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Listeria monocytogenes Contamination in Pork Can Originate from Farms

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ABSTRACT

The presence of *Listeria monocytogenes* in the pork production chain was followed from farm to slaughterhouse by examining the farm and slaughterhouse levels in the same 364 pigs, and finally by analyzing the cut meats from the same pig lots. Both organic and conventional farms were included in the study. Altogether, 1,962 samples were collected, and the 424 *L. monocytogenes* isolates were analyzed by pulsed-field gel electrophoresis. The results from microbial analyses were combined with data from an on-farm observation and a questionnaire to clarify the associations between farm factors and prevalence of *L. monocytogenes*. The prevalence of *L. monocytogenes* was 11, 1, 1, 24, 5, 1, and 4% in feed and litter, rectal swabs, intestinal contents, tonsils, pluck sets (including lungs, heart, liver, and kidney), carcasses, and meat cuts, respectively. The prevalence was significantly higher in organic than in conventional pig production at the farm and slaughterhouse level, but not in meat cuts. Similar *L. monocytogenes* genotypes were recovered in different steps of the production chain in pigs originating from the same farm. Specific farm management factors, i.e., large group size, contact with pet and pest animals, manure treatment, use of coarse feed, access to outdoor area, hygiene practices, and drinking from the trough, influenced the presence of *L. monocytogenes* in pigs. *L. monocytogenes* was present in the production chain, and transmission of the pathogen was possible throughout the chain, from the farm to pork. Good farm-level practices can therefore be utilized to reduce the prevalence of this pathogen.

In Europe, pork is the most frequently consumed meat, and *Listeria monocytogenes* is among the most severe biological hazards transmitted by pork in terms of lethality and hospitalization, as well as socioeconomic consequences *(19). L. monocytogenes* causes a life-threatening infection, listeriosis, in susceptible individuals, with a mortality of 20 to 30% or higher *(16, 44).* In addition, healthy adults may contract milder gastrointestinal illness due to the bacterium *(24, 34). L. monocytogenes* is frequently isolated from pork and processed pork products *(10, 28, 40, 42),* and sporadic cases and outbreaks of listeriosis have been associated with these food items *(14, 22, 27, 33).* Because of the potential risk to consumers, the presence of *L. monocytogenes* in pork and pork products needs to be controlled.

To control *L. monocytogenes* in meats, potential contamination routes throughout the pork production chain and factors affecting the presence of this bacterium must be evaluated. EU legislation *(3)* requires information from ''farm to fork'' to enhance consumers' protection regarding foodborne zoonotic hazards, i.e., *L. monocytogenes,* transmitted by pork. Healthy pigs are known to harbor *L. monocytogenes (7, 40, 43, 45).* Contamination of pig carcasses has been studied at both the slaughterhouse level *(4, 7, 11)* and in the processing plant *(12, 36, 41),* but contamination throughout the chain, from farms to meats, has not been investigated. The bacteria can potentially spread in the food chain all the way from the farm to retail level, and further to consumers. Some practices at the farm level have been shown to have impact on the prevalence of *L. monocytogenes,* but more studies are needed to reveal the correlation between infection of pigs on farms and contamination of carcasses at slaughter *(20).*

This study was conducted to evaluate the presence of *L. monocytogenes* throughout the pork production chain and to investigate points of contamination of the pathogen. To this end, we collected samples from farms and at slaughter, and then followed each pig during these steps. In addition, we collected meat cuts from the same slaughtered lots in meat cutting plants. We also evaluated farm management practices with the prevalence of *L. monocytogenes* to uncover the risk factors associated with the presence of *Listeria* at farm level. Because of the growing demands for more ethical and natural foods, to detect any differences between these production types, we included both organic and conventional farms in our study.

