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***Salmonella* enterica Serovar Typhi with CTX-M β-Lactamase, Germany**

To the Editor: Infection with *Salmonella enterica* serovar Typhi, the causative agent of typhoid fever, is an acute systemic illness with a high proportion of illness and deaths, especially in developing countries. In Europe, *S. enterica* ser. Typhi infections occur among travelers returning from disease-endemic areas. After emergence of multidrug-resistant *S. enterica* ser. Typhi strains that confer resistance to chloramphenicol, trimethoprim, and ampicillin, quinolones have become the primary drugs for treatment (1). Here we report the isolation of CTX-M–producing *S. enterica* ser. Typhi in Germany.

We isolated *S. enterica* ser. Typhi from blood and feces specimens from a 30-year-old Iraqi woman who was admitted to the hospital in Cologne in August 2008. The patient was febrile, dizzy, and had epigastric pain and headache. The symptoms began 2 weeks earlier, after she had returned from a month-long visit to her relatives in Sulaymaniya, the capital of As Sulaymaniyah Governorate in the northeastern Iraqi Kurdistan region. The interview indicated that the same symptoms had developed in other family members in Iraq. The patient was treated successfully with meropenem (1 g 3×/day) for 2 weeks, and

no relapse was observed in a follow-up period of 6 months.

The isolated strain was identified as *S. enterica* ser. Typhi with the VITEK2 system (VITEK2 GN-card; bioMérieux, Brussels, Belgium) and by slide agglutination with *Salmonella* antisera (SIFIN, Berlin, Germany) in accordance with the Kauffmann-White scheme. By using Vi-phage typing according to the International Federation for Enteric Phage Typing (L.R. Ward, pers. comm.), the strain was classified as *S. enterica* ser. Typhi Vi-phage type E9. Antimicrobial drug susceptibilities were determined according to the guidelines of the Clinical Laboratory Standards Institute with the VITEK2 AST-N021 card and Etest (bioMérieux). The extended-spectrum β-lactamase (ESBL) phenotype was confirmed with a combined disk diffusion test (MASTDISCS ID, Mast Diagnostica GmbH, Germany). PCR and sequence analyses were performed with universal primers for the ESBL genes *bla*_{CTX-M}, *bla*_{TEM}, and *bla*_{SHV} as described previously (2). Primer CTX-M-F 5'-G TTCGTCTCTCCAGAATAAGG-3' and primer CTX-M-R 5'-CAG-CACCTTTGCCGTCTAAG-3' were used for sequencing the entire *bla*_{CTX-M} gene. Investigation of the CTX-M environment was performed with primers IS26-F (5'-GCCCTGGTAAGCAG AGTTTTTG-3') and IS26-CTX-R (5'-ACAGCGGCACACTTCCTAA C-3'). The presence of plasmid-mediated quinolone resistance genes (*qnr*) was determined by PCR and sequencing of *qnrB* (3), *qnrS* (primer F, 5'-CGGCACCACAACCTTTTCAC-3'; primer R, 5'-CAACAATACCCAGT GCTTCG-3'), and *qnrA* (primer F, 5'-ATTTCTCACGCCAGGATTTG-3'; primer R, 5'-CGCAAAGGTTAGGT CACAG-3'). In addition, the nucleotide sequences of the quinolone resistance-determining regions of the *gyrA*, *gyrB*, *parC*, and *parE* genes were determined as previously described (4). Transfer of β-lactam resistance was tested by broth mating assays with a sodium azide–

resistant *Escherichia coli* J53 recipient. Selection of transconjugants was performed on Mueller-Hinton agar plates that contained sodium azide (200 µg/mL) and ampicillin (100 µg/mL). We isolated the plasmid DNA of donor and transconjugants using the QIAGEN Plasmid Mini Kit (QIAGEN, Hilden, Germany).

Phenotypically, the strain was resistant to ampicillin, ampicillin/sulbactam, piperacillin, cefotaxime, ceftazidime, cefepime, chloramphenicol, streptomycin, trimethoprim/sulfamethoxazole, azithromycin, and nalidixic acid. A reduced susceptibility to ciprofloxacin was detected (MIC_{CIP} = 1 µg/mL). The isolate was susceptible to imipenem, meropenem, gentamicin, tobramycin, and amikacin. PCR and sequence analyses displayed the presence of *bla*_{CTX-M-15}, *bla*_{TEM-1} and the *qnrB2* gene. We found an amino acid substitution in *gyrA* gene (83-Ser→Phe). No mutations were identified in the *gyrB*, *parC*, and *parE* genes. Sequencing of the insertion element (IS)26-F/R amplification product showed the location of IS26 *transposase A* gene (*tnpA*), followed by a truncated *ISEcp1* mobile element upstream of the *bla*_{CTX-M-15} gene. By conjugation, 1 plasmid of ≈50 kbp was successfully transferred into an *E. coli* J53 recipient (Figure). PCR-based replicon typing (5) showed an IncN-related plasmid. The *E. coli* J53 transconjugant mediated resistance to ampicillin, cefotaxime, ceftazidime, cefepime, trimethoprim/sulfamethazole, nalidixic acid and showed reduced susceptibility to ciprofloxacin (MIC = 0.5 µg/mL). Also, in the transconjugant, the *bla*_{CTX-M-15} and *qnrB2* genes were identified by PCR.

