

A shared molecular database for the surveillance of *Listeria monocytogenes* in the food chain in France

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Abstract

Listeria monocytogenes (*Lm*) is a ubiquitous bacterium responsible for a rare but serious infection: listeriosis. Transmitted through the consumption of contaminated food, listeriosis is fatal in 20% to 30% of cases. It mainly affects people with a weakened immune system. Therefore, the surveillance of strains isolated from the food chain and the environment is essential. An effective food chain surveillance system requires the centralisation of high-quality data and the production of useful and accessible information. ANSES, under its mandates as National Reference Laboratory (NRL) and European Union Reference Laboratory (EURL) for *Lm*, provides scientific and technical support prior to this data collection. In particular, it harmonises typing methods for strains isolated from the food chain, and organises training and inter-laboratory proficiency tests for laboratories in the French and European networks. In France, as part of the ARMADA Joint Technological Unit (UMT), ANSES and the French Pork and Pig Institute (IFIP) have been working for four years on the development of a national database for the centralisation and sharing of epidemiological and genetic data on the strains held by the two organisations. Over time, it will be shared with four other French technical institutes and the ANSES laboratories involved in *Lm* surveillance. This database is interconnected with the European database system developed by the EURL and the European Food Safety Authority, which makes it possible to report data collected nationwide at European level. The database of the ARMADA UMT currently contains 1,200 strains typed by PFGE, sharing 256 combined Apal/Ascl profiles. This tool is enhancing the surveillance of strains circulating in the various food sectors in France.

Keywords

Database, PFGE, *Listeria monocytogenes*, Molecular surveillance

Résumé

Une base de données moléculaires partagée pour améliorer la surveillance de *Listeria monocytogenes* dans la chaîne alimentaire en France

Listeria monocytogenes (*Lm*) est une bactérie ubiquitaire responsable d'une infection rare mais grave: la listériose. Transmise par la consommation d'aliments contaminés, la listériose s'avère mortelle dans 20 à 30 % des cas. Elle touche principalement les personnes immunitairement affaiblies. De ce fait, la surveillance des souches isolées de la chaîne alimentaire et de l'environnement de production est essentielle. Un dispositif efficace de surveillance sanitaire de la chaîne alimentaire nécessite la centralisation de données de qualité et la production d'informations utiles et accessibles. L'Anses, au titre de ses mandats de Laboratoire de référence national (LNR) et de l'Union européenne (LRUE) pour *Lm*, fournit un appui scientifique et technique en amont de cette collecte de données. Elle assure notamment l'harmonisation des méthodes de typage des souches isolées de la chaîne alimentaire, l'organisation de formations et d'essai inter-laboratoires d'aptitude pour les laboratoires des réseaux français et européen. En France, dans le cadre de l'unité mixte technologique (UMT) Armada, l'Anses et l'Institut du Porc (Ifip) ont travaillé depuis quatre ans au développement d'une base de données nationale pour la centralisation et le partage des données épidémiologiques et génétiques des souches détenues par les deux organismes. A terme, elle sera partagée avec quatre autres instituts techniques français ainsi que les laboratoires de l'Anses impliqués dans la surveillance de *Lm*. Cette base de données est interconnectée avec le système de base de données européen mis en place par le LRUE et l'Autorité européenne de sécurité des aliments et permet la remontée au niveau européen des données collectées au niveau national. La base de l'UMT Armada contient actuellement 1200 souches typées par PFGE, partageant 256 profils combinés Apal/Ascl. Cet outil permet une surveillance plus fine des souches circulant en France dans les différentes filières alimentaires.

Mots-clés

Base de données, PFGE, *Listeria monocytogenes*, surveillance moléculaire

This article describes the method of operation and features of a tool for collecting molecular typing data, used to:

- improve our knowledge of the structure of *Listeria monocytogenes* (*Lm*) populations circulating in France,
- monitor this pathogen nationwide.

