

Shigella* spp. Surveillance in Indonesia: the Emergence or Reemergence of *S. dysenteriae

**Decy Subekti,* Buhari A. Oyoyo,* Periska Tjaniadi,*
Andrew L. Corwin,* Wita Larasati,* Maily Putri,*
Cyrus H. Simanjuntak,† Narain H. Punjabi,* Jufri Taslim,‡
Budhi Setiawan,§ Anak Agung G.S. Djelantik,¶ Luh Sriwati,**
Atiek Sumardiati,†† Eka Putra,‡‡
James R. Campbell,* and Murad Lesmana***

*U.S. Naval Medical Research Unit No. 2, Jakarta, Indonesia; †National Institute of Health Research and Development, Jakarta, Indonesia; ‡Municipal Health Service, North Jakarta, Indonesia; §Friendship Hospital, Jakarta, Indonesia; ¶Sanglah Hospital, Denpasar, Bali, Indonesia; **Wangaya Hospital, Denpasar, Bali, Indonesia; ††Regional Office of Health Ministry, Pontianak, Indonesia; and ‡‡Otorita Hospital, Batam, Indonesia

From June 1998 through November 1999, *Shigella* spp. were isolated in 5% of samples from 3,848 children and adults with severe diarrheal illness in hospitals throughout Indonesia. *S. dysenteriae* has reemerged in Bali, Kalimantan, and Batam and was detected in Jakarta after a hiatus of 15 years.

Shigella spp. cause acute, debilitating diarrheal disease in humans (particularly young children) worldwide (1). In developing countries, where affected populations are immunologically compromised by poor nutrition and background infections, deaths attributed to shigellosis are common. Four *Shigella* species are recognized as pathogenic to humans: *S. sonnei*, *S. boydii*, *S. flexneri*, and *S. dysenteriae*. Both *S. sonnei* and *S. boydii* are usually associated with mild illness of short duration in which the stool may be watery or bloody (2). *S. flexneri* is generally more severe, lasts longer, and causes blood in stools. *S. dysenteriae*, particularly type 1, causes the most severe diarrheal illness, reflected in high death rates (3). *S. flexneri* is a principal cause of endemic shigellosis in many developing countries, while shigellosis in both endemic and epidemic form has been attributed to *S. dysenteriae* type 1 (2). Changes in the worldwide epidemiology of *Shigella* spp. have

been documented in the last decades of the 20th century. In industrialized regions, *S. dysenteriae* was first replaced by *S. flexneri*, and then by *S. sonnei* (4,5); *S. flexneri* remains the leading cause of shigellosis in most of the developing world (2,6-8).

In Indonesia, the last cases of *S. dysenteriae* diarrheal disease were reported in 1985 from Jakarta (8,9). This report, based on a study using a systematic surveillance approach that included a standardized detailed bacteriologic examination, provides an Indonesia-wide geographic profile of *Shigella* spp.

The Study

From June 1998 through November 1999, a total of 3,848 children and adults seeking treatment for debilitating diarrheal disease were identified from eight hospital sites in Medan, North Sumatra; Padang, West Sumatra; Batam, Riau Island; Jakarta, Java Island; Denpasar, Bali (two hospitals); Pontianak, West Kalimantan; and Makassar, South Sulawesi. Rectal swabs were obtained from patients in the study before antibiotic therapy was administered. Specimens were placed in Cary-Blair transport medium,

Address for correspondence: LCDR Buhari A. Oyoyo, American Embassy Jakarta, Unit 8132 NAMRU TWO, FPO, AP 965208132, Indonesia; telephone: 62-21-421-4460; fax: 62-21-424-4507; e-mail: oyoyo@namru2.org.

held at 4°C, and sent on wet ice within 2 to 4 days after collection to the U.S. Naval Medical Research Unit No. 2, Jakarta. Bacteriologic evaluation was performed by standard culture method (10). Species was confirmed by using API 20E (Biomérieux, Marcy l'Etoile, France) and slide agglutination with specific *Shigella* antisera (Difco Laboratories, Detroit, MI). Antibiotic susceptibility testing was accomplished by the disk-diffusion method (11).

