Ruminant-associated *Listeria monocytogenes* isolates belong preferentially to dairy-related hypervirulent clones: a longitudinal study in 19 farms

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ABSTRACT

The increasing prevalence of *Listeria monocytogenes* infections is a public health issue. Although studies have shown that ruminants constitute reservoirs of this foodborne pathogen, little is known about its epidemiology and genetic diversity within ruminant farms. Here we conducted a large-scale genomic and epidemiologic longitudinal study of *Listeria* spp. in dairy ruminants and their environments, comprising 19 farms monitored for three consecutive seasons (N=3251 samples). *L. innocua* was the most prevalent *Listeria* spp, followed by *L. monocytogenes*. *L. monocytogenes* was detected in 52.6% of farms (prevalence in feces samples 3.8%, in farm environment samples 2.5%) and more frequently in cattle (4.1%) and sheep (4.5%) than in goat farms (0.2%). Lineage I accounted for 69% of *L. monocytogenes* isolates. Among animal samples, the most prevalent sublineages (SL) and clonal complexes (CC) were SL1/CC1, SL219/CC4, SL26/CC26 and SL87/CC87, whereas SL666/CC666 was prevalent in environmental samples. 61 different *L. monocytogenes* CTs (cgMLST sequence types) were found, 17 of them (27.9%) common to different animals and/or surfaces within the same farms. *L. monocytogenes* prevalence was not affected by farm hygiene but by season: the overall prevalence of *L. monocytogenes* in cattle farms was higher during winter, and in sheep farms was higher during winter and spring. Cows in their second lactation had a higher probability of *L. monocytogenes* fecal shedding than other lactating cows. This study highlights that dairy farms constitute a reservoir for hypervirulent *L. monocytogenes* and the importance of continuous animal surveillance to reduce the burden of human listeriosis.

IMPORTANCE

Listeria monocytogenes is a bacterial pathogen responsible for listeriosis, the foodborne disease with the highest hospitalization and case-fatality rate. Despite increasing evidence that dairy products and ruminant farms are important reservoirs of *L. monocytogenes*, little is known about the epidemiology and genetic diversity of *Listeria* spp. within dairy ruminant farms. We report the largest *Listeria* spp. longitudinal study in individual domestic animals, and the first using whole-genome sequencing for a deep isolate characterization. Here, we show that domestic ruminants can be asymptomatic carriers of pathogenic *Listeria*, that *L. monocytogenes* fecal shedding is often intermittent, and that hypervirulent *L. monocytogenes* clones are overrepresented in dairy farms. Moreover, we uncover the effect of seasons and lactation number on the prevalence of *L. monocytogenes* in ruminants. Our study highlights the need for *Listeria* spp. monitoring in farm animals to control the spread of hypervirulent *L. monocytogenes* and reduce the burden of human listeriosis.

INTRODUCTION

The genus *Listeria* currently includes 26 recognized species of ubiquitous small rod-shaped gram-positive bacteria (1, 2). Only two of these species, *L. monocytogenes* (*L. monocytogenes*) and *L. ivanovii*, are considered pathogens (3). *L. monocytogenes* is an important foodborne pathogen that can cause human and animal listeriosis, a severe invasive infection with high hospitalization and fatality rates in humans (20–30%) (4). In

immunocompromised individuals and the elderly, listeriosis manifests mostly as septicemia and central nervous system (CNS) infections. In pregnant women, listeriosis can lead to fetal or neonatal complications (4, 5).

Domestic ruminants can become infected by *L. monocytogenes* through ingestion of contaminated silage (3), which can result in rhombencephalitis, septicemia, and abortion. Animals may also be asymptomatic carriers and shed the bacterium in their feces (6–11). In dairy ruminants, *L. monocytogenes* can be transmitted to bulk tank milk (BTM) from fecal or environmental contamination of the udder surface (9, 12–15), as a consequence of poor hygiene in the milking parlor or as a consequence of intramammary infection (14, 15). The prevalence of *L. monocytogenes* in BTM of dairy cow farms can range between 1.2 and 16% (9, 16–18) and contaminated milk poses several risks for producers and consumers, namely: (i) the development of listeriosis after consumption of raw milk contaminated products; (ii) the development of biofilms in the milking equipment that contributes to persistent contamination of the BTM and (iii) cross-contamination of dairy processing plants, pasteurized dairy products or other food associated environments (19–23). Fecal shedding of *L. monocytogenes* also poses a risk for inter-animal transmission in dairy farms and contamination of agricultural environments and raw vegetables at the pre-harvest stages (24).

L. monocytogenes population is heterogeneous and can be classified into lineages (25), PCR genoserogroups (26), clonal complexes (CCs or clones) and sequence types (STs) as defined by multilocus sequence typing (MLST) (27), and sublineages (SLs) and cgMLST types (CTs), as defined by core genome MLST (cgMLST) (28). *L. monocytogenes* genetic heterogeneity also reflects

different pathogenic potential among *L. monocytogenes* isolates, with some clones being more frequently isolated from human (e.g. CC1, CC2, CC4, and CC6) (29, 30) and ruminants (e.g. CC1) (31) clinical cases. Despite increasing evidence that dairy products and ruminant farms are important reservoirs of *L. monocytogenes* (7–11, 30, 32–34), little is still known about the genetic diversity, transmission dynamics and persistence of pathogenic *L. monocytogenes* in farm environments.

The objectives of the present study were: (i) to determine the prevalence of *Listeria* spp. in individual dairy ruminants and the farm environment in Spanish farms by a longitudinal study design; (ii) to characterize the genetic diversity and population structure of *L. monocytogenes* in dairy farms using whole genome sequencing; and (iii) to understand the transmission of *L. monocytogenes* at the farm level and the risk factors (season, production hygiene, lactation number and the days in milk (DIM) of current lactation) that influence it.

RESULTS

Prevalence of *Listeria* spp. in dairy farms

A total of 3,251 samples were collected from 19 Spanish dairy farms over three consecutive seasons (Figure 1, Table S1): 2,081 from animals (2,080 feces and 1 CNS infection case) and 1,170 from the surrounding farm environment (195 feed, 390 food and water troughs, 195 beddings, 195 milk filters, and 195 milking station floor). Each farm was sampled one time per season except farm “Sheep B” which was subjected to 8 additional samplings from 2019 to 2020 (extra samples $n=400$; farm environment $n=144$; animal feces $n=256$, see M&M

and Figure 1). None of the farms reported listeriosis cases, except one farm (“Sheep C”), where a listeriosis outbreak occurred on the last season sampled (Spring 2020).

Listeria spp. was detected in 94.7% (18/19) of farms and in all sampling seasons (Fig. 1). Overall, *Listeria* spp. prevalence was 11.2% (318/2850), and similar in feces samples (10.2%; 186/1824) and farm environment samples (12.9%; 132/1026) (Figure 1, Table S2). Prevalence varied significantly between farms from 0% to 43.3% and was overall higher in cattle and sheep farms (Table S2). The most prevalent species were *L. innocua* (64.7%; 275/425) and *L. monocytogenes* (30.6%; 130/425) (Table 1). Co-occurrence of the two *Listeria* species was detected in 0.8% (14/1824) of individual animal feces and 1.1% (11/1026) environmental samples (Table S3). *L. monocytogenes* was detected in 52.6% of farms (10/19), and prevalence in positive farms ranged between 0.7% and 21.3%, and was frequently higher for cattle farms (Fig. 1B, Table S2). *L. monocytogenes* prevalence was also comparable in feces samples (3.8%; 70/1824) and farm environment samples (2.5%; 26/1026), although in some farms, *L. monocytogenes* was most frequently present in feces samples compared to environmental samples in a specific season (Fig. 1B). *L. innocua* was present in 6.7% (123/1824) of feces samples and in 10.8% (111/1026) of farm environmental samples (Table S3). Among environmental samples, *L. monocytogenes* was detected in all sampled sites except in the milking station floor where other *Listeria* spp. were present (8 *L. innocua* and 1 *L. newyorkensis*). *L. monocytogenes* occurred on food troughs (5.8%), beddings (3.5%), feed (2.9%), milk filter socks (MFS) (2.3%), and the water troughs (0.6%) (Tables S2 and S3). Of note, no *L. monocytogenes* was

detected in feed, food troughs and water troughs from 4 out of 9 of the farms where fecal shedders were detected.

Among animals, different seasonal patterns of *L. monocytogenes* shedding were observed (Fig. 1B). While no *L. monocytogenes* was detected in animals from farm “Cattle B” during autumn and winter, it increased sharply in the spring season (28.1%). Farm “Cattle G” was characterized by a high *L. monocytogenes* prevalence of fecal shedders during autumn and winter (21.9% in both seasons), but none was detected in spring. In farm “Cattle I”, although no *L. monocytogenes* was detected in autumn, it increased sharply to 31.2% in winter and disappeared in the spring sampling. Finally, while none of the tested sheep shed *L. monocytogenes* during autumn in farm “Sheep B”, the prevalence increased to 34.3% during winter and to 50% during spring (Fig. 1B).

Interestingly, in farm “Sheep C”, where an 8-week listeriosis outbreak occurred in the spring of 2020, no *L. monocytogenes* was isolated from any of the feces or environmental samples collected. The outbreak caused 89 abortions (from a total of 974 pregnant sheep) and CNS symptoms (inappetence, recumbency, difficulties in swallowing, drooping eyelid, ear and lip, head-tilt and circling) in 6 animals (1.6% total mortality). On samples taken *post-mortem* from the bedding surfaces, feces and the brainstem of one diseased sheep, *L. monocytogenes* was isolated from the brainstem and from one bedding sample but only *L. innocua* was detected on the feces (Table S3).

Population structure and genetic diversity of *Listeria* spp. in dairy farms

Altogether, 425 *Listeria* spp. isolates were obtained from the farm environment (176/425, 41.4%) and animal samples (249/425, 58.6%) and further characterized at the genomic level. Eight different *Listeria* species were identified: *L. monocytogenes* ($n=130$, 30.6%), *L. innocua* ($n=275$, 64.7%), *L. valentina* ($n=6$, 1.4%), *L. newyorkensis* ($n=5$, 1.2%), *L. fleischmannii* subsp. *coloradonensis* ($n=4$, 0.9%), *L. aquatica* ($n=3$; 0.7%), *L. seeligeri* ($n=1$, 0.2%) and *L. thailandensis* ($n=1$, 0.2%) (Fig. 1, Fig. 2, and Table 1). *L. monocytogenes* belonged to lineages I ($n=91$; 70%; genoserogroups IVb, $n=70$ and IIb, $n = 21$) and II ($n=39$; 30%; genoserogroup IIa) (Fig. 2 and Fig. 3). Among animal samples, the most prevalent SLs and CCs were SL1/CC1 ($n=18$, 13.8%), SL219/CC4 ($n=14$, 10.8%), SL26/CC26 ($n=10$, 7.7%) and SL87/CC87 ($n=12$, 9.2%), whereas SL666/CC666 ($n=12$, 9.2%) was prevalent in environmental samples (Fig. 2A, Table 2). Sixty-one different cgMLST types were detected: 44 (72.1%) comprising only one isolate and 17 (27.9%) comprising 2 to 16 isolates sharing 0-6 allelic differences (Table 2, Fig. 2B). Up to 5 and 8 different CTs could be isolated from environmental and fecal materials, respectively, on a single sampling day (Table S3). Overall, a higher diversity was found in animal fecal samples than environmental samples (Shannon indexes 3.4 vs 2.8). The Hutcheson t-test showed a highly significant difference in terms of community composition of *L. monocytogenes* CTs ($P=0.006$), in the two categories (animal feces vs. environmental samples). No CTs were common to multiple farms, except for L1-SL219-ST219-CT5814 which was detected in farms “Sheep B” and “Cattle B”, separated by 73 km and sampled 7 days apart (Table S3). 16.4% (10/61) CTs were common to both environmental and animal samples from the same farm, 3

of them collected at different time points (Tables 2 and S3). Persistent *L. monocytogenes* strains (*i.e.* continued presence of a given CT over time, at a specific location (35)) were identified in 6 dairy farms (Table 2) and in one sheep (Tables S3 and S4).

Listeria pathogenic islands LIPI-3 and LIPI-4, were present in 50% (65/130) and 32.3% (42/130) *L. monocytogenes*, whereas all isolates carried LIPI-1, which is part of the *L. monocytogenes* core genome (Fig. 3). Acquired resistance traits towards antibiotics, disinfectants or other stress conditions, were rare (Table 3, Table S3 and Fig. 3). Two isolates (1.5%, cgMLST types L1-SL2-ST2-CT6147 and L1-SL2-ST2-CT6148) harbored genes conferring resistance to macrolides (*ermG*, *mefA* and *msrD* genes) or to benzalkonium chloride (*bcrABC* and *Tn6188::ermC*; cgMLST type L2-SL313-ST325-CT1188 and L2-SL121-ST121-CT909, respectively). SSI-1 (32/130 isolates, 24.6%, tolerance to low pH and high salt), SSI-2 (1/130, 0.7%; tolerance to alkaline and oxidative stress conditions) and LGI-3 (1/130, 0.7%; tolerance to cadmium) genomic regions were also present (Table 3). Acquired resistance genes were also present in *L. innocua* (19/275, 6.9%) and *L. aquatica* (1/3, 33.3%), with *tetM* (resistance to tetracyclines) being the most prevalent resistance trait detected (Table 3 and Table S3). The most prevalent CTs *L. monocytogenes* detected in this study (L1-SL87-ST1591-CT5545, *n*=12; L1-SL666-ST666-CT5281, *n*=10; L1-SL219-ST219-CT5814, *n*=8; and L2-SL26-ST26-CT2445, *n*=16) harbored at least one of the following genomic regions: LIPI-3, LIPI-4 or SSI-1 (Table 2, Fig. 3).

