Angiostrongyliasis in the Americas

To the Editor: We read with special interest the article by Hochberg et al. about angiostrongyliasis in Hawaii (*1*). *Angiostrongylus cantonensis* meningitis in the Americas was reported by Aguiar et al. in Cuba in 1981 (*2*), and we have studied this zoonosis during the ensuing 25 years. We agree with the authors about the difficulty in obtaining a specific immunoassay for detection of antibodies to *A. cantonensis* antigens. In Cuba, as in Hawaii, no other cause of eosinophilic meningitis was identified.

To improve accuracy of the diagnosis we investigated immunoglobulin (Ig) E intrathecal synthesis during the first diagnostic lumbar puncture. We also confirmed this synthesis as either a 2-class response (IgG + IgA) or a 3-class response (IgG + IgA + IgM) that appeared 8 days later in cerebrospinal fluid (*3*).

Since 1991, our records show that the major incidence of the disease is during the second quarter of the year. We detected 32% of the cases during the rainy season when rats come into houses in rural and semirural areas and snails and slugs appear more often in gardens and yards where children play. Ethnicity data show that 52% of those affected were Caucasian and 32% were African. The median interval from onset of symptoms to lumbar puncture was 1–3 days. Although no children died, 6 (23%) of 26 adult patients died. The clinical signs and symptoms of the Cuban patients are similar to those in Hawaii (*4,5*). We congratulate the authors for systematically determining incidence rates of *A. cantonensis* meningoencephalitis, a severe but preventable infection.

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Increase in Group G Streptococcal Infections in a Community Hospital, New York, USA

To the Editor: Identified in 1935 by Lancefield and Hare, group G streptococci (GGS) are part of the normal flora of the pharynx, gastrointestinal tract, genital tract, and skin (*1–3*). However, previous case reports have indicated that GGS also could cause complicated infections, including cellulitis, osteomyelitis, septic arthritis, meningitis, endocarditis, and bacteremia (*3–6*). Since the mid-1980s, several studies worldwide have reported an increasing incidence of GGS bacteremia (*1,5–8*), but no recent study has been conducted in the United States to determine the incidence of overall GGS infection.

We noticed that an increasing number of patients with GGS have been admitted to Long Island College Hospital in Brooklyn, New York, USA, during the past few years. To better understand the trend of GGS infection in our institution, we retrospectively reviewed charts of patients admitted from January 2003 through December 2007 who had microbiologically proven GGS infection. Inclusion criteria were clinically and microbiologically documented GGS infection in patients who received appropriate antimicrobial drugs and were ≥18 years of age. Lancefield GGS were identified in the laboratory by latex agglutination test; resistance profiles were not done for GGS.

A total of 73 persons with GGS were admitted to the hospital during the 5-year study period; the number of patients admitted increased yearly (Figure). Mean age of patients was 53 years; most (77%) were <65 years of age; 52% were women, and most (61%) patients were African American. Thirty (41%) patients had polymicrobial infections; other identi-

fied organisms included methicillin-susceptible *Staphylococcus aureus* (8 [11%]), methicillin-resistant *S. aureus* (MRSA) (9 [12%]), and gram-negative or anaerobic organisms (13 [18%]).

The spectrum of GGS infections ranged from mild skin and soft tissue infection (34 [46%]) to invasive diseases, including urogenital infection (7 [10%]); lower respiratory tract infection (7 [10%]); pharyngitis (6 [8%]); endocarditis and catheter infection (5 [7%]); and others (14 [19%]), such as peritonitis, pelvic abscess, rectal abscess, and septic arthritis. Four of the 6 persons with pharyngitis were assumed to be colonized with the organism. Eight (24%) of 34 skin and soft tissue infections were associated with bacteremia, 5 (15%) with osteomyelitis, and 20 (59%) with polymicrobial infections. Six persons with lower respiratory tract infections and 1 each with endocarditis, genital tract infection, pelvic abscess, and dental abscess also had polymicrobial infections.

Eighteen persons had bacteremia, the trend of which also increased yearly. Of these, 8 had skin and soft tissue infections, 4 had endocarditis, 2 had urinary tract infections, 1 had possible spontaneous bacteria peritonitis, and 1 had hemodialysis catheter infection; 2 were of unknown source. Of the patients with endocarditis, 2 had vegetations on the native valves, 1 had a pacemaker infection, and 1 had prosthetic valve vegetation. One case of native valve endocarditis occurred in a tricuspid valve in an injection drug user. Another case occurred in a patient in which an epidural abscess was associated with an aortic valve vegetation.

Most of the patients had underlying medical conditions; 34% had diabetes mellitus. In contrast to previous reports, which stated that malignancy was the most common underlying disease (*2,3*), only 7 (10%) of the patients in our study group had underlying malignancy, of whom 4 had active malignancy and the rest had had previous malignancy. Nine patients with a history of injection drug use and 5 with HIV infection were identified; the patient with bacteremia secondary to hemodialysis catheter infection had a history of both HIV and intravenous drug use.

Three (4%) patients died; their deaths were unlikely to be attributable to GGS because all were elderly (78–92 years) and had underlying coexisting conditions and co-infections. All 4 persons with endocarditis and the patient with the catheter infection survived. Five patients who were co-infected with MRSA were treated with vancomycin or daptomycin; the remainder were treated with β-lactam antimicrobial drugs and had the sources of infection (catheter or pacemaker) removed. When infections caused by gram-negative or anaerobe organisms were identified, they were also treated with appropriate antimicrobial drugs. The overall average length of stay for all patients with GGS was 9.4 days, with longer stays for those with underlying diabetes mellitus (14.6 days) than for those without diabetes (6.7 days).

