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The revolving door between hospital and community: extended-spectrum beta-lactamase-producing Escherichia coli in Dublin.

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The revolving door between hospital and community. ESBL-producing *Escherichia coli* in Dublin

Running title: ESBL-producing *Escherichia coli* in Dublin

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Summary

Background

Escherichia coli that produce extended-spectrum beta-lactamases (ESBLs) are an increasing cause of healthcare-associated infection and community healthcare facilities may be a reservoir for important epidemic clones.

Aim

To retrospectively characterise and investigate the epidemiology of ESBL-producing *E. coli* collected in a Dublin hospital, during 2009 and 2010, and to investigate the dissemination of specific clones within hospital and community healthcare facilities.

Methods

Pulsed field gel electrophoresis (PFGE) was used to determine the genetic relatedness of 100 ESBL-producing *E. coli* isolates. Phylogenetic groups were determined and the O25b-ST131 clone identified in the collection. The genetic data was correlated with antimicrobial susceptibility, clinical and demographic data to explore the epidemiology of specific clones.

Findings

Phylogenetic groups B2 (62%) and D (18%) were the most common and were associated with non-urinary isolates (P<0.0001 by Fisher's exact test). Pulsed-field gel electrophoresis (PFGE) revealed twelve clusters (≥80 % similarity), the largest of which clustered with the epidemic UK strain A. Residents of long-term care facilities (LTCFs)

in the community exclusively carried the O25b-ST131 clone and phylogenetic groups B2 and D.

Conclusion

E. coli O25b-ST131 is largely responsible for ESBL-producing *E. coli* in LTCFs in Dublin. The distribution of ESBL-producing *E. coli* in our hospital and community highlights a 'revolving door' through which these resistant bacteria spread and disseminate.

Key words: Extended-spectrum beta-lactamase, *Escherichia coli*, O25b-ST131 clone

Introduction

Since 2000, strains of *Escherichia coli* are the dominant extended-spectrum beta-lactamase (ESBL) producers worldwide, with CTX-M-15 the most widely disseminated of the ESBL enzymes.[1-2] According to the 2009 European Antibiotic Resistance Surveillance Network (EARS-Net) report, the prevalence of invasive *E. coli* resistant to third generation cephalosporins in Europe has increased from 1.7% in 2002 to 8% in 2009 ($P<0.001$) in 22 countries.[3] ESBL-producers are increasingly prevalent in non-ICU settings which may be due to increased admission of patients with urinary tract or bloodstream infections from nursing homes and other community healthcare facilities.[4-5] Risk factors for infection with an ESBL-producer includes recurring urinary tract

infections (UTI) and underlying renal pathology, old age, nursing home residence and recent exposure to β-lactams or fluoroquinolones.[6]

Transmission of ESBL genes is facilitated by their frequent location on conjugative multiresistance plasmids and the association of these plasmids with local and epidemic clones of Enterobacteriaceae. The most notable of these is *E. coli* O25b-ST131, a fluoroquinolone-resistant strain of the B2 phylogenetic group, associated with the global dissemination of CTX-M-15.[7-8] This pandemic clone comprises five closely related clusters in the United Kingdom (UK strains A-E), UK strain A is epidemic in the UK and is widespread among Irish hospitals and Belfast nursing homes.[9-11] Nursing homes may be reservoirs of these clones in the Republic of Ireland. Similarly, the clinical characteristics of patients with ESBL-producing *E. coli* (ESBL-EC) in Ireland have not been extensively investigated.

We characterised 100 ESBL-EC collected in a Dublin hospital, during 2009 and 2010, to determine their genetic relatedness and to investigate the dissemination of specific clones within hospital and community healthcare facilities. Clinical data, patient demographic data and antimicrobial susceptibility data relating to the isolates were analyzed to investigate the epidemiology of ESBL-EC.

Materials and methods

Study setting

Beaumont Hospital is a 700-bed tertiary referral hospital in Dublin, Ireland providing emergency and acute care to the local community of approximately 300 000 people. The microbiology laboratory receives specimens from the hospital and community healthcare facilities including general practitioners (GPs) and nursing homes.