MATERIALS AND METHODS

Sampling. A total of 15 farms (5 organic and 10 conventional) were selected from southwestern Finland. Five of the conventional farms had production capacity similar to the organic farms studied, i.e., under 1,000 fattening pigs (median, 350), and 5 had production capacity of over 1,000 fattening pigs (median, 2,600). Organic farms were registered as such and

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inspected according to EU regulations *(1)*. For each farm, 21 to 26 pigs were selected for sampling. Samples were taken in farms, slaughterhouses, and meat cutting plants; altogether, 1,962 samples were collected. Samples collected from pigs in farms and slaughterhouses were logistically connected to the corresponding pig, and meat samples were connected to the corresponding farm. At farms, 364 rectal swabs with sterile cotton swabs were collected into tubes containing half-Fraser broth (Oxoid, Ltd., Basingstoke, UK), and pigs were ear tagged. In addition, 37 samples of feed and litter were collected. At the slaughterhouse, the same pigs were recognized from ear tags, and intestinal content ($n = 358$), tonsil ($n = 350$), pluck set ($n = 354$), and carcass ($n = 359$) samples were collected after meat inspection. All samples from ear-tagged pigs at slaughterhouse level could not be collected because some pigs were not in the same slaughtering lot with others, and some samples were lost in the slaughtering process before meat inspection. Intestinal content was collected from an incision to a bowl with a sterile spoon. The pluck sets were sampled by swabbing the surface of lungs, heart, liver, and kidneys with gauze moistened with peptone water. Moisturized gauze was also used for swabbing the total surface of the thoracic and pelvic cavities of both halves of the carcass. The time between farm and slaughterhouse sampling was 1 to 2 weeks. Altogether, 140 meat samples were sent for investigations in cold storage directly from the cutting facilities. Meat samples were from nine of the farms investigated.

Determination of *L. monocytogenes*. Detection of *L. monocytogenes* was performed according to International Organization for Standardization method *(2),* with some modifications. Samples were initially enriched in half-Fraser broth for 24 h at 30°C, and then in Fraser broth (Oxoid, Ltd.) for 48 h at 37°C. After primary and secondary enrichments, samples were streaked onto PALCAM (Oxoid, Ltd.) and *L. monocytogenes* blood agar plates (LAB M, Lancashire, UK). Five typical colonies from each selective agar plate were cultured on blood agar, and *L. monocytogenes* was confirmed by catalase test, Gram staining, and the API *Listeria* kit (bioMérieux, Marcy l'Etoile, France). One identified *L. monocytogenes* isolate was collected from each selective plate, i.e., one to four isolates were collected from each positive sample.

PFGE. All *L. monocytogenes* isolates were genotyped by pulsed-field gel electrophoresis (PFGE). DNA isolation and PFGE were performed as described by Autio et al. *(5, 6),* with use of Pronase (Roche Diagnostics GmbH, Mannheim, Germany) instead of proteinase K. A single colony from blood agar was inoculated into brain heart infusion broth (Difco, Becton Dickenson, Sparks, MD), and cells were harvested from 2 ml of the broth after overnight incubation. Cells were embedded into 2% low-melting point agarose (InCert agarose, FMC BioProducts, Rockland, ME), lysed for 3 h at 37°C, and washed with 0.5 mol/liter EDTA (pH 8.0), 10% sodium laurolyl sarcosine, and 1 mg/ml Pronase for 1 h at 50°C. Digestion of agar-embedded DNA was performed by restriction endonucleases *Apa*I and *Asc*I (New England Biolabs, Beverly, MA), as described by the manufacturer. Samples were electrophoresed according to Autio et al. *(5),* in a Gene Navigator system with a hexagonal electrode (Pharmacia, Uppsala, Sweden). The pulse time ramped from 1 s to 30 s or 35 s for *Apa*I and *Asc*I, respectively, for 18 h. Low-Range PFG Marker (New England Biolabs) was used for fragment size determination. The gels were stained with ethidium bromide and then digitally photographed with an Alpha Imager 2000 documentation system (Alpha Innotech, San Leandro, CA). Macrorestriction patterns were analyzed by BioNumerics, version 4.61, software (Applied Maths, Sint-Martens-Platen, Kortrijk, Belgium). The similarities among restriction patterns based on band position were expressed as Dice coefficient correlations. A composite data set was created by averaging the results obtained by both enzymes. All differences in macrorestriction patterns were considered different genotypes. Genotypes were coded according to internal typing scheme in Department of Food and Environmental Hygiene.

