and provides a clear example of how epidemiologic baseline information on virus host range and tropism in animals may provide indications for the presence of similar viruses in the same organ system of humans. To clarify the epidemiology and pathogenicity of picobirnaviruses in humans, additional surveillance should be carried out in persons with and without respiratory and enteric disease.

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New Delhi Metallo-β-Lactamase 4–producing *Escherichia coli* in Cameroon

To the Editor: The metallo-β-lactamase (MBL) group of enzymes inactivates many β-lactam antimicrobial drugs. First identified from a *Klebsiella pneumoniae* strain recovered from a patient hospitalized in India, the New Delhi metallo-β-lactamase-1 (NDM-1), particularly in *Enterobacteriaceae*, is now the focus of worldwide attention (*1*). Whereas India and Pakistan were considered as the main reservoirs of the $bla_{\text{NDM-1}}$ gene (*2*) that produces this MBL, several NDM-1–producing *Enterobacteriaceae* isolates have been reported from the Balkan states and the Middle East, suggesting that those areas might be secondary reservoirs (*2*).

Since 2010, 3 NDM-1 point-mutation variants have been described (*3*–*5*). The first variant, NDM-2, was identified from an *Acinetobacter baumannii* isolate collected from a patient transferred from a hospital in Egypt to Germany (*4*). Subsequently, a clonal dissemination of NDM-2–producing *A. baumanni* was described in Israel (*6*). The second variant, NDM-4, which was identified in *Escherichia coli* from a patient hospitalized in India, possessed a higher carbapenemase activity compared with NDM-1 (*5*). The most recent variant, NDM-5, was identified in *E. coli* from a patient who had a history of hospitalization in India (*3*).

As recommended for the detection of carbapenemase producers (*7*), a rectal swab specimen was collected from a patient transferred from Cameroon to France. The *E. coli* strain FEK was isolated from the specimen.

He had been hospitalized for 1 month in Douala for an inflammatory syndrome associated with a kidney failure before his transfer to Paris. No history of travel in India was reported for this patient. Susceptibility testing was performed by disk diffusion assay (Sanofi-Diagnostic Pasteur, Marnes-la-Coquette, France), and results were interpreted according to the updated guidelines of the Clinical and Laboratory Standards Institute (Wayne, PA, USA; www.clsi.org). The MICs were determined by using Etest (bioMérieux, La Balmes-Les-Grottes, France) on Mueller-Hinton agar at 37°C.

E. coli FEK was fully resistant to all β-lactam antimicrobial drugs, including imipenem, meropenem, ertapenem, and doripenem (MICs >32 mg/L for all carbapenems). This isolate was also resistant to aminoglycosides, except amikacin, and to fluoroquinolones. We performed PCR amplification followed by sequencing on whole-cell DNA, as described (*8*). We identified the bla_{NDM-4}, $bla_{CTX-M-15}$, and bla_{OXA-1} genes. *E. coli* FEK also harbored the *aacA4* gene encoding the AAC(6′)-Ib acetyltransferase that confers high-level resistance to aminoglycosides, except amikacin. Results of multilocus sequence typing analysis performed as described (*5*) showed that the isolate belonged to sequence type (ST) ST405. Identification of this ST type among NDM-producing *E. coli*, compared with NDM-4– and NDM-5–producing *E. coli* in ST648, demonstrated that the spread of NDM-4 occurred among unrelated *E. coli* clonal backgrounds (*3*,*5*).

Plasmid DNA of *E. coli* FEK was extracted and analyzed as described (*5*). A single, ≈120-kb plasmid was identified. Direct transfer of the β-lactam resistance marker into *E. coli* J53 was attempted by liquid mating-out assays at 37°C. With the exception of the aminoglycoside amikin, transconjugants from *E. coli* were resistant to β-lactam antimicrobial drugs. MICs of imipenem, meropenem, ertapenem, and doripenem were 6, 3, 6, and 4 mg/L, respectively. The transconjugants harbored an 120-kb plasmid carrying bla_{NDM-4} and the $bla_{CTX-M-15}$, bla_{OXA-1}, and *aacA4* genes. We performed PCR-based replicon typing as described (*5*) and showed that this bla_{NDM-4}–positive plasmid belonged to the IncFIA incompatibility group. The IncF incompatibility group was previously reported to be associated with bla_{NDM-4} and bla_{NDM-5} (*3*,*5*).

By analyzing genetic structures surrounding the bla_{NDM-4} gene, performed by PCR mapping as described (*8*), we identified insertion sequence IS*Aba125* upstream and the bleomycin resistance gene ble_{MBL} downstream of the bla_{NDM-4} gene. The same genetic environment has been observed for most NDM-1–positive enterobacterial isolates (*8*). We showed in previous research that expression of ble_{MBL} conferred high-level resistance to bleomycin and bleomycin-like molecules (*9*); accordingly, the *E. coli* clinical isolate and its transconjugant were highly resistant to bleomycin (MIC >512 μg/mL) (*9*).

