INTRODUCTION

The production of extended-spectrum beta-lactamases (ESBLs) is one of the most significant mechanisms of resistance to oximinocephalosporin antibiotics in *E. coli* (Pitout and Laupland, 2008). Among these enzymes, the CTX-M type ESBLs have emerged worldwide, they have progressively replaced the TEM and SHV families (Bonnet, 2004). To date, 123 *bla*<sub>CTX-M</sub> genes have been reported, the corresponding CTX-M enzymes are clustered in five groups, group 1, 9, and 2 being predominant. The producing organisms are sometimes involved in nosocomial infections but are widely encountered in community settings (Arpin et al., 2009; Woerther et al., 2010). Their rate of dissemination might suggest the occurrence of environmental reservoirs potentially leading to human contamination through water, food consumption or direct contact with animals (Leverstein-Van Hall et al., 2011). There are many descriptions of fecal carriage of such organisms among food-producing animals especially poultry (broilers) and pigs (Costa et al., 2008; Bortolaia et al., 2010; Cortes et al., 2010). The reports concerning livestock cattle are much less abundant (Horton et al., 2011), and there is no published data about the prevalence of CTX-M producing *E. coli* in soils. Nevertheless cultivated soils are frequently fertilized with agricultural or urban organic residues that may contain antibiotic resistant microorganisms (Moodley and Guardabassi, 2009; Reinthaler et al., 2010) and thus might act as environmental reservoirs.

The aim of this study was to develop an integrated approach encompassing soils, livestock, and farm environment in a whole region (Burgundy, France). A systematic large scale study was conducted using a molecular detection approach to detect *bla*<sub>CTX-M</sub> directly from soil DNA extracts. Conventional bacteriological methods were used to isolate ESBL-producing *E. coli* from cattle feces from 182 farms. When positive animals were detected, the corresponding farm environment, i.e., cultivated and pasture soils as well as composted manure were recovered from within two of these farms. The genotypic analysis revealed that environmental and animal strains were clonally related. Our study confirms the occurrence of CTX-M producing *E. coli* in cattle and reports for the first time the occurrence of such strains in cultivated soils. The environmental competence of such strains has to be determined and might explain their long term survival since CTX-M isolates were recovered from a soil that was last amended with manure 1 year before sampling.

**Keywords:** extended-spectrum beta-lactamase, CTX-M, cattle, soil, Burgundy, farm environment

MATERIALS AND METHODS

SOIL SAMPLING

Soils were sampled in the “Réseau de Mesures de la Qualité des Sols” (RMQS = French Soil Quality Monitoring Network) which is a network based on the sampling of soil with a 16 × 16 km systematic grid covering the whole French territory (Arrouays et al., 2002). The RMQS consisted in 2200 monitoring sites, which are located close to the center of each 16 × 16 km cell. Corresponding
land covers were recorded and categorized as: large scale crops, pastures, orchards, vineyards, natural vegetation such as forests or meadows. Each site is geo-positioned with a precision of <0.5 m. Twenty five individual core samples were collected from the top soil (0–30 cm) using a stratified random sampling design within a 20 m × 20 m area. Core samples were bulked to obtain a composite sample for each site. Soil samples were air-dried and sieved to 2 mm before analysis. For this study 120 soil samples corresponding to the Burgundy region (four departments Côte d’Or, Saône et Loire, Yonne, and Nièvre) were analysed.

BOVINE FECES SAMPLING

From April 2009 to June 2009, a total of 271 fecal swabs of cattle were collected from 182 farms located in three departments of the Burgundy region, namely Côte d’Or, Nièvre, and Saône et Loire. Three groups of animals were sampled: (i) healthy adults (218), (ii) enteric diseased calves (35), and healthy adults linked with sick calves (18). Swabs (COPAN, CML, France) were immediately transferred into tubes containing Amies agar gel transport medium. Bacteriological analyses of the fecal swabs were performed within 3 days after sampling. In farm 2 where positive animals had been detected in 2009, feces samples of the whole cow herd were analyzed (90 animals) in July 2010 as described above.

