

## Characterization of Enteropathogenic and Enteroaggregative *Escherichia coli* Isolated from Diarrheal Outbreaks

Jun Yatsuyanagi,<sup>1\*</sup> Shioko Saito,<sup>1</sup> Hiroyasu Sato,<sup>1</sup> Yoshimichi Miyajima,<sup>1</sup> Ken-Ichi Amano,<sup>2</sup> and Katsuhiko Enomoto<sup>3</sup>

Akita Prefectural Institute of Public Health, 6-6 Sensyu kubota-machi, Akita 010-0874,<sup>1</sup> and Central Research Laboratory<sup>2</sup> and Department of Pathology,<sup>3</sup> Akita University School of Medicine, 1-1-1 Hondo, Akita 010-8543, Japan

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**Virulence characteristics of diarrheal outbreak-associated *Escherichia coli* O55:NM, O126:NM, and O111:NM were examined. The *E. coli* O55:NM strains were atypical enteropathogenic *E. coli* (EPEC), while the *E. coli* O126:NM and O111:NM strains should be classified as enteroaggregative *E. coli* (EAggEC). The contributions of EPEC and EAggEC to the human disease burden in Japan might be significantly greater than is currently appreciated.**

There are six categories of *Escherichia coli* that cause diarrhea: enterotoxigenic *E. coli* (ETEC), enteropathogenic *E. coli* (EPEC), enterohemorrhagic *E. coli*, enteroaggregative *E. coli* (EAggEC), enteroinvasive *E. coli*, and diffusely adherent *E. coli* (21). EPEC causes characteristic attaching-and-effacing lesions (A/E), which can be observed by intestinal biopsy in both human patient (19) and animal (29) models. A/E is characterized by loss of microvilli, intimate adherence of bacteria between epithelial cell membranes (27, 30), and cytoskeletal changes such as actin polymerization directly beneath the adherent bacteria (15). Generally, EPEC causes infantile diarrhea in developing countries and sporadic diarrhea in developed countries (21). EAggEC, on the other hand, is an enteric pathogen defined by its distinctive aggregative or “stacked-brick” pattern of adherence to cultured human epithelial cells (22). EAggEC associates mainly with persistent diarrhea in developing countries (21). Only two reports in Japan have described diarrheal outbreaks caused by EAggEC or EPEC. Itoh et al. (11) reported the isolation of EAggEC from the stools of patients with severe diarrhea in elementary and junior high schools. Makino et al. (18) reported the isolation of EPEC from a mass outbreak. In this paper, we describe three cases of diarrheal outbreaks in Japan caused by *E. coli* belonging to the traditional EPEC serotype.

Chromosomal DNA-embedded agarose plugs for pulsed-field gel electrophoresis (PFGE) analysis were prepared by using the CHEF Bacterial DNA Plug Kit (Bio-Rad, Hercules, Calif.) and were digested with *Xba*I (Nippon gene; Osaka, Japan) at a concentration of 30 U/plug for 4 h at 37°C. The plugs were applied to a 1% PFC Grade Agarose (Bio-Rad) gel. Electrophoresis was performed in 0.5× Tris-Borate EDTA buffer at 14°C using a CHEF DR-II PFGE apparatus (Bio-Rad) under the following conditions: voltage, 6 V/cm; block 1, 11 h, with initial switching time of 4 s to final switching time of 8 s; block 2, 9 h, with initial switching time of 8 s to final switching time of 50 s. The HEP-2 cell assay was performed

following the method described by Craviotto et al. (4), with modifications involving 3 or 6 h of incubation (15). The *E. coli* isolates were examined for the presence of the following virulence genes by PCR: *stx1* (Shiga toxin) and *stx2* (16), *eaeA* (*E. coli* attaching and effacing) (12), *bfpA* (bundle-forming pilus) (9), *perA* (EPEC plasmid-encoded regulatory region) (8), *astA* (EAggEC heat-stable enterotoxin) (28), *aggR* (transcriptional activator for EAggEC aggregative adherence fimbria I expression) (20), and *pet* (EAggEC plasmid-encoded heat-labile toxin) (6) using the primers listed in Table 1. EPEC E2348/69 and EAggEC 17-2 were kindly provided by James B. Kaper, and EAggEC 042 was kindly provided by James P. Nataro, University of Maryland School of Medicine, Baltimore, Md.