Bacterial strains

The American Type Culture Collection (ATCC) strains *E. coli* ATCC 25922, *E. coli* ATCC 35218 and *K. pneumoniae* ATCC 700603 are ESBL-negative, ESBL-positive and *bla*$_{SHV}$ ESBL-producing controls respectively. *Salmonella enterica* serovar Braenderup H9812 was a molecular weight reference strain for PFGE. The National Collection of Type Cultures (NCTC) strain *E. coli* NC13441 (UK strain A) was a comparison strain for PFGE.[12] One hundred ESBL-EC clinical isolates recovered from samples received by the diagnostic microbiology laboratory between January 2009 and December 2010 were studied. These were selected from all *E. coli* isolates (468) identified as ESBL-producers within the time period and selection was based on prioritization of serious infections (e.g. bloodstream isolates) with an even temporal distribution of isolates. One representative isolate per patient was selected. Isolates were confirmed as ESBL-producers phenotypically using *Brilliance*™ ESBL Agar (Oxoid Ltd., Cambridge, UK).

Determination of the *E. coli* phylogenetic group and detection of *E. coli* O25b-ST131 clone

E. coli clinical isolates and reference strains were assigned to phylogenetic groups A, B1, B2 or D using the triplex PCR method of Clermont *et al.*[13] Strains not yielding PCR products were scored as unassigned.[14] An allele-specific PCR of the *pabB* gene was used to identify clone O25b-ST131 among B2 phylogenetic group members as previously described.[15]

Pulsed-field gel electrophoresis (PFGE) of *E. coli* clinical isolates

Xba I-digested genomic DNA from *E. coli* isolates and UK strain A were subjected to PFGE according to the PulseNet standardized laboratory protocol for *E. coli* [16] Electrophoresis was performed in a 1% (w/v) SeaKem agarose gel with 0.5 X Tris-Borate-EDTA (TBE) buffer for 19h in a CHEF-DR III apparatus (Bio-Rad), (initial switch time 2.2 s, final switch time 54.2 s, 6 V, included angle of 120°, 14°C). Where DNA degradation occurred, electrophoresis was repeated with thiourea (50 µM) in the running buffer.[17] Macrorestriction patterns were analysed using GelCompar II® software (Ver. 6.5, Applied Maths NV, Saint-Martens-Latem, Belgium). Variability was determined by the Dice coefficient using a tolerance of 1%. Strains were clustered according to the unweighted pair group average method. Clonal groups were assigned based on a similarity of ≥80% (≤6 band difference in restriction profile) as previously described.[18] Isolates indistinguishable by PFGE were assigned the same alpha-numerical PFGE type.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was carried out in the diagnostic microbiology laboratory of Beaumont Hospital using the BD Phoenix™ Automated Microbiology System and results were interpreted according to Clinical and Laboratory Standards Institute (CLSI) guidelines.[19]

Data collection

Patient demographic data, clinical data and antimicrobial susceptibility data for ESBL-EC isolates were obtained by retrospective analysis of computerized hospital medical records. Clinical details, including patient outcome, were unavailable for community patients with ESBL-EC.

Statistical analysis

Numerical data were expressed as mean ± standard deviation (SD) or standard error of the mean (SEM) and inter-quartile range. Fisher's exact test was used to compare categorical data. Tests were performed using Prism 4 for Windows and were two-tailed.