Impact of farm type, season, and farming practices in the prevalence of *L. monocytogenes*

L. monocytogenes was detected more frequently in cattle (7/10 positive farms, prevalence 4.1%) than in sheep (2/5 positive farms, prevalence 4.5%) and goat farms (1/4 positive farms, prevalence 0.2%) (Table S2). Although *L. monocytogenes* was detected more frequently in “Cattle G” and “Sheep B” farms, no remarkable differences in management practices were detected compared to other farms of the same species where the prevalence of *Listeria* spp. was lower (Table S1). Since only 1 out of 4 goat farms was positive for *L. monocytogenes* (Fig. 1C), and the prevalence was extremely low in this farm (0.7%), goat farms were not included in further statistical analyses.

L. monocytogenes presence in consecutive seasons was only detected in farm “Cattle G” (Fig. 1A). In cattle farms the overall prevalence was higher in winter than in autumn ($P<0.05$) (Fig. 1B and Fig. 4A). In sheep farms the overall prevalence was higher in winter and spring than in autumn ($P<0.05$) (Fig. 1B and Fig. 4B). Interestingly, cows were more likely to shed *L. monocytogenes* on the second lactation than on the first, forth or higher lactations ($P<0.05$) (Fig. 4C), but DIM did not impact the frequency of *L. monocytogenes* fecal shedding (Fig. 4D). In sheep, no significant association was found between the lactation number and frequency of *L. monocytogenes* fecal shedding (Fig. 4E).

Differences in production hygiene were observed between both cattle and sheep farms, but there was no significant correlation between hygiene scores and *L. monocytogenes* prevalence (Table S5).

Genotypes isolated from feces samples did not occur in MFS, indicating that pre-milking teat disinfection used in these farms was effective to prevent *L.*

monocytogenes milk contamination, with exception for farm “Sheep B”, in which this procedure was not typically performed (similarly to all small ruminants’ dairy farms). Accordingly, L2-SL7-ST7-CT5782 isolated from sheep feces samples was identified in MFS in the farm “Sheep B”.

Although all farms reported usage of antibiotics for treatment purposes (Table S1), acquired genetic traits of antibiotic resistance were rare in *L.*

monocytogenes. Interestingly, among *L. innocua*, 19 isolates harbored *tetM* genes, 13 (68.4%) of which were isolated from farms using tetracyclines.

DISCUSSION

Understanding *L. monocytogenes* population dynamics and its biodiversity is essential for effective disease surveillance and the development of control strategies. To the best of our knowledge, this is the largest longitudinal study on the prevalence, ecology and genomic characteristics of *L. monocytogenes* in individual dairy ruminants and the farm environment. Other reports have either applied a longitudinal study design with a reduced number of farms (one to three farms) (7, 9, 10, 36) and/or analyzed feces samples from randomly chosen farm ruminants, which limits the understanding of global and individual fecal shedding patterns over time (9, 10).

In this study, the prevalence of *L. monocytogenes* detected in dairy farms (3.8% in feces samples and 2.5% in farm environment samples) was lower than previously reported in dairy farms with no clinical listeriosis cases (fecal sample prevalence of 0-60% in cattle and 14.2% in sheep) in farms from USA and Europe (6–9, 34, 36). Differences in climate and farm management (e.g., feed used) between different geographical regions may account for the low

prevalence of *L. monocytogenes* in our study compared to previous studies performed in northern countries (37–39). *L. monocytogenes* was detected more frequently in cattle farms than in small-ruminant farms, which is coherent with previous studies regarding the epidemiology of listeriosis among cattle and small ruminants (8, 11, 34, 40). Interestingly, the pathogenic species *L. ivanovii*, reported in small ruminants in previous studies (40–42) was not detected in any of our farms, which could be due to its relative low prevalence (42, 43) or to possible biases of isolation protocols that have typically been optimized for recovery of *L. monocytogenes* (42). Our results are in line with reports showing that the incidence of *L. innocua* in ruminants feces is higher (9.7–22.7%) than that of *L. monocytogenes* (1.8–9.3%) (17, 44). Of note, it has been previously shown that competitive *L. innocua* strains could mask detection of *L. monocytogenes* during enrichment protocols (45).

Although consumption of spoiled silage is thought to be the principal source of infection for ruminants (3), there is no evident link between listeriosis and silage feeding in up to a third of animal listeriosis cases (46). In this study, in 50% of the farms where fecal shedders were detected, no *L. monocytogenes* could be detected in feed, food troughs or water troughs. It has been suggested that contaminated water or feed by wildlife, birds, insects, farm staff, visitors, farm transport of animals, or farm equipment could vehiculate *L. monocytogenes* to farms (10, 13, 34, 47, 48). Moreover, introduction of new animals could be a potential source for the introduction of new *Listeria* strains into the farm, which can be transmitted via fecal-oral contact to other animals of the herd.

The majority of isolates retrieved here belonged to lineage I (particularly to SL1/CC1, SL219/CC4 and SL87/CC87) which is significantly associated with a clinical origin both in humans and animals (29, 49, 50). CC1 has been shown to be highly associated with dairy products (30, 51) and cause human listeriosis outbreaks (52, 53). CC1 is hypervirulent and colonizes better the intestinal lumen and invades more intestinal tissues than hypovirulent clones (CC9 and CC121) (30, 31, 50). CC87 has been previously reported as predominant in foodborne and clinical isolates in China and related to two outbreaks in Northern Spain (54–56).

Previously, *L. monocytogenes* isolates of identical or nearly identical genotypes (based on “multivirulence” locus sequence typing or pulsed-field gel electrophoresis) have been described to occur for years on dairy farms, although the majority of the genotypes were sporadic (9, 10, 57). In the present study, by using a genome-based approach, the same genotypes were found in multiple animals and surfaces within the same farms. Interestingly, with exception for one sheep, identical genotypes could not be detected in the same animal along different seasons, suggesting that fecal shedding period is shorter than the time frame between samplings dates. Indeed, previous experimental studies have shown that fecal shedding lasted 10 days in sheep inoculated orally with a high dose of *L. monocytogenes* (10^{10} colony forming units) (58).

Accordingly, fecal carriage of *L. monocytogenes* in healthy human adults is reported to be transient (59). However, studies in wild and domestic ruminants suggest that animals can silently carry *L. monocytogenes* in tonsils even without fecal shedding (58, 60). We hypothesize that these silent carriers could under certain circumstances (i.e. immunosuppression, stress factors) shed this

bacterium from the tonsils to the environment through feces leading to intermittent shedding. Tonsil infection may also be a portal of entry for infection in animals and may explain why *L. monocytogenes* was not identified in the feces of sheep herd where a listeriosis outbreak occurred.

Although *L. monocytogenes* could be isolated from cattle all year round, the overall prevalence of *L. monocytogenes* in cattle farms was significantly higher in samples collected during winter which is in line with previous reports (9, 61, 62). Cows in their second lactation had a higher probability of *L. monocytogenes* fecal shedding than cows on the first, forth or higher lactations. An inadequate transition from the first to the second lactation with a poor body condition score could impair immune function (63) and predispose to *L. monocytogenes* colonization. Interestingly, *tetM* genes were detected more frequently in *L. innocua* isolates from farms using tetracycline than in farms not using this antibiotic, highlighting the importance of antibiotic stewardship in veterinary medicine.

In summary, our data show that i) *L. innocua* and *L. monocytogenes* were the most prevalent *Listeria* spp. in both dairy ruminant feces and farm-associated environments; (ii) single ruminants can harbor *L. monocytogenes* alone or together with *L. innocua* without clinical signs of infection; (iii) *L. monocytogenes* could be isolated from half of the dairy farms sampled; (iv) *L. monocytogenes* fecal shedding can present high levels of month-to-month variation and could occur as an isolated sporadic case or as a high-number of fecal shedders case; (v) except one isolated case, there was no evidence of transmission of *L. monocytogenes* CTs between farms, indicating intra-farm transmission dynamics; (vi) CC1 and CC4 hypervirulent *L. monocytogenes* clones, which are

among the most common *L. monocytogenes* CCs responsible for human infection, represented 30% of the *L. monocytogenes* isolates retrieved in this study and were mainly obtained from host associated samples (feces); (vii) the overall *L. monocytogenes* prevalence was higher in winter than in autumn in cattle farms and higher in winter and spring than autumn in sheep farms; and (viii) cows were more likely to shed *L. monocytogenes* on the second lactation than on the first, forth or higher lactations.

Our data are consistent with the hypothesis that dairy farms may be sites that favor the selection of invasive *L. monocytogenes* clones, which are indeed shed in the feces more efficiently than hypovirulent clones (30), and constitute a reservoir for hypervirulent strains that can colonize dairy products. This study improves the understanding of *Listeria* spp. prevalence and ecology in the dairy ruminant environment and may contribute to the development of effective disease surveillance and control strategies to reduce the number of both human and animal listeriosis cases.

MATERIALS AND METHODS

Farms

The study population consisted of 19 dairy ruminant farms (10 cattle, 5 sheep, and 4 goat) with different housing systems, management practices, and herd sizes located in the provinces (administrative division in Spain) of Valencia, Alicante, Castellón, Murcia, and Albacete (mid-east and south-east of Spain) (Table S1).

No history of clinical listeriosis had been observed in any of the farms before and/or during the sampling period, except for farm “Sheep C” which suffered a listeriosis outbreak in the last season sampled (spring 2020).

Sample collection

During the sampling period (winter 2018 to spring 2019 and winter 2019 to spring 2020), each farm was visited once per season (autumn, winter, and spring), for a total of 3 visits per farm. Farm characteristics, sampling dates, and *Listeria* spp. isolated are indicated on Tables S1 and S3. Farm “Sheep B” was sampled 11 times during 7 consecutive seasons from autumn 2018 to spring 2020 for *Listeria* genomic diversity analysis due to the discovery of the new species *L. valentina* in the February/2019 sampling (1). For consistency with data from other farms, only data from three consecutive seasons (autumn 2018-Nov-07, winter 2019-Feb-27, and spring 2019-Apr-10) in this farm were considered for prevalence and statistics calculations.

On each farm visit, 50 samples (32 samples of feces from individual animals, 3 samples of feed, 3 samples of bedding, 3 MFS, and 9 surface swabs (3 from milking station floor, 3 from water troughs, 3 from food troughs) were collected during three consecutive seasons (autumn, winter, and spring) amounting to 150 samples per farm. The same 32 animals sampled during the first farm visit, were monitored in the course of followings evaluations (three seasons total) by veterinarians during the usual handling of the animals, following the guidelines of European Union Directive 2010/63/EU for the protection of animals used for scientific purposes (64). Cows, sheep, or goats that were sold in the intervals between the sampling periods were replaced in the study with a new animal.

MFS were selected for sampling since the prevalence of *L. monocytogenes* is twice that in BTM(9). Each sample was collected into a sterile bag by the use of clean gloves or sampling utensils. Rectal fecal grab samples were collected from randomly selected animals in each farm to have a representation of all lactation numbers. Fecal samples were obtained by rectal grab to avoid cross-contamination among animals. This routine veterinary practice does not require the approval of the Animal Ethics and Experimentation Committee. Bedding samples, food troughs samples, water troughs samples, and milking station floor samples were collected from diverse locations on each farm. All samples were collected using disposable gloves by aseptic conditions and stored in clean coolers with ice packs for transit to the laboratory. Samples were processed within 2-12 h of collection.

Animal cleanliness and production hygiene

A numerical scoring system for assessing animal cleanliness of 5 body areas (tail head, ventral abdomen, udder, upper rear limb, and lower rear limb) was used for the individual animals as previously described (scale of 1 to 5, where score 1 = very clean, score 5 = heavily soiled) (65). Production hygiene was evaluated based on the cleanliness of the premises (milk room, milking station, feed troughs, water troughs and beddings) on farm visits on a scale of 1 to 3 as previously described (9). A score of “1” corresponded to a major deficit in production hygiene, “2” to a minor deficit in production hygiene, and “3” to no notable deficit in production hygiene.

***Listeria* spp. isolation and identification**

Listeria spp. were isolated as previously described (1, 60). Briefly, 8 g of rectal fecal samples or bedding samples were diluted 1/10 in Half-Fraser broth (Scharlab, Spain), homogenized and incubated at 30 °C for 24 h for enrichment. Swab samples (feed troughs, water troughs, and milking station floor) were placed in 10 ml Half Fraser broth, vortexed for 2 min, and incubated at 30 °C for 24 h for enrichment. Entire MFS socks or 8 g of feed samples were used as sample material for primary enrichment in Half Fraser broth (30 °C, 24h). Samples were homogenized manually for 1 min until the solid matter was completely suspended in the enrichment solution. One hundred microlitres of the incubated suspension were transferred to 10 ml Fraser broth (Scharlab, Spain) and incubated at 37 °C for 24 h. After the second enrichment, 100 µl enriched culture and two tenfold dilutions were transferred to RAPID'*L.mono* plates (BioRad, USA) and incubated at 37 °C for 24 h. Characteristic *Listeria* spp. colonies (colonies were blue or white, with or without a yellow halo, round, convex, 1 to 2 mm) were confirmed in selective Oxford agar plates for *Listeria* (Scharlab, Spain) (colonies were approximately 2 mm in diameter, grey-green with a black sunken center and a black halo) and Columbia CNA agar with 5% sheep blood agar plates (colonies were opaque, flat, 1 to 2 mm). From each positive sample, one isolate colony was obtained and preserved in glycerol at -80°C and sent to the World Health Organization Collaborating Centre (WHOCC) for *Listeria*, Institut Pasteur, Paris, France, for species identification and characterization. *Listeria* isolates were identified with matrix-assisted laser desorption ionization-time of flight mass spectrometry using the MicroFlex LT system with the last MBT library DB-7854 (Bruker Daltonics, Germany), as

previously described (66) and by whole genome sequencing as previously described (1).