The diarrheal patients were junior high school students in case 1, adults who attended a party in case 2, and infants of a day care center in case 3. The only diarrheagenic bacterial pathogens isolated from the patients were three *E. coli* O126:NM isolates from four of nine patients in case 1, nine *E. coli* O111:NM isolates from 9 of 21 patients in case 2, and four *E. coli* O55:NM isolates from four of four patients in case 3. As shown in Fig. 1, *E. coli* strains isolated within the same case showed identical PFGE patterns, suggesting that the strains originated from the common infectious sources in the respective cases. These results indicated that these *E. coli* strains were the causative agents of the diarrheal outbreak cases. As shown in Fig. 2, *E. coli* O55:NM possessed *eaeA* and showed a localized HEP-2 cell adherence pattern only in the 6-h assays but was negative for *bfpA* and *perA*, indicating that *E. coli* O55:NM is an atypical EPEC. The *E. coli* O55:NM isolate was negative for *aggR*, *astA*, and *pet*. On the other hand, both *E. coli* O126:NM and O111:NM strains were negative for the *eaeA*, *bfpA*, and *perA* genes but positive for the *aggR* and *astA* genes and showed an aggregative HEP-2 cell adherence pattern, indicating that they should be classified as EAggEC, displaying features of the traditional EPEC serotypes. The *E. coli* O126:NM was *pet* positive, while *E. coli* O111:NM was negative for this gene. All three *E. coli* isolates were negative for both *stx1* and *stx2* genes.

At the Second International Symposium on EPEC (13), a consensus on the basic characteristics of EPEC infection was

\* Corresponding author. Mailing address: Akita Prefectural Institute of Public Health, 6-6 Sensyu kubota-machi, Akita 010-0874, Japan. Phone: 81-18-832-5005. Fax: 81-18-832-5938. E-mail: jyatsun@spica.freemail.ne.jp.

TABLE 1. PCR primers used in this study

Designation	Location	Sequence (5' to 3')	Target gene	Amplicon size (bp)	Reference
V1 V5	213–230 1013–1029	AGT-TAA-TGT-GGT-GGC-GAA GAC-TCT-TCC-ATC-TGC-CG	<i>stx1</i>	817	16
V3 V4	289–306 745–762	TTC-GGT-ATC-CTA-TTC-CCG TCT-CTG-GTC-ATT-GTA-TTA	<i>stx2</i>	474	16
EA-1 EA-2	1846–1865 2280–2299	AAA-CAG-GTG-AAA-CTG-TTG-CC CTC-TGC-AGA-TTA-ACC-TCT-GC	<i>eaeA</i>	454	This study
EP-1 EP-2	2773–2793 3076–3096	AAT-GGT-GCT-TGC-GCT-TGC-TGC GCC-GCT-TTA-TCC-AAC-CTG-GTA	<i>bfpA</i>	324	9
PerAS PerAAS	522–541 856–875	TGT-CAT-CCT-TAG-TGC-TTC-AT GGC-AAT-GTT-CCT-TGT-GTA-AT	<i>perA</i>	354	This study
EAST-1S EAST-1AS	63–82 149–168	GCC-ATC-AAC-ACA-GTA-TAT-CC GAG-TGA-CGG-CTT-TGT-AGT-CC	<i>astA</i>	106	This study
AggRks1 AggRkas2	100–120 353–334	GTA-TAC-ACA-AAA-GAA-GGA-AGC ACA-GAA-TCG-TCA-GCA-TCA-GC	<i>aggR</i>	254	26
PetS PetAS	557–576 979–998	TCA-TTT-CCA-GCA-CTT-CCT-GT CTC-CGA-CAG-TAT-TTG-CTC-GT	<i>pet</i>	442	This study