Overall, bacterial isolates of *Shigella* spp. were identified in 180 (5%) of 3,848 rectal swabs. The proportional contribution of *S. flexneri*, *S. sonnei*, and *S. dysenteriae* among shigellosis cases was 80%, 12%, and 8%, respectively. No *S. boydii* was detected. The percentage of representation among the three species did not vary substantially by geographic location. Notable was the reemergence of *S. dysenteriae* in Bali, West Kalimantan, and Batam, as well as in Jakarta after a hiatus of >15 years (Table). The proportional distribution of *S. flexneri*, *S. sonnei*, and *S. dysenteriae* for the 5- to 12-year-old and >12-year-old groups was similar. There appeared to be no consistency in the seasonal distribution patterns of *Shigella* spp. (Figure). *S. flexneri* was the most frequently isolated organism, followed by *S. sonnei* and *S. dysenteriae*.

Other enteric pathogens isolated were *Salmonella* spp. (95, 2.5%), *Vibrio cholerae* (80, 2.1%), *V. parahaemolyticus* (38, 1%), *V. cholerae* non-O1 (9, 0.2%), and *Campylobacter* spp. (27, 0.7%). Enterotoxigenic *Escherichia coli* were detected in 225 (18.1%) of 1,240 specimens tested by the GM1 enzyme-linked immunoassay (12). Of the 541 specimens examined for rotavirus in the age groups ≤ 5 years, 191 (35.3%) were positive. Tests to detect parasites showed *Ascaris lumbricoides* in 8 (2%), *Blastocystis hominis* in 23 (5.6%), *Giardia lamblia* in 3 (0.7%), and *Endolimax nana* in 2 (0.5%) of 407 stool specimens examined.

Clinical presentations associated with non-*S. dysenteriae* included abdominal cramping (79%), vomiting (56%), and fever (48%); for *S. dysenteriae*, percentages of the same symptoms were 100%, 64%, and 27%, respectively. Stool samples from patients with *S. flexneri*, *S. sonnei*, and *S. dysenteriae* were principally characterized by mucus in the absence of blood (45%) or mucus and visible blood (27%).

Overall, antibiotic susceptibility patterns showed greater resistance to ampicillin, trimethoprim-sulfamethoxazole, chloramphenicol, and tetracycline for *S. flexneri* (85%, 59%, 82%, and 98%, respectively, from examination of 144 isolates) and *S. sonnei* (32%, 79%, 37%, and 100%, respectively, from examination of 22 isolates), than for *S. dysenteriae* (36%, 43%, 7%, and 29%, respectively, from examination of 14 isolates). There was no evidence of resistance to ceftriaxone, norfloxacin, ciprofloxacin, or nalidixic acid, regardless of *Shigella* species. Antimicrobial resistance was only apparent among isolates obtained from Jakarta, Bali, and Pontianak.

Conclusions

Our study showed that a substantial proportion (5%) of acute, debilitating diarrheal illness throughout Indonesia can be ascribed to shigellosis; moreover, *S. dysenteriae* was documented from various geographic locations. Both findings suggest that greater attention should be paid to highlighting the endemic and epidemic community impact of this pathogen and that laboratory detection capabilities need to be enhanced. Recognition of emerging and or reemerging disease pathogens requires reliable baseline and ongoing surveillance data.

Shifting patterns of antimicrobial-drug resistance, particularly in much of the developing world, are generally a function of overuse and

Table. Distribution of *Shigella* spp. from patients with diarrhea in Indonesia, June 1998 through November 1999

Sites	No. specimens tested	No. pos. for <i>Shigella</i> (%)	Proportional distribution of <i>Shigella</i> spp. (%)		
			<i>S. flexneri</i>	<i>S. sonnei</i>	<i>S. dysenteriae</i>
Jakarta	2495	122 (5)	97 (80)	17 (14)	8 (6)
Makassar	146	4 (3)	3 (75)	1 (25)	0 (0)
Denpasar (2)	607	35 (6)	29 (83)	2 (6)	4 (11)
Pontianak	330	16 (5)	13 (81)	2 (13)	1 (6)
Batam	99	1 (1)	0 (0)	0 (0)	1 (100)
Padang	51	2 (4)	2 (100)	0 (0)	0 (0)
Medan	120	0 (0)	0 (0)	0 (0)	0 (0)
Total	3848	180 (5)	144 (80)	22 (12)	14 (8)