Genome sequencing and assembly

DNA extraction was carried out with the NucleoSpin Tissue purification kit (Macherey-Nagel, Germany) from 0.9 mL Brain heart infusion (Difco, USA) cultures grown overnight at 35°C. DNA libraries were prepared using the Nextera XT DNA Sample kit (Illumina, USA), and sequenced in a NextSeq 500 platform (Illumina, USA) using 2 x 150 bp runs, according to the manufacturer's protocol. Raw reads were trimmed with fqCleaner v.3.0 (Alexis Criscuolo, Institut Pasteur, Paris) as previously described (1, 60), and assembled with SPAdes v.3.12.0 (67) using automatic k-mer selection and the --only-assembler and --careful options.

Molecular typing and phylogenetic analysis

In silico typing was performed from the assemblies using the genoserogrouping (26), MLST (7 loci (27)), cgMLST profiles (1,748 loci (28)), resistance and virulence schemes (244 loci) implemented at using BIGSdb-*L. monocytogenes* v.1.30 (<https://bigsdb.pasteur.fr/listeria>; (28, 68)). Genes were scanned at BIGSdb-*L. monocytogenes* using the BLASTN algorithm, with minimum nucleotide identity and alignment length coverage of 70% and word size of 10, as previously described (28). MLST profiles were classified into ST and grouped into CCs as previously described (27). cgMLST profiles were grouped into CTs and SLs, using the cut-offs of 7 and 150 allelic mismatches, respectively, as previously described (28). Minimum spanning trees and single linkage

dendrograms were built from cgMLST profiles using Bionumerics 7.6 software (Applied Maths, Belgium) and annotated with iTol v.4.2 (69). Assemblies were also screened for antimicrobial resistance genes and the presence of plasmids using ABRicate v.1.0.1 (70–74) and MOB-suite v.2.0.1 (75), respectively.

Statistical analysis

For DIM analysis cows were grouped into different categories considering the dairy cattle lactation curve and classified in Early lactation (0 -120 days), Mid-lactation (121 – 240 days), Late lactation (241 – 360) and End of Lactation (> 361 DIM). DIM were not analyzed in sheep farms since all the ewes in the same farm were synchronized using intravaginal sponges and delivered approximately the same day. Shannon diversity indices and Hutcheson T-test were calculated using the web <https://www.dataanalytics.org.uk/comparing-diversity/> (76). The rest of statistical analyses were conducted with IBM SPSS Statistics version 25. The significance level for all statistical tests was $P < 0.05$. Chi-square tests were performed to determine the effect of season, the number of lactation and DIM on the number of *L. monocytogenes* fecal shedders. Spearman's rank-order correlations were done to evaluate the association between the farm hygiene score and *L. monocytogenes* prevalence.

Data availability

Sequences obtained in this study will be made publicly available at the European Nucleotide Archive (BioProjects PRJEB45781 and PRJEB36008) and BIGSdb-*Listeria* (bigsdb.pasteur.fr/listeria) upon publication. The accession numbers are detailed in Table S3.

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Figure legends

Figure 1. A) *Listeria* spp. isolated in this study from dairy cattle, sheep and goat farms during three consecutive seasons. Farm “Sheep B” was sampled 11 times during 7 consecutive seasons from autumn 2018 to spring 2020 (see Material and methods). Circle size is proportional to the number of isolates. B) Prevalence of *L. monocytogenes* in feces samples and the farm environment during three consecutive seasons. For consistency among farms, only data from three consecutive seasons (autumn 2018-Nov-07, winter 2019-Feb-27, and spring 2019-Apr-10) were considered for prevalence calculation on farm “Sheep B”.

Figure 2. Diversity of *L. monocytogenes* isolates collected in this study ($n=130$) based on cgMLST (1748 loci) analyses. A) Distribution of sublineages in animals, feed and farm environmental sources. Corresponding clonal complexes (CCs), defined on the basis of 7-locus MLST, are shown in brackets. B) Minimum spanning tree based on the cgMLST profiles *L. monocytogenes* observed in each farm sampled in this study. Farms with only one *L. monocytogenes* isolate (“Cattle A” and “Goat A”) are omitted. Circle sizes are proportional to the number of isolates and are colored by source type, as in panel A. Values shown in connecting lines denote the number of allelic differences between profiles. Grey zones delimitate isolates within the same cgMLST type (cut-off of 7-allelic differences (28)) and types common to more than 1 isolate are labeled.

Figure 3. Genetic diversity of the 130 *L. monocytogenes* isolates sequenced in this study. A) cgMLST single linkage dendrogram. Branches are colored by phylogenetic lineage (L1, red; L2, blue) and labelled by sublineages.

Corresponding clonal complexes (CCs), defined on the basis of 7-locus MLST, are shown in brackets. Isolates' names, type of sample and cgMLST types are shown in tips. Colored boxes indicate the sampling farm, season and source, colored according with the key panel, respectively. Color-filled dark blue boxes indicate the presence of selected genetic traits: *Listeria* pathogenic islands (LIPI-1, LIPI-3 and LIPI-4), internalins (*inlA*, *inlB*), intrinsic antibiotic resistance (*fosX*, *lin*, *norB*, *sul*) and acquired resistance loci towards antibiotics (*aphA*, *ermG*, *mefA*, *msrD*), benzalkonium chloride (*bcrABC*, *ermC*), pH or oxidative stress (SSI-1, SSI-2) and metals (LGI-3). White-filled blue boxes represent genes with truncations leading to premature stop codons.

Figure 4. Impact of seasons, lactation number and days in milk (DIM) in the number of *L. monocytogenes* fecal shedders. A, B) Number of *L. monocytogenes* fecal shedders per season in cattle and sheep farms, respectively. C, E) Number of *L. monocytogenes* fecal shedders per lactation in cattle and sheep farms, respectively. D) Number of *L. monocytogenes* fecal shedders per DIM range in cattle farms. Statistically significant differences were evaluated by Chi-square tests. Stars denote P-values < 0.05.

Tables

Table 1. Number of isolates obtained in this study (N=425).

<i>Listeria</i> species	Animal	Farm env.	Feed	Total
<i>L. monocytogenes</i>	89 (20.9%)	32 (7.5%)	9 (2.1%)	130 (30.6%)
<i>L. innocua</i>	150 (35.3%)	92 (21.6%)	33 (7.8%)	275 (64.7%)
<i>L. valentina</i>	5 (1.2%)	1 (0.2%)		6 (1.4%)
<i>L. newyorkensis</i>		5 (1.2%)		5 (1.2%)
<i>L. fleischmannii</i> subsp. <i>coloradonensis</i>	1 (0.2%)	2 (0.5%)	1 (0.2%)	4 (0.9%)
<i>L. aquatica</i>	3 (0.7%)			3 (0.7%)
<i>L. seeligeri</i>		1 (0.2%)		1 (0.2%)
<i>L. thailandensis</i>	1 (0.2%)			1 (0.2%)

Table 2. *L. monocytogenes* cgMLST types detected comprising 2 or more isolates (n=17 types out of 61).

cgMLST type	No. isolates	Farm(s)	Season(s)	Source(s)	Sources description	Traits
<i>Lineage I</i>						
L1-SL87-ST1591-CT5545 (CC87, IIb)	12	Sheep B	Spring 2019 (Apr, May)	A,E	feces (11), bedding (1)	LIPI-1,LIPI-4
L1-SL666-ST666-CT5281 (CC666, IVb)	10	Sheep B	Winter 2019 (Feb, Mar), Spring 2019 (Apr, May), Summer 2019 (Jun), Autumn 2019 (Sep)	E	milk filter (10)	LIPI-1,LIPI-3
L1-SL219-ST219-CT5814 (CC4, IVb)	8	Sheep B, Cattle B	Spring 2019 (May)	A,E	feces (7), feed (1)	LIPI-1,LIPI-3,LIPI-4
L1-SL1-ST1-CT5280 (CC1, IVb)	6	Sheep B	Winter 2019 (Feb), Spring 2019 (Apr)	A	feces (6)	LIPI-1,LIPI-3
L1-SL1-ST1-CT5546 (CC1, IVb)	4	Sheep B	Spring 2019 (Apr)	A	feces (4)	LIPI-1,LIPI-3
L1-SL219-ST219-CT2246 (CC4, IVb)	4	Cattle G	Autumn 2019 (Oct)	A,E	feces (2), food trough (2)	LIPI-1,LIPI-3,LIPI-4
L1-SL219-ST219-CT5797 (CC4, IVb)	3	Cattle E	Spring 2019 (Apr)	A	feces (3)	LIPI-1,LIPI-3,LIPI-4
L1-SL6-ST6-CT5517 (CC6, IVb)	3	Sheep B	Winter 2019 (Mar)	A,E	feces (1), feed (1), bedding (1)	LIPI-1,LIPI-3
L1-SL1-ST1-CT2060 (CC1, IVb)	2	Cattle G	Winter 2020 (Feb)	A	feces (2)	LIPI-1,LIPI-3
L1-SL6-ST6-CT5393 (CC6, IVb)	2	Sheep B	Winter 2019 (Feb, Mar)	A	feces (2)	LIPI-1,LIPI-3
L1-SL392-ST392-CT7234 (CC392, IIb)	2	Sheep B	Winter 2020 (Jan)	A	feces (2)	LIPI-1
L1-SL387-ST388-CT5390 (CC388, IVb)	2	Sheep B	Winter 2019 (Feb)	A,E	feces (1), feed (1)	LIPI-1,LIPI-4
L1-SL1-ST1-CT8169 (CC1, IVb)	2	Sheep C	Spring 2020 (May)	A,E	brain (1), bedding (1)	LIPI-1,LIPI-3
<i>Lineage II</i>						
L2-SL26-ST26-CT2445 (CC26, IIa)	16	Cattle I	Winter 2020 (Feb), Spring 2020 (May)	A,E	feces (10), feed (1), food trough (3), bedding (2)	LIPI-1, SSI-1
L2-SL7-ST7-CT5782 (CC7, IIa)	5	Sheep B	Spring 2019 (Apr, May)	A,E	feces (4), milk filter (1)	LIPI-1, SSI-1
L2-SL7-ST7-CT1679 (CC7, IIa)	3	Cattle B	Spring 2019 (May)	A,E	feces (2), bedding (1)	LIPI-1, SSI-1
L2-SL37-ST37-CT1830 (CC37, IIa)	2	Cattle G	Winter 2020 (Feb)	A,E	feces (1), food trough (1)	LIPI-1

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Table 3. Acquired antibiotic resistance genes detected in this study.

<i>Listeria</i> species	No. isolates	Genes ¹	Farm(s)	Season(s)	Source(s)	Source description
<i>L. monocytogenes</i>	2	<i>mefA,msrD,ermG</i>	Cattle G	Autumn 2019 (Oct)	A,E	feces (1), feed (1)
	1	<i>aphA</i>	Goat A	Autumn 2018 (Nov)	A	feces (1)
<i>L. innocua</i>	13	<i>tetM</i>	Cattle A, E, G, J; Sheep A, E	Spring 2019 (Apr, May), Autumn 2019 (Dec), Spring 2020 (Jun), Winter 2020 (Jan, Feb)	A,E	feces (6), feed (1), bedding (4), food trough (2)
	4	<i>dfrD,lnuA,tetM</i>	Sheep E	Autumn 2019 (Dec), Winter 2020 (Mar), Spring 2020 (Jun)	A,E	feces (1), bedding (2), food trough (1)
	1	<i>dfrD,lnuA,tetS,tetM</i>	Goat D	Winter 2020 (Mar)	A	feces (1)
	1	<i>lnuA,tetM</i>	Cattle J	Autumn 2019 (Dec)	E	feed (1)
<i>L. aquatica</i>	1	<i>dfrK</i>	Sheep A	Spring 2019 (May)	A	feces (1)

¹gene traits of antibiotic resistance towards: folate inhibitors (*dfrD*, *dfrK*); lincosamides (*lnuA*); macrolides (*ermG,mefA,msrD*); tetracyclines (*tetM*, *tetS*)

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Supplementary table legends

Table S1. Characteristics and management practices of the investigated dairy farms.

Table S2. Prevalence of non-pathogenic *Listeria*, *L. monocytogenes*, and total *Listeria* spp. in feces samples and the farm environment from 19 Spanish dairy farms.

Table S3. *Listeria* isolates characterized in this study.

