one (1.2 per cent) of the isolates, 
respectively (table 1). None of strains tested positive for 
aggR, afa, eae, LT, yfa, STh, STp or stx2.

Antimicrobial susceptibility testing

The prevalence of resistant, intermediate and suscept-
ible strains among the bovine mastitis E. coli isolates 
is summarised in figure 2. Overall, the majority (n=56; 
68.3 per cent) of the isolates were fully susceptible to all 
antimicrobials tested in this study (online supplementary 
table S1). The highest rate of resistance was observed 
for AM (n=18; 22 per cent), followed by TE (n=12; 14.6 
per cent), SXT (n=8; 9.8 per cent) and CN (n=3; 3.7 per
Table 1  Distribution of virulence factors among the phylogenetic groups of 82 Escherichia coli causing bovine mastitis

<table>
<thead>
<tr>
<th>Gene or marker*</th>
<th>Prevalence by phylogenetic group (n, %)</th>
<th>A (n=25)</th>
<th>B1 (n=34)</th>
<th>B2 (n=2)</th>
<th>C (n=9)</th>
<th>D (n=8)</th>
<th>E (n=2)</th>
<th>F (n=2)</th>
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</thead>
<tbody>
<tr>
<td>ExPEC-associated genes</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>papAH</td>
<td>2 (8.0)</td>
<td>2 (5.9)</td>
<td>–</td>
<td>3 (33.3)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>papC</td>
<td>2 (8.0)</td>
<td>2 (5.9)</td>
<td>–</td>
<td>3 (33.3)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>papEF</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>1 (11.1)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>yfcv</td>
<td>–</td>
<td>–</td>
<td>2 (100)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>hlyA</td>
<td>1 (4.0)</td>
<td>12 (35.3)</td>
<td>1 (50)</td>
<td>–</td>
<td>1 (12.5)</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>vat</td>
<td>1 (50)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>2 (100)</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>fyuA</td>
<td>6 (24.0)</td>
<td>8 (23.5)</td>
<td>1 (50)</td>
<td>6 (66.7)</td>
<td>–</td>
<td>–</td>
<td>2 (100)</td>
<td>–</td>
</tr>
<tr>
<td>iutA</td>
<td>3 (12.0)</td>
<td>5 (14.7)</td>
<td>1 (50)</td>
<td>5 (55.6)</td>
<td>1 (12.5)</td>
<td>–</td>
<td>2 (100)</td>
<td>–</td>
</tr>
<tr>
<td>KpsMII</td>
<td>–</td>
<td>–</td>
<td>1 (50)</td>
<td>–</td>
<td>1 (12.5)</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td>PAI</td>
<td>–</td>
<td>–</td>
<td>1 (50)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>traT</td>
<td>14 (56.0)</td>
<td>27 (79.4)</td>
<td>2 (100)</td>
<td>8 (88.9)</td>
<td>4 (50)</td>
<td>2 (100)</td>
<td>2 (100)</td>
<td>–</td>
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<tr>
<td>Virulence factor score (median, range)</td>
<td>1, 0–4</td>
<td>2, 0–5</td>
<td>5, 2–8</td>
<td>3, 0–6</td>
<td>0.5, 0–3</td>
<td>1, 1–1</td>
<td>4, 4–4</td>
<td>–</td>
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<tr>
<td>IPEC-associated genes</td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>stx1a</td>
<td>2 (8.0)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>subAB</td>
<td>–</td>
<td>1 (2.9)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

*aggR, afa, eae, LT, sfa, STh, STp and stx2 genes were not identified in any of the isolates.
–, not detected; ExPEC, extraintestinal pathogenic E. coli; fyuA, ferric yersiniabactin uptake protein; hlyA, haemolysin; IPEC, intestinal pathogenic E. coli; iutA, aerobactin siderophore receptor; KpsMII, group 2 polysaccharide capsule; PAI, right-hand terminus of pathogenicity island; papAH, pyelonephritis-associated major pilin protein; papC, outer membrane usher protein; papEF, fimbrial protein subunit; stx1a, Shiga toxin subunit; subAB, subtilase cytotoxin; traT, lipoprotein involved in serum resistance; vat, vacuolating autotransporter toxin; yfcv, major subunit of a chaperone-usher fimbria.

cent). Resistance rates were low for AMC (n=2; 2.4 per cent) and EFT (n=1; 1.2 per cent), respectively. Notably, for EFT, seven strains were categorised intermediate resistant (figure 2). Eight strains (9.8 per cent) were resistant to three or more classes of antibiotics (MDR). The MDR phenotype AM/TE/SXT represented the most common pattern (six isolates), followed by AM/AMC/CN/TE and AM/CN/TE/SXT (one isolate each, respectively).

