have stated that introduction of fluoroquinolones for use in veterinary practice has been associated with a dramatic rise in Campylobacter strains showing resistance to these drugs (9). Increasing antimicrobial drug resistance limits the number of therapeutic options, which makes empirical treatment more difficult. Therefore, constant monitoring of Campylobacter susceptibility to antimicrobial agents is essential. We could not detect any allele of plasmid-mediated quinolone resistance genes (qnr) among C. jejuni isolates and the different class of mobile genetic elements that generally carry the antimicrobial resistance gene cassettes. However, we found that most of the C. jejuni isolates had a mutation in the quinolone-resistance determining region of gyrA (Thr-86 to Ile), which led the isolates to become resistant for quinolone and fluoroquinolones.

Recent microbiome analysis of the gut of a malnourished child residing in an urban slum in Kolkata showed 35 times more Campylobacter bacteria than in healthy child in the same setting (10). This finding suggests that intestinal inflammation may directly influence malabsorption of nutrients. Hence, it is essential to examine the effect of Campylobacter infection in the developing world in the context of many recent developments in the human gut microbiome.

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To the Editor: Among Enterobacteriaceae, Verona integron-encoded metallo–β-lactamase 1 in Enterobacteria, Ontario, Canada

Verona Integron–encoded Metallo-β-Lactamase 1 in Enterobacteria, Ontario, Canada

To the Editor: Among Enterobacteriaceae, Verona integron–encoded metallo–β-lactamase 1 (VIM-1) has been found only in Klebsiella pneumoniae in North America (1). We report 4 VIM-1–producing Enterobacteriaceae isolated from 4 patients at 3 hospitals in Ontario, Canada.

Patient 1, a 61-year-old man, was initially hospitalized in Italy for presumed pneumonia and was treated with levofloxacin during his 6-month stay in Italy. Upon returning to Ontario, Canada, he was admitted to hospital 1 in August 2010 because of diabetic ketoacidosis and began empiric treatment with metronidazole and gentamicin. Urine cultures were positive for a carbapenem-resistant Escherichia coli (strain GN531). Two days later, the patient had a fever and a blood culture was positive for E. coli (strain GN532), which was also resistant to carbapenems. During his hospitalization, the patient was isolated and received droplet precaution because of his travel history until he was discharged home.

Patient 2, a 76-year-old man, was admitted to hospital 2 in May 2011 because of a recurrent urinary tract...
infection (urine was positive for *E. coli*). The patient was given ciprofloxacin. On day 49, a carbapenem-sensitive *Enterobacter cloacae* was isolated from urine. On day 61, a carbapenem-resistant *E. cloacae* was isolated from urine culture (strain GN719). Contact precautions were used until the patient was discharged to a long-term care facility on day 80.

Patient 3, an 81-year-old man, was admitted to hospital 2 (November 2011) 2 months after patient 2 was discharged. Urine culture at admission was positive for a carbapenem-resistant *E. cloacae* (strain GN825).

The patient was given ceftriaxone and metronidazole and then ceftriaxone and a carbapenem. The patient died on day 110. Patients 2 and 3 had no hospital room in common during their admissions and both received contact precautions for methicillin-resistant *Staphylococcus aureus* before isolation of the carbapenem-resistant isolates.

Patient 4, a 90-year-old woman, was admitted to hospital 3 in November 2011 because of nausea, vomiting, and diarrhea. In the preceding 6-month period, she had recurrent *Clostridium difficile*–associated diarrhea. At admission, a carbapenem-susceptible *Proteus* spp. was isolated from a urine culture. The patient was given a 3-day course of ciprofloxacin and vancomycin. On day 17, a carbapenem-resistant *E. cloacae* was isolated from urine (strain GN738). Because this organism was also isolated from a rectal swab specimen, it was assumed that the urine sample might be contaminated by her feces. Therefore, the patient did not receive additional treatment other than that for recurrent *C. difficile*–associated diarrhea.

Patients 2, 3, and 4 had no history of travel outside Canada. All 5

Table. VIM-1–producing *Escherichia coli* and *Enterobacter cloacae* clinical isolates, derivative transconjugants, and transformants, Ontario, Canada*