Results

Clinical features and patient demographics

Amongst 633 isolates identified as ESBL-producers during the study period 468 were *E. coli*, 57 were *Klebsiella spp.* and 18 were other *Enterobacteriaceae* (eg, *Pseudomonas spp., Proteus spp., Morganella morganii*). Patient demographic and clinical characteristics for 100 ESBL-EC isolates studied are outlined in Table I. Almost two thirds (65%) of patients were inpatients at the time of isolation of ESBL-EC. A further 22 patient samples were from community healthcare facilities including nursing homes (NH; 9 %) and GPs (13%). Urinary isolates made up the majority of ESBL-EC (68%), with 38/68 (56%) from inpatients. Isolates cultured from blood (8), fluid (5), surgical theatre specimens (2), catheter/cannula tips (2) and nine of 12 respiratory isolates were from hospital inpatients. All GP and Emergency Department (ED) samples and 7/9 NH samples were urinary, with the remainder being wound swabs. Outpatient samples were urinary (4) and respiratory (3). Among inpatients, median length of stay (LOS) was 23d and in-hospital mortality was 20%. Two thirds of inpatients were on medical wards, the most common specialities being geriatric medicine (14%), respiratory medicine (11%), nephrology (9%), gastroenterology (8%) and rheumatology (8%).

All isolates were multidrug-resistant (MDR) according to the definition of the European Centre for Disease Control and Prevention.[20] Although all isolates were susceptible to meropenem, there was almost complete resistance to several beta-lactam antimicrobials including amoxicillin (100%), aztreonam (99%), cefuroxime (100%), cefazolin (100%), cefotaxime (97%), ceftazidime (99%) and cephalothin (100%). A relatively high resistance rate to other commonly used Gram-negative antimicrobials was evident, with the majority of isolates co-resistant to ciprofloxacin (73%), co-trimoxazole (78%) and amoxicillin-clavulanic acid (72%). Overall, 64% of clinical

isolates showed reduced susceptibility to 3 or more non-β-lactam/combination antimicrobials.

Genetic relatedness of isolates

The relatedness of *E. coli* clinical isolates is represented in Figure 1. Phylogenetic groups were successfully assigned to 97% of *E. coli* clinical isolates. The most prevalent phylogenetic groups were B2 (62%) and D (18%). The other isolates comprised group A (10%) and group B1 (7%), most of which were recovered from urine samples (13/17; 76.5%). A significant association was found between group B2 and D isolates and non-urinary types with 26/32 isolates (81%) belonging to these groups versus four non-urinary isolates involving group A or B1 isolates (P<0.0001, Fisher's exact test). Isolates responsible for bloodstream infections belonged to phylogenetic groups B2 or D. Of the 62 B2 phylogenetic group isolates, 54 (87%) belonged to the O25b-ST131 epidemic clone.

PFGE analysis of 100 isolates revealed 87 distinct types of which 64 isolates were clonally related and comprised 12 clusters (A-L) based on a similarity of ≥80%. Cluster A was the largest group (n=34), all belonging to the O25b-ST131 epidemic clone and clustering with the epidemic UK strain A. Clusters B, C and D (n=5, 6 and 2 respectively) also belonged to the O25b-ST131 clone but were <80% similar to UK strain A. Members of the remaining clusters also shared the same phylogenetic backgrounds, with clusters E, F and J belonging to group B2; clusters G, H and I belonging to group D and clusters K and L belonging to groups A and B1.

Epidemiology of clonal groups The epidemiological and antimicrobial resistance patterns of the clonal groups are summarised in Table II. Cluster A isolates demonstrated distinctive resistance profiles to ciprofloxacin, trimethoprim, amoxicillin-clavulanic acid and co-trimoxazole. Cluster G isolates displayed resistance to gentamicin, not evident in other clusters. The clusters with the most resistance to common Gram-negative antimicrobials were B2 phylogenetic group clusters J (resistant to 67% of six antimicrobials) and A (63%). Cluster L, containing group B1 isolates had the lowest proportion of co-resistances (25%). O25b-ST131 isolates comprised 21/27 (78%) of piperacillin-tazobactam-resistant isolates and 10/11 (91%) of amikacin-resistant isolates.