reached, identifying them as the presence of A/E histopathology and the absence of Shiga toxin. The A/E phenotype is closely related to the localized adherence phenomenon displayed by EPEC (14). DNA probes and PCR primers have been developed and used for the evaluation of the three major characteristics of EPEC: A/E (12), the presence of a ca. 60-MDa plasmid designated EPEC adherence factor plasmid (EAF) (23), and lack of Shiga toxin (16). Some EPEC strains possess EAF-encoding bundle-forming pilus (BFP) (5). Typical EPEC strains possess the *eaeA* for A/E and the EAF or *bfpA*, while atypical EPEC strains possess the *eaeA* gene only, and there is some controversy over whether atypical EPEC strains are true diarrheagenic pathogens (13). On the other

hand, EAggEC infection is diagnosed definitively by isolation from the stools of patients of *E. coli* showing the aggregative HEp-2 cell adherence pattern (21). EAggEC strains possess the *aggA* gene that encodes the aggregative adherent fimbria I (AAF/I) protein (24), the *aggR* gene for transcriptional activation of AAF/I expression (20), and the *astA* gene that encodes the enteroaggregative *E. coli* heat-stable enterotoxin I protein (28). In this study, we examined *E. coli* isolated from patients with diarrhea from three outbreak cases. Serotyping of *E. coli* isolates showed the pathogenic strains to be O55:NM, O111:NM, and O126:NM, representing traditional EPEC serotypes. Based on phenotypic and genotypic tests, the O55:NM strain was identified as an atypical EPEC; it showed localized adher-

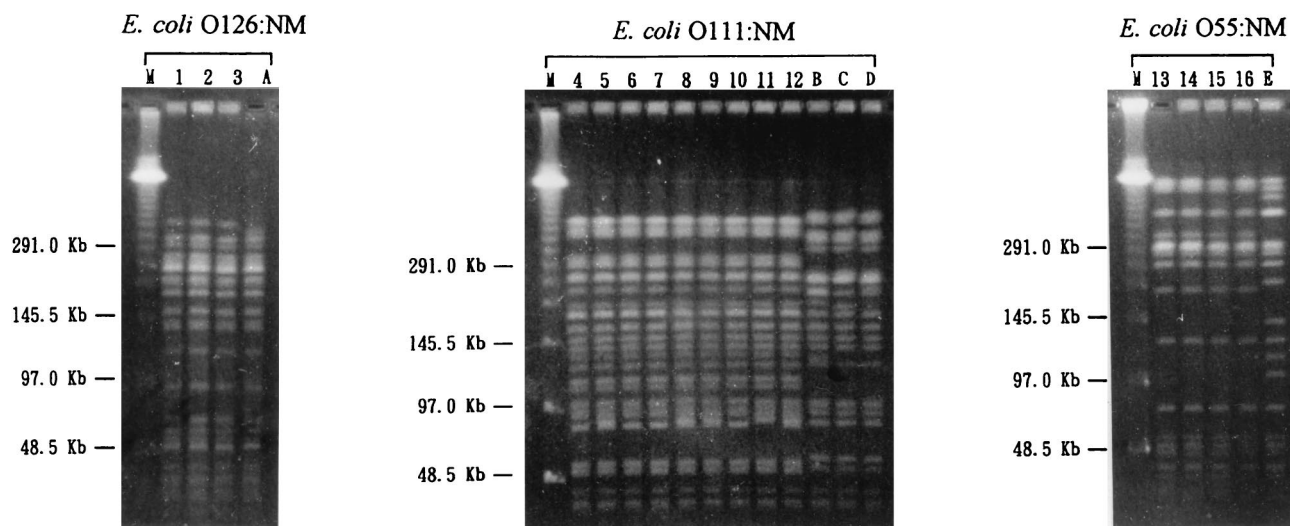


FIG. 1. PFGE patterns of the diarrheal isolates. Lanes: M, lambda molecular weight ladder; 1 to 3 (case 1, *E. coli* O126:NM); 4 to 12 (case 2, O111:NM isolates); 13 to 16 (case 3, O55:NM isolates); A to E (sporadic isolates of respective organisms).