Listeria and listeriosis: reminders

Lm is an environmental bacterium responsible for listeriosis. This infection is characterised by i) the severity of its symptoms, ii) the high disease mortality rate, ranging from 20% to 30% of cases, and iii) a preference for immune-deficient subjects, pregnant women, and their children (Tourdjman *et al.*, 2014). Listeriosis is contracted through the consumption of contaminated foods. Foods can be contaminated by a raw material of animal or plant origin, or by the

food processing and distribution environment ("resident" bacteria). *Lm* can persist in

products all along the food chain, multiplying at refrigeration temperatures, resisting cleaning and disinfection procedures, and contaminating food processing plants. The principal food sectors are monitored, in particular the pork and pig sector, which has been affected by several health crises involving *Lm* (Giovannacci *et al.*, 1999; Hong *et al.*, 2007).

The French regulations require the withdrawal from the market of foods contaminated at concentrations above 100 CFU/g as well as foods contaminated at lower concentrations but enabling the growth of *Listeria* to values of above 100 CFU/g at the end of their shelf life. The high number of sporadic cases in France (Tourdjman *et al.*, 2014) provides grounds for improving knowledge of circulating strains and their reservoirs.

Pulsed field gel electrophoresis (PFGE) remains the reference method in France and internationally for surveillance of clinical and food-borne strains of *Lm* (Tourdjman *et al.*, 2014).

Methods based on whole genome sequencing (WGS) are expected to replace PFGE in the very near future. However, WGS typing is not yet routinely used by all of the laboratories involved in the surveillance of this bacterium.

The *Lm* species is divided into four phylogenetic lineages and 13 separate serotypes. Two of these lineages and four of these serotypes are primarily associated with human listeriosis: 4b, 1/2b (lineage I), 1/2a and 1/2c (lineage II). The genetic diversity of the species has been widely studied over the past few years, in particular by the research group of Institut Pasteur (NRC and WHO CC for *Listeria*) using the MLST (Multi-Locus Sequence Typing) technique. (Ragon *et al.*, 2008). This can characterise strains based on their "sequence type" (ST) obtained from the sequencing of seven housekeeping genes. STs can be grouped into clonal complexes (CCs). A CC is a group of STs with at least six alleles in common (Ragon *et al.*, 2008). These MLST data provided the foundation for a French and international reference nomenclature. They are now essential for analysing the structure of populations and for exchanging surveillance information. Certain clonal complexes (CC1, CC2, CC4 and CC6) are commonly found in cases of human listeriosis in France and around the world (Ragon *et al.*, 2008; Chenal-Francois *et al.*, 2011). The strains in these clonal complexes were recently recognised as being hyper-virulent, with the particular capacity to attack the brain and foetus, whereas the strains of other CCs such as CC9 and CC121 have very little or no virulence (Maury *et al.*, 2016).

Under their mandates, the European Union Reference Laboratory (EURL) and the National Reference Laboratory (NRL)(1) for *Lm* have built an exceptional collection, by virtue of its size (more than 10,000 strains including 3000 that have been typed by PFGE) and the diversity of the field strains it contains (from a variety of food sectors, isolated for more than 20 years). These strains were received as part of self-inspections, French and European surveillance programmes (Roussel *et al.*, 2012; Roussel *et al.*, 2014), and research projects undertaken jointly with INRA, technical centres, and European NRLs. Part of the collection has been characterised genotypically, by serotyping and PFGE (Félix *et al.*, 2012a,b, 2013; Michelon *et al.*, 2014; Roussel *et al.*, 2014). Some strains have also been characterised phenotypically (antimicrobial resistance, ability of strains to survive in extreme conditions, ability to form biofilms, virulence).

Information from these collections has been structured in shared molecular databases, in collaboration with all the partners. In 2012, as part of the activities of the EURL for *Lm*, a database shared with the European NRLs, the "EURL for *Lm* DB", was created. The various stages of this tool's development, as well as its operation, are described in detail in two articles published in 2014 (Félix *et al.*, 2014 and 2015). The same approach was used to set up a French database during a five-year project undertaken in close collaboration with the French Pork and Pig Institute (IFIP), as part of the Armada Joint Technological Unit (UMT). This database is shared by the UMT's various stakeholders that will use the tool: French agro-industrial technical institutes (ITAls) (IFIP, Aériel, Actalia La Roche-sur-Foron and Adria Développement) and three ANSES laboratories (Ploufragan-Plouzané Laboratory, the Boulogne-sur-Mer and Maisons-Alfort sites of the Laboratory for Food Safety). The objective of the tool is to centralise the main molecular profiles of *Lm* circulating in France in the various food sectors.

