Listeria monocytogenes (Lm) is an ubiquitous bacterium that causes a severe and often lethal foodborne illness. The pork sector has been concerned by several health crisis in 1992 (1), 1993 (2), 1999 (3) and 2000 (3). Thus, efficient surveillance tools for strains circulating throughout the pork chain are of major interest.

Anses hosts the French National Reference Laboratory (NRL) and the European Union Reference Laboratory for Lm. The NRL, collect and typed isolated from various food chains for decades. Typing and epidemiological data are centralized in the NRL molecular database. The EURL has developed an expertise in the setup of molecular databases (4) and is currently involved in the development of the EFSA/ECDC molecular typing database (5).

The French Institute for Pig and Pork Industry (Ifip) owns an Lm database gathering data of strains coming from own checks of pork processing plants.

For 3 years, Ifip and Anses have been working together in the frame of the ARMADA joint technological unit, a national collaborative project. It enabled the two partners to harmonize their typing method according to standard operating procedures for PFGE (6) and PFGE profile interpretation (6). The need for exchanging typing data recently resulted in the creation of a joint national molecular typing database. Its objective is to share and compare epidemiological and typing data (serotyping, PFGE, MLST) related to strains owned by both Anses and Ifip. Ultimately, this database will be shared between the French technical institutes and Anses units involved in the national surveillance of Lm. This database contains 800 strains all type by PFGE sharing 206 combined ApaI-AscI PFGE pulsotypes. 200 strains were typed by MLST. This database represents a key tool for the efficient surveillance of strains circulating throughout the pork food chain and molecular surveillance.

We will describe here the different steps in the development of this database and its content.


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