FARM ENVIRONMENT SAMPLING

For three farms (farms 1, 2 and 3), where CTX-M-producing E. coli occurred in animals, we conducted further analysis of several environmental samples during the autumn 2009. These farms were chosen on the basis of the willingness of the farmers to cooperate to the study. In each farm one cropped and one pasture soils were sampled by taking three individual cores in the top soil (using a 7 cm width disinfected auger) that were pooled to obtain a composite sample. Manure samples were collected in the three farms using the same equipment (disinfected auger). All samples were kept moist in single use plastic bags at room temperature. Bacteriological analyses were performed on these samples within 3 days after sampling.

SOIL MICROBIAL COMMUNITY DNA EXTRACTION

Microbial DNA was extracted from bulk RMQS soil samples according to the method described by Ranjard et al. (2003). Briefly, 1.5 g of each soil was mixed with 5 ml of a solution containing 100 mM Tris (pH 8.0), 100 mM EDTA (pH 8.0), 100 mM NaCl, and 2% (w/v) sodium dodecyl sulfate. Two grams of 106 µm diameter glass beads and eight glass beads of 2-mm diameter were added in a bead-beater tube. The samples were then homogenized for 30 s at 1,600 rpm in a mini bead-beater cell disruptor (Mikrodismembrator; S.B. Braun Biotech International) and centrifuged at 7,000 × g for 5 min at 4˚C after 30 min incubation at 70˚C. The collected supernatants were incubated for 10 min on ice after adding 1/10 volume of 3 M potassium acetate (pH 5.5) and centrifuged at 14,000 × g for 5 min. After precipitation with one volume of ice-cold isopropanol, the nucleic acids were washed with 70% ethanol. DNA extracts were purified on polyvinyl polypyrrolidone minicolumns (Bio-Rad, France) by centrifugation at 1,000 × g for 2 min at 10˚C. Residual impurities from DNA extracts were finally removed by using a GeneCleen Turbo kit as recommended by the manufacturer (Q Biogene®, Illkirch, France). DNAs were quantified by agarose gel electrophoresis (1% agarose in TBE buffer) using calf thymus DNA dilutions as standards and the ImageQuant software (Applied Biosystems). Five nanograms of DNA were used per PCR reaction.