In this article, we describe the database of the Armada UMT; in particular, we explain how it works and the data it contains. Lastly, we illustrate potential uses of this database by providing a few examples.

1. Scientific and technical activities managed by the *Listeria* team of the SEL (*Salmonella-E. coli-Listeria*) Unit of the Laboratory for Food Safety, Maisons-Alfort site, ANSES.

Box.

Objectives

The database of the Armada UMT enables agro-industrial technical institutes (ITAls) and agri-food professionals to pool, with ANSES, molecular profiles of *Listeria monocytogenes* (*Lm*) collected in France in order to track and detect sources of contamination in production chains. In this sense, the database will be used as a supporting tool for the definition of actions to prevent contamination. It will be easy to share the submitted profiles and validate their quality because of the validation criteria applied to the data submitted. This will ensure the immediate availability of typing data as needed.

Regulatory requirement

Molecular profiles of strains and related epidemiological information are submitted to the database of the Armada UMT on a voluntary basis. The NRL submits molecular profiles of strains resulting from the control and surveillance plans implemented by the monitoring authorities as described by Roussel *et al.* (2012). ITAls submit profiles for strains in their collections, most of which have been isolated during specific studies.

Protocol

The Armada UMT's database centralises the PFGE molecular profiles of *Lm* strains and related epidemiological information. It provides users with access to data while ensuring the anonymity of the strains' origins and geographic regions of isolation as described in Félix *et al.* (2014; 2015; 2016). The data can be consulted, for example, to compare a molecular profile with those in the database. Submitted data are validated at the European level and made available at the national level via a cascading synchronisation system between the database of the Armada UMT and those of its users.

The Armada UMT's database currently contains the strain typing data from IFIP and ANSES and will be available to the ANSES Ploufragan-Plouzané Laboratory, the Boulogne-sur-Mer and Maisons-Alfort sites of the Laboratory for Food Safety, and four ITAls (IFIP, Aériel, Actalia La Roche-sur-Foron and ADRIA Développement).

Definition of a "case"

The database contains molecular profiles and epidemiological information related to *Lm* strains isolated from samples collected from animals (asymptomatic carriage or sick animals), food or the food production environment.

Materials and methods

Harmonised typing methods between partners

The activities undertaken by the EURL over the past few years have made a major contribution to enhancing typing capacities in the NRL network, thanks to ongoing training, theory and practical courses, annual meetings, and Inter-Laboratory Proficiency Tests (ILPTs) (Félix *et al.*, 2012; Félix *et al.*, 2013). This experience has contributed to the nationwide organisation, by the French NRL, of training sessions on PFGE and PFGE profile interpretation, for the various partners of the Armada UMT. In addition, the two ILPTs organised by IFIP, in the framework of the UMT, provided validation of the typing capacities of the UMT's stakeholders and helped improve the quality of the profiles obtained following the corrective actions taken.

A technical platform organised and administered by ANSES

Data are exchanged between the various users via a web server (BN Server Web Edition, version 7, Applied Maths, Sint-Martens-Latem, Belgium). This enables several database networks to be managed simultaneously. It currently manages the EURL *Lm* DB and the Armada UMT's database.

ANSES is the administrator of these databases and is responsible for validating the PFGE profiles submitted to the

EURL *Lm* DB. ANSES is also in charge of the storage and continuity of the submitted data.

Who can submit profiles to the database?

Molecular profiles are submitted to the Armada UMT's database on a voluntary basis. Users must first have been i) trained in PFGE according to standardised protocols (Roussel *et al.*, 2014) and ii) assessed for the achievement of satisfactory results when participating in the ILPTs organised by IFIP every other year. In addition, IFIP and ANSES have established a charter of use for the database, whose users are the signatories. This charter defines the conditions under which users can populate the database and ANSES can make its data available. It also specifies data ownership and confidentiality.