GGS was an important etiologic agent for a wide spectrum of infections. Its impressive increase in our institution during the past 5 years raises concerns because other types of β-hemolytic streptococcal infection have increased recently. Group A and B (*9,10*) increased substantially during the 1980s. A multicenter analysis may confirm GGS as an emerging human pathogen and may help us better understand the reason for this increase.

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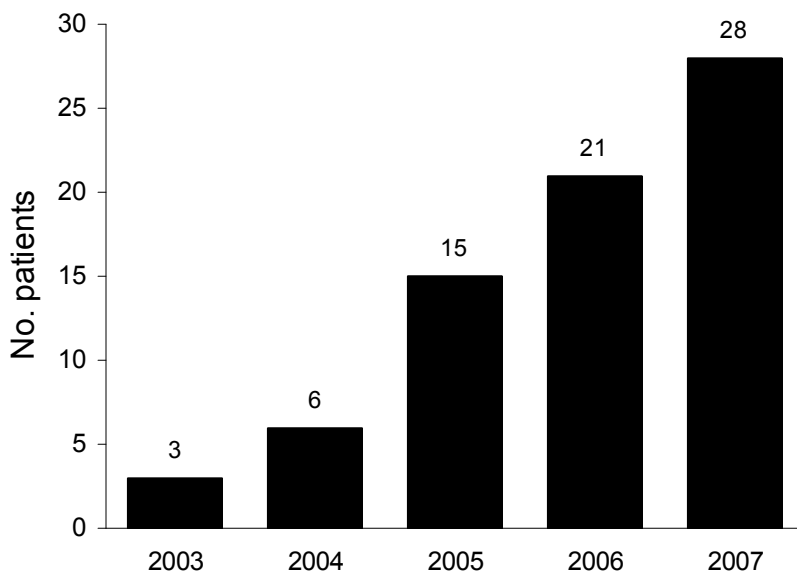Author affiliation: Long Island College Hospital, Brooklyn, New York, USA

Figure. Annual number of patients with group G streptococcal infections admitted to Long Island College Hospital, Brooklyn, New York, USA, 2003–2007.

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New Saffold Cardiovirus in Children, China

To the Editor: A new member of the genus *Cardiovirus*, termed *Saffold virus* (SAFV), was discovered recently in stool specimens and nasopharyngeal aspirate samples from patients with fever of unknown origin, respiratory symptoms, or gastroenteritis; these have been considered the first documented reports of cardiovirus infection in humans (*1–4*). However, the epidemiologic characteristics and pathogenic role of the virus are not fully understood.

From July 2006 through June 2008, stool specimens were collected from 631 hospitalized children with diarrhea and 161 asymptomatic controls in Lanzhou, People's Republic of China. All children were <5 years of age (median age 8 months, range 0–60 months). Diarrhea was defined as ≥3 loose stools in the previous 24–72 h. Controls were asymptomatic children who had been brought to the First Hospital of Lanzhou University Pediatric Primary Care Center for a routine checkup and had not had fever, diarrhea, vomiting, or a respiratory illness in the previous 3 weeks. The stool specimens were then transported to the Chinese Center for Disease Control and Prevention, Beijing, to undergo screening for common enteric viruses. The specimens were tested for rotavirus by using a commercially available ELISA kit (IDEIA Rotavirus; DAKO, Glostrup, Denmark), and PCR and reverse transcription PCR (*5*) were used to screen for other common enteric viruses, including norovirus, sapovirus, astrovirus, and adenovirus.

Viral RNA and DNA were extracted from 140 μL of 10% fecal suspension in phosphate-buffered saline by using QIAamp Viral RNA Mini Kit (QIAGEN, Hilden, Germany); viral RNA and DNA was supposed to be extracted simultaneously, according

to the manufacturer's instructions. Extracts of nucleic acid were tested for SAFV by a nested PCR that targeted the 5′ untranslated region (UTR) gene as described by Drexler et al. (*4*). The viral protein 1 (VP1) gene from positive samples was amplified as described by Chiu et al. (*3*). Positive bands were cloned and sequenced in both directions.

By confirming sequences of the 5′ UTR gene, 3 (0.5%) specimens from the 631 children with diarrhea (LZ50419, LZ52903, LZ53879) and 1 (0.6%) from the 161 asymptomatic children (LZ53010) were found to be positive for SAFV. Of the 4 positive specimens, 2 were collected in October, 1 in September, and 1 in June. The median age of the 4 patients with positive specimens was 6 months (range 2–25 months). Viral co-infection was detected in the 3 children with diarrhea who had SAFV-positive specimens; 2 were co-infected with rotavirus and 1 with norovirus. No co-infection was detected in the asymptomatic child with SAFV-positive results.

The 0.5% detection rate of SAFV in children with diarrhea in our study is lower than the 1.2% reported by Chiu et al. (*3*). One possible reason could be that the patients in our study were younger (median age 8 months), but in other studies, the median age was 20 months for all patients with confirmed cases. Nonetheless, the seasonal distribution of the positive cases in our study is in accordance with the result of Drexler et al. (*4*), namely, in late summer and early fall.

The 5′ UTR sequences of the 4 positive samples were deposited in GenBank (accession nos. FJ586238, FJ586239, FJ610244, and FJ623968). After several trials, only the VP1 sequence of sample LZ50419 was amplified (accession no. FJ586240). The obtained sequences were analyzed by using the DNASTAR software package (DNASTAR, Madison, WI, USA). A BLAST search (http://blast.ncbi.nlm.nih.gov/Blast.cgi) demon-