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Emergence of a Novel Extended-Spectrum-β-Lactamase (ESBL)-Producing, Fluoroquinolone-Resistant Clone of Extraintestinal Pathogenic *Escherichia coli* in Kumasi, Ghana

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Beginning in 2007, we began noticing a high level (~80%) of resistance to ampicillin and co-trimoxazole among Gram-negative urinary tract isolates from inpatients at the Komfo Anokye Teaching Hospital (KATH) in Kumasi, Ghana (1). Also, we noticed resistance to expanded-spectrum cephalosporins among urinary tract isolates from outpatients in the community. To investigate whether specific pathogenic genotypes were associated with resistance, we characterized 156 *Escherichia coli* isolates from blood, urine, sputum, and wound swab specimens as well as infected body site aspirates (collected February to April 2008 and March to July 2009). This study was approved by the Joint Committee on Human Research Publications and Ethics of the School of Medical Sciences at the Kwame Nkrumah University of Science and Technology, only patients with a diagnosed infection were considered, and only a single isolate per patient was obtained.

Over half of all isolates were resistant to amoxicillin-clavulanic acid (67%), ampicillin (92%), cefpodoxime (65%), cefuroxime (58%), gentamicin (56%), nalidixic acid (62%), co-trimoxazole (90%), and chloramphenicol (76%), and roughly half (49%) carried bla_{TEM}, bla_{SHV}, bla_{CTX-M}, or some combination of these genes. Extended-spectrum β-lactamase (ESBL) production was found in 77 of the 156 (49.4%) isolates and was significantly associated (chi-square test; $P = 0.009$) with nosocomial cases (53 of 91 isolates; 58.2%) compared to outpatient cases (24 of 65 isolates; 36.9%) but was not associated with patient age, gender, or the source of the clinical sample ($P = 0.101$).

Due to the widespread dissemination of the ESBL-producing extraintestinal pathogenic *E. coli* (ExPEC) clone, identified by multilocus sequence typing (MLST) as sequence type 131 (ST131) (2, 3), we selected 29 ESBL-producing *E. coli* isolates at random for MLST. All isolates were identical and belonged to a previously identified sequence type, ST88, according to the STEC Center database (http://www.shigatox.net). ST88 belongs to the *E. coli* B1 phylogroup (Fig. 1) and includes a pyelonephritis strain, *E. coli* reference (ECOR) strain 72 (ECOR-72). Screening for the presence of 37 virulence genes (4–6) confirmed the presence of fimbrial genes (c1936, *fimA*, *ppdD*, and *yehA*) previously shown to be associated with attachment and virulence in the urinary tract (4, 6).

ECOR-72 has been circulating in humans for some time (7, 8) and was shown to be sensitive to 14 antibiotics (9). Susceptibility testing (Vitek 2; bioMérieux Inc., Durham, NC) of 22 randomly selected ST88 isolates from this study, however, indicated that all were resistant to ampicillin and ampicillin-clavulanic acid as well as narrow-spectrum and expanded-spectrum cephalosporins (cefazolin and ceftriaxone), 2 of the 3 aminoglycosides (gentamicin and tobramycin), and, with a single exception, fluoroquinolones (ciprofloxacin and moxifloxacin).

There is growing concern over the emergence of non-ST131, fluoroquinolone-resistant (FQ^r) ExPEC (10). Given that all ST88 KATH isolates tested but one were resistant to both ciprofloxacin and moxifloxacin, it seems they may be an important reservoir of fluoroquinolone resistance genes. More data are needed to determine the directionality of these events and whether resistant ST88 ExPEC strains are common in other regions. Regardless, the widespread availability of antibiotics without prescription in the Kumasi area may have contributed to the fact that ~37% of all community-acquired and ~60% of all nosocomial, clinical ExPEC isolates at our center are now ESBL-producing ST88.