Four ITAls (IFIP, AÉrial, Actalia La Roche-sur-Foron and Adria Développement) and two ANSES laboratories (Ploufragan-Plouzané Laboratory, the Boulogne-sur-Mer and Maisons-Alfort sites of the Laboratory for Food Safety) can currently use the Armada UMT's database.

The database is monitored by a steering committee made up of the founding members of the Armada UMT (ANSES, IFIP, Actalia La Roche-sur-Foron) and the database's administrators.

Two key points: management of sensitive data and nomenclature

BN Server randomly generates a registration number for each strain when data are submitted (a unique identification code containing 33 alphabetic characters); this number serves as an ID in the database. Strains are identified by two other fields: the first contains the identity of the user submitting the data, in the form of a numerical code, and the second is the strain number initially assigned by the user. To ensure the anonymity of the user providing the data, other users do not have access to the identifying numerical code or the initial strain number. Similarly, geographic data can be submitted but are not visible to other users. The pulsotype nomenclature has been established according to the PulseNet USA pulsotype format (Gerner-Smidt *et al.*, 2006) identified with the "EU" tag. For example, for a "GX6A16.0001.EU" *Ascl* profile, "GX6" means *Lm*, "A16" refers to the *Ascl* restriction enzyme, "0001" is the pulsotype number, and "EU" is the European tag. Each pulsotype is associated with information about its occurrence in the entire database (ratio of the number of strains belonging to the same *Ascl* + *Apal* pulsotypes to the total database population).

An epidemiological classification in agreement with the European Food Safety Authority (EFSA)

Related epidemiological data are recorded according to a detailed classification (Figure 1) containing several consecutive fields associated with lists of choices predefined in the software. The structure of this epidemiological classification is based on all the data required by EFSA's epidemiological reporting system (EFSA, 2012). However, to simplify its use, the epidemiological data contained in the Armada UMT's database have been limited to the classification of foods generally used for the assessment of risks related to *Lm*.

A system for the automatic conversion of epidemiological data, based on the sample descriptors used at the European level by EFSA (FoodEx2) (EFSA, 2015), has been developed in close collaboration with EFSA. This system automatically generates a code and a standard description based on the descriptions in

the Armada UMT's database (e.g. A0EYM#F01.A057F Charcuterie meat products, SOURCE= Pig (live animals) corresponds to...). This system has been designed to evolve if new terms are added to the epidemiological classification of the Armada UMT's database. It anticipates the database's connection to the future database being set up by EFSA and ECDC, whose pilot was launched in 2016 (Figure 1) (EFSA, 2014).

Interconnection of database systems and validation of typing data

Molecular profiles of strains are submitted by the Armada UMT's members. The profiles are then sent to a European database (EURL

Lm DB until 2017 and then the EFSA database (Box)). This system enables available molecular profiles to be grouped at the national level and then submitted at the European level (Figure 2). PFGE profiles are validated at the European level, together with the profiles submitted by other NRLs. A synchronisation system enables typing data to be returned after validation (modified molecular profiles, assessor comments and nomenclature). All of the changes made by the operator in charge of validating and integrating profiles in the database are tracked and can be downloaded by users for their own profiles. Thus, the Armada UMT's database regularly uploads data for validated profiles that have been submitted at the European level. Profiles appearing in the databases of national users can also be synchronised when they have been submitted to the Armada UMT's database (Figure 2).

What is a curator?

The operator responsible for validating each new molecular profile in a typing database is referred to as a "curator". The curator can directly modify processing parameters for gel images and the marking of bands on profiles. Each profile is analysed and identified according to an innovative protocol for the interpretation of PFGE profiles developed by the *Lm* EURL (Felix *et al.*, 2012) and used and enhanced by EFSA (Roussel *et al.*, 2014). Curation occurs through an interpretation system divided into identification groups. The curator's technical competences, for the interpretation of PFGE gels, are regularly updated and verified as part of an internal evaluation process that determines suitability for the position of curator. After processing, the curator rates the profiles as follows: "confirmed" or "unsatisfactory". In the current system, the interconnection of databases provides for centralised curation in the EURL *Lm* DB. This system will be transposed to the EFSA database in 2017.

