

were isolated by differential culture and serotyped. A total of 200 samples were collected from 50 markets between May and August 2003. Of the 200 samples tested, 121 (61%) were positive for at least one *Salmonella* spp. serogroup. A total of 175 *Salmonella* spp. were isolated. The most common serovar was *S. Anatum* followed by *S. Corvallis* and *S. Derby*. *Campylobacter* spp. was found in 31 (15.5%) of 200 samples. *C. jejuni* was isolated from 15% of fresh market chicken samples and 35% of supermarket chicken samples. *Arcobacter* spp. was isolated from 42 (21%) of the total specimens; fresh market chicken had significantly higher *A. butzleri* contamination than supermarket chicken. The presence of *Enterococcus* spp., an indication of fecal contamination, was detected in 188 (94%) samples, including 100% of the beef and pork sources. Few studies have examined retail food contamination in Thailand. In particular, the finding of large amounts of *Arcobacter* spp. on food warrants further study to determine pathogenicity.

Abstract of the International Conference on Emerging Infectious Diseases. Atlanta, Georgia, U.S.A. 29 February – 3 March 2004. Poster Board 57:78.

DETECTION OF *SHIGELLA* BY A PCR ASSAY TARGETING THE *IPAH* GENE SUGGESTS INCREASED PREVALENCE OF SHIGELLOSIS IN NHA TRANG, VIETNAM

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Shigella spp. are exquisitely fastidious gram-negative organisms which frequently escape detection by traditional culture methods. To get a more complete understanding of the disease burden caused by *Shigella* in Nha Trang, Vietnam, real-time PCR was used to detect *Shigella* DNA. Randomly selected rectal swab specimens from 60 *Shigella* culture-positive patients and 500 *Shigella* culture-negative patients detected by population-based surveillance of patients seeking care for diarrhea were processed by real-time PCR. The target of the primer pair is the invasion plasmid antigen H gene sequence (*ipaH*), carried by all four *Shigella* species and enteroinvasive *Escherichia coli*. *Shigella* spp. could be isolated from the rectal swabs of 547 of 19,206 (3%) patients with diarrhea. *IpaH* was detected in 55 of 60 (93%) *Shigella* culture-positive specimens, whereas it was detected in 87 of 245 (36%) culture-negative patients free of dysentery ($P < 0.001$). The number of PCR cycles required to detect a PCR product was highest for culture-negative, nonbloody diarrheal specimens (mean number of cycles to detection, 36.6) and was lowest for children with culture-positive, bloody diarrheal specimens (mean number of cycles, 25.3) ($P < 0.001$). The data from real-time PCR amplification indicate that the culture-proven prevalence of *Shigella* among patients with diarrhea may underestimate the prevalence of *Shigella* infections. The clinical presentation of shigellosis may be directly related to the bacterial load.

J Clin Microbiol. 2004; 42(5): 2031-5.
