Setting up a French molecular sub-typing database for *Salmonella* surveillance in the pig and pork industry

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INTRODUCTION

In 2008, salmonellosis was the second most frequently reported zoonotic disease in humans in Europe, accounting for more than 131,000 confirmed cases. Moreover, *Salmonella* was one of the leading causes of food poisoning outbreaks in France and Europe in 2008 (2). EFSA has shown that pork meat and products accounted for 10.2% of *Salmonella* food sources. In addition, EFSA’s survey of *Salmonella* in slaughtered pigs in 2006-2007 showed a significant prevalence of 17.6% on pig carcasses in France (1). In this context, IFIP, the French Pork Institute, has since 2006 been developing a database of epidemiological information, serotyping data and PFGE profiles of 550 representative *Salmonella* strains specifically isolated from the pig and pork industry. This database aims to establish how *Salmonella* strains circulate from pig farming to finished products in order to better control the hazard, and to develop a monitoring tool for the pork sector. Moreover, since 1997, through the “Salmonella network”, AFSSA-LERQAP has been developing a national database for strains isolated from the entire agro-food chain. This database includes the most frequently detected *Salmonella* serotypes and contains 3500 PFGE profiles of strains isolated from food, animals and the environment. This database is regularly consulted by public health and food authorities during investigations and outbreaks. In order to improve the national surveillance of *Salmonella* in pig production, both institutes, IFIP and AFSSA-LERQAP, plan to share their PFGE databases. This may allow the identification of common clusters and improve the ability to react in case of outbreaks. In the present work, we report on trends in serovar and intra-serovar diversity of 550 *Salmonella* strains constituting the current pig and pork sector database, and make a preliminary comparison of 216 *Salmonella* strains from this database with the AFSSA-LERQAP database.

MATERIAL AND METHODS

*Salmonella* strains collected by IFIP came either from pork product self testing by the pork sector operators or from studies performed in pork production (pig farming, slaughterhouses). They were isolated from pigs, pork products or the environment at a national level and were not epidemiologically related. All strains were serotyped at AFSSA-LERQAP according to the Kauffmann-White scheme (4). PFGE using the XbaI restriction endonuclease was carried out with a CHEF-DR III system (Bio-Rad) according to the Salm-gene and PulseNet standardized protocol (6). Because of the instability of the extracted DNA of some serovars (Cerro, Panama...), hepes and thiourea were added to the run (5). *S. enterica* serovar Braenderup H9812 was used as the molecular size marker in the PFGE experiment (3). Banding patterns were viewed under UV light after staining with ethidium bromide. DNA patterns were analysed with BioNumerics software v. 5.1 (Applied Maths, Kortrijk, Belgium), using the Dice coefficient (and the unweighted pair group method with arithmetic means (UPGMA) with a 1% tolerance limit and 1% optimization. The profile comparison was performed based on exchange of image gels.

RESULTS

Pig and pork sector database

Since 2006, 18 different serovars have been identified with two predominant serovars, Typhimurium and Derby that accounted for
43.6% and 38.4% of the 550 strain panel respectively. Other serovars are represented as follows: Infantis (3.6%), London (3%), Kedougou (1.5%), Rissen and Kapemba (1.2%). Serovars Brandenburg, Anatum, Panama, Lansing, Agona, Ohio and incomplete serovars accounted for less than 1% of the strain panel. Since 2006, the proportion of serovars Typhimurium and Derby has not varied from one year to another. However, we showed the predominance of serovar Derby in pig farming while serovar Typhimurium was predominant in pig and pork product samples. PFGE divided the 550 strains into 95 representative profiles. The 240 strains of serovar Typhimurium were divided into 35 distinct PFGE profiles with a major profile, named Ty-01, represented by 49 strains (20.3%). The 211 strains of serovar Derby were divided into 24 distinct PFGE profiles with a major profile, named Der-03 that accounted for 18.2% of the panel (38 strains). Comparison with AFSSA database profiles 216 strains were considered for this comparison from which 130 strains (60%) were of serovar Derby and 57 (26%) were of serovar Typhimurium. The remaining strains exhibited the following serovars: Bredeney (10 strains), Brandenburg (7 strains), Infantis (6 strains), Kedougou (3 strains), Cerro (1 strain), Livingstone (1 strain) and Duisburg (1 strain). PFGE divided the 216 strains into 42 distinct PFGE profiles. Each of them comprised strains of the same serovar. The 130 strains of the Derby serovar were divided into 15 distinct PFGE profiles, with the major profile Der-03 composed of 61 strains. The 57 strains of the Typhimurium serovar were divided into 11 distinct PFGE profiles, with the major profile Ty-01 composed of 36 strains. The two major profiles observed for Derby and Typhimurium serovars were observed for strains isolated from various sectors (cattle, sheep and poultry) and were not specific to the pig and pork sector. Among the 42 observed distinct profiles, 16 have already been observed in the AFSSA database for strains isolated from various foods. Thus, none of these 16 profiles were specific to the pig and pork sector. On the contrary, the remaining 26 profiles were specific to the pig and pork sector.

PERSPECTIVES

In the coming months, profile exchanges will be pursued and performed from xml profiles. Standardized protocols for PFGE typing and profile interpretation will be used. Indeed, this standardization will make comparisons easier. Eventually, a new multi-sector national database will be created, that will be helpful for (i) monitoring strain transmission from animal husbandry to finished products, (ii) identifying strains that are relevant to public health and (iii) responding more effectively to food-borne diseases.

REFERENCES


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