| Characteristic | E. coli GN531 | E. cloacae GN719 | E. cloacae GN738 | E. cloacae GN825 | E. coli J-531 | E. coli T-719 | E. coli 825 | E. coli Top10 | E. coli J53 |
|---------------|--------------|-----------------|-----------------|-----------------|--------------|--------------|------------|-------------|------------|
| Drug, MIC (mg/L)† |              |                 |                 |                 |              |              |            |             |            |
| Ampicillin    | ≥256         | ≥256            | ≥256            | ≥256            | ≥256         | ≥256         | ≥256       | 3           | 6          |
| Ceftoxin      | ≥256         | ≥256            | ≥256            | ≥256            | 64           | ≥256         | ≥256       | 6           | 8          |
| Ceftazidime   | ≥256         | ≥256            | ≥256            | ≥256            | ≥256         | ≥256         | ≥256       | 0.19        | 0.19       |
| Ceftoxime     | ≥256         | ≥256            | ≥256            | ≥256            | 96           | 128          | ≥256       | 0.094       | 0.094      |
| Cefepime      | 256          | 32              | 192             | 256             | 12           | 12           | 24         | <0.016      | 0.064      |
| Ertapenem     | 2            | 2               | 8               | 24              | 0.125        | 0.25         | 0.25       | 0.004       | 0.008      |
| Meropenem     | 1.5          | 6               | 16              | 0.5             | 0.5          | 0.5          | 0.023      | 0.023       |            |
| Imipenem      | 4            | 6               | 6               | 8               | 2            | 2            | 1.5        | 0.19        | 0.38       |
| Aztreonam     | ≥256         | 0.19            | 4               | 1.5             | 192          | 0.125        | 0.125      | 0.125       | 0.125      |
| Amikacin      | 8            | 2               | 3               | 2               | 3            | 1.5          | 1.5        | 2           | 1.5        |
| Gentamicin    | 96           | 12              | 2               | 96              | 0.75         | 2            | 0.064      | 1.5         |            |
| Tobramycin    | 32           | 48              | 6               | 32              | 12           | 4            | 4          | 0.25        | 1          |
| Nalidixic acid| ≥256         | ≥256            | ≥256            | ≥256            | 32           | 2            | 1          | 3           |            |
| Ciprofloxacin | ≥32          | ≥32             | ≥32             | ≥32             | 0.5          | 0.125        | <0.002     | <0.002      | 0.012      |
| Levofloxacin  | ≥8           | ≥32             | ≥32             | 8               | 0.094        | 0.002        | 0.003      | 0.016       |            |
| Tetracycline  | ≤4           | 192             | 2               | 256             | 0.5          | 32           | 32         | 0.75        | 1          |
| Tigecycline   | 0.094        | 1               | 0.5             | 1               | 0.047        | 0.064        | 0.094      | 0.032       | 0.047      |
| Colistin      | 0.064        | 0.094           | 0.094           | 0.125           | 0.047       | 0.023        | 0.016      | 0.016       | 0.047      |
| Co-trimoxazole| ≥32          | ≥32             | ≥32             | ≥32             | ≥32          | 0.047        | 0.023      | 0.064       |            |
| Drug resistance gene‡ | + | + | + | + | + | + | + | NA | NA |
| bla<sub>VIM-1</sub> | + | + | + | + | + | + | + | NA | NA |
| bla<sub>CTX-M-15</sub> | + | + | + | + | + | + | + | NA | NA |
| bla<sub>TEM-1</sub> | + | + | + | + | + | + | + | NA | NA |
| bla<sub>ACC-1</sub> | + | + | + | + | + | + | + | NA | NA |
| bla<sub>OXA-1</sub>i & & & | + | + | + | + | + | + | + | NA | NA |
| gnrS1 | + | + | + | + | + | + | + | NA | NA |

*VIM-1, Verona integrase–encoded metallo-β-lactamase 1; E. coli J-531, E. coli transconjugant derived from GN531; E. coli T-719 and T-825, E. coli transformants derived from GN719 and GN825, respectively; E. coli J53 and TOP10, recipient E. coli J53 and TOP10, respectively; bla, β-lactamase; +, positive; NA, not applicable (only genes and replicons detected by molecular screening are included); −, negative; qnr, quinolone resistance; Inc, incompatibility.
†Drug susceptibility results were determined by using Etest (bioMérieux, Marcy l’Etoile, France) and the agar dilution method and interpreted by using Clinical and Laboratory Standards Institute guidelines (3).
‡Sequence of whole genes was performed in samples positive by PCR. PCR included screening for *bla<sub>TEM</sub>*; *bla<sub>SHV</sub>*; *bla<sub>OXA-1</sub>*; *bla<sub>CTX-M</sub>* groups 1, 2, and 9; *bla<sub>AC</sub>*; *bla<sub>GES</sub>*; *bla<sub>QPC</sub>*; *bla<sub>TEM-1</sub>*; and 6 groups of *bla<sub>AMPc</sub>* genes (4).
§Obtained by using the replicon typing approach of Carattoli et al. (5).
isolates were submitted for reference purposes to the Public Health Ontario Laboratories. Pulsed-field gel electrophoresis showed that *E. coli* GN531 and GN532 were indistinguishable (GN531 was selected for further studies), and the 3 *E. cloacae* isolates had similar fingerprint patterns. All strains displayed synergy in presence of meropenem disks plus dipicolinic acid, which is indicative of metallo-β-lactamase inhibition (2). The 4 clinical strains displayed a multidrug resistance phenotype, and were susceptible only to tigecycline transformation with plasmid extracts from *E. cloacae* GN738 was unsuccessful. Pulsed-field gel electrophoresis with S1 nuclease (9) and Southern blot analysis identified VIM-1-containing plasmids; estimated sizes were 65 kb (*E. coli* GN531), 50 kb (*E. cloacae* GN738), and 30 kb (*E. cloacae* GN719 and GN825).

In conclusion, VIM-1 was found among *Enterobacteriaceae* from 3 geographically distant nosocomial units in Ontario, Canada. Although *E. cloacae* strains were clonally related, there were no clear epidemiologic links between these patients, suggesting that the clone or resistance gene might circulating in the province on a greater scale than believed. Emergence of *E. coli* ST131, a pandemic multidrug-resistant clone that causes cases predominantly community-onset infections (7), and produces simultaneously CTX-M-15 and VIM-1, could be a serious threat for the dissemination of these drug-resistance elements.

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