ESBL-producing non-Typhi serotypes of *S. enterica* are an increasing problem worldwide. In Europe and Asia, CTX-M-group ESBLs are prevalent in *S. enterica*, and in North America, domestically acquired CTX-M ESBLs were recently identified in *S. enterica* ser. Typhimurium

(6). In *S. enterica* ser. Typhi, reports of ESBLs have been rare. The CTX-M-15 type that we found has been reported only once previously in *S. enterica* ser. Typhi from Indian patients hospitalized in Kuwait (7). In addition to cephalosporin resistance mediated by ESBLs, the reduced susceptibility to quinolones in *S. enterica* is of concern. In the study isolate, this reduced susceptibility was due to a known mutation 83-Ser→Phe in *gyrA* (8) and the acquisition of a *qnrB2* gene. Plasmid-mediated Qnr determinants have been identified in *S. enterica* of different non-Typhi serovars (9), whereas in *S. enterica* ser. Typhi, only mutations in gyrase and topoisomerase genes leading to quinolone resistance had been observed previously (8).

In our isolate of *S. enterica* ser. Typhi that contained *bla*_{CTX-15} and *qnrB2*, resistance to cephalosporins as well as the reduced quinolone susceptibility was easily transferable by con-

jugation into *E. coli*. This occurrence is alarming because the dissemination of such strains with acquired resistances will further limit the therapeutic options for treatment of typhoid fever.

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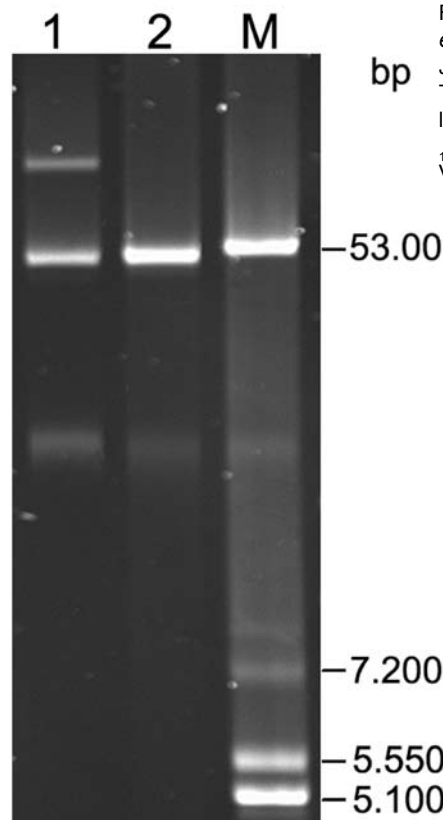


Figure. Plasmids isolated from *Salmonella enterica* serovar Typhi and *Escherichia coli* J53 transconjugant. Lane 1, *S. enterica* ser. Typhi 218/08 (*bla*_{CTX-M-15} + *bla*_{TEM-1} + *qnrB2*); lane 2, *E. coli* J53 transconjugant (*bla*_{CTX-M-15} + *qnrB2*); lane M, plasmid marker *E. coli* V517.

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***Gordonia sputi* Bacteremia**

To the Editor: In November 2007, a 69-year-old man with fever was hospitalized at the Northern Hospital in Marseilles, France. He also had diabetes, high blood pressure, and alcohol and tobacco addictions. In September 2007, he had received a diagnosis of laryngeal cancer, which required 2 chemotherapy treatments through a central venous catheter (CVC), the second of which he had received 6 days before his November visit. Prostatic cancer, diagnosed 1.5 years earlier, had been treated by radiotherapy. At the time of the November admission, he had leukopenia (1.77×10^9 leukocytes/L with 0.49×10^9 polymorphonuclear cells/L) and an elevated C-reactive protein level (151 mg/L). The patient was admitted with a preliminary diagnosis of drug-induced febrile granulocytosis; the origin of his fever remained unclear. Blood for culture was first collected from a peripheral vein and on the next day was collected from a peripheral vein and from the CVC. Gram-positive rods grew in the aerobic bottle from the CVC sample. The microorganism was identified by biochemical tests using API Coryne strip (bioMérieux, Marcy-l'Étoile, France) as *Rhodococcus* spp. (94% similarity). The day after hospital admission, the patient was empirically treated with intravenous ticarcillin-clavulanate, 5 g 3×/day; ciprofloxacin, 200 mg 2×/day; and granulocyte colony-stimulating factor. One day later, fever resolved and the polymorphonuclear cell count was within normal limits. Oral antimi-

crobial drug therapy was continued for 1 week.

Bacterial identification of the strain was performed by 16S rRNA sequencing. We obtained a 1,464-bp sequence, which was found to differ at only 2 nt positions from that of *Gordonia sputi* (GenBank accession no. X80634). We concluded that our patient had catheter-related bacteremia caused by *G. sputi* because he was immunocompromised and had a CVC. We ruled out a contaminant because the organism did not belong to the normal flora of human skin and because fever resolved after treatment with antimicrobial drugs.

The genus *Gordonia* was first described in 1971, for coryneform bacteria isolated from sputum of patients with pulmonary disease or from soil (1). It is a member of the mycolic acid-containing group consisting of genera *Corynebacterium*, *Dietzia*, *Gordonia*, *Mycobacterium*, *Nocardia*, *Rhodococcus*, and *Tsukamurella*. The genus has been revised several times by rearrangements with the genera *Rhodococcus* and *Nocardia*, and the name *Gordonia* was changed to *Gordonia* in 1997. The genus belongs to suborder *Corynebacterineae* within the order *Actinomycetales* and currently contains 27 recognized species; only 7 have been described in human disease. Species are identified by molecular analysis.

Gordonia spp. cause a wide spectrum of disease in humans (2–10; Table). Neurologic and vascular infections in immunocompromised and immunocompetent patients have been reported. Cutaneous and respiratory infections, otitis externa, osteitis, and arthritis have reportedly occurred only in immunocompetent patients. Bacteria have most often been isolated from blood samples. Bacteremia has started from underlying disease such as a sequestered lung (4) or acute cholecystitis (5) or has been related to coronary artery surgery (2) and frequently to CVCs (2,3,6). Catheter removal has been recommended for treatment of