All twenty patients that normally resided in LTCFs/NH in the community, eleven of which were hospitalised during the study period, carried clonal isolates. Seventeen were O25b-ST131 (including twelve cluster A isolates), and the remainder were phylogenetic groups B2 (1) and D (2). Clonal ESBL-EC from clusters A (3), C (2) and I (1) were isolated from six of eleven hospitalised NH residents on the day of hospital admission. Members of six clonal groups were isolated from both NH residents and hospital inpatients during the study period (Table II). Isolates belonging to cluster A were detected in residents of six long-term care facilities over 23 months and from 17 hospital wards. Cluster A isolates were also recovered from six different specimen sources and from all patient categories. The pandemic O25b-ST131 clone was less prevalent in patients that normally resided at home than in NH residents (37/80; 46% versus 17/20;

85%) *P* = 0.0022. Also all patients with sporadic ESBL-EC strains normally resided at home. The O25b-ST131 clone accounted for 33/65 (51%) of ESBL-EC recovered from hospital inpatients. Amongst GP urine samples 54% were positive for O25b-ST131 and belonged to clusters A(2), B(2) and D(1).

Discussion

This study reports a molecular investigation into ESBL-producing *E. coli* and their associated patient characteristics. *E. coli* accounted for 86% of ESBL-positive Enterobacteriaceae isolated during 2009 and 2010 in our hospital. Although bloodstream and respiratory isolates were prioritized to include those causing the most severe infections, the majority of isolates were of urinary origin, reflecting the increase in ESBL-producing *E. coli* UTI seen worldwide.[6] Over two thirds of patients carrying ESBL-EC were over 65 years old and almost three quarters were resident in a healthcare facility at the time of sample collection, either in hospital (65%) or in a nursing home (9%). The median length of stay for inpatients was relatively high (23d) matching the median LOS found for patients in a recent study from a Belgian hospital of similar size.[21] Extended hospital stay is a known risk factor for hospital-onset ESBL-producer infection.[6]

The majority of study isolates were non-susceptible to β-lactam antimicrobials but all were susceptible to meropenem. Frequent non-susceptibility to other antimicrobial

classes was observed with 64% of isolates non-susceptible to at least three of six non-β-lactam or β-lactam-inhibitor combination antimicrobials. The high level of resistance to β-lactam-inhibitor combination antimicrobials amoxicillin-clavulanic acid and piperacillin-tazobactam, suggests concomitant production of other beta-lactamase enzymes such as those belonging to Ambler classes A (e.g penicillins TEM-30 and SHV-10), C (e.g. AmpC) or D (OXA enzymes).[22-23] The variability in antimicrobial resistance observed between isolates of the same clonal group may be explained by differences in the content and structure of mobile genetic elements, such as resistance plasmids and integrons.

A previous Irish study of ESBL-producing *Enterobacteriaceae* isolates from 25 different laboratories over an 11 year period highlighted the high prevalence of resistance to ciprofloxacin and we found similar prevalence rates amongst *E. coli* (73 %).[9] Resistance to gentamicin was less prevalent at 24% of ESBL-EC (24/100) compared to 38% (176/462) of ESBL-producing *Enterobacteriaceae*, 85% of which were *E. coli*. The continuing trend towards multidrug resistance that limits empirical therapy choices for Gram-negative infections is evident. Excluding meropenem, only amikacin and nitrofurantoin were effective antimicrobials in terms of in-vitro susceptibility (97% and 90% of isolates).

Most isolates belonged to the B2 (62%) and D (18%) phylogenetic groups which contain virulent extra-intestinal strains.[24] In the present study, strains belonging to these groups were significantly associated with non-urinary isolates and all bloodstream isolates belonged to these groups. Phylogenetic groups A and B1, which are associated with

human and animal commensal strains, were represented by only 17 isolates, the majority being from urine samples (13/17, 76%).

The pandemic O25b-ST131 clone was predominant in the collection, represented by over half of all isolates and the majority of B2 phylogenetic group isolates (87%). This virulent uropathogenic strain is described in all five continents and is commonly co-resistant to fluoroquinolones.[25] In our collection, O25b-ST131 clone members were represented by five clusters (A-D and J), the largest containing 34 isolates and clustering with epidemic UK strain A. The distinctive antimicrobial resistance profile of UK strain A was also observed in cluster A, i.e. resistance including ciprofloxacin and trimethoprim and marked susceptibility to gentamicin.[12] The widespread dissemination of this strain is evidenced by its isolation from all patient categories.