Unlimited consultation of the database

All of the PFGE profiles available in the Armada UMT's database can be compared to the profiles appearing in user databases. For a given PFGE profile, users have access to the following information: 1) serotype, 2) food matrix, 3) sampling date, and 4) frequency at which the profile appears in the Armada UMT's database.

The database also contains a sub-set of 167 strains that have been typed by both PFGE and by Multi-Locus Sequence Typing (MLST). MLST data are available in two dedicated fields corresponding to the CC and ST.

In a study recently published by ANSES and DTU Food (Henri *et al.*, 2016), we achieved good congruence (ability of a method to predict the result of another method), for a panel of 396 strains, between the PFGE groups with 80% similarity (group established using the UPGMA dendrogram construction method based on the average similarity of the *Ascl* and *Apal* restriction profiles, Dice coefficient, tolerance and optimisation set at 1%) and the STs.

This sub-set may be used as a dictionary that gives to the users an indication of the CC and ST for some of their strains and enables them to link their PFGE results to MLST data.

Results

Key figures: current content of the Armada UMT's database

The Armada UMT's database contains the combined PFGE profiles of 1602 strains generated with the *Ascl* and *Apal* restriction enzymes. Of these profiles, 1136 have been submitted at the European level, for validation of their quality and linking to a pulsotype number. The other profiles are undergoing validation. Of the profiles already validated, the strains have been divided up by food origin: meat products (524 strains including 241 isolated from pork products), dairy products (189 strains), fishery products (179 strains), composite

products (elaborated products combining at least two products of different food origins - 213 strains), plants (59 strains), and non-food animal and environmental samples (45 strains).

The validated profiles include 93 submitted by IFIP, 1030 submitted by ANSES, and three submitted by other users. The profiles of these strains have been subdivided into PFGE groups with 80% similarity. The 14 main PFGE groups account for 86% of the submitted profiles. They are all observed in the four main food origins. These groups have been associated with clonal complexes (Table 1).

Discussions

Example of a practical use of the Armada UMT's database

Understanding the diversity of strains in a given sector

The Armada UMT has strengthened relations between IFIP, the Laboratory for Food Safety (LSA), and the ANSES Ploufragan-Plouzané Laboratory. These three entities recently pooled their knowledge and know-how in order to better assess the diversity of *Lm*