The patient had a history of Hodgkin lymphoma treated by 8 sessions of bleomycin chemotherapy 1 year before his hospitalization. This anticancer drug is widely distributed throughout the body following intravenous administration, and plasmatic concentrations increase in proportion with the increase of the dose (*10*). Because the patient was successively treated with 30 mg of bleomycin, the serum levels achieved (≈2–5 mg/mL) might have contributed to selection of the ble_{MBL} gene. Similarly, the multiple courses of antibacterial drug therapy administered in Cameroon (including carbapenems) could have contributed to selection of the bla_{NDM-4} gene.

By culturing rectal swab samples from the patient, we identified fecal carriage of *E. coli* carrying a plasmid-encoded bla_{NDM-1} gene. That strain had a distinct ST type (ST5) compared with the index strain. The plasmid carrying the bla_{NDM-1} gene with the bla_{OXA-1} and *aacA4* genes belonged to the IncFIA incompatibility group.

β-Lactamase NDM-4 displaying increased carbapenemase activity compared with NDM-1 was described in a patient hospitalized in India (*5*). This study shows that NDM-4 producers are also present in Africa; specifically, in the highly populated city of Douala, providing an environment that may promote the dissemination of those strains. We showed that the same patient was carrying strains expressing 2 NDM variants**,** possibly indicating ongoing evolution of NDM variants.

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Salmonella enterica Serovar Agbeni, British Columbia, Canada, 2011

To the Editor: Infection with *Salmonella enterica* serovar Agbeni is rare. In Canada, it was reported 8 times during 2000–2010 and never in the province of British Columbia (2011 population 4.5 million) (Public Health Agency of Canada, unpub. data). In June 2011, an outbreak of *S. enterica* ser. Agbeni affecting 8 persons was identified in British Columbia; pulsed-field gel electrophoresis patterns for all isolates were identical. Although no specific source was identified, 2 features were noted: 1) diagnosis through urine specimens for 3 of 8 persons and 2) a longer than typical incubation period for *Salmonella* spp. infection.

In British Columbia, public health authorities interview all reported *Salmonella* spp.–infected persons by using a standard questionnaire (www.bccdc.ca/discond/CDSurveillanceForms) to collect information about potential exposures during the 3 days before date of illness onset. Seven of the ill persons in British Columbia had attended the same wedding on May 14, 2011, which was outside the 3-day period about which they were asked. The person with the earliest reported case (May 16) was not associated with the wedding or with the other ill persons.

We reviewed wedding food sources and preparation. The 7 persons with wedding-associated illness were reinterviewed by using a menu-specific questionnaire; no obvious food source was implicated. The first wedding guest to be reported with enteric symptoms was visiting from outside British Columbia and had assisted with food preparation. In April and May 2011, five persons from the same jurisdiction outside British Columbia in which this wedding guest resided were identified with *S. enterica* ser. Agbeni infection; isolates from these persons had the same pulsed-field gel electrophoresis pattern as those in British Columbia. Also, the ill person who was not associated with the wedding had traveled to that same jurisdiction before onset of symptoms. The original source of infection was probably outside of British Columbia.

Average age of the 8 ill persons was 52.8 years (range 21–82 years). Six were men. One person reported hospital admission. No underlying conditions were documented in any of the 8 ill persons.

Culture results of urine samples were positive for 3 (38%) of the 8 ill persons; feces were not tested. All 3 persons had symptoms of urinary tract infection (UTI), and 2 had fever. All were men and were the oldest persons reported. Two had gastrointestinal (GI) symptoms before UTI symptoms. For 1 person, the interval between onset of GI and UTI symptoms was 15 days.

Approximately 1% of nontyphoidal *Salmonella* spp. infections are detected in urine (*1*,*2*). In British Columbia, ≈3% of *Salmonella* isolates submitted to the reference laboratory are isolated from urine (British Columbia Centre for Disease Control's Public Health Microbiology and Reference Laboratory, unpub. data). *Salmonella* spp. are more often recovered from urine in adults >60 years of age, children (*2*,*3*), and female patients (*2*,*4*). Immunocompromising conditions and urinary tract structural abnormalities also are risk factors for isolating the organism in urine (*2*,*3*). Also, certain *Salmonella* serogroups or serotypes are more likely than others to be isolated from urine (*2*,*3*). GI symptoms concurrent with or preceding UTI are rare (*4*,*5*). We found no literature to suggest whether *S. enterica* ser. Agbeni is more likely to cause systemic illness or UTI. The