Epidemiology and control of hazards in pork production chain – SAFEPORK

One health approach under a concept of farm to fork

Supported by a grant from the European Commission’s Directorate General for Health and Food Safety (DG SANTE).

(3) Ifip, French Institute for Pig and Pork Industry, Maisons-Alfort, France.
(2) Anses, Ploufragan Laboratory for Food Safety, Viral Genetic and Biosecurity Unit, Ploufragan, France.


Conclusion

This study is a bioinformatics and statistical challenge, with regard to the amount of data generated by WGS and the complex genetic background that drives persistence.

Acknowledgements

This work was conducted as part of the 2015 activities of the European Union Reference Laboratory for L. monocytogenes and was supported by a grant from the European Commission’s Directorate General for Health and Food Safety (DG SANTE).

References


Although pork is considered an important source of Salmonella infections, the introduction of control programs in pig farms is not obligatory in the EU. To resolve current epidemiological situation, monitoring of pig farms was introduced in Poland in 2014. The paper reports the first year outputs of the survey. Sampling plan targeted breeding and fattening herds (150 each) located in all regions of the country, proportionally to number and size of the farms. Convenience sampling of each herd included: 1) a pair of boots swabs taken during sampling of 2) dust and 3) slurry swabs. Samples were tested according to ISO 6579:2003/A1:2006 followed by serotyping according to White-Kaufman-Le Minor scheme. Salmonella were found in 50 out of 281 herds: 21 out of 147 breeding (14.3%) and 29 of 134 (21.6%) fattening herds. Positive results were more frequently noted in the herds: 1) located in the region with the highest density of pig farms, 2) originating from the biggest farms (≥5000 fatteners or ≥500 saws), 3) fed with commercial feeds, 4) with high health status, and 5) with AI/AO procedure. Irrelevant for Salmonella occurrence were: herd production type, previous record of salmonellosis, and antimicrobial usage. The pathogen was isolated from all three tested samples in seven herds. Two and single sample were positive in, respectively, 10 and 33 herds. Of 14 serovars noted, seven were found in breeding herds and 12 in fatteners. Two farms were contaminated with two serovars. Monophasic Salmonella Typhimurium was the most common serovar found in 32 samples and 21 herds, followed by S. Derby (9 herds) and S. Typhimurium (7 herds). The study revealed higher than expected frequency of Salmonella contamination of pig farms caused by diverse serovars of public health relevance. Some surprising risk factors will be further investigated.

*Anses, Moistons-Allot laboratory for Food Safety, Measons-Alfort, France.
*Anses, Plovfragan Laboratory for Food Safety, Viral Genetic and Biosecurity Unit, Plovfragan, France.
*Ifip, Means Institute for Pig and Pork Industry, Measons-Alfort, France.
*corresponding author: benjamin.felix@anses.fr