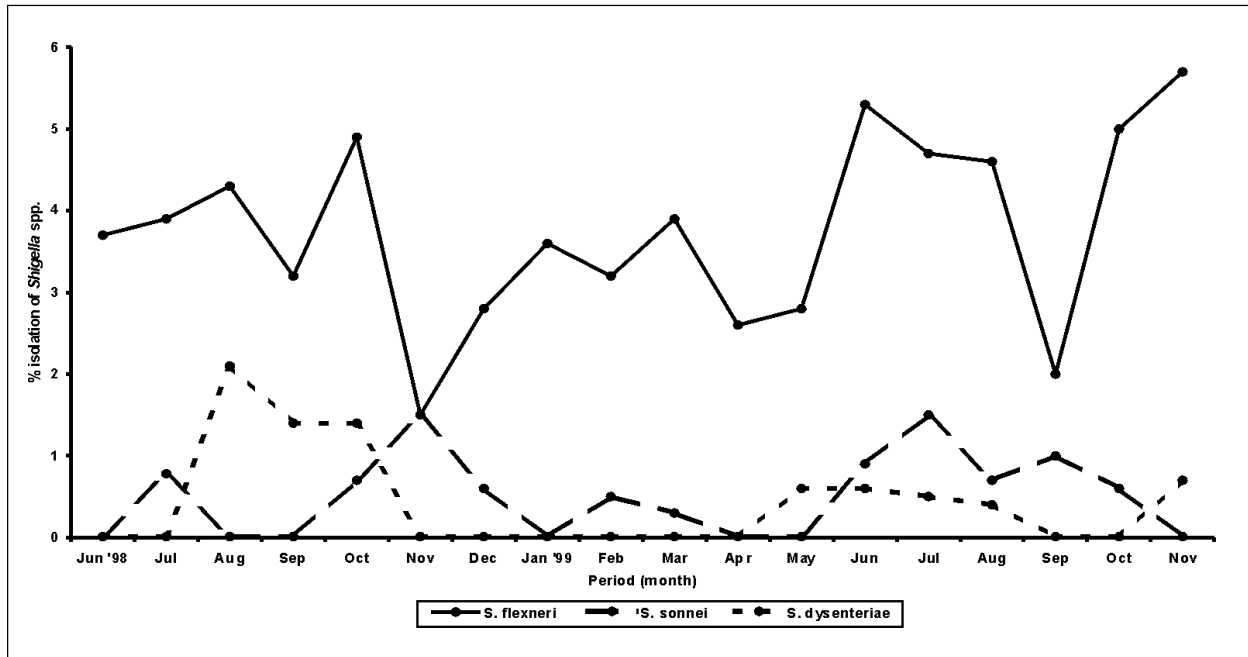


Figure. Seasonal isolates of *Shigella* spp. from patients with diarrhea in Indonesia (June 1998 - November 1999).

misuse of antibiotic drug therapies. The spread of drug resistance is the result of poorly regulated and enforced policies. Resistance to nalidixic acid (100%) among isolates of *S. dysenteriae* has been reported in Bangladesh (13); however, we found no such resistance. Nevertheless, other data from Indonesia indicate increasing resistance. In a previous report (8), 72% of *Shigella* spp. were resistant to tetracycline, but less than 30% were resistant to chloramphenicol, trimethoprim-sulfamethoxazole, or ampicillin. Previous studies from Bangladesh and Tanzania (13,6) showed that almost all tested isolates were resistant to the antibiotics used for treatment. Similar antimicrobial resistance profiles for *Shigella* spp. were reported from Thailand (14), where high resistance to ampicillin, trimethoprim-sulfamethoxazole, chloramphenicol, and tetracycline was documented.

The reemergence of *S. dysenteriae* from several locations in Indonesia should prove cause for concern to health officials, particularly in monitoring acute, debilitating diarrheal outbreaks. The epidemic potential attributed to *S. dysenteriae*, as documented in Central America, Asia, and Africa, in conjunction with notably high death rates, warrants close attention to this reemerging pathogen in Indonesia (13,15,16).

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Dr. Subekti is a microbiologist and medical research scientist who heads the Molecular Microbiology Section of the Enteric Diseases Program at U.S. Naval Medical Research Unit No. 2, Jakarta, Indonesia.

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