Short communication

Sequence-Based Characterization of *Listeria monocytogenes* Strains Isolated from Domestic Retail Meat in the Tokyo Metropolitan Area of Japan

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SUMMARY: The level of *Listeria monocytogenes* contamination of domestic retail meat in Tokyo, Japan, was assessed by comparison of isolates from 2004 to 2007 with those isolated before 2003. The overall prevalence of *L. monocytogenes* among these samples significantly diminished over time (1998–2003, 28.0%; 2004–2007, 17.6%) reflecting a significant decrease in the frequency of contamination of beef. Serotype 1/2a was isolated most frequently, reflecting a change in the predominant serotype in pork from 1/2c to 1/2a. We performed a simple genetic subtyping method based on 3 genes, *iap*, *sigB*, and *actA*, as well as traditional multilocus sequence typing to classify the allele types (ATs). No extensive variation among sequence types was detected. However, increased genetic diversity among the ATs of the 3 genes in the 2004–2007 isolates was evident. We identified AT 26 of the *iap* gene, which was not previously reported in Japanese isolates, and 6 ATs of the *sigB* gene, including 4 with nonsense mutations not currently registered in *L. monocytogenes* DNA databases. *sigB* is an evolutionally conserved gene that plays a role in the stress response. Our results indicate that the *sigB* gene may be relatively unstable among *L. monocytogenes* strains circulating in Japan.

Listeria monocytogenes is widely distributed in nature and causes listeriosis in humans. Listeriosis often exhibits severe symptoms and is associated with high mortality rates in immunocompromised individuals. Outbreaks of food-mediated listeriosis occasionally occur in the United States and Europe (1). In Japan, although the level of contamination with *L. monocytogenes* is similar to that reported in other countries, human listeriosis cases are usually sporadic. The reason for this discrepancy remains to be determined. However, the surveillance of *L. monocytogenes* in food remains important for the maintenance of food hygiene and to limit the risk of human listeriosis.

This study was conducted to assess the levels of contamination by *L. monocytogenes* in domestic retail meat sold in Japan after the establishment of the Food Safety Basic Act in 2003 and the revision of the Food Sanitation Act in the same year. The data were compared with that obtained from 1998 to 2003. We collected 170 samples including 57 beef, 57 pork, and 56 chicken from 2004 to 2007 using a previously described sampling procedure (2). For the isolation of *Listeria*, 10 g of each meat sample was incubated with 90 ml of UVM-modified *Listeria* enrichment broth (BD, Franklin Lakes, NJ, USA) at 30°C for up to 48 h. Each bacterial culture

was then streaked onto PALCAM agar (Merck, Darmstadt, Germany) and incubated at 37°C for 48 h. *Listeria*-like colonies were identified as *L. monocytogenes* as described by Takahashi et al. (3). In total, 137 *L. monocytogenes* isolates were detected from 30 of the 170 (17.6%) meat samples. The detection rates for each type of meat were as follows: beef 1/57 (1.8%), pork 12/57 (21.1%), and chicken 17/56 (30.4%) (Table 1). The frequency of isolation of *L. monocytogenes* was significantly diminished compared with previously reported levels (106/379, 28.0% for 1998–2003, $p < 0.05$; all statistical analyses were performed with the chi-square test) (2) because the frequency of isolation from beef samples

Table 1. Prevalence of *L. monocytogenes* during 2004–2007

Type of meat	No. of samples	No. of positive samples	Prevalence (%)
Beef	57	1	1.8
Pork	57	12	21.1
Chicken	56	17	30.4
Total	170	30	17.6

Table 2. Prevalence of *L. monocytogenes* serotype

Type of meat	No. of samples	No. of serotypes (prevalence, %)				No. of serotyped strains
		1/2a	1/2b	1/2c	4b	
Beef	57	0 (0)	0 (0)	1 (1.8)	0 (0)	1
Pork	57	7 (12.3)	1 (1.8)	4 (7.0)	1 (1.8)	13
Chicken	56	8 (14.3)	7 (12.5)	1 (1.8)	8 (14.3)	24
Total	170	15 (8.8)	8 (4.7)	6 (3.5)	9 (5.3)	38

Received January 5, 2018. Accepted May 7, 2018.

J-STAGE Advance Publication May 31, 2018.