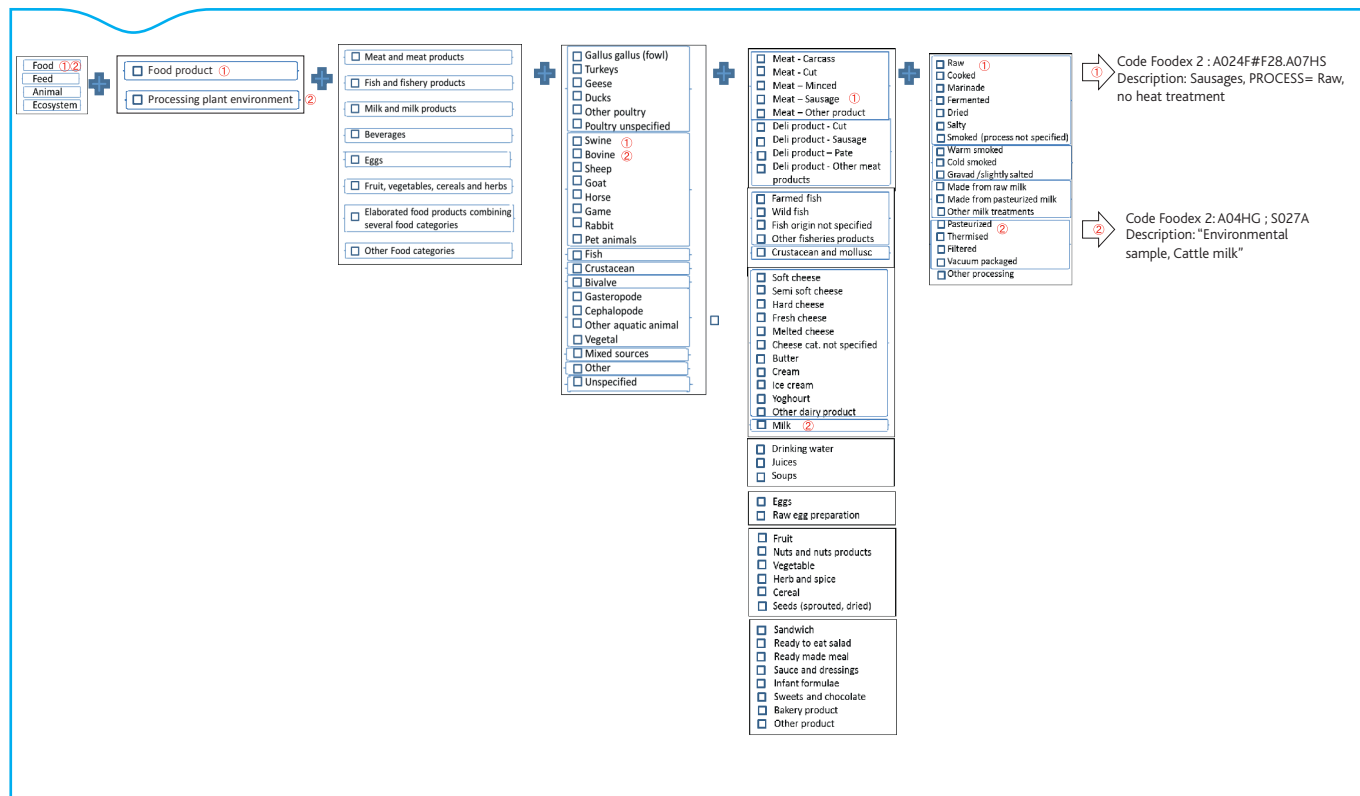


Figure 1. Standard food description used in the Armada UMT's database and automatic correspondence with the FoodEx2 epidemiological scheme (EFSA, 2015).