DEVELOPMENT AND USE OF A REAL-TIME PCR ASSAY FOR blaCTX-M DETECTION FROM SOIL EXTRACTED DNA

Twenty seven blaCTX-M genes sequences were aligned using the ClustalW program. Sequences were chosen to be representative from the five distinct groups of CTX-M enzymes described by Bonnet (2004). Seven sequences from CTX-M-1 group were used (GenBank accession numbers: DQ658221, X92506, EU921825, NC004464, Y10278, NC005327, and AY238472) corresponding to CTX-M-12, CTX-M-1, CTX-M-32, CTX-M-3, CTX-M-15, CTX-M-33, respectively. Four sequences from CTX-M-9 group (GenBank accession numbers: AF174129, EU916273, EU921824, and EU921826) corresponding to CTX-M-9, CTX-M-27, CTX-M-24, and CTX-M-65, respectively. Three sequences from CTX-M-2 group were used (GenBank accession numbers: X92504, EF374097, and AM982521) corresponding to CTX-M-2, CTX-M-56, and CTX-M-77 respectively. Three sequences from CTX-M-25 group were used (GenBank accession numbers: AF518567, DQ023162, and AM982522) corresponding to CTX-M-25, CTX-M-41, and CTX-M-78 respectively. Two sequences from CTX-M-8 group were used (GenBank accession number: AF189721 and AY750914) corresponding to CTX-M-8 and CTX-M-40. From these alignments, primers and Taqman type probes specific for either blaCTX-M genes encoding CTX-M-1 or CTX-M-9 groups were selected using Primer Express software (Applied Biosystems). For CTX-M-1 group, primers were F469 (5′-CACCTGGGAGACGAAACGTT-3′) and R532 (5′-CGCGATATTTTTATTTTATTTTTAGT-3′) and the probe was S490 (5′-6FAM-CTGCAGCCGCGTACCGAGGCAC-TAMRA-3′) and R532 (5′-6FAM-CTGCAGCCGCGTACCGAGGCAC-TAMRA-3′) and the probe was S470 (5′-6FAM-CTGCAGCCGCGTACCGAGGCAC-TAMRA-3′). For the CTX-M-9 group, primers were F446 (5′-GAGCCGTGACCGGACGTCGACGAAAGC-3′) and R532 (5′-CTAGTTGTCACCACTGACACCG-3′) and the probe was S470 (5′-6FAM-GAGCCGTGACCGGACGTCGACGAAAGC-TAMRA-3′) and the probe was S470 (5′-6FAM-GAGCCGTGACCGGACGTCGACGAAAGC-TAMRA-3′). Duplicate real-time PCRs were run with the ABI Prism 7900 sequence detection system (Applied Biosystems, France) and Absolute QPCR ROX master mix (Thermo Scientific, France) in 25-µl reaction mixtures and under reaction conditions of 95˚C for 15 min (enzyme activation), and 40 two-step cycles consisting of 95˚C for 15 s and 60˚C for 1 min. Primers concentrations were 400 nM and Taqman type probe concentration was 200 nM, 1 µl of T4 GP32 (MP Biomedicals, France) was added per reaction. Five microliters of template DNA was added per reaction. PCR targets were cloned in pCR II-TOPO plasmid and recombinant linearized plasmids were used as standards. Gene copy numbers were calculated by amplifying six serial dilutions of the standard (105–109 copies per reaction mixture) in parallel with the samples. The specificity of the CTX-M detection systems has also been checked in silico using the BLASTn algorithm across the GenBank nucleotide database (NCBI website). The specificity of the CTX-M detection systems has also been validated by
Table 1 | Human clinical strains used to validate the CTX-M-1 group and CTX-M-9 group detection systems (clinical strains were collected between 2006 and 2007 at CHU Dijon, France).

| Strain | Strain origin | bla gene (CTX-M Group) | Detection by CTX-M-1 group PCR | Detection by CTX-M-9 group PCR |
|--------|---------------|------------------------|-------------------------------|-------------------------------|
| E. coli 913SE | CHU Dijon, bacteriology | CTX-M-1 (1) | +++ | – |
| E. coli 882SE | CHU Dijon, bacteriology | CTX-M-2 (2) | – | – |
| E. coli 886SE | CHU Dijon, bacteriology | CTX-M-3 (1) | +++ | – |
| E. coli 803SE | CHU Dijon, bacteriology | CTX-M-9 (9) | – | +++ |
| E. coli 912SE | CHU Dijon, bacteriology | CTX-M-14 (9) | – | +++ |
| E. coli 902SE | CHU Dijon, bacteriology | CTX-M-15 (1) | +++ | – |
| K. ascorbata 268SL | CHU Dijon, bacteriology | KLUA (2) | – | – |
| K. cryocrescens 254SL | CHU Dijon, bacteriology | KLUG-1 (8) | – | – |

E. coli, Escherichia coli; K. ascorbata, Kluyvera ascorbata; K. cryocrescens, Kluyvera cryocrescens.

FIGURE 1 | Detection levels of blaCTX-M genes by real-time PCR (CTX-M-1 group detection system) in soil microcosms spiked with increasing amounts of E. coli strain 913SE CTX-M-1. ND, not detected. Results are the means of two replicates and bars represent standard deviations.

using human clinical isolates harboring known blaCTX-M genes (Table 1). In order to determine the efficiency of these detection systems in soil, soil samples (2 g) were spiked with known titers of E. coli strain EC 913 SE carrying blaCTX-M-1, soil DNA was extracted immediately as described above and subjected to real-time PCR using the primers and probe specific for CTX-M-1 group (Figure 1).