DOI: 10.7883/yoken.JJID.2017.582

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was significantly decreased (15.5%, 1998–2003). These results suggested that chicken was the most likely source of contamination. Next, we performed serotyping of the *L. monocytogenes* isolates as previously described by Ueda et al. (4). The serotypes of all isolates were determined. A total of 38 serotyped strains were obtained. These strains were classified as serotype 1/2a (15/38, 39.5%), 1/2b (8/38, 21.1%), 1/2c (6/38, 15.8%), or 4b (9/38, 23.7%). The frequency of serotype 1/2a was significantly increased compared with previous results (25/122, 20.5%; $p < 0.05$) (2). This was due to a significant increase in the frequency of serotype 1/2a from pork (1998–2003, 3.1%; 2004–2007, 12.3%; $p < 0.05$) (Table 2). Significant differences were not observed for other serotypes. Serotype 1/2a was most frequently detected from chicken (8/56, 14.3%) and the data were similar to previously reported levels (18/129, 14.0% for 1998–2003) (2). 760P6 and 761C4 were processed at the same plant on the same day (Table 3). These results potentially indicate that the ecological niche of serotype 1/2a is expanding in nature or that cross-contamination from chicken to pork occurs during processing.

Genetic surveillance of pathogens is an informative tool to determine the source and route of infection at the time of an outbreak and to determine the evolutionary relationships between strains (5). In a previous study, we performed a simple nucleotide sequence-based typing method for *L. monocytogenes* using partial *iap*, *sigB*, and *actA* gene sequences (triple-locus sequence typing [TLST]), and confirmed identical allele types (ATs) among strains isolated from retail meat and human patients from 1996 to 2003 (6). The *iap* and *actA* genes encode known virulence factors of *L. monocytogenes*, whereas the *sigB* gene encodes a stress-responsive alternative sigma factor. In this study, we confirmed the genetic subtypes of isolates from 2004 to 2007 and compared these with previous results (2). The data obtained from TLST were then compared with traditional multilocus sequence typing (MLST) results. MLST is based on the sequences of 7 housekeeping genes: *abcZ*, *bglA*, *cat*, *dapE*, *dat*, *ldh*, and *lhcA* (7). The *L. monocytogenes* MLST database <<http://bigsdw.web.pasteur.fr/listeria>> is maintained by the Pasteur Institute (Paris, France). In the present study, DNA sequence-based subtyping was performed on *L. monocytogenes* strains (Table 3). Each strain was incubated in brain heart infusion broth at 37°C for 18 h. After incubation, bacterial cells were harvested by centrifugation, washed with sterilized MilliQ water, and suspended in 400 µl of TE solution (50 mM Tris-HCl and 1 mM EDTA, pH 8.0). The bacterial suspensions were boiled for 15 min, followed by centrifugation at 15,000 × g for 10 min at 4°C. The supernatant containing DNA was harvested and stored at –80°C until use. To determine the nucleotide sequence, partial *iap*, *sigB*, and *actA* gene sequences were amplified using the specific primer pairs, S13A/S14B (3), LMsigB15/LMsigB16 (8), and massF/massR (9), respectively. Sequence analyses were carried out using comparative sequences of the *iap*, *sigB*, and *actA* genes from the reference strain, EGD-e (serotype: 1/2a; GenBank accession no. AL591824, 407 bp, 662 bp, and 561 bp, respectively) isolated from a rabbit listeriosis outbreak (10). The ATs were then determined. All TLST sequence data have been registered at the DNA Data Bank of Japan