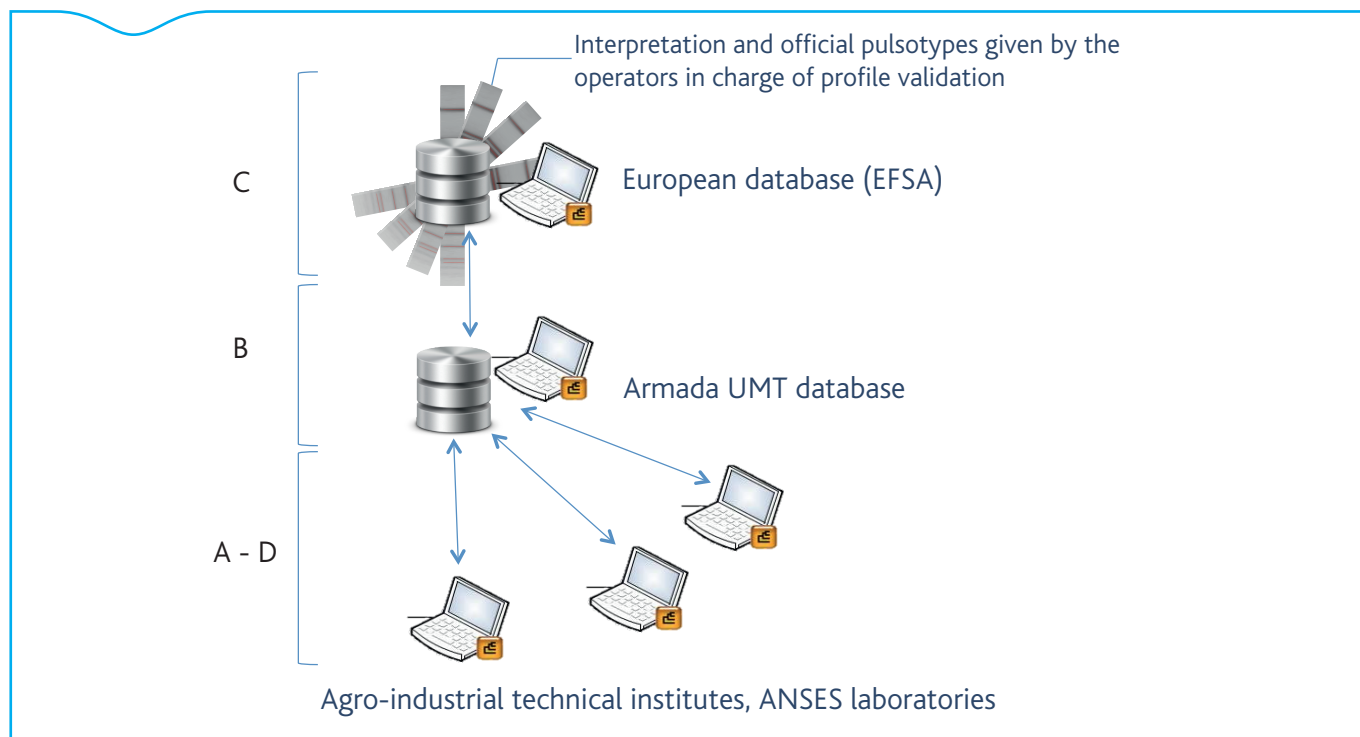


Figure 2. Information flows ensuring (A) the submission of molecular profiles, (B) the sharing of data between users of the Armada UMT's database, (C) data curation at the European level, and (D) the return of curation information to users

strain populations isolated from the pork and pig sector, from farm to finished product. The data provided by ANSES Ploufragan-Plouzané came from two field studies (Boscher *et al.*, 2008; Kerouanton *et al.*, 2011). The data provided by IFIP came from specific studies undertaken with professional partners. The data provided by the LSA in Maisons-Alfort came from DGCCRF surveillance and control plans for which strains have been typed since 2005 by the NRL, and from self-inspection strains collected between 2003 and 2016. Thanks to the Armada UMT's database, it was possible to compile, for the first time, the PFGE profiles of over 900 strains circulating in the pork and pig sector, from farm to distribution. The pooling of these strains collected in various isolation contexts helped broaden our knowledge of the genetic diversity of *Lm* over time and of the high number of colonisation sites for this bacterium in the pork and pig sector.

Example of use of the Armada UMT's database by ITAIs

For an ITAI, the Armada UMT's database can be used for the *Lm* surveillance undertaken by a corporate client of the institute. This surveillance can occur in its slaughter or cutting plants, or plants for the manufacture of processed products. This enables the company to characterise the diversity of strains circulating in its plant environments and link this diversity to that of strains isolated from raw materials or finished products, in order to better track sources of contamination for cuts of meat/finished products. Use of the multi-sector database allows the company to view the frequency at which the PFGE profiles of these strains are observed and compare this frequency to that of its own sector of activity as well as other food sectors. It can also enable it to assess the hazardous nature of the strains it isolates. Since the hyper-virulence of certain CCs has been described, it is possible to predict the CC based on the PFGE profile and obtain this information.

The Armada UMT's database can also be used for investigating contamination incidents on a production site. If the company monitors *Lm* in its plants every day, the detection of a contaminated product on a production line will be more quickly linked to a contamination source (equipment, raw material), by comparison with the typing data contained in the database. The company can then more quickly control the spread of this contamination and in some cases can report it to the supplier(s) of the contaminated raw materials.

This approach can also be used to assess the effectiveness of plant and equipment cleaning and disinfection procedures for circulating or persistent strains in a company.

Outlook

Several stakeholders with complementary roles are involved in the *Lm* surveillance undertaken by the public authorities in the food chain and the French population. The Armada UMT's database can be used by public stakeholders only as stipulated in Article R201-11 of the French Rural Code, i.e. when owners or analytical laboratories holding foodstuffs undergoing an epidemiological investigation further to a food-borne illness are required to submit samples or analytical results. It is therefore necessary to work with producers and their associated ITAIs to have access to the submitted data.