Table S4. Individual animals where *L. monocytogenes* were isolated repeatedly in different samplings

Table S5. Correlation of hygienic scores and prevalence of *L. monocytogenes* on the investigated dairy farms. Hygienic scores were calculated as described in Material and Methods to assess animal cleanliness and production hygiene.

Figure 1.

A

B

FIGURE 2

A)

B)

Cattle B ($n=11$)

Cattle C ($n=4$)

Cattle E ($n=4$)

Cattle H ($n=2$)

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Cattle G ($n=23$)

Cattle I ($n=16$)

Sheep B ($n=65$)

Sheep C ($n=3$)

FIGURE 3

Figure 4

Table S1. Characteristics and management practices of the investigated dairy farms.

Farm	Province	Herd size	Area per animal (m ²)	Silage	Bedding material	Sampling periods	Antibiotics used
Cattle A	Valencia	>400	17	Corn+Barley	Compost	2018-10-17 / 2019-02-11 / 2019-04-08	Penicillin, ceftiofur, trimethoprim, sulfonamide, tylosin, marbofloxacin
Cattle B	Valencia	>400	15	Corn	Compost	2018-11-14 / 2019-02-19 / 2019-05-27	Ceftiofur, penicillin, oxitetracycline
Cattle C	Murcia	>400	23	Corn	Compost	2018-11-15 / 2019-03-20 / 2019-05-13	Ceftiofur, marbofloxacin, amoxicillin
Cattle D	Albacete	40	8.1	Corn	Straw	2018-12-17 / 2019-02-08 / 2019-03-26	Ceftiofur, florfenicol
Cattle E	Valencia	124	8	No	Straw	2018-10-23 / 2019-02-27 / 2019-04-30	Ceftiofur, marbofloxacin, trimethoprim, sulfonamide, penicillin, dihydrostreptomycin, enrofloxacin
Cattle F	Albacete	190	263	Oats	Straw	2019-10-28 / 2020-02-21 / 2020-06-17	Florfenicol, trimethoprim, sulfonamide, penicillin
Cattle G	Murcia	>400	22	Oats	Compost	2019-10-28 / 2020-02-21 / 2020-06-17	Sulfonamide, marbofloxacin, tetracycline, enrofloxacin
Cattle H	Albacete	>400	3.3	Corn+Oats	Compost	2019-11-19 / 2020-02-28 / 2020-05-20	Trimethoprim, sulfonamide, penicillin, tylosin, oxitetracycline
Cattle I	Valencia	150	3.3	Corn	Mattress+wood-shavings	2019-12-10 / 2020-02-27 / 2020-05-26	Florfenicol, trimethoprim, sulfonamide, penicillin, tylosin, oxitetracycline
Cattle J	Valencia	>400	22.5	No	Straw	2019-12-16 / 2020-01-27 / 2020-05-26	Oxitetracycline
Sheep A	Albacete	1400	1.8	No	Straw	2018-11-23 / 2019-01-17 / 2019-05-06	Amoxicillin
Sheep B	Castellon	>2000	2	Alfalfa	Straw	2018-11-07 / 2019-02-27 / 2019-04-10	Amoxicillin, oxitetracycline, marbofloxacin, trimethoprim, sulfonamide, tulathromycin
Sheep C	Albacete	>2000	4	Corn	Straw	2019-11-05 / 2020-01-13 / 2020-05-15	Amoxicillin, oxytetracycline
Sheep D	Albacete	>2000	3	Corn	Straw	2019-12-03 / 2020-02-17 / 2020-05-20	Amoxicillin
Sheep E	Alicante	>2000	3	Wet brewery grains	Straw	2019-12-17 / 2020-03-09 / 2020-06-17	Cephalosporin, oxitetracycline, colistin
Goat A	Castellón	400	1.06	No	Straw	2018-11-01 / 2019-01-23 / 2019-04-16	Enrofloxacin, amoxicillin
Goat B	Murcia	600	3	No	Straw	2018-12-10 / 2019-04-01 / 2019-05-10	Enrofloxacin, oxitetracycline, tylosin, erythromycin
Goat C	Albacete	750	1.64	Corn	Straw	2019-11-05 / 2020-01-27 / 2020-05-20	Terramycin
Goat D	Murcia	>2000	4	Corn	Straw	2019-11-26 / 2020-03-13 / 2020-06-19	Amoxicillin, gentamycin, ceftiofur, enrofloxacin

All farms had an open-air barn structure, a parlor milking system, and used a conventional farming system except farm “Cattle F” that followed an organic farming system. All farms used a loose housing system (bedded-pack), except farms “Cattle H” and “Cattle I” which used a free stall system. All farms used a mechanic scrape as a feces removal system.

Table S2. Prevalence of non-pathogenic *Listeria* , *L. monocytogenes* (*Lm*), and total *Listeria* spp. in feces samples and the farm environment from 19 Spanish dairy farms.

Farm		No. (%) of non- <i>Lm</i> , <i>Lm</i> and total positive samples collected																							
		FECES (n =96)			FEED/SILAGE (n =9)			FOOD TROUGH (n =9)			WATER TROUGH (n =9)			BEDDING (n =9)			MILK FILTER (n =9)			MILK STATION FLOOR (n =9)			ALL SAMPLES (n =150)		
		non- <i>Lm</i>	<i>Lm</i>	Total	non- <i>Lm</i>	<i>Lm</i>	Total	non- <i>Lm</i>	<i>Lm</i>	Total	non- <i>Lm</i>	<i>Lm</i>	Total	non- <i>Lm</i>	<i>Lm</i>	Total	non- <i>Lm</i>	<i>Lm</i>	Total	non- <i>Lm</i>	<i>Lm</i>	Total	non- <i>Lm</i>	<i>Lm</i>	Total
Cattle	Cattle A	0 (0,0)	0 (0,0)	0 (0,0)	1 (11,1)	0 (0,0)	1 (11,1)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	3 (33,3)	1 (11,1)	3 (33,3)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	4 (2,7)	1 (0,7)	4 (2,7)
	Cattle B	1 (1,0)	9 (9,4)	10 (10,4)	1 (11,1)	0 (0,0)	1 (11,1)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	2 (22,2)	2 (22,2)	4 (44,4)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	4 (2,7)	11 (7,3)	15 (10,0)
	Cattle C	0 (0,0)	3 (3,1)	3 (3,1)	1 (11,1)	0 (0,0)	1 (11,1)	1 (11,1)	1 (11,1)	1 (11,1)	2 (22,2)	0 (0,0)	2 (22,2)	3 (33,3)	0 (0,0)	3 (33,3)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	7 (4,7)	4 (2,7)	10 (6,7)
	Cattle D	6 (6,3)	0 (0,0)	6 (6,3)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	2 (22,2)	0 (0,0)	2 (22,2)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	8 (5,3)	0 (0,0)	8 (5,3)
	Cattle E	2 (2,1)	4 (4,2)	6 (6,3)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	2 (22,2)	0 (0,0)	2 (22,2)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	4 (2,7)	4 (2,7)	8 (5,3)
	Cattle F	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	1 (11,1)	0 (0,0)	1 (11,1)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	1 (0,7)	0 (0,0)	1 (0,7)
	Cattle G	16 (16,7)	14 (14,6)	25 (26,0)	5 (55,6)	3 (33,3)	6 (66,7)	9 (100,0)	6 (66,7)	9 (100,0)	1 (11,1)	0 (0,0)	1 (11,1)	2 (22,2)	0 (0,0)	2 (22,2)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	33 (22,0)	23 (15,3)	43 (28,7)
	Cattle H	23 (24,0)	1 (1,0)	24 (25,0)	4 (44,4)	0 (0,0)	4 (44,4)	5 (55,6)	0 (0,0)	5 (55,6)	3 (33,3)	1 (11,1)	4 (44,4)	5 (55,6)	0 (0,0)	5 (55,6)	0 (0,0)	0 (0,0)	0 (0,0)	1 (11,1)	0 (0,0)	1 (11,1)	41 (27,3)	2 (1,3)	43 (28,7)
	Cattle I	9 (9,4)	10 (10,4)	19 (19,8)	5 (55,6)	1 (11,1)	5 (55,6)	3 (33,3)	3 (33,3)	6 (66,7)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	2 (22,2)	2 (22,2)	1 (11,1)	0 (0,0)	1 (11,1)	0 (0,0)	0 (0,0)	0 (0,0)	18 (12,0)	16 (10,7)	33 (22,0)
	Cattle J	0 (0,0)	0 (0,0)	0 (0,0)	4 (44,4)	0 (0,0)	4 (44,4)	0 (0,0)	0 (0,0)	0 (0,0)	1 (11,1)	0 (0,0)	1 (11,1)	3 (33,3)	0 (0,0)	3 (33,3)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	8 (5,3)	0 (0,0)	8 (5,3)
	Total	57 (5,9)	41 (4,3)	93 (9,7)	21 (23,3)	4 (4,4)	22 (24,4)	19 (21,1)	10 (11,1)	22 (24,4)	7 (7,8)	1 (1,1)	8 (8,9)	22 (24,4)	5 (5,6)	26 (28,9)	1 (1,1)	0 (0,0)	1 (1,1)	1 (1,1)	0 (0,0)	1 (1,1)	128 (8,5)	61 (4,1)	173 (11,5)
Sheep	Sheep A	11 (11,5)	0 (0,0)	11 (11,5)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	1 (11,1)	0 (0,0)	1 (11,1)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	12 (8,0)	0 (0,0)	12 (8,0)
	Sheep B	14 (14,6)	27 (28,1)	32 (33,3)	0 (0,0)	1 (11,1)	1 (11,1)	0 (0,0)	0 (0,0)	0 (0,0)	1 (11,1)	0 (0,0)	1 (11,1)	3 (33,3)	0 (0,0)	3 (33,3)	0 (0,0)	4 (44,4)	4 (44,4)	0 (0,0)	0 (0,0)	0 (0,0)	18 (12,0)	32 (21,3)	41 (27,3)
	Sheep C	1 (1,0)	1 (1,0)	2 (2,1)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	1 (11,1)	1 (11,1)	2 (22,2)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	2 (1,3)	2 (1,3)	4 (2,7)
	Sheep D	37 (38,5)	0 (0,0)	37 (38,5)	3 (33,3)	0 (0,0)	3 (33,3)	2 (22,2)	0 (0,0)	2 (22,2)	6 (66,7)	0 (0,0)	6 (66,7)	6 (66,7)	0 (0,0)	6 (66,7)	4 (44,4)	0 (0,0)	4 (44,4)	7 (77,8)	0 (0,0)	7 (77,8)	65 (43,3)	0 (0,0)	65 (43,3)
	Sheep E	8 (8,3)	0 (0,0)	8 (8,3)	2 (22,2)	0 (0,0)	2 (22,2)	3 (33,3)	0 (0,0)	3 (33,3)	0 (0,0)	0 (0,0)	0 (0,0)	6 (66,7)	0 (0,0)	6 (66,7)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	19 (12,7)	0 (0,0)	19 (12,7)
	Total	71 (14,8)	28 (5,8)	90 (18,8)	5 (11,1)	1 (2,2)	6 (13,3)	5 (11,1)	0 (0,0)	5 (11,1)	7 (15,6)	0 (0,0)	7 (15,6)	17 (37,8)	1 (2,2)	18 (40,0)	4 (8,9)	4 (8,9)	8 (17,8)	7 (15,6)	0 (0,0)	7 (15,6)	116 (15,5)	34 (4,5)	141 (18,8)
Goat	Goat A	0 (0,0)	1 (1,0)	1 (1,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	1 (0,7)	1 (0,7)
	Goat B	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)
	Goat C	1 (1,0)	0 (0,0)	1 (1,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	1 (0,7)	0 (0,0)	1 (0,7)
	Goat D	1 (1,0)	0 (0,0)	1 (1,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	1 (11,1)	0 (0,0)	1 (11,1)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	2 (1,3)	0 (0,0)	2 (1,3)
	Total	2 (0,5)	1 (0,3)	3 (0,8)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	1 (2,8)	0 (0,0)	1 (2,8)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	0 (0,0)	3 (0,5)	1 (0,2)	4 (0,7)
All Farms	Total	130 (7,1)	70 (3,8)	186 (10,2)	26 (15,2)	5 (2,9)	28 (16,4)	24 (14,0)	10 (5,8)	27 (15,8)	14 (8,2)	1 (0,6)	15 (8,8)	40 (23,4)	6 (3,5)	45 (26,3)	5 (2,9)	4 (2,3)	9 (5,3)	8 (4,7)	0 (0,0)	8 (4,7)	247 (8,7)	96 (3,4)	318 (11,2)

For consistency with data from the rest of the farms, for the farm “Sheep B” only data from three consecutive seasons (Autumn 2018-Nov-07, Winter 2019-Feb-27, and Spring 2019-Apr-10) were considered for prevalence calculation.

Table S3. *Listeria* isolates characterized in this study.