(Mishima, Japan) under the accession numbers indicated in Table 3. Alignments and phylogenetic analyses of TLST and MLST were conducted using MEGA software, version 7.0 (11). Based on the data, both phylogenetic trees were divided into 2 large clades, representing lineage I (Fig. 1, lower clade) and lineage II (Fig. 1, upper clade). The ATs of *iap* and *actA* in almost all the strains isolated from 2004 to 2007 were consistent with those reported for the strains isolated from domestic meat from 1996 to 2003 (2,12,13), with the exception of *iap* AT 26 (Table 3). The *iap* ATs 0, 2, 8, and 26 (e.g., EGD-e, 78P1, 104P5, and 726P4/778P6, respectively) differed only in the number of tandem repeat sequences (ACAAAT). The number of tandem repeats increased by one in the order of ATs 8, 0, 2, and 26. The *iap* AT 26 sequence was a new type in Japanese isolates. In the Pasteur Institute database, 235 *iap* alleles are currently registered. However, for many of the registered strains (3,261 strains), the sequence of *iap* remains undetermined, and 38 *iap* alleles have been found in only 127 strains. Fortunately, *iap* AT 26 corresponds with Pasteur *iap* allele id 40. CLIP 2009/00942 isolated from an animal possesses this allele. Further analyses are needed to determine whether the strain possessing *iap* AT 26 originally existed in Japan or whether the repeat sequence has increased in more recent isolates. Four strains showed nonsense mutations in the *sigB* gene (698C1, 709C1, 720P1, and 727C4). In other strains isolated from the same sample (698C2, 709C5, 720P3, and 727C2), the same ATs were detected in the *iap*, *actA*, and traditional MLST genes. We previously reported that 2 strains, 76P1 (Table 3) and 1E1 (*sigB* AT 37; derived from the skin of beef cattle), possessed nonsense mutations in the *sigB* gene (6). According to genetic analysis of the *sigB* allele, this sequence was found to be relatively conserved in *L. monocytogenes* (14). We confirmed that only 2 strains, FSL J1-0086 (AT 103, isolate source: human sporadic listeriosis) and FSL J2-0076 (AT 105, isolate source: ready-to-eat turkey), have nonsense mutations in this gene using the Food Microbe Tracker database <www.pathogentracker.net> maintained by Cornell University (Ithaca, NY, USA) (14,15). In addition to these nonsense mutation-containing types of *sigB* (ATs 36, 37, 39–41, and 43), a new type of *sigB* (ATs 38 and 42) was identified that is not currently registered in either of the databases at the Pasteur Institute or Cornell University. The expression of *sigB* affects not only bacterial adaptation under stress conditions (e.g., acid, heat, and hyperosmolarity) but also the transcription of virulence factors (16,17). Furthermore, *sigB* contributes to the persistence of *L. monocytogenes* in food processing plants and on equipment by conferring resistance to desiccation and acid and tolerance to disinfectants (18). These data raise a question as to whether *sigB* deficient mutants can survive during the environmental changes that accompany listeriosis. In fact, FSL J1-0086 was isolated from a case of human listeriosis. Therefore, further studies should investigate the phenotypes associated with *sigB* variants in Japanese isolates, and the correlation with stress tolerance in these strains. Our data will contribute to the sequencing data for *L. monocytogenes* that is crucial for subtyping new isolates.

Conflict of interest None to declare.

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Table 3. Comparison of the genetic classification of *L. monocytogenes* strains between 1996–2003 and 2004–2007