Serotyping. One isolate of each genotype was subjected to multiplex PCR, as described by Doumith et al. *(15),* to separate four serovar groups (1/2a [including 1/2a and 3a], 1/2b [1/2b, 3b, and 7], 1/2c [1/2c and 3c], and 4b [4b, 4d, and 4e]). In addition, commercial O antisera (Denka Seiken, Tokyo, Japan) were used according to the manufacturer's instructions to identify each serotype in the serovar group obtained by PCR.

Statistical analyses. A 95% confidence interval for prevalence of *L. monocytogenes* was calculated, assuming randomized sampling (exact binomial estimate) and considering the fact that 21 to 26 pigs were sampled from each farm (Fleiss quadratic considering the design effect of sampling in clusters) by using the Epi Info 6 program *(13).* Data about farm management practices were collected from the farms with a questionnaire and from on-farm observations, as described earlier *(39).* To assess different features associated with the presence of *L. monocytogenes* in pigs, correlations between farm factors and the prevalence of *L. monocytogenes* were calculated (SPSS 12.0.1, SPSS, Inc., Chicago, IL). In addition, a two-level (farm and pig) multivariate logistic regression model was constructed (MLwiN 2.02, Centre for Multilevel Modelling, University of Bristol, UK). Associations between *L. monocytogenes* and farm factors were tested with combined on-farm rectal swab and tonsil sample results. A pig was considered positive if either or both of the above-mentioned samples were positive. A pig was excluded from analyses if either the rectal or the tonsil sample was missing. A total of 14 pigs were excluded.

RESULTS

Altogether, 119 (6%) of 1,962 samples investigated were *L. monocytogenes* positive (Tables 1 through 3). In addition, *L. monocytogenes* was isolated from all organic farms and from 7 of the 10 conventional farms. The overall prevalence of *L. monocytogenes* was significantly higher on organic farms than on conventional farms, both when samples were assumed to be random (chi-square test, $P < 0.001$) and when samples were clustered according to farms (Mann-Whitney U test, $P < 0.01$). Prevalence in all sample types was higher in organic pork production than in conventional production, except in meat samples. *L. monocytogenes* prevalence within all farms in rectal swabs, intestinal contents, tonsils, pluck sets, carcass samples, and meat varied from 0 to 17, 0 to 8, 0 to 63, 0 to 38, 0 to 8, and 0 to 20%, respectively. Prevalence was significantly higher in tonsil samples than in other samples from pigs (chi-square test, $P < 0.001$). High- and low-capacity conventional farms had similar prevalence of *L. monocytogenes,* i.e., 2 and 3% for all samples, respectively.

Altogether, 424 *L. monocytogenes* isolates were genotyped by PFGE. Restriction enzyme *Asc*I revealed 34 restriction patterns, and *Apa*I revealed 30 restriction patterns, resulting in 36 PFGE genotypes. Thirteen PFGE

TABLE 1. *Prevalence of* Listeria monocytogenes *in farm-level conventional and organic pig production*

	Rectal swab				Feed/litter			
			95% CI[a]				95% CI	
Production	*n*	Positive (%)	Random[b]	Clustering[c]	*n*	Positive (%)	Random	Clustering
Organic	121	4 (3)	1–8	0–20	15	3 (20)	4–48	1–74
Conventional	243	0 (0)	0–2	NC[d]	23	1 (4)	0–22	1–18
Total	364	4 (1)	0–3	0–7	38	4 (11)	3–25	2–34