BACTERIOLOGICAL METHODS AND ANTIBIOTIC RESISTANCE TESTING

All fecal samples from the cows and all environmental samples have been inoculated on ESBL screening agar plates containing Drigalsky medium supplemented with either cefotaxime (4 mg/l) or ceftazidime (4 mg/l). The antibiotic susceptibility tests have been performed by the disk diffusion method. A range of antibiotics including penicillins, cephalosporins, carbapenem (imipenem), aminoglycosides (kanamycin, tobramycin, gentamycin, streptomycin, amikacin, netilmicin), chloramphenicol, quinolones (ciprofloxacin, ofloxacin), doxycycline, cotrimoxazol, and colistin was used to determine antibiotic susceptibility patterns of the isolates and the production of ESBL was assessed by the double-disk synergy test (Jarlier et al., 1988). Guidelines for the interpretation of antibiotic susceptibility testing were from the Clinical and Laboratory Standards Institute (CLSI, 2010).

IDENTIFICATION OF ESBL TYPES

The characterization of the bla gene was performed by PCR on isolates with a positive double-disk synergy test by using primers specific for the genes encoding ESBL from TEM, SHV, and CTX-M families (Chenal et al., 1992; Neuwirth et al., 1995; Sabate et al., 2002). PCR products were sequenced on both strands using ABI PRISM 3100 (Applied Biosystems, France).

GENOTYPING BY THE DIVERSILAB SYSTEM (BIOMÉRIEUX)

The Diversilab system is a typing technique which is based on the repetitive-sequence-based PCR (rep-PCR) and proved to be a useful method for genotyping of E. coli (Fluit et al., 2010). All reagents, automates and software used for this study were provided by bioMérieux, France. DNA was extracted from E. coli colonies using an UltraClean Microbial DNA isolation kit and following the manufacturer’s instructions. The extracted DNA was amplified using a Diversilab Escherichia DNA fingerprinting kit. Electrophoresis of the amplified fragments using a microfluidics LabChip with an Agilent 2100 Bioanalyzer and analysis were performed according to the protocol of the manufacturer. Isolates with a similarity of <95% were considered different, and isolates with a similarity of >98% were considered indistinguishable.

MLST TYPING OF E. COLI STRAINS

MLST typing of E. coli strains was done according to recommendations found at http://mlst.ucc.ie/mlst/dbs/Ecoli/documents/primersColi_html. The E. coli MLST scheme uses internal fragments of the following seven house-keeping genes: adk (adenylate kinase), fumC (fumarate hydratase), gyrB (DNA gyrase), icd (isocitrate/isopropylmalate dehydrogenase), mdh (malate dehydrogenase), purA (adenylosuccinate dehydrogenase), recA (ATP/GTP binding motif). MLST typing was done at the Institute of Microbiology and Epizootics, Freie Universität Berlin, Berlin, Germany, by Dr. Sebastian Guenther.
RESULTS

bla\textsubscript{CTX-M} DETECTION IN SOILS

The method of real-time PCR detection of \textit{bla\textsubscript{CTX-M}} has been validated on the basis of amplification of DNA from pure strains or from inoculated soil DNA. The two detection systems proved to be sensitive and specific of \textit{bla\textsubscript{CTX-M}} genes encoding group 1 and group 9 enzymes. Detection threshold was estimated to be one copy per PCR reaction. Detection limit in soil samples was estimated to be 10\textsuperscript{-3} copies per gram of soil (Figure 1). Out of the 120 soil extracted DNAs from Burgundy, 22 were found to be positive using one or two detection systems (Figure 2). The proportion of positive soil for occurrence of \textit{bla\textsubscript{CTX-M 1 or 9}} was of 3.3% in Yonne, 6.2% in Côte d’Or, 16.0% in Nièvre, and 24.2% in Saône et Loire. These results demonstrate the wide distribution of some \textit{bla\textsubscript{CTX-M}} genes in soils from Burgundy. No obvious correlation was found between soil physical and chemical properties and the occurrence of \textit{bla\textsubscript{CTX-M}} genes [analysis by principal component analysis (PCA), data not shown]. The causes of the higher prevalence of \textit{bla\textsubscript{CTX-M}} genes in soils from Saône et Loire remain to be deciphered.