Strain	Year	Meat class	Serotype	Triple-locus sequence typing [6]						Traditional MLST [7]										Lineage	Ref.
				<i>iap</i>		<i>sigB</i>		<i>actA</i>		ST ²⁾	<i>abcZ</i>	<i>bglA</i>	<i>cat</i>	<i>dapE</i>	<i>dat</i>	<i>ldh</i>	<i>lhkA</i>	ST	CC ³⁾		
				AT ¹⁾	Acc.#	AT	Acc.#	AT	Acc.#												
23C1	1996	Chicken	1/2c	3	AB365669	1	LC158698	68	LC158765	9	7	14	10	6	1	27	1	196	193	II	(12)
42C1	1997	Chicken	4b	12	AB365719	2	LC158699	16	LC158766	24	1	1	11	11	2	1	5	2	2	I	(13)
63P1	1997	Pork	1/2b	14	AB365676	5	LC158700	14	LC158767	20	34	39	11	60	3	1	2	330	288	I	(12)
72C1	1998	Chicken	1/2b	12	AB365670	5	LC158703	12	LC158770	21	11	1	12	16	3	1	7	59	59	I	(2)
76P1	1998	Pork	1/2c	2	AB365666	36	LC158705	1	LC158772	6	6	5	6	4	1	4	1	9	9	II	(2)
76P2	1998	Pork	1/2a	4	AB365649	12	LC158706	21	LC158773	15	7	6	8	8	6	37	1	121	121	II	(2)
78P1	1998	Pork	1/2c	2	AB365667	1	LC158707	1	LC158774	2	6	5	6	4	1	4	1	9	9	II	(2)
80C1	1998	Chicken	1/2a	5	AB365655	1	LC158710	1	LC158777	16	7	10	16	7	5	2	1	155	155	II	(2)
93C1	1998	Chicken	1/2b	13	AB365748	5	LC158714	9	LC158781	22	4	4	4	3	2	1	5	3	3	I	(2)
104P5	1998	Pork	1/2a	8	AB517745	1	LC158716	1	LC158783	3	5	6	8	62	6	7	34	321	321	II	(2)
114P3	1998	Pork	1/2b	13	AB365744	3	LC158718	8	LC158785	19	2	1	11	3	3	1	7	5	5	I	(2)
186C1	1999	Chicken	1/2a	10	AB365664	1	LC158721	1	LC158788	5	5	6	2	29	5	3	1	120	8	II	(2)
241C1	2000	Chicken	4b	24	AB517776	2	LC158726	69	LC158793	25	3	18	27	3	4	1	5	194	315	I	(2)
265C1	2000	Chicken	1/2a	6	AB365657	12	LC158727	27	LC158794	13	7	6	10	6	1	2	1	11	11	II	(2)
268C1	2000	Chicken	1/2a	7	AB365658	1	LC158728	1	LC158795	14	5	6	8	62	6	7	34	321	321	II	(2)
393P1	2002	Pork	4b	16	AB457603	2	LC158730	2	LC158797	27	3	1	1	1	3	1	3	1	1	I	(2)
508C6	2003	Chicken	4b	25	AB517769	6	LC158734	11	LC158801	29	3	9	9	3	3	1	5	6	6	I	(2)
565C1	2004	Chicken	1/2a	4	LC336459	12	LC336545	21	LC336502	15	7	6	8	8	6	37	1	121	121	II	
633C3	2004	Chicken	1/2a	8	LC336460	38	LC336546	1	LC336503	30	5	194	8	62	6	7	34	1250	321	II	
633C5	2004	Chicken	4b/4e	16	LC336461	2	LC336547	2	LC336504	27	3	1	1	1	3	1	3	1	1	I	
635P1	2004	Pork	1/2a	5	LC336462	1	LC336548	1	LC336505	16	7	10	16	7	5	2	1	155	155	II	
668C2	2005	Chicken	4b/4e	12	LC336463	2	LC336549	16	LC336506	24	1	1	11	11	2	1	5	2	2	I	
698C1	2005	Chicken	4b/4e	12	LC336464	43	LC336550	16	LC336507	38	1	1	11	11	2	1	5	2	2	I	
698C2	2005	Chicken	4b/4e	12	LC336465	2	LC336551	16	LC336508	24	1	1	11	11	2	1	5	2	2	I	
702P6	2006	Pork	4b/4e	16	LC336466	2	LC336552	2	LC336509	27	3	1	1	1	3	1	3	1	1	I	
702P7	2006	Pork	1/2a	4	LC336467	12	LC336553	21	LC336510	15	7	6	8	8	6	37	1	121	121	II	
703C5	2006	Chicken	1/2b	14	LC336468	5	LC336554	14	LC336511	20	34	39	11	60	3	1	2	330	288	I	
706C6	2006	Chicken	1/2a	4	LC336469	12	LC336555	21	LC336512	15	7	6	8	8	6	37	1	121	121	II	
706C7	2006	Chicken	4b/4e	16	LC336470	2	LC336556	2	LC336513	27	3	1	1	1	3	1	3	1	1	I	
709C1	2006	Chicken	1/2a	6	LC336471	39	LC336557	27	LC336514	31	7	6	10	6	1	2	1	11	11	II	
709C5	2006	Chicken	1/2a	6	LC336472	12	LC336558	27	LC336515	13	7	6	10	6	1	2	1	11	11	II	