[a] CI, confidence interval.
[b] Random, 95% CI of prevalence when sampling assumed to be random.
[c] Clustering, 95% CI of prevalence when the fact that 21 to 26 pigs sampled from each farm was considered.
[d] NC, could not be calculated.

types were recovered only once, i.e., each from one sample. Twenty-three PFGE types were recovered from 2 or more samples, including 4 PFGE types that were recovered from 10 or more samples. Altogether, 18 samples harbored two or three genotypes, i.e., 15 samples harbored two genotypes, and 3 samples three types. All of these samples were collected from organic farms. Thirty-five genotypes comprised serotype 1/2a and one serotype 1/2c.

Distributions of *L. monocytogenes* genotypes in farms and in pigs that had more than one positive sample are presented in Tables 4 and 5. The highest number of different genotypes was recovered from farm III, which also had the highest prevalence of *L. monocytogenes*. Overall, all genotypes detected in feed or litter were also recovered from pig samples. Six of the seven genotypes detected in pluck sets were also found in tonsils, and 16 of the 17 pigs that had *L. monocytogenes* in more than one sample had the bacterium in the tonsils. The two *L. monocytogenes*–positive carcass samples harbored the genotypes that were also found previously from pigs of the same farm.

In correlation and logistic regression analyses, large group size and contact with pet and pest animals were associated with high prevalence of *L. monocytogenes* on farms (Tables 6 and 7). In correlation analyses, organic production, hygiene conditions, and farm management practices, i.e., management of manure, use of coarse feed, access to outdoor area, and drinking from the trough, were also associated with a high prevalence of *L. monocytogenes* (Table 6).

DISCUSSION

L. monocytogenes was found less frequently in carcass and pork cuts than in tonsils, where it was a common finding. *L. monocytogenes* genotypes found in pluck sets were similar to those in tonsils, indicating direct contact and contamination during slaughter between tonsils and pluck sets. Tonsils and pluck sets are removed at same time during slaughter, thus enabling the above-mentioned contamination. Carcass samples contaminated with *L. monocytogenes* harbored the same genotypes as did the pluck sets; thus, the carcass likely becomes contaminated during slaughter, although this is not as common as contamination of pluck sets. Further, the same genotype in carcasses was detected in cut meats, indicating that contamination of meats may originate from carcasses. Transmission of *L. monocytogenes* has been suspected to occur mainly via the slaughterhouse environment, not primarily via animals *(11).* As shown in this study, direct contamination during slaughter from tonsils to pluck sets and carcasses is also possible.

Farms with the highest prevalence of *L. monocytogenes* had no contaminated carcasses. This shows that a high prevalence of *L. monocytogenes* in pigs does not inevitably lead to highly contaminated meats. Several preventive actions can be utilized in the slaughtering process to reduce contamination of pathogenic bacteria, including proper cleaning and disinfection of equipment and good operating protocols *(11).* With good manufacturing practices, contamination from pigs to the food chain may be substantially reduced, and thus, solid hygienic practices are of the utmost importance during slaughter.

Similar genotypes were frequently found in different pigs of the same farm. This indicates that the pigs of one farm probably have the same origin of *L. monocytogenes*. Feed and litter were found to be contaminated with *L. monocytogenes,* and *L. monocytogenes* genotypes found in feed or litter were also detected in pig samples. Animal feeds and the farm environment commonly harbor *L. monocytogenes (17, 26, 35),* thus serving as a contamination source. This contamination may be the origin of the bacterium further along in the food chain. In addition to a common origin, bacterial spreading from pig to pig on farms is possible, since pigs are reared in close contact with one other. Contamination of tonsils and pluck sets could also occur from pig to pig in the slaughterhouse, since the same equipment is used in the slaughtering line *(7, 36).* However, rectal swabs collected already on farms had similar strains to those later isolated from pigs in the slaughterhouse, and thus, at least part of the contamination detected at the slaughterhouse originates from farms. Further, we demonstrated here that *L. monocytogenes* in pigs might spread all the way from the farm to meat cuts, as similar genotypes were found in samples from pigs, carcass, and meat. In addition, *L. monocytogenes* was also detected in meats from farms where no contaminated carcasses were detected, and those strains were not found in other samples. This indicates that contamination most likely occurred from cutting facility environments, which are often known to be a source of contamination *(30).*