The prevalence of antimicrobial resistance was high among isolates belonging to ST58 and ST88 and low among ST10 and ST1125 (table 3). Among the remaining STs, antimicrobial resistance was found predominantly among ST117 and ST167, respectively (online supplementary table S1).

None of the E. coli isolates yielded growth on ESBL plates.

**DISCUSSION**

Bovine mastitis caused by E. coli is generally considered to include typically commensal strains of intestinal or environmental origin. Commensal strains have been shown by phylogenetic analyses to position within phylogenetic groups A, B1 or C, while virulent extraintestinal E. coli strains belong mainly to group B2, and to a lesser extent to groups D, E or F.

In line with previous reports, the isolates from the present study were mainly of phylogenetic groups A and B1, with the exception of isolates belonging to phylogroup C, which were not identified in earlier studies that restricted classifications to four main phylogenetic groups A, B1, B2 and D. Phylogroup C is closely related to group B1, but before its recognition as a distinct phylogroup its members were classified within group A. Consequently, the prevalence of phylogroup A mastitis strains may have been overestimated in the past. Furthermore, mastitis isolates belonging to phylogroups E and F were detected in the current study. While phylogroup F comprises strains that were formerly classified group D, phylogroup E includes a small number of E. coli, to which EHEC O157:H7 and its ancestor O55:H7 belong. Similar to previously described mastitis strains belonging to phylogroup F, both isolates in the current study lacked virulence traits that characterise EHEC strains, and their significance among mastitis isolates, although remarkable, remains unclear.

In agreement with previous studies that document the absence of specific genotypes to characterise mastitis E. coli, a wide variety of STs were observed, indicating high
heterogeneity. Even most isolates from multiple cows on the same farms displayed diverse STs, with a maximum of two isolates from any one farm belonging to the same ST. Nevertheless, _E. coli_ ST10, ST58 and ST1125, which were among the most common STs from this collection of isolates, were also frequent among mastitis strains isolated previously in Israel. _E. coli_ ST1125 has also been described among mastitis strains from cattle in Germany and Ireland. Taken together, these findings indicate that notwithstanding the high genetic variability, certain STs may predominate among bovine mastitis strains. _E. coli_ ST10, which occurs frequently among livestock, food and healthy human beings, is significantly more prevalent among mastitis isolates compared with environmental isolates. ST58 and ST88, although also isolated globally from a wide variety of sources, may cause disease in human beings, including urinary tract infection and sepsis. Several STs less frequently identified in this study have also been described among human clinical isolates, diseased animals and livestock, and represent typical ExPEC. For instance, _E. coli_ ST69, isolated from three mastitis cases in this study, is accountable for community-acquired and healthcare-associated urinary tract infections worldwide, and _E. coli_ ST117, detected in two cases, has been identified among APEC strains causing colibacillosis in broilers. Nevertheless, an association of these STs with severity of mastitis was not investigated, which may be considered a limitation of this study. Interestingly, _E. coli_ ST69 was recently identified in faecal samples of dairy cows in Washington state in USA, and in raw milk cheese in Egypt, suggesting that this pandemic human disease-associated ST may be circulating in dairy cattle worldwide.