A nationwide study of 69 Irish LTCFs in June 2010 revealed a prevalence of healthcare associated infection (HCAI) of 3.7% among 4170 patients. Over one third (35.8%) of antibiotic prescriptions were intended for prophylaxis of UTI; however UTI remained the most common HCAI (40%). It is possible that the practice of prophylactic prescription for UTI may have contributed to the success of the MDR ESBL-EC strains in Irish LTCFs, especially the uropathogenic O25b-ST131 clone.[26] In the present study all twenty patients normally residing in LTCFs had clonal ESBL isolates belonging to phylogenetic groups B2 and D and 17/20 were O25b-ST131. This suggests that *E. coli* O25b-ST131 and some other virulent clones may be largely responsible for ESBL-EC infections/carriage in LTCFs. In contrast patients with sporadic strains all normally resided in their home, which suggests that a greater variety of ESBL-EC strains

circulate in the community compared to LTCFs. However the high proportion of O25b-ST131 amongst ESBL-EC positive inpatients (51%) and GP urine samples (54%) suggests this clone is dominant in hospital and community settings.

Although difficult to identify definitive transmission events based on the recovery of indistinguishable PFGE types alone, we can speculate that ESBL-EC strains may have disseminated throughout the hospital and from LTCFs in the community to the hospital. For example, three isolates from cluster A2 (0026-0028) were isolated within three days of each other from patients on three geographically separate wards. Two of these patients originated from the same nursing home and an ESBL-EC was isolated from one of these patients upon hospitalization. The recovery of identical strains (F1 (0041 and 0042) may indicate cross infection with the postulated route of spread from an ED patient to a surgery patient. However certain clonal strains including UK strain A may be endemic in the hospital and this may account for their recovery from multiple hospital patients over extended time periods. For example PFGE type A2 isolates were recovered from five geriatric patients, all from different hospital wards over 18 months. Although the origin of the strains is not clear, it is evident that both the hospital and LTCFs in the community are now a reservoir for many of the same ESBL-EC clones.

There are limitations to the study. Due to time and resource constraints consecutive isolates were not studied. Therefore the isolate collection represents just over one fifth of ESBL-EC isolates recovered during the study period. Bloodstream and respiratory isolates were prioritised and therefore are over-represented in this study. This may have introduced bias to certain clinical characteristics. Limited reliable data on previous

hospital contacts for this patient cohort precluded the definition of infections as healthcare-associated or community-associated.

This study describes the epidemiology and molecular characteristics of ESBL-EC clones in an Irish hospital. Similar to the pattern observed in other European countries and world-wide, our study highlights the importance of the epidemic O25b-ST131 clone as the major category of ESBL-producing *E. coli* in our hospital and local community.[25, 27] The dissemination of clones throughout the hospital and between several LTCFs in the local community and the hospital is supported by the identification of highly similar or identical PFGE types among hospital and NH patients and the predominance of the O25b-ST131 clone in both settings. This indicates the potential for continuous recirculation of this clone between healthcare facilities. This 'revolving door' mechanism for the spread of ESBL-EC in our catchment area highlights the challenges faced in preventing and controlling their spread.

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405 **Table I.** Demographic and clinical data of 100 patients with ESBL-producing *E. coli*.

Characteristic	Value
Patient demographics	
Male: female	37:63
Mean age, *y ±SD [SEM] (range)*	67± 21[2](11-100)
Residents of nursing homes or long term care facilities	20
Patient types	
Hospital inpatients	65
Emergency Department patients	6
Outpatients	7
GP referral patients	13
Nursing home patients	9
Length of stay^	
Mean LOS *d ±SD(SEM)*	97.5 ± 232(28.8)
Range *d*	0.5-1434
Inter-quartile range *d*	8-49
Median LOS *d*	23
Time from admission to collection of ESBL-EC ^	
Mean time *d ±SD(SEM)*	63.5 ± 178.5(22.3)
<7d *n(%)*	32(49)
≤30d *n(%)*	50(77)
>30d *n(%)*	15(23)
Clinical specimen type	
Blood	8
Urine	68
Respiratory	12
Wound Swab	3
Fluid	5
Others	4
Inpatient outcome^	
Discharged home *n(%)*	33(51)
Discharged to nursing home *n(%)*	10(15)
Transferred to other hospital *n(%)*	6(9)
Deceased *n(%)*	13(20)
Other *n(%)*	3(5)

406 ^ = Inpatients only (65/100 patients), LOS = length of stay

Table II. Phenotypic and epidemiological characteristics of clonal groups.