TABLE 2. *Prevalence of* Listeria monocytogenes *in pigs at slaughterhouse level in conventional and organic production*

	Intestinal content				Tonsil				Pluck set			Carcass		
			95% CI[a]				95% CI			95% CI		95% CI		
Production	*n*	Positive (%)	Random[b]	Clustering[c]	*n*	Positive (%)	Random	Clustering	*n*	Positive (%)	Random	Clustering	*n*	Positive (%)	Random	Clustering
Organic	119	4 (3)	1–8	1–8	119	56 (47)	38–56	23–72	120	15 (13)	7–20	3–34	120	2 (2)	0–6	0–9
Conventional	239	1 (0)	0–2	0–3	231	27 (12)	8–17	5–24	234	2 (1)	0–3	0–3	239	0 (0)	0–2	NC[d]
Total	358	5 (1)	0–3	0–4	350	83 (24)	19–29	12–40	354	17 (5)	3–8	1–14	359	2 (1)	0–2	0–3

[a] CI, confidence interval.
[b] Random, 95% CI of prevalence when sampling assumed to be random.
[c] Clustering, 95% CI of prevalence when the fact that 21 to 26 pigs sampled from each farm was considered.
[d] NC, could not be calculated.

TABLE 3. *Prevalence of* Listeria monocytogenes *in cut pork meats in conventional and organic production*

	Meat			
			95% CI[a]	
Production	*n*	Positive (%)	Random[b]	Clustering[c]
Organic	60	2 (3)	0–12	0–19
Conventional	80	3 (4)	1–11	0–19
Total	140	5 (4)	1–8	1–13

[a] CI, confidence interval.
[b] Random, 95% CI of prevalence when sampling assumed to be random.
[c] Clustering, 95% CI of prevalence when the fact that 21 to 26 pigs sampled from each farm was considered.

Almost all isolated *L. monocytogenes* strains were serotype 1/2a. Because of the very low diversity of serotypes, some *L. monocytogenes* types may be better adapted to pork production environments than are others. Adaptation of a certain group of *L. monocytogenes,* including serotype 1/2a, to that niche has also been discussed previously *(21, 25).*

Overall, the prevalence of *L. monocytogenes* in pigs is consistent with earlier findings, except the high prevalence observed in tonsils and pluck sets of pigs from organic farms. In fecal and carcass samples, the prevalence of *L. monocytogenes* has been low, 0 to 2% *(18, 29, 31, 32, 38, 40).* In tonsil samples, the prevalence has been somewhat higher (7 to 14%) than in other pig samples *(4, 7, 29, 40).*

The prevalence of *L. monocytogenes* was higher in organic than in conventional pig production, and *L. monocytogenes* was isolated from pigs of all organic farms. Certain practices on organic farms, such as large group size, access to outdoor areas, and use of coarse feed, seem to explain this higher prevalence. Large numbers of pigs in one pen facilitate contact with more pigs, thus spreading the bacterium. Moreover, because *L. monocytogenes* is common in the environment *(35, 37),* outdoor areas may be a source of contamination. Finally, coarse feed is frequently contaminated with *L. monocytogenes (17, 26).* Although these practices appear to be associated with the prevalence of *L. monocytogenes,* they may otherwise be advantageous with regard to pig welfare, which is one aim in organic production, and some of these practices are also required by law (according to organic production regulations in the European Union *(1),* pigs must have access to outdoor areas and must be given coarse feed daily).