BIGSdb id	isolate	aliases	species	isolation date	season	farm	source	source details	no. paired reads (after trimming)	final coverage	no. contigs	genome length (bp)	NSO contig length (bp)	G+C content (%)	cgMLST loci called (%)	plasmids contigs (bp)	phylogenetic lineage	genosereogroup	CC (MLST)	ST (MLST)	SL (cgMLST)	CT (cgMLST)	pathogenic islands	ΔinA	intrinsic resistance	acquired resistance	other genomic regions	
42361	CLIP 2019/01686	LISVAL251	<i>L. aquatica</i>	2019-05-06	Spring 2019	Sheep A	Animal	Sheep 39	1,588±06	163	98	2,886±06	7,606±04	39.3	n.a.	n.a.	n.a.	L	n.a.	n.a.	n.a.	n.a.					dfxK	
43885	CLIP 2019/02397	LISVAL253	<i>L. aquatica</i>	2019-09-16	Autumn 2019	Sheep B	Animal	Sheep 43	2,500±06	259	69	2,800±06	1,211±05	39.2	n.a.	n.a.	n.a.	L	n.a.	n.a.	n.a.	n.a.						
49068	CLIP 2020/01417	LISVAL422	<i>L. aquatica</i>	2020-01-29	Winter 2020	Sheep B	Animal	Sheep 36	2,800±06	192	62	2,800±06	1,211±05	39.2	n.a.	n.a.	n.a.	L	n.a.	n.a.	n.a.	n.a.						
43838	CLIP 2019/02931	LISVAL247	<i>ischianmami coloradon</i>	2019-07-15	Summer 2019	Sheep B	Feed	Feed 2	2,332±06	240	66	3,076±06	1,355±05	38.4	n.a.	n.a.	n.a.	L	n.a.	n.a.	n.a.	n.a.						
43839	CLIP 2019/02932	LISVAL248	<i>ischianmami coloradon</i>	2019-07-15	Summer 2019	Sheep B	Animal	Sheep 23	1,900±06	197	71	3,076±06	1,211±05	38.4	n.a.	n.a.	n.a.	L	n.a.	n.a.	n.a.	n.a.						
46817	CLIP 2020/00405	LISVAL407	<i>ischianmami coloradon</i>	2020-01-13	Winter 2020	Sheep C	Farm environment	Bedding 1	1,644±06	170	100	1,717±06	1,067±05	38.5	n.a.	n.a.	n.a.	L	n.a.	n.a.	n.a.	n.a.						
46077	CLIP 2020/00426	LISVAL431	<i>ischianmami coloradon</i>	2020-01-29	Winter 2020	Sheep B	Farm environment	Bedding 3	2,100±06	245	68	2,100±06	9,931±04	38.4	n.a.	n.a.	n.a.	L	n.a.	n.a.	n.a.	n.a.						
40563	CLIP 2019/00555	LISVAL92	<i>L. innocua</i>	2019-02-11	Winter 2019	Sheep A	Farm environment	Bedding 2	1,200±06	124	40	2,844±06	1,771±05	37.4	n.a.	n.a.	n.a.	L	CC1609	ST1609	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
40842	CLIP 2019/00575	LISVAL113	<i>L. innocua</i>	2019-02-27	Winter 2019	Sheep B	Farm environment	Bedding 3	6,871±05	71	145	2,851±06	5,771±04	37.3	n.a.	n.a.	n.a.	L	CC1480	ST1480	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
40852	CLIP 2019/00573	LISVAL111	<i>L. innocua</i>	2019-02-27	Winter 2019	Sheep B	Farm environment	Bedding 2	8,931±05	92	67	2,871±06	9,861±04	37.4	n.a.	n.a.	n.a.	L	CC1609	ST1609	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
40855	CLIP 2019/00578	LISVAL116	<i>L. innocua</i>	2019-02-27	Winter 2019	Sheep B	Farm environment	Bedding 3	9,831±05	126	102	2,911±06	5,871±04	37.4	n.a.	2037, 6825, 5806, 10288	n.a.	L	CC500	ST503	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
41305	CLIP 2019/01602	LISVAL134	<i>L. innocua</i>	2019-03-26	Spring 2019	Cattle D	Animal	Cow 25	1,131±06	117	45	2,781±06	1,651±05	37.4	n.a.	n.a.	n.a.	L	ST599	ST599	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41364	CLIP 2019/01587	LISVAL119	<i>L. innocua</i>	2019-02-27	Winter 2019	Sheep B	Farm environment	Bedding 1	1,351±06	139	36	2,841±06	3,341±05	37.4	n.a.	n.a.	n.a.	L	CC1609	ST1609	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41371	CLIP 2019/01594	LISVAL126	<i>L. innocua</i>	2019-03-13	Winter 2019	Sheep B	Feed	Feed 2	1,211±06	125	33	2,811±06	4,671±05	37.4	n.a.	n.a.	n.a.	L	CC133	ST536	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41372	CLIP 2019/01595	LISVAL127	<i>L. innocua</i>	2019-03-13	Winter 2019	Sheep B	Animal	Sheep 52	1,281±06	132	34	2,841±06	3,341±05	37.4	n.a.	n.a.	n.a.	L	CC1609	ST1620	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
41373	CLIP 2019/01596	LISVAL128	<i>L. innocua</i>	2019-03-26	Spring 2019	Cattle D	Farm environment	Bedding 3	1,011±06	105	41	2,791±06	2,501±05	37.4	n.a.	n.a.	n.a.	L	ST599	ST599	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41374	CLIP 2019/01597	LISVAL129	<i>L. innocua</i>	2019-03-26	Spring 2019	Cattle D	Farm environment	Bedding 2	1,431±06	147	47	2,791±06	2,931±05	37.5	n.a.	n.a.	n.a.	L	ST599	ST599	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41375	CLIP 2019/01598	LISVAL130	<i>L. innocua</i>	2019-03-26	Spring 2019	Cattle D	Animal	Cow 24	1,421±06	147	48	2,791±06	3,331±05	37.4	n.a.	n.a.	n.a.	L	ST599	ST599	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41376	CLIP 2019/01599	LISVAL131	<i>L. innocua</i>	2019-03-26	Spring 2019	Cattle D	Animal	Cow 19	1,461±06	152	34	2,791±06	3,181±05	37.4	n.a.	n.a.	n.a.	L	ST599	ST599	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41377	CLIP 2019/01600	LISVAL132	<i>L. innocua</i>	2019-03-26	Spring 2019	Cattle D	Animal	Cow 16	2,021±06	208	33	2,791±06	3,821±05	37.4	n.a.	n.a.	n.a.	L	ST599	ST599	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41378	CLIP 2019/01601	LISVAL133	<i>L. innocua</i>	2019-03-26	Spring 2019	Cattle D	Animal	Cow 12	1,861±06	192	34	2,791±06	3,701±05	37.4	n.a.	n.a.	n.a.	L	ST599	ST599	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41379	CLIP 2019/01603	LISVAL135	<i>L. innocua</i>	2019-03-26	Spring 2019	Cattle D	Animal	Cow 8	1,801±06	186	33	2,791±06	3,331±05	37.4	n.a.	n.a.	n.a.	L	ST599	ST599	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41611	CLIP 2019/01607	LISVAL139	<i>L. innocua</i>	2019-03-20	Winter 2019	Cattle C	Farm environment	Food trough 1	8,601±05	89	102	2,891±06	7,411±04	37.4	n.a.	5948, 9152	n.a.	L	CC493	ST1614	n.a.	n.a.	LP1-3, LP1-4					<i>foxK1in, noB, noS</i>
41612	CLIP 2019/01608	LISVAL140	<i>L. innocua</i>	2019-03-20	Winter 2019	Cattle C	Farm environment	Bedding 1	8,461±05	87	42	2,891±06	1,581±05	37.4	n.a.	6041, 9152	n.a.	L	ST1482	ST1482	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41643	CLIP 2019/01609	LISVAL141	<i>L. innocua</i>	2019-03-20	Winter 2019	Cattle C	Animal	Sheep 26	2,861±06	109	26	2,861±06	5,141±04	37.3	n.a.	n.a.	n.a.	L	ST1482	ST1482	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
41614	CLIP 2019/01610	LISVAL142	<i>L. innocua</i>	2019-03-20	Winter 2019	Cattle C	Farm environment	Bedding 2	1,871±06	193	15	2,781±06	5,361±05	37.4	n.a.	n.a.	n.a.	L	n.a.	n.a.	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
41645	CLIP 2019/01612	LISVAL144	<i>L. innocua</i>	2019-04-08	Spring 2019	Sheep A	Feed	Feed 1	9,021±05	93	89	2,841±06	9,431±04	37.4	n.a.	12305, 11843	n.a.	L	CC448	ST448	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
42244	CLIP 2019/01633	LISVAL165	<i>L. innocua</i>	2019-04-10	Spring 2019	Sheep B	Animal	Sheep 1	1,311±06	135	21	2,751±06	2,841±05	37.4	n.a.	n.a.	n.a.	L	ST1621	ST1621	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
42245	CLIP 2019/01634	LISVAL166	<i>L. innocua</i>	2019-04-10	Spring 2019	Sheep B	Animal	Sheep 10	9,281±05	92	96	2,841±06	2,941±05	37.4	n.a.	n.a.	n.a.	L	CC1609	ST1609	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
42246	CLIP 2019/01635	LISVAL167	<i>L. innocua</i>	2019-04-10	Spring 2019	Sheep B	Animal	Sheep 10	1,271±06	131	27	2,716±06	2,901±05	37.3	n.a.	n.a.	n.a.	L	ST1616	ST1616	n.a.	n.a.	LP1-3					<i>foxK1in, noB, noS</i>
42247	CLIP 2019/01636	LISVAL168	<i>L. innocua</i>	2019-04-10	Spring 2019	Sheep B	Animal	Sheep 25	1,091±06	113	41	2,831±06	1,291±05	37.3	n.a.	n.a.	n.a.	L	ST1616	ST1616	n.a.	n.a.	LP1-3					<i>foxK1in, noB, noS</i>
42248	CLIP 2019/01637	LISVAL169	<i>L. innocua</i>	2019-04-10	Spring 2019	Sheep B	Animal	Sheep 26	1,271±06	132	132	2,791±06	2,961±05	37.4	n.a.	n.a.	n.a.	L	ST1621	ST1621	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
42249	CLIP 2019/01638	LISVAL170	<i>L. innocua</i>	2019-04-10	Spring 2019	Sheep B	Animal	Sheep 38	8,541±05	88	48	3,311±04	3,741±04	37.4	n.a.	n.a.	n.a.	L	ST1621	ST1621	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
42278	CLIP 2019/01639	LISVAL171	<i>L. innocua</i>	2019-04-10	Spring 2019	Sheep B	Animal	Sheep 40	9,091±05	94	n.a.	n.a.	2,121±05	37.3	n.a.	n.a.	n.a.	L	CC133	ST536	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
42279	CLIP 2019/01640	LISVAL172	<i>L. innocua</i>	2019-04-10	Spring 2019	Sheep B	Animal	Sheep 43	9,481±05	98	35	2,881±06	2,331±05	37.3	n.a.	n.a.	n.a.	L	CC1609	ST1609	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
42280	CLIP 2019/01641	LISVAL173	<i>L. innocua</i>	2019-04-10	Spring 2019	Sheep B	Animal	Sheep 43	9,281±05	93	93	2,861±06	2,331±05	37.3	n.a.	n.a.	n.a.	L	ST1619	ST1619	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
42284	CLIP 2019/01645	LISVAL177	<i>L. innocua</i>	2019-04-30	Spring 2019	Cattle E	Farm environment	Bedding 1	8,951±05	93	23	2,831±06	1,871±05	37.4	n.a.	n.a.	n.a.	L	CC133	ST536	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
42285	CLIP 2019/01646	LISVAL178	<i>L. innocua</i>	2019-04-30	Spring 2019	Cattle E	Farm environment	Cow 6	9,261±06	96	25	2,831±06	2,581±05	37.4	n.a.	n.a.	n.a.	L	ST1482	ST1482	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
42286	CLIP 2019/01647	LISVAL179	<i>L. innocua</i>	2019-04-30	Spring 2019	Cattle E	Farm environment	Cow 30	9,431±05	98	37	2,831±06	1,221±05	37.4	n.a.	n.a.	n.a.	L	ST1482	ST1482	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
42287	CLIP 2019/01658	LISVAL180	<i>L. innocua</i>	2019-05-02	Spring 2019	Cattle E	Feed	Feed 2	9,041±05	94	94	2,841±06	2,291±05	37.4	n.a.	n.a.	n.a.	L	CC1609	ST1609	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
42298	CLIP 2019/01659	LISVAL191	<i>L. innocua</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 7	1,081±06	112	32	2,791±06	2,141±05	37.4	n.a.	n.a.	n.a.	L	CC492	ST492	n.a.	n.a.	LP1-3, LP1-4					<i>foxK1in, noB, noS</i>
42300	CLIP 2019/01661	LISVAL193	<i>L. innocua</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 51	7,401±05	77	125	2,871±06	5,991±04	37.3	n.a.	n.a.	n.a.	L	ST1622	ST1622	n.a.	n.a.	LP1-3					<i>foxK1in, noB, noS</i>
42302	CLIP 2019/01663	LISVAL195	<i>L. innocua</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 25	1,831±06	102	36	2,801±06	1,881±05	37.3	n.a.	n.a.	n.a.	L	CC133	ST536	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
42303	CLIP 2019/01664	LISVAL196	<i>L. innocua</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 36	9,811±05	91	99	3,801±06	1,271±05	37.4	n.a.	n.a.	n.a.	L	ST1717	ST1717	n.a.	n.a.	LP1-3 (partial), LP1-4					<i>foxK1in, noB, noS</i>
42305	CLIP 2019/01666	LISVAL198	<i>L. innocua</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 3	6,501±05	67	80	2,801±06	7,591±04	37.4	n.a.	n.a.	n.a.	L	CC1609	ST1609	n.a.	n.a.	LP1-4					<i>foxK1in, noB, noS</i>
42307	CL																											