PFGE cluster (No. of isolates)	Antimicrobial resistance[a]	Antimicrobial susceptibility[b]	Percentage of co-resistance[c]	Patient categories (No. of isolates) [d]	NH residents[e]
A (34)	CIP TMP AMC SXT	GEN	63	E(1) GP(2) I(23) O(2) NH(6)	12
B (5)	CIP	TZP AMK	43	GP(2) I(3)	1
C (6)	CIP	AMK	42	I(4) O(1) NH(1)	3
D (2)	-	TZP AMK	33	GP(1) I(1)	0
E (2)	TMP SXT	CIP GEN AMK	33	E(1) NH(1)	1
F (2)	TMP AMC SXT	CIP GEN AMK TZP	33	E(1) I(1)	0
G (3)	GEN TMP SXT	CIP TZP AMK	39	I(3)	1
H (2)	-	TZP AMK	33	I(1) O(1)	0
I (2)	TMP AMC SXT	TZP AMK	50	I(2)	1
J (2)	TMP TZP AMC SXT	GEN	67	I(1) NH(1)	1
K (2)	CIP SXT	GEN AMK	50	I(1) O(1)	0
L (2)	-	GEN TZP AMK	25	I(2)	0

[a] = >90% of strains tested were resistant to the listed antibiotics.

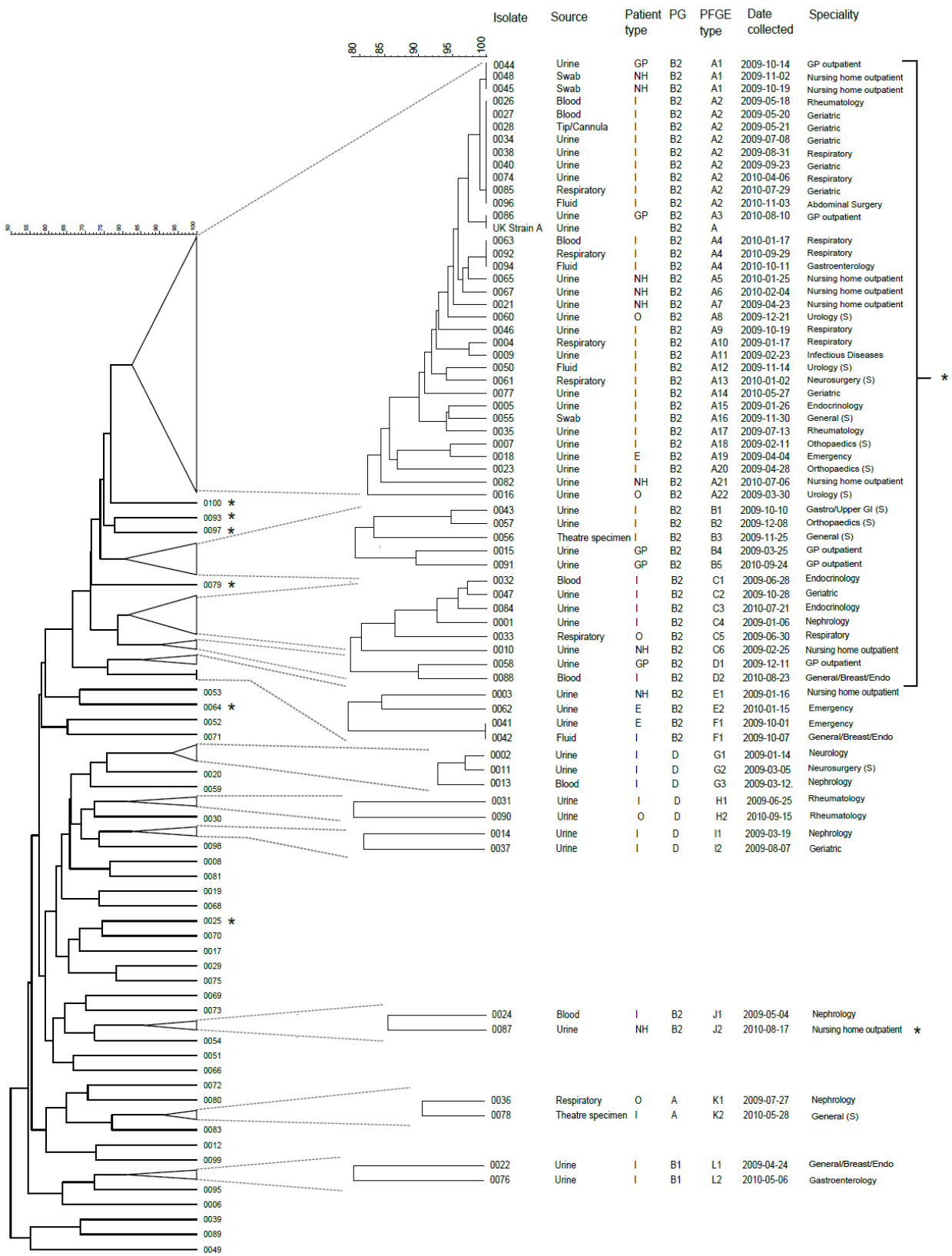
[b] = 100% of strains tested were susceptible