Even within the same production system, a wide range of prevalence existed between farms, suggesting that some farm-specific factors affect the presence of *L. monocytogenes.* These farm factors include large group size, contact of pigs with pet and pest animals, treatment of manure, hygiene practices, and drinking from a trough. In large groups, the bacterium may spread from one pig to many others, and thus, smaller groups in pens may be advantageous. Pet and pest animals may spread the bacterium into the farm environment or contaminate feeds, e.g., birds frequently harbor *L.*

TABLE 4. *Distribution of* Listeria monocytogenes *genotypes on farms*[a]

Farm	Production	Feed/litter	Rectal swab	Intestinal content	Tonsils	Pluck set	Carcass	Meat	Total
I	Conventional				134 (5)	134 (1)			134 (6)
II	Organic	70 (1)		26 (1)	26 (1)				26 (2)
				50 (1)	67 (2)				50 (1)
					151 (3)				67 (2)
									70 (1)
									151 (3)
III	Organic	10B (1)	71 (2)	162A (1)	10A (2)	162A (3)			10A (2)
		162A (2)	82 (1)		10B (9)				10B (10)
			162A (2)		31 (3)				31 (3)
			195 (1)		82 (3)				71 (2)
			205 (1)		160 (2)				82 (4)
					162A (7)				160 (2)
					162B (2)				162A (15)
					188 (1)				162B (2)
									188 (1)
									195 (1)
									205 (1)
IV	Conventional				185 (1)				185 (1)
V	Conventional	70 (1)			88 (1)				70 (1)
		78 (1)			186 (1)				78 (1)
									88 (1)
									186 (1)
VI	Organic				16 (1)	38 (2)	38 (1)	70 (2)	16 (1)
					26 (1)	70 (8)	70 (1)		26 (1)
					38 (2)				38 (5)
					170 (1)				70 (11)
									170 (1)
VII	Conventional				7 (1)				7 (1)
					31 (9)				31 (9)
VIII	Organic			31 (1)	27 (1)	33 (1)			27 (1)
				91 (2)	31 (12)				31 (13)
					33 (1)				33 (2)
					91 (7)				91 (8)
					93 (1)				93 (1)
XI	Conventional				92 (5)			5 (2)	5 (2)
					183 (1)			99 (1)	92 (5)
									99 (1)
									183 (1)
XII	Conventional				16 (1)	50 (1)			16 (1)
					50 (2)				50 (3)
XIII	Organic				51 (1)	78 (1)			51 (1)
					66 (2)				66 (2)
					78 (1)				78 (2)
					209 (5)				209 (5)
XV	Conventional				33 (1)				33 (1)

[a] Genotypes are numbered according to internal coding scheme of the Department of Food and Environmental Hygiene. The number of samples harboring the genotype is in parentheses.

monocytogenes in their intestines and may spread the pathogen *(23)*. Thus, controlling pest animals and restricting the entrance of pets and birds into piggeries reduces the prevalence of *L. monocytogenes*. Drinking water can easily be contaminated when pigs drink from a common trough; using nipple drinkers may be prudent. In addition, liquid manure compared with solid manure as well as mechanical removal of manure reduces the prevalence of *L. monocytogenes*. Some earlier studies have reported similar results, showing that farm management practices, such as specific pathogen–free herds *(40)* and type of feed *(8, 9),* influence the prevalence of *L. monocytogenes*. In this study, some of these practices were specified.

In conclusion, *L. monocytogenes* is found in the pork production chain, and transmission of the bacterium from the farm to pork is possible. However, contamination is not inevitable, and presence of the bacterium during slaughter and production may be reduced. Pigs that harbor *L. monocytogenes* on farm can carry the pathogen into the slaughterhouse, where they may provide a direct source of contamination for carcasses and raw meat cuts during slaughter. Pork-based smallgoods and delicatessen products

TABLE 5. *Distribution of* Listeria monocytogenes *genotypes in pigs harboring the pathogen in more than one sample*[a]

