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An Outbreak of Diarrhea Caused by *Escherichia coli* Serogroup O169:HNM Harboring a Coding Gene for Enteroaggregative *E. coli* Heat-Stable Enterotoxin 1 (*astA*) in Fukui Prefecture

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In Japan, the first outbreak of gastroenteritis caused by a strain of *Escherichia coli* having a coding gene for enteroaggregative *E. coli* heat-stable enterotoxin 1 (*astA*) occurred in Osaka Prefecture in 1996 (1). Outbreaks of diarrhea due to the same strain have since been reported in Hiroshima city and Oita Prefecture (2,3). The strain was also implicated in a food-poisoning outbreak that occurred in a school dormitory in Fukui Prefecture on 19 to 22 August 2004, in which 69 of 95 exposed individuals (82 students and 13 teaching staffs) were symptomatic. Lunches that were served on 19 or 20 August were the only food stuffs ingested in common by all these patients, although no portions of the lunches remained for examination. The clinical symptoms recorded were as follows: explosive diarrhea (68 people), abdominal pain (55), fever (17), headache (12), and nausea (10).

Stool samples were collected from 15 students and 1 teaching staff of 69 patients and 3 food-handlers (1 of those food handlers was clinically symptomatic) during 23-24 August, and were examined for bacteriological inspection. *E. coli* O169:HNM were isolated from all samples. A PCR-based assay for genes encoding *astA*, *aggR*, *eae*, *LT*, *ST*, *invE*, and *stx* (4-6) revealed that all 19 strains were positive for *astA* and negative for *aggR*, *eae*, *LT*, *ST*, *invE*, and *stx*, as previously described (data not shown). When 13 of the 19 strains were tested for their sensitivity to tetracyclin (TC), fosfomycin (FOM), ampicillin (ABPC), streptomycin (SM), ciprofloxacin (CPFX), kanamycin (KM), cefotaxime (CTX), chloramphenicol (CP), sulfamethoxazole-trimethoprim (ST), gentamycin (GM), nalidixic acid (NA), and sulfisoxazole (Su) by using Sensi Disc (Becton Dickinson Microbiology Systems, Cockeysville, Md., USA), all were resistant to TC, and intermediately resistant to FOM and ABPC (data not shown).

These 13 isolates were also examined by pulsed-field gel electrophoresis (PFGE) using a Gene Path Typing System (Program No. 22; Nippon Bio Rad, Tokyo, Japan). The PFGE patterns of *Xba*I- (Nippon Bio Rad) or *Bln*I- (Roche Diagnostics, Mannheim, Germany) digested chromosomal DNAs were identical among all the isolates examined (Fig. 1). The plasmid profiles were also identical among these isolates (data not shown). As referring, 1,730 strains of O-serotyped *E. coli* isolates from sporadic diarrhea cases at 2 hospitals in Fukui

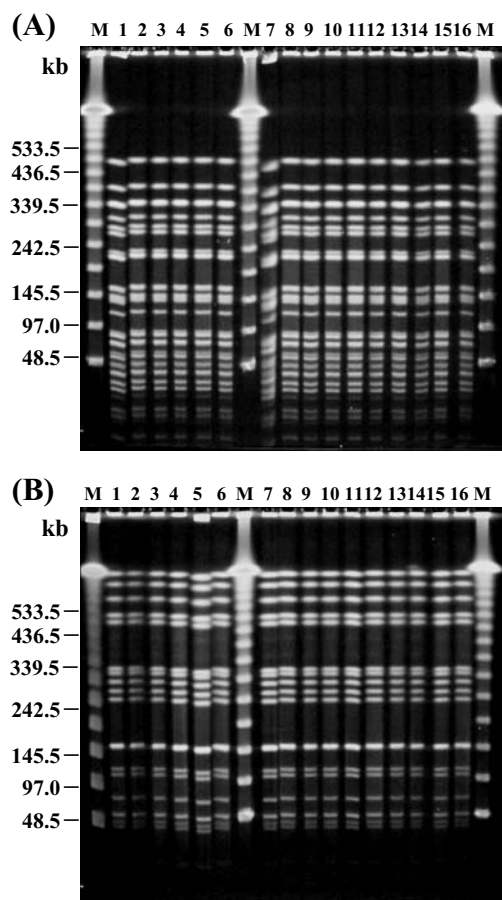


Fig. 1. PFGE patterns of *Xba*I- and *Bln*I-digests of chromosomal DNA of *Escherichia coli* O169:HNM (*astA* positive) isolates. (A) *Xba*I-digests and (B) *Bln*I-digests. Lane 1-2, Isolates from food-handler A; Lane 3-4, Isolates from food-handler B; Lane 5-6, Isolates from food-handler C; Lane 7, Isolate from a staff of patient; Lane 8-16, Isolates from students of patient; M, λ DNA ladder.

from 1997 to 2004, only 3 strains were found to be *E. coli* O169:HNM, and 2 of these were positive for *astA*.

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