DETECTION OF ESBL-PRODUCING \textit{E. coli} FROM LIVESTOCK

Out of the 271 feces samples analyzed in 2009, 13 proved to contain ESBL-producing \textit{E. coli} (Table 2). Five isolates harbored the TEM-71-ESBL. Interestingly all these isolates were originated from “Nièvre.” Four isolates were genotypically indistinguishable. Among them isolates 32 and 101 were originated from two farms located in the same village. The others (92 and 107) were recovered in animals from farms located 16 km apart. The eight remaining isolates harbored CTX-M-1. The CTX-M-1 producing isolates have been isolated in three departments (Nièvre, Saône et Loire, and Côte d’Or). The genotypical analysis performed by rep-PCR with Diversilab revealed a wide diversity among the strains isolated from different farms. However, the strains 234 and 235 originated from two animals sampled in a same farm (farm 2) were clonally related (not distinguishable).

One year later (July 2010), feces samples of the whole cow herd from farm 2 were analyzed (90 animals), and CTX-M-1 producing \textit{E.coli} isolates were detected from two animals. Strains V71 and V9 were genotyped and were different from the strains 234 and 235 isolated in June 2009 (Table 2).

DETECTION OF ESBL \textit{E. coli} ISOLATES IN ENVIRONMENTAL SAMPLES

The environments of three farms where positive animals have been detected were chosen for further investigations. In the farm 1, no ESBL-producing \textit{E. coli} were found in the farm environment. On the contrary, 4 and 6 CTX-M-1 producing \textit{E. coli} were detected in farms 2 and 3 respectively (Table 2). In farm 2, a cultivated soil amended one year before with liquid cow manure from the farm was found to contain CTX-M harboring \textit{E. coli} strains. These isolates were genotypically indistinguishable from the animal strains F2/CO/234 and F2/CO/235. Interestingly the soil sampling site was located 3 km away from the cattle barn. In farm 3 the positive samples were: pasture soil, and composted manure. In that case, composted manure isolate was identical to the animal isolate, whereas one soil isolate had a different genotype.

DISCUSSION

The worldwide emergence of CTX-M producing \textit{E. coli} in human clinical samples is a public health concern (Pitout and Laupland, 2008) and raises several interrogations regarding their high dissemination rate. These strains are also widely described in animals (pets, farm animals; Costa et al., 2009; Bortolaia et al., 2010; Cortes et al., 2010). It can be hypothesized that there is a cross-transmission between the human being and the animals (Leverstein-Van Hall et al., 2011), or that there are common environmental sources leading to human and animal contaminations. The treatment regimes for eradication of infections caused by such strains are sometimes very limited, i.e., when the CTX-M production is associated with the production of aminoglycosides modifying enzymes and gyrase mutations (fluoroquinolones resistance). We report in this study our findings concerning the prevalence of fecal carriage of \textit{E. coli} CTX-M producing in cattle as well as the contamination of the farm environment.

DETECTION OF ESBL-PRODUCING \textit{E. coli} IN LIVESTOCK

We have detected ESBL-producing \textit{E. coli} in livestock (5% of the animals tested). In Europe such strains have been only sporadically described in cattle: in Germany (Guerra et al., 2007), England (Horton et al., 2011), and Spain (Brinas et al., 2005). To our best knowledge this is the second report of ESBL-producing \textit{E. coli} in cattle in France where Meunier et al. (2006) reported three isolates (carrying either CTX-M-1 or CTX-M-15 ESBL) responsible for infections in cow. Our results demonstrate that ESBL-producing \textit{E.
Table 2 | Characteristics of the E. coli strains isolated from animals, manure and soils.