The Armada UMT's database has been designed to incorporate various types of data, especially those obtained using cutting-edge technologies such as whole genome sequencing (WGS). This new technology enables previously inaccessible genetic information to be used. It considerably increases the discriminating power of typing, and also eliminates genetic artefacts inherent in methods based on the analysis of molecular profiles such as PFGE. WGS thus promises to make the detection of outbreaks more relevant and advanced. Several European and international laboratories now use techniques based on WGS for the typing of clinical and food-borne strains. The methodologies used differ from one laboratory to the next (Moura *et al.*, 2016; Hyden *et al.*, 2016; Painset *et al.*, 2016; Gerner-Smidt *et al.*, 2016; Nielsen *et al.*, 2016). A current limitation of WGS is the bio-informatic processing of data. In the United States where WGS

Box. The fate of the EURL *Lm* DB

The EURL *Lm* DB is an integral part of the *Listeria* surveillance system at the national and European levels. It is currently seen as a European surveillance tool for circulating clones. It can be accessed by European NRLs to direct their investigations to a food sector or product category. However, it is not meant to be used unless there is a suspicion of an international outbreak.

The development of this database has enabled the laboratory and ANSES to establish its expertise and position itself in relation to key stakeholders involved in *Lm* surveillance: i) in Europe (ECDC, EFSA, SSI), ii) in the United States (CDC), and iii) internationally (PulseNet International).

The database set up by EFSA and ECDC, currently in the pilot phase, should be operational in 2017 (EFSA, 2014). It will contain all the profiles of food, animal, and environmental strains as well as those of human strains of *Lm*, *Salmonella* and VTEC. It will thus replace the EURL *Lm* DB for the collection of typing data of non-human origin. Users of the EURL *Lm* DB will recover data related to their molecular profiles by synchronisation. They will then install the features of the EFSA-ECDC database and will submit the molecular profiles of their strains. The EFSA-ECDC database has been developed to maintain the same features as the EURL *Lm* DB, in particular by enabling profiles to be synchronised after curation. The EURL *Lm* DB curation team will be an integral part of the steering committee for the EFSA-ECDC database and will be in charge of curating data related to *Lm* of non-human origin in this new system.

In France, the competent authorities (DGAL, DGCCRF and DGS) are to appoint the laboratory responsible for submitting French molecular typing data to the EFSA-ECDC database. NRLs are the laboratories identified for this task. One possibility is to enable the grouping and submission of all of the national typing data of users of the Armada UMT's database.

Table 1. Breakdown of the main PFGE groups in relation to the main food origins of the strains submitted to the Armada UMT's database by ANSES and IFIP

PFGE group*	Fishery products	Dairy products	Composite products	Meat products	Total	MLST clonal complexes demonstrated by PFGE
A	70	8	48	120	246	CC121
B	7	3	70	94	174	CC9
C	15	3	5	40	63	CC5
D	12	33	15	36	96	CC8
E	7	7	13	35	62	CC1
F	15	66	17	31	129	CC4
G	5	18	10	21	54	CC31
H	0	9	0	12	21	CC204
I	5	4	6	12	27	CC20
J	0	6	5	9	20	CC37
K	9	0	5	7	21	CC121
L	1	5	3	7	16	CC155
M	9	4	3	4	20	CC77 - CC54
N	11	2	8	4	25	CC14
Total	166	168	208	432	974	

* group established by UPGMA based on the average similarity between *Ascl* and *Apal* profiles above 80%, Dice coefficient, tolerance and optimisation set at 1%

is becoming widespread, computer equipment with the computing power required to analyse WGS data is hosted by the laboratory responsible for surveillance (Jackson *et al.*, 2016; Allard *et al.*, 2016). This ensures harmonised data analysis for national laboratory users. In France, this solution could be proposed by ANSES for the development of the Armada UMT's database.

Conclusion

The Armada UMT's database has encouraged the use of molecular typing for *Lm* in the French network. The development of this database was proposed as an innovative project created by ANSES in close collaboration with national stakeholders in the agri-food sector, in particular IFIP. This project helped establish the interconnection between the Armada UMT's database and the one currently being developed by EFSA and ECDC.

It was agreed with the database's users that profiles would be validated at the European level, in order to enable typing data to be reported to the European surveillance system. In France, the Armada UMT's database can be accessed by the authorities only when producers are officially required to report information as specified in Article R201-11 of the French Rural Code. Beyond the harmonisation of typing methods, the joint use of a database system is a way to rally *Lm* surveillance stakeholders at the national and European levels.

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