46687	CLIP 2020/00338	LISVAL326	L. innocua	2019-11-19	Autumn 2019	Cattle H	Animal	Cow 26	5,77E+06	597	18	2,86E+06	1,44E+06	374	n.a.		n.a.	L	CC493	ST493	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46688	CLIP 2020/00339	LISVAL327	L. innocua	2019-11-19	Autumn 2019	Cattle H	Animal	Cow 30	4,93E+06	569	18	2,86E+06	1,44E+06	374	n.a.		n.a.	L	CC493	ST493	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46689	CLIP 2020/00340	LISVAL328	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 7	5,58E+06	577	22	2,85E+06	1,43E+06	374	n.a.	9152, 11976	n.a.	L	ST1482	ST1482	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46690	CLIP 2020/00341	LISVAL329	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Milking floor	1,55E+06	261	26	2,85E+06	3,70E+05	374	n.a.	9152, 11713	n.a.	L	ST1482	ST1482	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46691	CLIP 2020/00342	LISVAL330	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 27	1,71E+06	277	27	3,04E+06	2,74E+05	374	n.a.	54879	n.a.	L	ST1008	ST1008	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46692	CLIP 2020/00343	LISVAL331	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 12	1,38E+06	142	17	2,81E+06	3,26E+05	374	n.a.	235797	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46693	CLIP 2020/00344	LISVAL332	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 32	2,63E+06	270	18	2,81E+06	4,66E+05	375	n.a.	1404743	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46694	CLIP 2020/00345	LISVAL333	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 13	1,38E+06	142	56	2,85E+06	1,88E+05	374	n.a.	5909, 9152	n.a.	L	ST1482	ST1482	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46695	CLIP 2020/00346	LISVAL334	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Water trough 1	2,43E+06	249	24	2,85E+06	3,65E+05	374	n.a.	6159, 9152	n.a.	L	ST1482	ST1482	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46696	CLIP 2020/00347	LISVAL335	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 135	1,93E+06	19	306	2,81E+06	4,66E+05	374	n.a.	1155153	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46697	CLIP 2020/00348	LISVAL336	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 31	2,44E+06	252	34	3,04E+06	2,87E+05	372	n.a.	91899	n.a.	L	ST1008	ST1008	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46698	CLIP 2020/00349	LISVAL337	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Water trough 1	2,43E+06	251	20	2,81E+06	3,47E+05	374	n.a.	825163	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46699	CLIP 2020/00350	LISVAL338	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Bedding 1	2,82E+06	291	20	2,85E+06	3,64E+05	374	n.a.	9152, 11976	n.a.	L	ST1482	ST1482	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46700	CLIP 2020/00351	LISVAL339	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Food trough 3	1,46E+06	151	17	2,81E+06	3,64E+05	374	n.a.	598085	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46701	CLIP 2020/00352	LISVAL340	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Milk filter 1	1,72E+06	178	26	2,81E+06	4,66E+05	374	n.a.	844560	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46721	CLIP 2020/00353	LISVAL341	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Bedding 2	1,77E+06	183	19	2,81E+06	3,64E+05	374	n.a.	845069	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46722	CLIP 2020/00354	LISVAL342	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 39	1,24E+06	128	39	2,95E+06	2,58E+05	374	n.a.	1155153	n.a.	L	ST1008	ST1008	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46723	CLIP 2020/00355	LISVAL343	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Feed 2	1,58E+06	164	37	2,81E+06	3,14E+05	374	n.a.	313741	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46748	CLIP 2020/00356	LISVAL344	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 15	1,89E+06	195	31	2,84E+06	3,57E+05	373	n.a.		n.a.	L	ST1008	ST1008	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46749	CLIP 2020/00357	LISVAL345	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Food trough 1	2,06E+06	213	25	2,81E+06	3,14E+05	374	n.a.	314295	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46750	CLIP 2020/00358	LISVAL346	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 6	1,87E+06	194	33	2,81E+06	4,66E+05	375	n.a.	551921	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46751	CLIP 2020/00359	LISVAL347	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Milk filter 2	2,00E+06	207	32	2,78E+06	3,33E+05	374	n.a.		n.a.	L	ST1263	ST1263	n.a.	n.a.	UPI-4	fox,lin,neob,sl	SSI-2
46752	CLIP 2020/00360	LISVAL348	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 22	1,07E+06	111	12	2,81E+06	1,40E+06	374	n.a.	1404310	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46753	CLIP 2020/00361	LISVAL349	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 19	2,25E+06	233	15	2,81E+06	4,66E+05	374	n.a.	825598	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46754	CLIP 2020/00362	LISVAL350	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Water trough 3	1,32E+06	219	26	2,94E+06	2,92E+05	373	n.a.		n.a.	L	ST1008	ST1008	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46755	CLIP 2020/00363	LISVAL351	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 12	2,11E+06	218	21	2,85E+06	3,65E+05	374	n.a.	9152, 11976	n.a.	L	ST1482	ST1482	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46756	CLIP 2020/00364	LISVAL352	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 26	1,88E+06	195	20	2,81E+06	3,64E+05	374	n.a.	825239	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46757	CLIP 2020/00365	LISVAL353	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 14	2,37E+06	245	23	2,40E+06	3,70E+05	374	n.a.	91899	n.a.	L	ST1008	ST1008	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46758	CLIP 2020/00366	LISVAL354	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 30	2,70E+06	279	14	2,81E+06	4,66E+05	374	n.a.	423354	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46759	CLIP 2020/00367	LISVAL355	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Milking floor 3	2,47E+06	255	14	2,81E+06	5,60E+05	373	n.a.	845093	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46760	CLIP 2020/00368	LISVAL356	L. innocua	2019-12-03	Autumn 2019	Sheep D	Farm environment	Bedding 3	2,10E+06	218	17	2,94E+06	1,50E+06	373	n.a.		n.a.	L	ST1008	ST1008	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46761	CLIP 2020/00369	LISVAL357	L. innocua	2019-12-03	Autumn 2019	Sheep D	Animal	Sheep 17	2,81E+06	240	17	2,81E+06	3,64E+05	374	n.a.	598109	n.a.	L	ST1087	ST1087	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46762	CLIP 2020/00370	LISVAL358	L. innocua	2019-12-10	Autumn 2019	Cattle I	Animal	Cow 11	2,42E+06	250	12	2,82E+06	5,20E+05	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46763	CLIP 2020/00371	LISVAL359	L. innocua	2019-12-10	Autumn 2019	Cattle I	Animal	Cow 8	2,45E+06	253	17	2,82E+06	5,09E+05	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46764	CLIP 2020/00372	LISVAL360	L. innocua	2019-12-10	Autumn 2019	Cattle I	Feed	Feed 2	2,51E+06	259	17	2,82E+06	5,09E+05	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46765	CLIP 2020/00373	LISVAL361	L. innocua	2019-12-10	Autumn 2019	Cattle I	Animal	Sheep 1	2,51E+06	260	14	2,82E+06	4,44E+06	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46766	CLIP 2020/00374	LISVAL362	L. innocua	2019-12-10	Autumn 2019	Cattle I	Animal	Cow 18	2,88E+06	298	21	2,82E+06	3,32E+05	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46767	CLIP 2020/00375	LISVAL363	L. innocua	2019-12-10	Autumn 2019	Cattle I	Animal	Cow 27	2,17E+06	224	18	2,82E+06	4,10E+05	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46768	CLIP 2020/00376	LISVAL364	L. innocua	2019-12-10	Autumn 2019	Cattle I	Animal	Sheep 12	2,83E+06	223	20	2,82E+06	3,33E+05	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46769	CLIP 2020/00377	LISVAL365	L. innocua	2019-12-10	Autumn 2019	Cattle I	Farm environment	Milk filter 1	2,11E+06	218	17	2,82E+06	5,09E+05	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46786	CLIP 2020/00378	LISVAL366	L. innocua	2019-12-10	Autumn 2019	Cattle I	Animal	Cow 30	8,74E+05	90	32	2,82E+06	1,74E+05	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46787	CLIP 2020/00379	LISVAL367	L. innocua	2019-12-10	Autumn 2019	Cattle I	Animal	Cow 30	9,72E+05	101	19	2,82E+06	4,04E+05	374	n.a.		n.a.	L	CC731	ST1262	n.a.	n.a.	UPI-3,UPI-4	fox,lin,neob,sl	SSI-2
46788	CLIP 2020/00381	LISVAL373	L. innocua	2019-12-16	Autumn 2019	Cattle I	Feed	Feed 1	6,39E+05	64	41	2,90E+06	1,98E+05	373	n.a.	5361, 8568, 40991	n.a.	L	CC609	ST603	n.a.	n.a.	UPI-4	fox,lin,neob,sl	SSI-2
46789	CLIP 2020/00382	LISVAL374	L. innocua	2019-12-16	Autumn 2019	Cattle I	Feed	Feed 2	9,70E+05	38	38	2,90E+06	2,59E+05	374	n.a.	26139, 39771	n.a.	L	CC609	ST603	n.a.	n.a.	UPI-4	fox,lin,neob,sl	SSI-2
46790	CLIP 2020/00383	LISVAL375	L. innocua	2019-12-16	Autumn 2019	Cattle I	Feed	Feed 3	9,93E+05	103	42	2,90E+06	1,20E+05	374	n.a.		n.a.	L	CC529	ST610	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46812	CLIP 2020/00400	LISVAL402	L. innocua	2019-12-17	Autumn 2019	Sheep E	Sheep E	Sheep 5	3,00E+06	310	310	2,82E+06	1,45E+05	374	n.a.		n.a.	L	ST163	ST619	n.a.	n.a.	UPI-3 (partial),UPI-4	fox,lin,neob,sl	SSI-2
46813	CLIP 2020/00401	LISVAL403	L. innocua	2019-12-17	Autumn 2019	Sheep E	Farm environment	Sheep 15	2,65E+06	274	26	2,82E+06	4,52E+05	373	n.a.	5014, 72912	n.a.	L	CC609	ST603	n.a.	n.a.	UPI-4	fox,lin,neob,sl	SSI-2
46814	CLIP 2020/00402	LISVAL404	L. innocua	2019-12-17	Autumn 2019	Sheep E	Farm environment	Food trough 3	2,46E+06	254	25	2,86E+06	4,52E+05	373	n.a.	5014, 72912	n.a.	L	CC609	ST603	n.a.	n.a.	UPI-4	fox,lin,neob,sl	SSI-2
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47967	CLIP 2020/00453	LSVAL470	<i>L. innocua</i>	2020-02-17	Winter 2020	Sheep D	Farm environment	Milk filter 2	1,676+06	173	26	2,85E+06	3,45E+05	374	n.a.	9152, 11473	n.a.	L	ST1482	ST1482	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
47970	CLIP 2020/00515	LSVAL532	<i>L. innocua</i>	2020-02-28	Winter 2020	Cattle H	Farm environment	Bedding 1	1,844+06	190	30	2,87E+06	3,50E+05	373	n.a.		n.a.	L	CC43	ST0275	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
47971	CLIP 2020/00521	LSVAL538	<i>L. innocua</i>	2020-02-28	Winter 2020	Cattle H	Farm environment	Food trough 1	1,832+06	189	29	2,77E+06	2,47E+05	374	n.a.		n.a.	L	ST530	ST530	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
47972	CLIP 2020/00522	LSVAL539	<i>L. innocua</i>	2020-02-28	Winter 2020	Cattle H	Farm environment	Food trough 2	2,12E+06	219	17	2,77E+06	3,49E+05	374	n.a.		n.a.	L	ST530	ST530	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
47973	CLIP 2020/00524	LSVAL541	<i>L. innocua</i>	2020-02-28	Winter 2020	Cattle H	Feed	Feed 1	1,69E+06	175	15	2,86E+06	3,50E+05	373	n.a.		n.a.	L	CC43	ST0275	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
47974	CLIP 2020/00526	LSVAL543	<i>L. innocua</i>	2020-02-28	Winter 2020	Cattle H	Farm environment	Food trough 1	1,37E+06	172	37	2,17E+06	3,52E+05	374	n.a.		n.a.	L	CC43	ST0275	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48002	CLIP 2020/00523	LSVAL540	<i>L. innocua</i>	2020-02-28	Winter 2020	Cattle H	Farm environment	Food trough 3	1,48E+06	153	33	2,77E+06	2,06E+05	374	n.a.		n.a.	L	ST530	ST530	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48148	CLIP 2020/01266	LSVAL547	<i>L. innocua</i>	2020-03-09	Winter 2020	Sheep E	Feed	Feed 1	2,62E+06	272	19	2,82E+06	4,65E+05	374	n.a.		n.a.	L	CC235	ST2345	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48149	CLIP 2020/01267	LSVAL548	<i>L. innocua</i>	2020-03-09	Winter 2020	Sheep E	Farm environment	Bedding 1	2,45E+06	254	22	2,78E+06	3,65E+05	373	n.a.		n.a.	L	CC605	ST1613	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48150	CLIP 2020/01268	LSVAL549	<i>L. innocua</i>	2020-03-09	Winter 2020	Sheep E	Farm environment	Bedding 2	2,98E+06	30	169	2,98E+06	3,90E+05	373	n.a.	5014, 72826		L	CC248	ST1448	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48151	CLIP 2020/01269	LSVAL550	<i>L. innocua</i>	2020-03-09	Winter 2020	Sheep E	Farm environment	Bedding 3	2,90E+06	300	11	2,83E+06	1,45E+06	374	n.a.		n.a.	L	ST1619	ST1619	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48152	CLIP 2020/01270	LSVAL551	<i>L. innocua</i>	2020-03-09	Winter 2020	Sheep E	Feed	Feed 2	1,66E+06	171	21	2,62E+06	3,74E+05	374	n.a.		n.a.	L	CC235	ST2346	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48153	CLIP 2020/01271	LSVAL552	<i>L. innocua</i>	2020-03-09	Winter 2020	Sheep E	Animal	Goat 4	2,95E+06	305	18	2,78E+06	1,44E+06	374	n.a.		n.a.	L	CC731	ST1247	n.a.	n.a.	UP1-3,UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48154	CLIP 2020/01272	LSVAL553	<i>L. innocua</i>	2020-03-09	Winter 2020	Sheep E	Animal	Goat 11	1,29E+06	134	24	2,78E+06	2,65E+05	374	n.a.		n.a.	L	ST1619	ST1619	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48155	CLIP 2020/01273	LSVAL554	<i>L. innocua</i>	2020-03-09	Winter 2020	Sheep E	Animal	Goat 12	1,88E+06	195	19	2,88E+06	3,32E+05	374	n.a.		n.a.	L	ST1619	ST1619	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48156	CLIP 2020/01274	LSVAL555	<i>L. innocua</i>	2020-03-09	Winter 2020	Sheep E	Animal	Goat 19	2,68E+06	278	12	2,83E+06	1,45E+06	374	n.a.		n.a.	L	ST1619	ST1619	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48158	CLIP 2020/01276	LSVAL557	<i>L. innocua</i>	2020-03-13	Winter 2020	Sheep D	Animal	Goat 14	1,48E+06	153	37	2,98E+06	2,76E+05	373	n.a.		n.a.	L	CC448	ST1448	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48159	CLIP 2020/01283	LSVAL564	<i>L. innocua</i>	2020-05-15	Spring 2020	Sheep C	Animal	Sheep 12	1,33E+06	135	31	2,83E+06	3,20E+05	374	n.a.	4334, 78971		L	CC493	ST493	n.a.	n.a.	UP1-3,UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48160	CLIP 2020/01284	LSVAL565	<i>L. innocua</i>	2020-05-20	Spring 2020	Cattle H	Farm environment	Water trough 2	1,52E+06	158	27	2,85E+06	2,29E+05	374	n.a.		n.a.	L	CC2074	ST2074	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48161	CLIP 2020/01285	LSVAL566	<i>L. innocua</i>	2020-05-20	Spring 2020	Cattle H	Farm environment	Milking floor 2	2,53E+06	162	34	2,71E+06	4,41E+05	374	n.a.		n.a.	L	ST1256	ST1256	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48162	CLIP 2020/01286	LSVAL567	<i>L. innocua</i>	2020-05-20	Spring 2020	Cattle H	Farm environment	Food trough 1	1,46E+06	151	24	2,85E+06	2,95E+05	374	n.a.		n.a.	L	CC2074	ST2074	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48204	CLIP 2020/01291	LSVAL572	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Farm environment	Water trough 2	1,69E+06	175	12	2,76E+06	5,35E+05	374	n.a.		n.a.	L	ST527	ST527	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48205	CLIP 2020/01292	LSVAL573	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Farm environment	Milking floor 1	1,45E+06	150	14	2,83E+06	1,42E+06	374	n.a.		n.a.	L	ST1621	ST1621	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48206	CLIP 2020/01293	LSVAL574	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Farm environment	Milking floor 2	1,87E+06	194	10	2,76E+06	4,72E+05	374	n.a.		n.a.	L	ST527	ST527	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48207	CLIP 2020/01294	LSVAL575	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Farm environment	Milking floor 3	1,67E+06	173	9	2,81E+06	6,80E+05	374	n.a.	679764		L	ST1087	ST1087	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48208	CLIP 2020/01295	LSVAL576	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 13	1,75E+06	182	17	2,84E+06	4,66E+05	374	n.a.	487514		L	ST1087	ST1087	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48210	CLIP 2020/01297	LSVAL578	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 12	1,12E+06	116	26	2,76E+06	4,30E+05	374	n.a.		n.a.	L	ST527	ST527	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48211	CLIP 2020/01298	LSVAL579	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 13	1,41E+06	145	26	2,73E+06	5,73E+05	374	n.a.	9152, 9768		L	ST1482	ST1482	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48212	CLIP 2020/01299	LSVAL580	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 28	1,48E+06	153	15	2,76E+06	4,72E+05	374	n.a.		n.a.	L	ST527	ST527	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48213	CLIP 2020/01300	LSVAL581	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 9	7,85E+05	81	27	2,95E+06	4,82E+05	373	n.a.		n.a.	L	ST1008	ST1008	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48214	CLIP 2020/01301	LSVAL582	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 22	1,08E+06	111	32	2,83E+06	2,20E+05	374	n.a.		n.a.	L	ST1621	ST1621	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48215	CLIP 2020/01302	LSVAL583	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 12	1,38E+06	142	24	2,84E+06	2,49E+05	374	n.a.		n.a.	L	ST1621	ST1621	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48216	CLIP 2020/01303	LSVAL584	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 15	1,49E+06	154	23	2,85E+06	5,74E+05	374	n.a.	9152, 11736		L	ST1482	ST1482	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48217	CLIP 2020/01304	LSVAL585	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 36	8,87E+05	92	29	2,84E+06	2,10E+05	374	n.a.		n.a.	L	ST1621	ST1621	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48597	CLIP 2020/01305	LSVAL586	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 5	1,334E+06	138	17	2,81E+06	3,64E+05	374	n.a.	431782		L	ST1087	ST1087	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48598	CLIP 2020/01306	LSVAL587	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 12	8,54E+05	88	30	2,83E+06	1,70E+05	374	n.a.		n.a.	L	ST1621	ST1621	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48599	CLIP 2020/01307	LSVAL588	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 34	9,93E+05	103	46	2,83E+06	1,74E+05	374	n.a.	1078, 3141, 6963, 9249		L	ST1087	ST1087	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48600	CLIP 2020/01308	LSVAL589	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 3	1,335E+06	139	23	2,83E+06	2,43E+05	374	n.a.		n.a.	L	ST1621	ST1621	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48601	CLIP 2020/01309	LSVAL590	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 13	9,51E+05	104	33	2,52E+06	2,10E+05	374	n.a.	38545		L	ST1087	ST1087	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48602	CLIP 2020/01310	LSVAL591	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 30	1,52E+06	157	25	2,76E+06	2,95E+05	374	n.a.		n.a.	L	ST527	ST527	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48603	CLIP 2020/01311	LSVAL592	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 38	1,16E+06	120	44	2,83E+06	1,43E+05	374	n.a.		n.a.	L	ST1621	ST1621	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48604	CLIP 2020/01312	LSVAL593	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 37	1,23E+06	127	28	2,73E+06	2,63E+05	374	n.a.		n.a.	L	ST527	ST527	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48605	CLIP 2020/01313	LSVAL594	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 25	1,23E+06	131	24	2,83E+06	2,25E+05	374	n.a.		n.a.	L	ST1621	ST1621	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48606	CLIP 2020/01314	LSVAL595	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 26	1,30E+06	135	18	2,83E+06	3,44E+05	374	n.a.		n.a.	L	ST1621	ST1621	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48607	CLIP 2020/01315	LSVAL596	<i>L. innocua</i>	2020-05-20	Spring 2020	Sheep D	Animal	Sheep 20	1,50E+06	155	102	2,81E+06	3,49E+05	374	n.a.		n.a.	L	ST527	ST527	n.a.	n.a.	UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48608	CLIP 2020/01316	LSVAL597	<i>L. innocua</i>	2020-05-26	Spring 2020	Sheep D	Feed	Feed 3	1,13E+06	117	26	2,86E+06	2,68E+05	374	n.a.		n.a.	L	ST485	ST485	n.a.	n.a.	UP1-3 (partial),UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48807	CLIP 2020/01318	LSVAL599	<i>L. innocua</i>	2020-05-26	Spring 2020	Cattle I	Feed	Feed 2	1,82E+06	141	42	2,78E+06	1,78E+05	374	n.a.		n.a.	L	CC731	ST2162	n.a.	n.a.	UP1-3,UP1-4	<i>foxK.lin.noB.usl</i>	SSI-2
48808	CLIP 2020/01319	LSVAL600	<i>L. innocua</i>	2020-05-26	Spring 2020	Cattle I	Feed	Feed 3	1,83E+06	189	52	2,83E+06	1,58E+05	374	n.a.										