| Strain designation, farm number/department/isolate number | Origin | Type of ESBL | Rep-PCR genotype (Diversilab) | Associated non-beta-lactam antibiotic resistance | ST<sup>d</sup> |
|-----------------------------------------------------------|--------|--------------|------------------------------|---------------------------------------------|-----------|
| F1/SL/250 Animal EDC                                      |        | CTX-M-1      | E                            | CIP-G                                       |           |
| F2/CO/234 Animal H                                        |        | CTX-M-1      | A                            | SXT                                         |           |
| F2/CO/235 Animal H                                        |        | CTX-M-1      | A                            | SXT                                         | 2497      |
| F2/CO/RET12 Cultivated soil                              |        | CTX-M-1      | A                            | SXT                                         | 155       |
| F2/CO/RET15 Cultivated soil                              |        | CTX-M-1      | A                            | SXT                                         |           |
| F2/CO/RET20 Cultivated soil                              |        | CTX-M-1      | A                            | SXT                                         | 155       |
| F2/CO/RET21 Cultivated soil                              |        | CTX-M-1      | A                            | SXT                                         |           |
| F2/CO/V9 (2010) Animal H                                 |        | CTX-M-1      | F                            | SXT                                         |           |
| F2/CO/V71 (2010) Animal H                                |        | CTX-M-1      | G                            | SXT                                         |           |
| F3/CO/241 Animal H                                        |        | CTX-M-1      | B                            | SXT                                         | 2498      |
| F3/CO/RET23 Pasture soil                                |        | CTX-M-1      | H                            | CIP-Cm-SXT                                   | 58        |
| F3/CO/RET24 Pasture soil                                |        | CTX-M-1      | B                            | SXT                                         | 58        |
| F3/CO/RET25 Pasture soil                                |        | CTX-M-1      | B                            | SXT                                         | 58        |
| F3/CO/RET26 Pasture soil                                |        | CTX-M-1      | B                            | SXT                                         | 58        |
| F3/CO/RET27 Composted manure                            |        | CTX-M-1      | B                            | SXT                                         | 2498      |
| F3/CO/RET28 Composted manure                            |        | CTX-M-1      | B                            | SXT                                         |           |
| F3/CO/RET29 Pasture soil                                |        | CTX-M-1      | B                            | Cm-SXT                                      | 2499      |
| F4/N/32 Animal HLEDC                                     |        | TEM-71       | C                            | CIP-G-Cm-SXT                                 |           |
| F5/N/87 Animal H                                        |        | CTX-M-1      | I                            | CIP-G-Cm-SXT                                 |           |
| F6/N/92 Animal EDC                                      |        | TEM-71       | C                            | CIP-G-Cm-SXT                                 |           |
| F7/N/101 Animal HLEDC                                   |        | TEM-71       | C                            | CIP-G-Cm-SXT                                 | 178       |
| F8/N/105 Animal H                                        |        | TEM-71       | J                            | CIP-G-Cm-SXT                                 |           |
| F9/N/107 Animal H                                        |        | TEM-71       | C                            | CIP-G-Cm-SXT                                 |           |
| F10/SL/190 Animal EDC                                    |        | CTX-M-1      | K                            | CIP-Cm-SXT                                   |           |
| F11/CO/240 Animal H                                     |        | CTX-M-1      | D                            | SXT                                         |           |
| F12/CO/245 Animal H                                     |        | CTX-M-1      | D                            | SXT                                         |           |

<sup>a</sup>SL, department of Saône et Loire; CO, department of Côte d’Or; N, department of Nièvre. For farms 2 and 3, isolates from cattle and from environment were listed together to allow strain comparison. In farm 2, the two isolates isolated in 2010 are indicated.

<sup>b</sup>Strains were isolated from animal feces, manure or soil. H, healthy animal; EDC, enteric disease calf; HLEDC, healthy animal linked with an enteric disease calf.

<sup>c</sup>Associated antibiotic resistances: CIP, ciprofloxacin; G, gentamicin; Cm, chloramphenicol; SXT, Cotrimoxazol.

<sup>d</sup>ST, sequence type from MLST analysis as defined at University College Cork (UCC, Ireland) http://mlst.ucc.ie/mlst/dbs/Ecoli/GetTableInfo_html

coli strain are carried indifferently by sick and healthy animals. Our results are in agreement with previously reported data: CTX-M-1 is the ESBL which is the most frequently encountered in animals (Girlich et al., 2007; Bonnedahl et al., 2009; Bortolaia et al., 2010).

