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Comparison by Pulsed-Field Gel Electrophoresis of Salmonella Enteritidis Genotypes from Various Food Poisoning Outbreaks from 1997 to 1999 in Hyogo Prefecture

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Salmonella serovar Enteritidis has become the most prevalent among the Salmonellae serotypes in Japan since 1989 (1). From 1997 to 1999, Hyogo Prefecture experienced 21 known food poisoning outbreaks caused by the serovar. To determine the genetic characters of the strains involved in Hyogo Prefecture, we determined the phage types and genotypes of representative isolates from the 21 outbreaks (2, 3) (Table).

The 21 isolated strains showed various phage types (PTs), such as 1, 4, 5, 6, 6a, 34, and RDNC (Reaction Does Not Conform). All were prevalent in Japan (1), but RDNC (4) emerged abruptly in 1998 in Hyogo Prefecture. They were examined by pulsed-field gel electrophoresis (PFGE) by using a Gene Path Typing System (Nippon Bio-Rad, Tokyo) (Fig. 1, 2). There were five PFGE patterns revealed by the BlnI chromosomal DNA digests. There was no correlation between PFGE pattern and phage type.

A major PFGE pattern, group A, exhibited one PT 1 (Hyogo-S058) (Table 1). A separate experiment indicated that the PFGE patterns with both BlnI and XbaI were essentially the same as those of Hyogo-S058 in case 9.

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Fig. 1. PFGE pattern of BlnI-digests of chromosomal DNA of Salmonella Enteritidis isolates.

(A) Salmonella Enteritidis isolates with RDNC phagetypes.

(B) Salmonella Enteritidis isolates with other phagetypes.

Fig. 2. PFGE pattern of XbaI-digests of chromosomal DNA of Salmonella Enteritidis isolates.

(A) Salmonella Enteritidis isolates with RDNC phagetypes.

(B) Salmonella Enteritidis isolates with other phagetypes.

SE005, lane 11 in Fig. 1A and lane 3 in Fig. 1B), five PT4s (Nishinomiya-01, lane 2 in Fig. 1B; Hyogo-SE058, lane 5 in Fig. 1B; Hyogo-SE073, lane 13 in Fig. 1A and lane 6 in Fig. 1B; Hyogo-SE138, lane 8 in Fig. 1B; and Hyogo-072, data not shown), and eight RDNCs (Hyogo-SE017, lane 2 in Fig. 1A and lane 13 in Fig. 1B; Hyogo-SE026, lane 3 in Fig. 1A, Hyogo-SE028, lane 4 in Fig. 1A; Hyogo-SE096, lane 6 in Fig. 1A; Hyogo-SE106, lane 7 in Fig. 1A; Hyogo-SE116, lane 8 in Fig. 1A; Hyogo-SE129, lane 9 in Fig. 1A; and Hyogo-SE143, lane 10 in Fig. 1A). The PFGE pattern quite similar to group A but having an extra band unique to each strain was named A'. It consisted of one PT6 (Hyogo-SE008, case 5, lane 4 in Fig. 1B) with an extra band just below 48.5 kb, one PT6a (Hyogo-SE103, case 14, lane 14 in Fig. 1A and lane 9 in Fig. 1B) with an extra band of 194 - 243 kb, and one PT5 (Hyogo-SE127, case 17, lane 7 in Fig. 1B) with an extra band far below 48.5 kb. In groups A and A', all the non-RDNC strains except Hyogo-SE103 (case 14) had a common extra band slightly larger than 630 kb.

The remaining four strains exhibited unique PFGE patterns.
They were classified as groups B-E; a strain of RDNC, Hyogo-SE065 (case 10) as group B (Fig. 1A, lane 5 and Fig. 1B, lane 14); a strain of PT1, Hyogo-SE151 (case 20) as group C (Fig. 1B, lane 12); a strain of PT34, Kakogawa-A03 (case 1) as group D (Fig. 1B, lane 10); and a strain of PT4, Sumoto-21 (case 3) as group E (Fig. 1A, lane 12 and Fig. 1B, lane 11). The PFGE patterns of XbaI digests were similar for all the isolates (Fig. 2). The PFGE pattern grouped as above for each isolate is shown in Table together with other descriptions.

We have thus described a PFGE analysis of Salmonella Enteritidis from the recent 21 food poisoning outbreaks. Five distinct patterns were detected upon PFGE. No correlation with phage type was detected.

REFERENCES