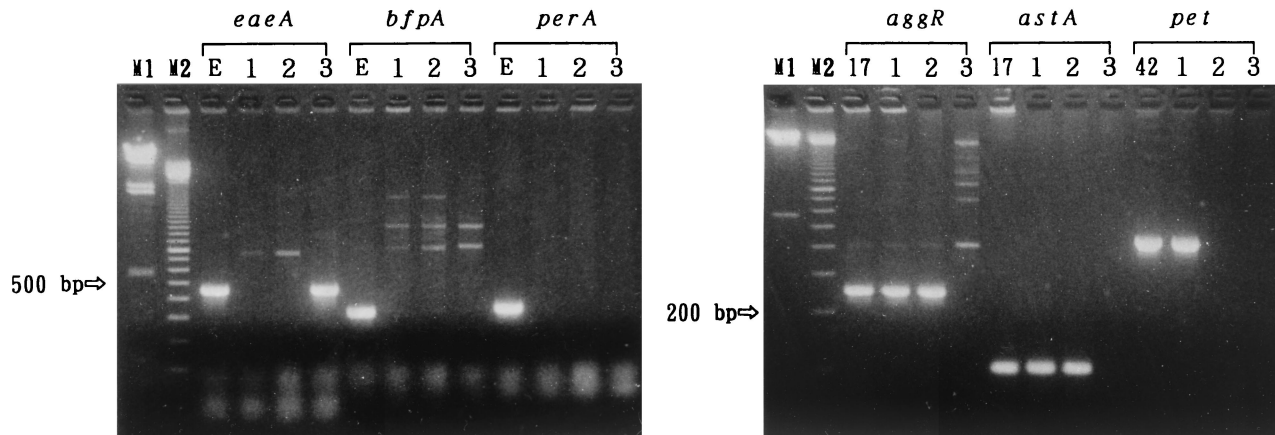


FIG. 2. Agarose gel electrophoresis of the PCR products of *E. coli* virulence genes showing virulence traits of the *E. coli* isolates from three outbreak cases. Lanes: M1, lambda/*Hind*III molecular weight marker; M2, 100-bp-ladder molecular weight marker; 1, *E. coli* O126:NM EC-152 from case 1; 2, *E. coli* O111:NM EC-560 from case 2; 3, *E. coli* O55:NM EC-1045 from case 3; E, EPEC E2348/69; 17, EAggEC 17-2; 42, EAggEC 042.

ence and possessed the *eaeA* without the EAF. However, *E. coli* isolates from the other two cases were identified as EAggEC, because they showed aggregative adherence and possessed *astA* and *aggR* but not *eaeA* or EAF. In general, EPEC infection is primarily a disease of infants younger than two years old (17), and EAggEC is associated with persistent diarrhea (1). Several outbreaks of diarrhea due to EPEC have been reported in the United States, the United Kingdom, Finland, and other developed countries. These outbreaks frequently occur in day care centers (2, 25) and occasionally occur in pediatric wards (10). However, reports of outbreaks due to atypical EPEC are infrequent. Recently, Hedberg et al. (10) reported an outbreak caused by an atypical EPEC among adults who ate at a gourmet buffet in the United States. This atypical EPEC strain was unique, because its serotype was O39:NM, which did not belong to any of the traditional EPEC serotypes, and it was positive for *astA* along with *eaeA* but negative for the EAF. Our present data, along with Hedberg's observation, suggest that atypical EPEC is a diarrheic pathogen. Furthermore, the number of reports describing outbreaks due to EAggEC is increasing (3, 7). In Japan, there are only two reports describing outbreaks of diarrhea involving EPEC and EAggEC (11, 18). Based on our cases and the two reports just mentioned, the contribution of EPEC and EAggEC to the human disease burden in Japan might be significantly greater than is currently appreciated.

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