Although the pathogenesis mechanisms of many _E. coli_ genotypes are well described for other epithelial systems, VFs enabling adherence and survival within the bovine mammary gland remain, to a large extent, undefined. In the present study, _traT_ was the only VF to characterise the majority (72 per cent) of the strains. This plasmid-located determinant encodes an outer membrane protein thought to block the membrane attack complex present in the serum of the host. Although serum resistance has repeatedly been reported in _E. coli_ mastitis isolates, it is currently considered to be an unspecific feature of mastitis isolates. Therefore, although the _traT_ gene is prevalent among human, avian and porcine ExPEC, and has also been described in mastitis _E. coli_ in previous studies, the significance of _traT_ among mastitis _E. coli_ remains unclear. In addition to _traT_, only two other VFs, _fyuA_ and _iutA_, were found to be prevalent among the isolates from this study. Both genes encode ferric acquisition proteins that allow bacteria to grow in environments with limited concentrations of free iron, such as in tissues and fluids of the host. The _fyuA_ gene encodes a ferric yersiniabactin uptake protein and is strongly associated with uropathogenicity in human beings. It has been suggested that the presence of _fyuA_ is not essential for survival of _E. coli_ in mammalian guts, but that its presence may contribute to the ability to utilise iron from lactoferrin, one of the main iron sources available to bacteria in milk. Similarly, _iutA_, encoding for an aerobactin receptor, is frequently associated with ExPEC but not, so far, with mastitis strains. In this study, a limited number of VF genes were analysed. Despite this constraint, the wide variation of aggregate VF scores among the phylogenetically diverse strains in this study lends support to previous data that there exists no distinct bovine mastitis _E. coli_ pathotype.

The prevalence of IPEC-associated virulence genes was low among the isolates, which is remarkable because cattle are considered a major reservoir for EPEC, STEC and EHEC. Moreover, a recent study evaluating the global prevalence of STEC in bovine mastitis cases estimated that in Europe, STEC occurs in 0.5–13.7 per cent of mastitic milk, and suggested that the prevalence of STEC in mastitis may be underestimated. Only two (2.4 per cent) of the isolates in the present study, both belonging to phylogenetic group A and ST730, were _stx1_ and _stx2_-positive, and they did not encode the intimin gene _eae_. Interestingly, the occurrence of _subAB_ in an isolate that did not contain _stx1_ or _stx2_ was observed. This is one of very few reports of non-STECC harbouring _subAB_. Overall, these data show that susceptibility to antimicrobials remains high among the study’s sample population of mastitis _E. coli_ in Switzerland. Utmost caution should be applied when comparing AST results...
Table 2  Distribution of virulence factors among four main sequence types of 82 Escherichia coli causing bovine mastitis

<table>
<thead>
<tr>
<th>Gene or marker*</th>
<th>Prevalence by sequence type (n, %)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>ST10 (n=7)</td>
</tr>
<tr>
<td>ExPEC-associated genes</td>
<td></td>
</tr>
<tr>
<td>papAH</td>
<td>–</td>
</tr>
<tr>
<td>papC</td>
<td>–</td>
</tr>
<tr>
<td>papEF</td>
<td>–</td>
</tr>
<tr>
<td>yfcv</td>
<td>–</td>
</tr>
<tr>
<td>hlyA</td>
<td>–</td>
</tr>
<tr>
<td>vat</td>
<td>–</td>
</tr>
<tr>
<td>fyvA</td>
<td>3 (42.9)</td>
</tr>
<tr>
<td>iutA</td>
<td>–</td>
</tr>
<tr>
<td>KpsMII</td>
<td>–</td>
</tr>
<tr>
<td>PAI</td>
<td>–</td>
</tr>
<tr>
<td>traT</td>
<td>2 (29.6)</td>
</tr>
<tr>
<td>Virulence factor score (median, range)</td>
<td>1, 0–1</td>
</tr>
<tr>
<td>IPEC-associated genes</td>
<td></td>
</tr>
<tr>
<td>stx1a</td>
<td>–</td>
</tr>
<tr>
<td>subAB</td>
<td>–</td>
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</tbody>
</table>

*aggR, afa, eae, LT, sfa, STh, STp and stx2 genes were not identified in any of the isolates.
–, not detected; ExPEC, extraintestinal pathogenic E. coli; fyvA, ferric yersiniabactin uptake protein; hlyA, haemolysin; IPEC, intestinal pathogenic E. coli; iutA, aerobactin siderophore receptor; KpsMII, group two polysaccharide capsule; PAI, right-hand terminus of pathogenicity island; papAH, pyelonephritis-associated major pilin protein; papC, outer membrane usher protein; papEF, fimbrial protein subunit; stx1a, Shiga toxin subunit; subAB, subtilase cytotoxin; traT, lipoprotein involved in serum resistance; vat, vacuolating autotransporter toxin; yfcv, major subunit of a chaperone-usher fimbria.

obtained across different strain collections, countries and settings. A comparison with earlier data from Switzerland obtained using identical methodologies and interpretive criteria showed no major shift in antibiotic resistance. Moreover, using identical CLSI interpretation criteria, resistance data from this study are similar to those from the German antimicrobial resistance monitoring programme GermVet, with the exception of EFT.

