

Bicout's letter), Bicout shows that more time is required to detect a bioterror attack than when exponential infection growth is assumed (Figure accompanying Bicout's letter). The number of persons infected over time under the logistic model will be fewer than the number of persons infected if exponential growth is assumed; therefore, screening blood donors to detect a bioterror attack is even less attractive than using our best-case assumptions. The take-home message from our article was and is: It makes little sense to screen blood donors to detect a bioterror attack.

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Aeromonas spp. and Infectious Diarrhea, Hong Kong

To the Editor: Vila et al. reported the prevalence of *Aeromonas* spp. associated with traveler's diarrhea in Spain (1). Some of the patients described in this study had traveled to countries in Asia, such as Thailand and India. This report details the

prevalence of this pathogen in patients with acute infectious diarrhea who were treated in emergency department settings in Hong Kong.

Over a 12-month period, we retrospectively studied all adult patients who showed clinical features of acute infectious diarrhea, were treated as outpatients with or without observation in the emergency department, and had a positive stool culture (2-4). Our data were collected at an urban university-affiliated hospital with 1,400 beds and an emergency department with an annual census of 190,000 patient visits. *Aeromonas* spp. were isolated from stool samples by standard culture procedures, which included introduction onto xylose lysine desoxycholate agar plate and thiosulphate citrate bile sucrose plate, and subsequent screening by triple iron sugar slant (acid butt with no H₂S), positive oxidase, negative urease, fermentation of mannitol but not dulcitol and inositol, resistance to vibriostatic agent 0/129, and ability to grow at 0% NaCl. The main species of *Aeromonas* were identified by the differential biochemical reactions of gas production from D-glucose, arginine dihydrolase, ornithine and lysine decarboxylase; esculin hydrolysis; Voges Proskauer reaction; fermentation from arabinose, sucrose, mannitol, salacin, and D-sorbitol; and citrate and glycerol utilization (5).

Of 130 patients with positive stool cultures, *Aeromonas* spp. were isolated in 9 patients (6.9%), including *A. caviae* in 4 patients, *A. hydrophila* in 2 patients, and *A. veronii* in 3 patients. The cases were not epidemiologically linked. In one of these isolates (*A. caviae*), another enteropathogen (*Vibrio parahaemolyticus*) was also isolated. None of the patients reported recent travel abroad or to mainland China before treatment.

Our review of the clinical features of these nine patients found that the mean highest body temperature at the time of treatment or during the

patient's stay in the emergency department was 37.4°C (95% confidence interval [CI] 36.9-38.0). Two patients (both with *A. caviae* isolated) had temperatures >37.5°C. Bloody diarrhea was present in two patients (one with *A. veronii* and one with *A. caviae*). The mean number of unformed stools per day was 8.6 (95% CI 4.0-13.2). Abdominal pain in eight patients and vomiting in four patients was reported. Five patients required admission to the emergency department's observation unit before discharge. Of these, four patients needed intravenous fluid therapy. Empiric ciprofloxacin was given to one patient with a temperature of 38.3°C. Stool culture results were available within 3 days for positive isolation of *Aeromonas*. All *Aeromonas* strains were susceptible to ciprofloxacin, cefotaxime, cotrimoxazole, and chloramphenicol, while two of nine isolates (one *A. caviae* strain and one *A. hydrophila* strain) were susceptible to ampicillin. All patients had recovered satisfactorily by the time stool culture results were available, and antimicrobial therapy was not necessary, except for the patient who was given ciprofloxacin empirically.

In conclusion, *Aeromonas* spp. are responsible for a small proportion of cases of bacterial gastroenteritis encountered in an urban emergency department setting in Hong Kong. Patients affected do not necessarily have a history of travel to a nonindustrialized region. In a substantial proportion of cases, the symptoms are severe enough to require intravenous fluid therapy and observation. However, symptoms generally would have resolved by the time the pathogen was isolated from stool culture. In contrast to the report of Vila et al., persistent diarrhea is uncommon, and antimicrobial therapy is usually unnecessary in our particular setting. *Aeromonas* spp. are susceptible to a wide range of antimicrobial drugs, except ampicillin. Whether empiric antimicrobial drugs given at the time of treatment would

have significantly shortened the duration of the symptoms is not known.

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Trichinella papuae in Saltwater Crocodiles (*Crocodylus* *porosus*) of Papua New Guinea

To the Editor: Until 1995, reptiles

were not known to be hosts of *Trichinella*; however, in that year *Trichinella* was detected in 40% of farm-raised crocodiles (*Crocodylus niloticus*) in Zimbabwe. These crocodiles were infected with a new species, *T. zimbabwensis*, which was experimentally infective in mammals, including primates (1).

The infection of reptiles with *Trichinella* species that are potentially infective for humans has become more important since demand for the meat of crocodiles, caimans, and alligators has increased in many areas of the world. This trend has resulted in the development of national breeding programs in more than 30 countries in North, Central, and South America; Africa; Asia; and Australia (2), which generated an income of approximately \$60 million in 1998 (3).

In 1999 in Papua New Guinea, wild and domestic pigs infected with a new species, *T. papuae*, were found (4,5); this new species was capable of completing its life cycle in reptiles that were infected experimentally (6). *Trichinella* infection has also been found in farm-raised saltwater crocodiles (*C. porosus*) in Papua New Guinea, where a national program for crocodile meat and skin products exists.

Papua New Guinea has one crocodile breeding farm that processes approximately 6,000 animals per year. Following the discovery of *Trichinella*-infected crocodiles in Zimbabwe, the Australian government requested that Papua New Guinea conduct *Trichinella* testing on the crocodile meat exported to Australia. Muscle samples from crocodiles were digested by pepsin and HCl solution according to the standard technique (7). When available, approximately 100 larvae from each infected crocodile were given by mouth to laboratory rats, and 10–20 larvae were stored in 90% ethyl alcohol for molecular identification. Multiplex polymerase chain reaction

(PCR) was used to characterize the larvae, according to a published protocol (8). The primer set oTsr1 and oTsr4 was used to amplify the expansion segment V of the large subunit ribosomal RNA (9). The larvae of all *Trichinella* reference strains were used as controls. PCR products were gel-purified and directly sequenced by using the same primers as those used for PCR amplification. All sequences were aligned by using the Clustal W program from OMIGA 2.0 (Accelrys, San Diego, CA). Final alignment of the expansion segment V sequences was performed manually so microsatellites could be compared.

Muscle samples from 118 saltwater crocodiles (46 farm-born, 71 wild-born and farm-raised, and 1 killed in the wild near the Bensbach River) were tested. All samples from the farm-born crocodiles were negative for *Trichinella*. Of the samples from the 72 wild-born crocodiles (including the 1 killed in the wild), 16 (22.2%) were positive for *Trichinella* larvae, with an average of 7 larvae/g in the biceps. All of the infected crocodiles originated in the Kikori area (Figure). The prevalence of *Trichinella* infection in crocodiles from this area was 32.0% (16/50). Samples from the remaining 21 wild-born and farm-raised crocodiles, and the 1 killed in the wild, were negative for *Trichinella*. These crocodiles originated in nine different locations (Figure).

PCR analysis showed that the parasites belonged to *T. papuae*. However, the crocodile isolates differed from the reference strain of this species by the deletion of a TG dinucleotide and by a single base mutation (G vs. A) in the expansion segment V sequence. Testing for *Trichinella* in crocodile meat has been conducted in Zimbabwe and Papua New Guinea only, and infected crocodiles have been found in both countries. Crocodiles in other parts of the world are also likely to be infected. Since