Nevertheless we have detected for the first time E. coli TEM-71-producing in five animals whereas they have been exceptionally reported in human infection (Wong-Beringer et al., 2001; Rasheed et al., 2002; De Champs et al., 2004). This finding is interesting from the epidemiological point of view because four isolates are genotypically related whereas they were originated from different farms (F4, F6, F7, and F9). This indicates that some clonal isolates are widespread or might circulate (through animal transfer) at a regional scale or that there is a common reservoir in the region. At the farm level, this might suggest a potential cross-contamination among cattle or the presence of a reservoir within the farm. Finally, this is the first description of TEM-71-producing E. coli in animals. It is noteworthy that the TEM-71 producing isolates are multiresistant to ciprofloxacin, gentamicin, chloramphenicol, and cotrimoxazol. On the opposite, most of the CTX-M-1 producing isolates harbor a single associated resistance to cotrimoxazol (Table 2). Therefore, cefotaxim resistant E. coli recovered from animals originated from different farms show significantly different antibiotic resistance patterns. This might reflect different exposition of the animals to antimicrobial agents or different sources of contamination.

In farm 2, strains isolated from cattle in 2010 have a different genotype compared to those isolated in 2009. Several hypothesis might explain this result: (i) horizontal gene transfer may occur between E. coli genotypes carried by cattle, since blaclCTX-M genes are carried by plasmids, (ii) new exogenous E. coli strains may have been disseminated in the farm environment.

DETECTION OF ESBL-PRODUCING E. COLI IN FARM ENVIRONMENT

Among the 12 farms where ESBL-producing E. coli were detected from animals, we chose three farms to further investigate the dissemination of these strains in the farm environment. Farms were chosen on the basis of which farmers will decide to cooperate to our study.

In two of the three farms where positive animals were reported, ESBL E. coli isolates were detected in environmental samples.
Interestingly, in farm 2 one of the soil sampling sites was a crop field that has been amended 1 year before (autumn 2008) with liquid manure collected in the barn. This crop field was located 3 km away from the cattle barn. In autumn 2009, we were able to isolate several CTX-M producing E. coli strains from this soil, indicating that such strains have the ability to survive at least 1 year after soil amendment under environmental conditions. In farm 3, the positive samples were: pasture soil, and composted manure. In that case, composted manure was identical to the animal isolate, whereas one soil isolate had a different genotype.

**FURTHER GENOTYPIC COMPARISON OF E. COLI STRAINS**

MLST typing of E. coli strains isolated from this study has been partially done. Preliminary results indicate that some E. coli strains isolated from animal and soil belong to previously described ST38, ST155, and ST178 as defined in the MLST database hosted at UCC2. Four strains appear to belong to new genotypes namely ST2497, ST2498, and ST2499. bla\textsubscript{CTX-M-1} genes were found in E. coli isolates with variable ST. ST8 and ST155 grouped strains from animal and human origin, some strains belonging to these ST are pathogenic for human or animals. Plasmids of four strains were sequenced (454 pyrosequencing), bla\textsubscript{CTX-M} genes were found on plasmids and located close to one copy of IS\textsubscript{Ecp}1 in each strain (data not shown).

**MOLECULAR DETECTION OF bla\textsubscript{CTX-M} GENES IN SOILS FROM BURGUNDY**

The origin of the bla\textsubscript{CTX-M} genes detected in soils remains to be elucidated, several hypotheses might be investigated. E. coli strains harboring bla\textsubscript{CTX-M} genes might have been disseminated in soils through manure application on cultivated soils (animal origin), sewage sludge application (human origin), or through irrigation with treated or untreated waste-water. As the progenitor bla\textsubscript{CTX-M} gene is the chromosomal bla genes of different species of K. pneumoniae (Decousser et al., 2001; Poirel et al., 2002) we can also hypothesize that bla genes detected in the studied soils might be harbored by bacterial species other than E. coli. These bacteria might thus act as potential environmental bla genes reservoirs. To our best knowledge, this is the first report about occurrence of bla\textsubscript{CTX-M} genes in soil.

The detection of CTX-M producing E. coli in soil was the major finding of this study. Our work demonstrated the survival of CTX-M producing E. coli in soil at least for one year. Future work will aim at linking bla\textsubscript{CTX-M} occurrence with the capacity of E. coli strains to survive under environmental conditions. Finally, potential risks for public health through water or vegetables contamination will have to be determined.

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