Figure 2  Antimicrobial susceptibility percentages among 82 Escherichia coli isolated from bovine mastitis milk in Switzerland during 2017. AM, ampicillin; AMC, amoxicillin/clavulanic acid; CN, gentamicin; EFT, ceftiofur; I, intermediate; R, resistant; S, susceptible; SXT, sulfamethoxazole/trimethoprim; TE, tetracycline.
Table 3  Distribution of antimicrobial resistance among four main sequence types of 82 Escherichia coli causing bovine mastitis

<table>
<thead>
<tr>
<th>Resistance*</th>
<th>ST10 (n=7)</th>
<th>ST58 (n=8)</th>
<th>ST88 (n=6)</th>
<th>ST1125 (n=9)</th>
<th>Other (n=52)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AM</td>
<td>–</td>
<td>4 (50.0)</td>
<td>3 (50.0)</td>
<td>1 (11.1)</td>
<td>10 (19.2)</td>
</tr>
<tr>
<td>AMC</td>
<td>–</td>
<td>1 (12.5)</td>
<td>1 (16.7)</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>EFT</td>
<td>1 (14.3)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>CN</td>
<td>–</td>
<td>2 (25.0)</td>
<td>1 (16.7)</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>TE</td>
<td>–</td>
<td>4 (50.0)</td>
<td>1 (16.7)</td>
<td>–</td>
<td>7 (13.5)</td>
</tr>
<tr>
<td>SXT</td>
<td>–</td>
<td>3 (37.5)</td>
<td>1 (16.7)</td>
<td>–</td>
<td>4 (7.7)</td>
</tr>
<tr>
<td>MDR</td>
<td>–</td>
<td>3 (37.5)</td>
<td>1 (16.7)</td>
<td>–</td>
<td>4 (7.7)</td>
</tr>
</tbody>
</table>

*Antimicrobial susceptibility was determined using the disk diffusion method according to the Clinical and Laboratory Standards Institute guidelines and breakpoints.36

−, no resistance detected; AM, ampicillin; AMC, amoxicillin/clavulanic acid; CN, gentamicin; EFT, ceftiofur; MDR, multidrug resistant (resistant to three or more classes of antimicrobials); SXT, sulfamethoxazole/trimethoprim; TE, tetracycline.

Regarding this antimicrobial, a lower rate of resistance compared with that reported by GermVet for the year 2016 was identified (1.2 per cent v 7.6 per cent). Notably, in the study presented here, seven (8.5 per cent) of the isolates were categorised intermediate resistant. This may be indicative of a shift towards a resistant phenotype and warrants future observation. An increase of resistance to EFT from 0.4 per cent in 2006 to 2.4 per cent in 2016 has been reported for mastitis isolates in France.69 By contrast, resistance rates among mastitis isolates are reportedly low in other countries, for example, Denmark,70 with resistance to AM reported in only 11.3 per cent and resistance in other countries, for example, Denmark,70 with resistance to AM reported in only 11.3 per cent and resistance to EFT and CN in 0 per cent. Nevertheless, the results presented here provide a means by which to monitor trends in antimicrobial susceptibility and to identify emerging resistance. To this end, quantitative data, such as the zone diameter measures provided in online supplementary table S1, could be helpful.

ConclusioNS

This work represents a study exploring the phenotypic and genotypic traits of E. coli involved in mastitis in Swiss dairy cows. The results highlight the clonal diversity of the isolates and suggest that certain STs such as ST58, ST88 and ST1125 may be more successful than others at colonising and infecting the mammary gland. Only a minority of the isolates represented typical ExPEC. Although no distinct virulence gene profile was detected among the isolates, traT was found in the majority of bovine E. coli mastitis cases. Therefore, traT may represent a virulence trait that favours pathogenesis in the bovine udder. Overall, antimicrobial susceptibility was high for β-lactams, CN, TE and SXT. Moreover, no ESBL-producing E. coli were detected.

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