

## PROJECT SUMMARY

Pig production has grown dramatically worldwide over the last 20 years, leading to increased herd sizes with weekly production cycles of piglets. In the meantime, the dynamics of infections with swine influenza A viruses (swIAV) have changed, from epizootic acute respiratory outbreaks to self-sustaining infected status of affected herds. Moreover, the genetic and antigenic diversity of swIAVs in European pig populations has dramatically increased in recent years, possibly driven by changes in rearing conditions and/or reverse zoonotic incursion of the H1N1 virus responsible for the 2009 human pandemic, which now is circulating concurrently with three formerly endemic swIAV lineages. Thus, novel reassortants and antigenic variants have emerged regionally, that can escape control strategies based on vaccines licensed for use in Europe.

The self-sustaining forms of swine influenza (SI) in large holdings adversely affect animal health and welfare, and prompts the excessive use of antibiotics when swIAV is associated with other respiratory pathogens in the porcine respiratory disease complex (PRDC), resulting in severe economic losses. Further, continuous exposure of humans to swIAVs in confined herds, including viruses that may have changed their inter-species transmission capabilities, constitutes an increasing risk for public health.

The conditions sustaining recurrent swIAV infections, by influencing swIAV transmission and spread, may depend on factors such as production systems, biosecurity level, housing conditions, co-infections, vaccination protocols, vaccine strain composition and pre-existing herd immunity, but many of them are poorly understood. Thus, there is an urgent need to increase knowledge of within-herd virus dynamics and evolution in order to design intervention and prevention measures to limit swIAV persistence in intensive herds and counteract continuous production losses and emergence of new swIAVs.

The objectives of the research project PIGIE are:

- to define the epidemiological and economic factors that drive the prevalence and dynamics of swIAV in large pig herds,
- to evaluate the impact that swIAV enzootic infections have on animal welfare, production parameters and economic productivity,
- to study the genetic and antigenic diversity of swIAV in Europe,
- to identify the host-pathogen factors that would foster swIAV evolution,
- to provide a better understanding of long-lasting and protective immunological memory responses developed in the infected hosts,
- to identify mitigation points in continuously infected herds,
- to implement and evaluate control strategies that would help to counter sustained infections in closed intensive herds.

Longitudinal studies will be implemented in selected herds typical for the production systems that face continuous swIAV infections in six European countries that produce up to 80% of pork or related products in the EU. They will provide epidemiological, virological and immunological data, while swIAV diversity will be studied at the genetic and antigenic levels. Mitigation points will be identified, linking viral diversity to production systems where possible. Then, control strategies will be implemented and evaluated through further longitudinal studies.

Thus, thanks to data sharing, integration and analysis, PIGIE will provide further understanding of the epidemiology and means of control of swIAVs in Europe, essential for sustainable and competitive pig production. Moreover, PIGIE data will be important for further development of more accurate diagnostic tools and relevant vaccines, which would take into account swIAV genetic and antigenic diversity.