[a, b] Antimicrobials: AMC; amoxicillin/clavulanate, AMK; amikacin, CIP; ciprofloxacin, GEN; gentamicin, SXT; trimethoprim/sulfamethoxazole, TZP; piperacillin/tazobactam, TMP; trimethoprim (urinary isolates only).

[c] Percentage of total antimicrobial susceptibility tests to the 6 antimicrobials listed above (excluding trimethoprim) with resistant result.

[d] E; emergency department patients, GP; GP patients, I; inpatients, O; outpatients, NH; nursing home/long term care facility patients.

[e] Patients normally residing in nursing homes/long-term care facilities.


Isolate
Source
Patient type
PG
PFGE type
Date collected
Speciality
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100
0044 Urine GP B2 A1 2009-10-14 GP outpatient
0048 Swab NH B2 A1 2009-11-02 Nursing home outpatient
0045 Swab NH B2 A1 2009-10-19 Nursing home outpatient
0026 Blood I B2 A2 2009-05-18 Rheumatology
0027 Blood I B2 A2 2009-05-20 Geriatric
0028 Tip/Cannula I B2 A2 2009-05-21 Geriatric
0034 Urine I B2 A2 2009-07-08 Geriatric
0038 Urine I B2 A2 2009-08-31 Respiratory
0040 Urine I B2 A2 2009-09-23 Geriatric
0074 Urine I B2 A2 2010-04-06 Respiratory
0085 Respiratory I B2 A2 2010-07-29 Geriatric
0096 Fluid I B2 A2 2010-11-03 Abdominal Surgery
0086 Urine GP B2 A3 2010-08-10 GP outpatient
UK Strain A Urine B2 A
0063 Blood I B2 A4 2010-01-17 Respiratory
0092 Respiratory I B2 A4 2010-09-29 Respiratory
0094 Fluid I B2 A4 2010-10-11 Gastroenterology
0065 Urine NH B2 A5 2010-01-25 Nursing home outpatient
0067 Urine NH B2 A6 2010-02-04 Nursing home outpatient
0021 Urine NH B2 A7 2009-04-23 Nursing home outpatient
0060 Urine O B2 A8 2009-12-21 Urology (S)
0046 Urine I B2 A9 2009-10-19 Respiratory
0004 Respiratory I B2 A10 2009-01-17 Respiratory
0009 Urine I B2 A11 2009-02-23 Infectious Diseases
0050 Fluid I B2 A12 2009-11-14 Urology (S)
0061 Respiratory I B2 A13 2010-01-02 Neurosurgery (S)
0077 Urine I B2 A14 2010-05-27 Geriatric
0005 Urine I B2 A15 2009-01-26 Endocrinology
0055 Swab I B2 A16 2009-11-30 General (S)
0035 Urine I B2 A17 2009-07-13 Rheumatology
0007 Urine I B2 A18 2009-02-11 Othopaedics (S)
0018 Urine E B2 A19 2009-04-04 Emergency
0023 Urine I B2 A20 2009-04-28 Orthopaedics (S)
0082 Urine NH B2 A21 2010-07-06 Nursing home outpatient
0016 Urine O B2 A22 2009-03-30 Urology (S)
0100 *
0093 *
0097 *
0043 Urine I B2 B1 2009-10-10 Gastro/Upper GI (S)
0057 Urine I B2 B2 2009-12-08 Orthopaedics (S)
0056 Theatre specimen I B2 B3 2009-11-25 General (S)