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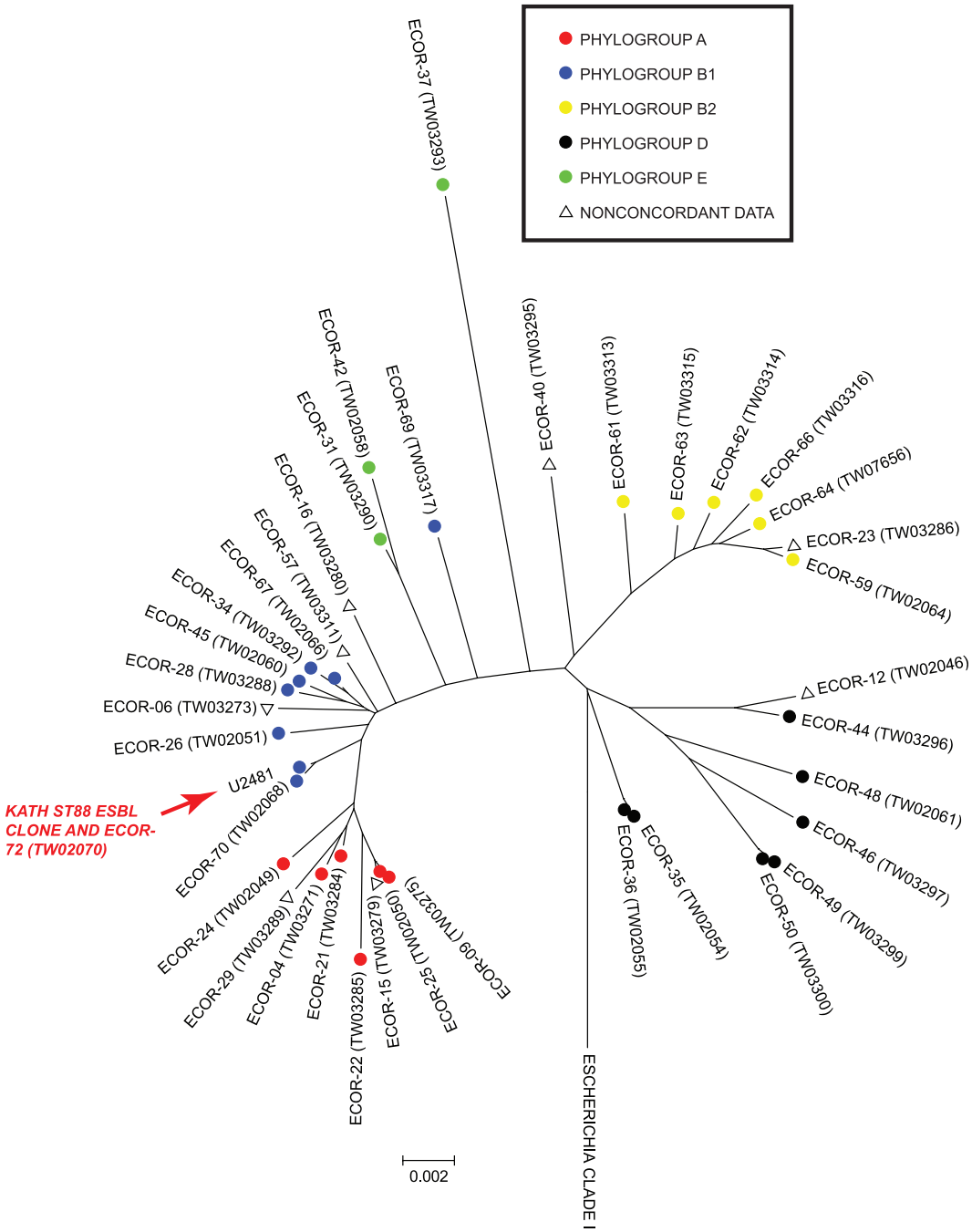

FIG 1 Phylogenetic relationships among isolates of the ECOR collection and the ESBL-producing ST88 clone from KATH (red arrow). Isolates are labeled according to ECOR numbers and STEC Center identification numbers ("TW"). Colors are used to indicate *E. coli* phylogroup designations, and only unique STs are shown (i.e., other ECOR representatives of the same ST are not shown). Inconsistencies between phylogroup designations between studies (11, 12) are labeled for reference with open triangles. A representative of the closest common ancestor to *E. coli* (*Escherichia* clade I) was used as an outgroup in the dendrogram (13).

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