42290	CLIP 2019/01651	LSVAL183	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 7	1,09E+06	113	39	2,89E+06	2,35E+05	37.9	99.9	I	Ilb	CC87	ST1591	S187	CT5545	UPH-1,UPH-4	<i>foxJ,lin,norB,suB</i>	
42291	CLIP 2019/01652	LSVAL184	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Farm environment	Bedding 3	9,48E+05	98	43	2,89E+06	1,57E+05	37.9	99.9	I	Ilb	CC87	ST1591	S187	CT5545	UPH-1,UPH-4	<i>foxJ,lin,norB,suB</i>	
42292	CLIP 2019/01653	LSVAL185	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 13	7,98E+05	77	88	2,89E+06	6,63E+04	37.9	99.8	I	Ilb	CC87	ST1591	S187	CT5545	UPH-1,UPH-4	<i>foxJ,lin,norB,suB</i>	
42293	CLIP 2019/01654	LSVAL186	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Farm environment	Filter 2	6,77E+05	70	167	2,94E+06	4,87E+04	37.9	99.1	I	NvB	CC666	ST666	S1666	CT5281	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
42294	CLIP 2019/01655	LSVAL187	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 40	8,15E+05	84	115	3,01E+06	9,15E+04	37.8	99.4	I	Ila	CC7	ST7	S17	CT5782	UPH-1	<i>foxJ,lin,norB,suB</i>	SSI-1
42295	CLIP 2019/01656	LSVAL188	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Feed	Feed	8,74E+05	90	67	2,89E+06	1,22E+05	37.9	99.9	I	NvB	CC666	ST666	S1666	CT5281	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	SSI-1
42296	CLIP 2019/01657	LSVAL189	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 3	8,70E+05	87	57	2,90E+06	7,61E+04	37.9	99.8	I	NvB	CC217	ST217	S1217	CT5798	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
42299	CLIP 2019/01660	LSVAL192	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 51	8,19E+05	85	64	2,89E+06	1,03E+05	37.9	99.9	I	Ilb	CC87	ST1591	S187	CT5545	UPH-1,UPH-4	<i>foxJ,lin,norB,suB</i>	
42301	CLIP 2019/01662	LSVAL194	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 25	1,30E+06	134	48	3,01E+06	4,37E+05	37.8	99.7	I	Ilb	CC7	ST7	S17	CT5812	UPH-1	<i>foxJ,lin,norB,suB</i>	
42302	CLIP 2019/01668	LSVAL200	<i>L. monocytogenes</i>	2019-05-02	Spring 2019	Sheep B	Animal	Sheep 14	1,53E+06	158	62	2,89E+06	1,13E+05	37.9	99.8	I	Ilb	CC87	ST1591	S187	CT5545	UPH-1,UPH-4	<i>foxJ,lin,norB,suB</i>	
42363	CLIP 2019/01687	LSVAL219	<i>L. monocytogenes</i>	2019-05-13	Spring 2019	Cattle C	Animal	Cow 24	2,80E+06	289	21	2,89E+06	1,50E+06	37.9	99.9	I	Ila	CC37	ST37	S137	CT5813	UPH-1	<i>foxJ,lin,norB,suB</i>	
42397	CLIP 2019/01690	LSVAL222	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Animal	Cow 3	7,43E+05	77	51	2,89E+06	1,21E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT5814	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
42398	CLIP 2019/01691	LSVAL223	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Animal	Cow 4	8,39E+05	87	58	2,89E+06	1,91E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT5814	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
42399	CLIP 2019/01692	LSVAL224	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Animal	Cow 5	9,42E+05	97	57	2,89E+06	1,38E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT5814	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
42400	CLIP 2019/01693	LSVAL225	<i>L. monocytogenes</i>	2019-05-20	Spring 2019	Sheep B	Feed	Feed 1	8,39E+05	85	58	2,89E+06	1,62E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT5814	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
42401	CLIP 2019/01694	LSVAL226	<i>L. monocytogenes</i>	2019-05-20	Spring 2019	Sheep B	Animal	Sheep 7	8,61E+05	89	24	2,87E+06	2,28E+05	37.9	99.9	I	NvB	CC1	ST612	S11	CT5815	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
42402	CLIP 2019/01698	LSVAL230	<i>L. monocytogenes</i>	2019-05-20	Spring 2019	Sheep B	Farm environment	Filter 3	7,55E+05	78	62	2,79E+06	1,79E+05	37.8	99.7	I	Ila	CC7	ST7	S17	CT5792	UPH-1	<i>foxJ,lin,norB,suB</i>	SSI-1
42403	CLIP 2019/01704	LSVAL236	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Animal	Cow 8	7,88E+05	82	36	2,89E+06	2,15E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT5815	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
42404	CLIP 2019/01705	LSVAL237	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Animal	Cow 10	9,00E+05	99	43	2,89E+06	1,31E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT5814	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
42741	CLIP 2019/01706	LSVAL238	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Animal	Cow 13	1,23E+06	127	42	2,89E+06	4,37E+05	37.9	99.9	I	Ila	CC7	ST7	S17	CT1679	UPH-1	<i>foxJ,lin,norB,suB</i>	SSI-1
42742	CLIP 2019/01707	LSVAL239	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Animal	Cow 16	1,33E+06	138	42	2,89E+06	1,98E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT5814	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
42743	CLIP 2019/01708	LSVAL240	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Animal	Cow 35	1,34E+06	138	39	2,98E+06	2,62E+05	37.9	99.9	I	Ila	CC7	ST7	S17	CT1679	UPH-1	<i>foxJ,lin,norB,suB</i>	
42744	CLIP 2019/01709	LSVAL241	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Animal	Cow 33	1,41E+06	146	34	2,89E+06	2,16E+05	37.9	99.9	I	NvB	CC4	ST219	S1219	CT5814	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
42745	CLIP 2019/01710	LSVAL242	<i>L. monocytogenes</i>	2019-05-27	Spring 2019	Cattle B	Farm environment	Bedding 2	1,47E+06	152	27	2,98E+06	3,63E+05	37.9	99.9	I	Ila	CC7	ST7	S17	CT1679	UPH-1	<i>foxJ,lin,norB,suB</i>	
42816	CLIP 2019/02615	LSVAL147	<i>L. monocytogenes</i>	2019-04-10	Spring 2019	Sheep B	Farm environment	Filter 1	8,54E+05	88	213	2,99E+06	9,39E+04	37.8	99.4	I	NvB	CC666	ST666	S1666	CT5281	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
43882	CLIP 2019/02934	LSVAL250	<i>L. monocytogenes</i>	2019-07-15	Summer 2019	Sheep B	Animal	Milk filter 2	3,03E+06	313	16	2,95E+06	5,57E+05	37.8	99.5	I	NvB	CC666	ST666	S1666	CT5281	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
43886	CLIP 2019/02938	LSVAL254	<i>L. monocytogenes</i>	2019-09-16	Autumn 2019	Sheep B	Farm environment	Milk filter 1	2,07E+06	214	19	2,95E+06	5,57E+05	37.8	99.5	I	NvB	CC666	ST666	S1666	CT5281	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
43925	CLIP 2019/02939	LSVAL255	<i>L. monocytogenes</i>	2019-09-16	Autumn 2019	Sheep B	Farm environment	Feed 1	2,95E+06	255	170	2,95E+06	1,69E+05	37.9	99.9	I	NvB	CC666	ST666	S1666	CT5281	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
43937	CLIP 2019/02949	LSVAL270	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Feed	Feed 1	1,29E+06	133	37	2,95E+06	1,82E+05	38	99.9	I	Ilb	CC3	ST3	S13	CT4309	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	SSI-1
43938	CLIP 2019/02950	LSVAL271	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Feed	Feed 2	1,36E+06	141	54	3,14E+06	1,55E+05	37.9	99.8	I	NvB	CC2	ST2	S12	CT6148	UPH-1	<i>foxJ,lin,norB,suB</i>	ermG_mefA,muB
43939	CLIP 2019/02951	LSVAL272	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Feed	Feed 3	1,54E+06	159	546	3,13E+06	3,06E+05	38.7	99.9	I	NvB	CC1	ST1	S11	CT6145	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
43940	CLIP 2019/02952	LSVAL273	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Farm environment	Food trough 1	1,12E+06	116	39	2,89E+06	1,80E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT6148	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
43941	CLIP 2019/02953	LSVAL274	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Farm environment	Food trough 3	8,96E+05	93	43	2,88E+06	1,81E+05	38	99.9	I	NvB	CC4	ST4	S14	CT6149	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
43942	CLIP 2019/02954	LSVAL275	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Farm environment	Food trough 2	1,01E+06	105	53	2,88E+06	1,59E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT2246	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
43943	CLIP 2019/02955	LSVAL276	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Animal	Cow 5	1,44E+06	151	42	2,89E+06	1,96E+05	38	100	I	NvB	CC4	ST219	S1219	CT6151	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
43944	CLIP 2019/02956	LSVAL277	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Animal	Cow 10	1,44E+06	149	21	3,97E+06	1,55E+05	37.9	99.8	I	NvB	CC87	ST87	S187	CT6148	UPH-1,UPH-4	<i>foxJ,lin,norB,suB</i>	
43945	CLIP 2019/02957	LSVAL278	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Animal	Cow 11	7,57E+05	78	39	2,91E+06	1,55E+05	37.9	99.8	I	NvB	CC1	ST1	S11	CT6150	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
43946	CLIP 2019/02958	LSVAL279	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Animal	Cow 12	7,85E+05	81	34	2,99E+06	2,36E+05	37.9	99.8	I	NvB	CC2	ST2	S12	CT6147	UPH-1	<i>foxJ,lin,norB,suB</i>	ermG_mefA,muB
43947	CLIP 2019/02959	LSVAL280	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Animal	Cow 13	7,45E+05	77	28	2,89E+06	1,81E+05	38	99.9	I	Ilb	CC3	ST3	S13	CT6149	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
43948	CLIP 2019/02960	LSVAL281	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Animal	Cow 22	1,10E+06	114	28	2,89E+06	3,48E+05	37.9	99.9	I	Ila	CC37	ST37	S137	CT6152	UPH-1	<i>foxJ,lin,norB,suB</i>	
43949	CLIP 2019/02961	LSVAL282	<i>L. monocytogenes</i>	2019-10-28	Autumn 2019	Cattle G	Animal	Cow 32	1,13E+06	116	36	2,89E+06	1,95E+05	38	99.9	I	NvB	CC4	ST219	S1219	CT2246	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
46816	CLIP 2020/00404	LSVAL406	<i>L. monocytogenes</i>	2020-01-13	Winter 2020	Sheep C	Animal	Sheep 31	1,99E+06	206	24	2,88E+06	5,09E+05	38	99.8	I	NvB	CC4	ST219	S1219	CT7210	UPH-1,UPH-3,UPH-4	<i>foxJ,lin,norB,suB</i>	
46863	CLIP 2020/00412	LSVAL417	<i>L. monocytogenes</i>	2020-01-29	Winter 2020	Sheep C	Feed	Feed 1	2,79E+06	27	88	2,89E+06	1,28E+05	37.9	99.7	I	Ilb	CC87	ST87	S187	CT7210	UPH-1,UPH-4	<i>foxJ,lin,norB,suB</i>	
46664	CLIP 2020/00413	LSVAL418	<i>L. monocytogenes</i>	2020-01-29	Winter 2020	Sheep B	Animal	Sheep 36	2,53E+06	261	34	2,92E+06	2,37E+05	37.9	99.9	I	Ilb	CC736	ST736	S1737	CT7233	UPH-1	<i>foxJ,lin,norB,suB</i>	
46665	CLIP 2020/00414	LSVAL419	<i>L. monocytogenes</i>	2020-01-29	Winter 2020	Sheep B	Animal	Sheep 7	2,19E+06	227	29	2,89E+06	2,38E+05	37.9	99.8	I	NvB	CC388	ST388	S1387	CT7231	UPH-1,UPH-4	<i>foxJ,lin,norB,suB</i>	
46666	CLIP 2020/00415	LSVAL420	<i>L. monocytogenes</i>	2020-01-29	Winter 2020	Sheep B	Farm environment	Water trough 3	2,57E+06	266	28	2,89E+06	4,45E+05	37.9	99.8	I	NvB	CC389	ST389	S1389	CT7232	UPH-1,UPH-3	<i>foxJ,lin,norB,suB</i>	
46881	CLIP 2020/00430	LSVAL435	<i>L. monocytogenes</i>	2020-01-29	Winter 2020	Sheep B	Animal	Sheep 62	1,95E+06	202	21	2,90E+06	5,02E+05	37.9	99.9	I	Ilb	CC392	ST392	S1392	CT7234	UPH-1	<	