0015 Urine GP B2 B4 2009-03-25 GP outpatient
0091 Urine GP B2 B5 2010-09-24 GP outpatient
0079 *
0032 Blood I B2 C1 2009-06-28 Endocrinology
0047 Urine I B2 C2 2009-10-28 Geriatric
0084 Urine I B2 C3 2010-07-21 Endocrinology
0001 Urine I B2 C4 2009-01-06 Nephrology
0033 Respiratory O B2 C5 2009-06-30 Respiratory
0010 Urine NH B2 C6 2009-02-25 Nursing home outpatient
0058 Urine GP B2 D1 2009-12-11 GP outpatient
0088 Blood I B2 D2 2010-08-23 General/Breast/Endo
0053
0064 *
0003 Urine NH B2 E1 2009-01-16 Nursing home outpatient
0062 Urine E B2 E2 2010-01-15 Emergency
0041 Urine E B2 F1 2009-10-01 Emergency
0042 Fluid I B2 F1 2009-10-07 General/Breast/Endo
0052
0071
0002 Urine I D G1 2009-01-14 Neurology
0011 Urine I D G2 2009-03-05 Neurosurgery (S)
0013 Blood I D G3 2009-03-12 Nephrology
0020
0059
0031 Urine I D H1 2009-06-25 Rheumatology
0090 Urine O D H2 2010-09-15 Rheumatology
0030
0014 Urine I D I1 2009-03-19 Nephrology
0098
0037 Urine I D I2 2009-08-07 Geriatric
0008
0081
0019
0068
0025 *
0070
0017
0029
0075
0069
0073
0024 Blood I B2 J1 2009-05-04 Nephrology
0087 Urine NH B2 J2 2010-08-17 Nursing home outpatient *
0054
0051
0066
0072
0080
0036 Respiratory O A K1 2009-07-27 Nephrology
0078 Theatre specimen I A K2 2010-05-28 General (S)
0083
0012
0099
0022 Urine I B1 L1 2009-04-24 General/Breast/Endo
0076 Urine I B1 L2 2010-05-06 Gastroenterology
0095
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0049
*

419

Figure 1. Dendrogram showing PFGE profile types (A-L) and *E. coli* phylogenetic groups (PG). Pairwise cluster analysis was performed using the Dice coefficient with an optimisation of 1% and a band matching tolerance of 1%. Columns L to R: Isolate = clinical isolate number; Source = source of clinical specimen; Patient type: I = inpatient, O = outpatient, E = emergency department patient, NH = nursing home patient, GP = GP patient; PG = phylogenetic group; PFGE type: clusters A to L were identified based on a similarity of ≥80% with distinguishable members numbered consecutively. Isolates that were indistinguishable by PFGE were given the same PFGE type code; Date collected = date of first isolation of *E. coli*; Speciality = medical speciality, (S) denotes surgical; * = O25b-ST131 positive by PCR.

Conflict of interest statement

HH has recent research collaborations with Steris Corporation, 3M, Inov8 Science, Pfizer & Cepheid. He has also recently received lecture & other fees from 3M, Novartis, Astra Zeneca and Astellas.