Farm	Pig	Rectal swab	Intestinal content	Tonsils	Pluck set	Carcass
I	23			134	134	
II	277		26, 50	26		
III	54			162A	162A	
	55			10B	162A	
	57	162A		10B, 31		
	66		162A	10B		
	68	71, 162A, 205		162A		
	71	82, 195		162A		
	74	71		82		
VI	157			38	38	38
	186			170	70	
	189				70	70
VIII	150		31, 91	31, 91		
	153			31, 91	33	
	154		91	27, 91		
XII	303			50	50	
XIII	335			78	78	

[a] Genotypes are numbered according to internal coding scheme of the Department of Food and Environmental Hygiene.

TABLE 6. *Farm factors associated with the prevalence of* Listeria monocytogenes *in herds according to correlation analyses*

Variable	All farms			Conventional			Organic		
	n/observed[a]	*r*[b]	*P* value	*n*/observed	*r*	*P* value	*n*/observed	*r*	*P* value
Large group size, >25 pigs/pen	15/2	0.818	0.000	10/0	NC[c]	NC	5/2	0.897	0.039
Solid or partly solid manure	15/5	0.782	0.001	10/1	0.774	0.009	5/4	0.446	0.451
Pigs have access to outdoor area	15/4	0.718	0.002	10/0	NC	NC	5/4	0.501	0.390
Organic production	15/5	0.687	0.004	10/0	NC	NC	5/5	NC	NC
Forage grass as coarse feed	15/2	0.663	0.007	10/0	NC	NC	5/2	0.578	0.307
Pigs drink from trough	15/8	0.653	0.008	10/4	0.774	0.009	5/4	0.798	0.106
Pen hygiene score[d,e]	15	−0.607	0.016	10	−0.662	0.037	5	−0.218	0.725
Low stocking density (m^2/pig)[e]	15	0.598	0.019	10	0.235	0.514	5	0.301	0.623
Hay as coarse feed	15/8	0.577	0.024	10/3	0.379	0.281	5/5	NC	NC
Manure spreading from pen to pen	15/12	−0.568	0.027	10/9	0.174	0.630	5/3	−0.897	0.039
Partial cleaning of pens	14/6	0.578	0.030	9/2	−0.028	0.942	5/4	0.562	0.324
Mechanical removal of manure	15/9	−0.554	0.032	10/9	0.187	0.605	5/0	NC	NC
Pets and birds have access to piggery	15/9	0.553	0.032	10/4	0.446	0.197	5/5	NC	NC
Rodents and birds have access to piggery	15/11	0.543	0.036	10/6	0.643	0.045	5/5	NC	NC
Cats have access to piggery	14/7	0.553	0.040	10/1	0.265	0.459	4/4	NC	NC
Straw as coarse feed	11/10	0.532	0.041	6/5	−0.289	0.418	5/5	NC	NC

[a] *n*, number of farms.
[b] Pearson correlation coefficient
[c] NC, could not be calculated.
[d] From Siekkinen et al. *(39).*
[e] Continuous variable.

TABLE 7. *Results of two-level multivariate logistic regression analyses for farm factors associated with the prevalence of* Listeria monocytogenes *in herds*[a]

Variable	Estimate	Odds ratio	95% CI of odds ratio[b]	*P* value
Constant	−2.636	0.072	0.017–0.310	0.000
Large group size, >25 pigs/pen	2.220	9.207	2.129–39.810	0.003
Pets and birds have access to piggery	1.515	4.549	1.420–14.574	0.011

[a] Herd variance (σ^2_{farm}), 0.646 (SE 0.363); $P = 0.076$ (Wald test); intraclass correlation coefficient, 0.099.
[b] CI, confidence interval.

have been implicated in cases of listeriosis *(14, 22, 27, 33),* and this study supports the need to consider incoming raw meat in the food safety risk management of these products. Reduction of the prevalence of *L. monocytogenes* on farm by control of appropriate risk factors will contribute to the overall reduction of human health risk from the consumption of pork products.

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