Table S4. Individual animals where *Listeria monocytogenes* were isolated repeateadly in different samplings

Farm	Animal	AUTUMN 2018	WINTER 2019			SPRING 2019		SUMMER 2019	AUTUMN 2019	WINTER 2020		SPRING 2020
		07-Nov-18	27-Feb-19	13-Mar-19	10-Apr-19	02-May-19	20-May-19	15-Jul-19	16-Sep-19	29-Jan-20	26-Feb-20	06-Jun-20
Sheep B	Sheep 3	n.d.	L1-SL1-ST1-CT5280	L1-SL6-ST6-CT5393	L1-SL1-ST1-CT5544	L1-SL217-ST217-CT5798	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	Sheep 7	n.d.	n.d.	n.d.	L1-SL87-ST1591-CT5545*	L1-SL87-ST1591-CT5545 *	L1-SL1-ST1612-CT5815	n.d.	n.d.	L1-SL387-ST388-CT7231	n.d.	n.d.
	Sheep 10	n.d.	L1-SL288-ST288-CT5282	n.d.	L1-SL87-ST1591-CT5545	sold						
	Sheep 21	n.d.	L1-SL1-ST1-CT5280	n.d.	L2-SL7-ST7-CT5650	n.d.	n.d.	n.d.	n.d.	n.d.	sold	
	Sheep 25	n.d.	L1-SL392-ST392-CT5391	n.d.	L2-SL7-ST7-CT5782	L2-SL7-ST7-CT5812	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	Sheep 33	n.s.	L1-SL387-ST388-CT5390	n.d.	L2-SL7-ST7-CT5782	n.d.	n.d.	n.d.	n.d.	sold		
	Sheep 36	n.s.	L1-SL1-ST1-CT5392	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	L1-SL737-ST736-CT7233	n.d.	n.d.
	Sheep 40	n.s.	n.s.	n.s.	L1-SL87-ST1591-CT5545	L2-SL7-ST7-CT5782	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	Sheep 43	n.s.	n.d.	n.d.	L1-SL1-ST1-CT5546	L1-SL87-ST1591-CT5545	n.d.	n.d.	Laq	sold		
	Sheep 51	n.s.	n.d.	n.d.	L2-SL7-ST7-CT5782	L1-SL87-ST1591-CT5545	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	Sheep 65	n.s.	L1-SL217-ST217-CT5518	n.d.	L1-SL666-ST666-CT5561	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Cattle G	Cow 12	28-Oct-19	21-Feb-20	17-Jun-20								
		L1-SL2-ST2-CT6147	L2-SL8-ST8-CT7720	n.d.								

* Sheep showing the same CT in two consecutive samplings
n.d. = not detected
n.s. = not sampled

Table S5. Correlation of hygienic scores and prevalence of *L. monocytogenes* on the investigated dairy farms. Hygienic scores were calculated as described in Material and Methods to assess animal cleanliness and production hygiene.

Farm	Prevalence <i>Lm</i> animals	Score animals	Prevalence <i>Lm</i> food trough	Score food trough	Prevalence <i>Lm</i> water trough	Score water trough	Prevalence <i>Lm</i> bedding	Score bedding	Prevalence <i>Lm</i> milk filter	Score milking tank	Prevalence <i>Lm</i> milk parlor	Score milking parlor
CATTLE A	0.00	2.1	0.0	3	0	3	11.1	1	0	3	0	2
CATTLE B	9.38	1.9	0.0	3	0	3	22.2	3	0	2	0	2
CATTLE C	3.13	2.1	11.1	3	0	3	0.0	2	0	3	0	3
CATTLE D	0.00	2.5	0.0	2	0	2	0.0	1	0	1	0	1
CATTLE E	4.17	4.1	0.0	3	0	2	0.0	1	0	3	0	1
CATTLE F	0.00	1.7	0.0	3	0	2	0.0	1	0	3	0	3
CATTLE G	14.58	3.0	66.7	3	0	1	0.0	2	0	2	0	3
CATTLE H	1.04	1.8	0.0	3	11.1	2	0.0	3	0	3	0	2
CATTLE I	10.42	1.5	33.3	3	0	2	22.2	3	0	2	0	3
CATTLE J	0.00	2.2	0.0	3	0	1	0.0	3	0	1	0	2
(P> 0.05) Spearman's rho	0.056		0.214		0.063		0.337		n.c.		n.c.	
SHEEP A	0,0	3	0,0	3	0,0	2	0	3	0,0	3	0,0	3
SHEEP B	28.1	3	0,0	2	0,0	1	0	1	44.4	3	0,0	3
SHEEP C	1,0	2.5	0,0	2	0,0	2	11.1	2	0,0	2,4	0,0	2,4
SHEEP D	0,0	2	0,0	3	0,0	3	0	3	0,0	3	0,0	3
SHEEP E	0,0	2	0,0	2	0,0	2	0	2	0,0	2	0,0	2
(P> 0.05) Spearman's rho	0.53		n.c.		n.c.		0.186		0.395		n.c.	
GOAT A	1.0	1	0,0	2	0,0	2	0,0	2	0,0	3	0,0	3
GOAT B	0,0	1	0,0	2	0,0	1	0,0	3	0,0	3	0,0	3
GOAT C	0,0	1	0,0	2	0,0	3	0,0	3	0,0	3	0,0	3
GOAT D	0,0	1	0,0	3	0,0	3	0,0	3	0,0	3	0,0	3

n.c., not calculated (prevalence = 0)