715C1	2006	Chicken	1/2b	13	LC336473	3	LC336559	8	LC336516	19	2	1	11	3	3	1	7	5	5	I	
720P1	2006	Pork	1/2a	5	LC336474	40	LC336560	1	LC336517	32	7	10	16	7	5	2	1	155	155	II	
720P3	2006	Pork	1/2a	5	LC336475	1	LC336561	1	LC336518	16	7	10	16	7	5	2	1	155	155	II	
724C4	2006	Chicken	1/2a	8	LC336476	1	LC336562	1	LC336519	3	5	6	8	62	6	7	34	321	321	II	
726P4	2006	Pork	1/2c	26	LC336477	1	LC336563	1	LC336520	33	6	5	6	4	1	4	1	9	9	II	
727C2	2006	Chicken	4b/4e	16	LC336478	2	LC336564	2	LC336521	27	3	1	1	1	3	1	3	1	1	I	
727C4	2006	Chicken	4b/4e	16	LC336479	41	LC336565	2	LC336522	34	3	1	1	1	3	1	3	1	1	I	
731C1	2006	Chicken	1/2b	13	LC336480	5	LC336566	9	LC336523	22	4	4	4	3	2	1	5	3	3	I	This study
732P1	2006	Pork	1/2a	4	LC336481	12	LC336567	21	LC336524	15	7	6	8	8	6	37	1	121	121	II	
738P5	2007	Pork	1/2a	4	LC336482	12	LC336568	21	LC336525	15	7	6	8	8	6	37	1	121	121	II	
742C1	2007	Chicken	1/2b	13	LC336483	5	LC336569	3	LC336526	17	12	1	4	14	3	39	4	87	87	I	
750P2	2007	Pork	1/2c	2	LC336484	1	LC336570	1	LC336527	2	6	5	6	4	1	4	1	9	9	II	
757P5	2007	Pork	1/2b	14	LC336485	42	LC336571	14	LC336528	35	34	12	11	15	3	1	2	323	288	I	
759B1	2007	Beef	1/2c	2	LC336486	1	LC336572	1	LC336529	2	6	5	6	4	1	4	1	9	9	II	
760P6	2007	Pork	1/2a	4	LC336487	12	LC336573	21	LC336530	15	7	6	8	8	6	37	1	121	121	II	
761C4	2007	Chicken	1/2a	4	LC336488	12	LC336574	21	LC336531	15	7	6	8	8	6	37	1	121	121	II	
761C7	2007	Chicken	1/2b	13	LC336489	5	LC336575	3	LC336532	17	12	1	4	14	3	39	4	87	87	I	
763P3	2007	Pork	1/2a	4	LC336490	12	LC336576	21	LC336533	15	7	6	8	8	6	37	1	121	121	II	
764C2	2007	Chicken	1/2b	14	LC336491	5	LC336577	14	LC336534	20	34	39	11	60	3	1	2	330	288	I	
764C5	2007	Chicken	4b/4e	12	LC336492	2	LC336578	16	LC336535	24	1	1	11	11	2	1	5	2	2	I	
769P6	2007	Pork	1/2c	2	LC336493	1	LC336579	1	LC336536	2	6	5	6	4	1	4	1	9	9	II	
770C1	2007	Chicken	4b/4e	16	LC336494	2	LC336580	2	LC336537	27	3	1	1	1	3	1	3	1	1	I	
770C2	2007	Chicken	1/2a	6	LC336495	12	LC336581	29	LC336538	36	7	6	10	6	1	2	1	11	11	II	
770C3	2007	Chicken	1/2c	2	LC336496	1	LC336582	1	LC336539	2	6	5	6	4	1	4	1	9	9	II	
778P6	2007	Pork	1/2c	26	LC336497	1	LC336583	1	LC336540	33	6	5	6	4	1	4	1	9	9	II	
779C2	2007	Chicken	1/2a	8	LC336498	38	LC336584	1	LC336541	30	5	6	8	62	6	7	34	321	321	II	
782C1	2007	Chicken	4b/4e	12	LC336499	2	LC336585	8	LC336542	37	1	1	11	11	2	1	5	2	2	I	
782C7	2007	Chicken	1/2b	14	LC336500	5	LC336586	14	LC336543	20	34	39	11	60	3	1	2	330	288	I	
782C8	2007	Chicken	4b/4e	12	LC336501	2	LC336587	16	LC336544	24	1	1	11	11	2	1	5	2	2	I	

This study

¹⁾: AT, Allele type.
²⁾: ST, Sequence type.
³⁾: CC, Clonal complex.

Fig. 1. Phylogenetic classification of 60 *L. monocytogenes* strains using TLST (A) and MLST (B). Phylogenetic analysis was performed using the maximum likelihood method. The strains isolated from 1996 to 2003 are boxed. The frequency (%) obtained from 1,000 bootstrap replications are shown for >70% of bootstrap replicates.

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