



Suckling piglets.
Source: University of Montreal

Epidemiology of porcine reproductive and respiratory syndrome virus (PRRSv) among swine herds, an applied research program supporting PRRS control projects

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Overview

Porcine reproductive and respiratory syndrome (PRRS) has a major economic impact on the swine industry. The important diversity observed in PRRS North American strains, combined with the multiple different ways it can be transmitted between herds, make the control of the disease very difficult. Virus sequencing is now viewed as an essential tool to better manage PRRS in Canada and, to help interpret results on sequences for surveillance purposes, a PRRS classification system is under development. This system will allow strains to be grouped to better observe their movements over time and help detect emerging strains. Moreover, through an improved integration of these laboratory results and epidemiological data, the most likely sources of infection of breeding herds will be identified to provide essential information to improve control strategies.

Highlights

PRRS Sequence Database

In 2016-2017, more than 545 virus sequences from herds in Quebec, along with information about locations, were validated and included in the PRRS sequence database in near real-time. PRRS virus reference strains from Europe, as well as some sequences from other Canadian provinces, were also included in the database. Since the beginning of the present study, a total of 2070 sequences have been included in that database.

PRRS Control Projects

This project aims to support ongoing PRRS Area Regional Control and Elimination (ARC&E) programs. In particular, the diversity of the PRRS virus within and outside some of these ARC&E programs is being studied. The diversity of the PRRS virus seems to have decreased globally within the studied ARC&E programs and this decrease seems to be mainly due to vaccination. Indeed, a higher proportion of PRRS vaccine-like strains were found in herds participating

in ARC&E programs. Also, albeit to a lesser extent, the diversity of circulating wild type strains in ARC&E program herds was lower than in other herds.

Most likely source of virus introduction into a herd

In the study, researchers examined how virus strains could enter into pig herds. They identified approximately 100 breeding sites on which a PRRS virus strain had recently been introduced. For each virus strain that was identified as ‘new’ to the herd, researchers checked the database and were able to identify and study two to three other herds that had a similar PRRS virus strain. Researchers discovered that more than half the time when there was ‘new’ strain identified in a herd, the closest herd having a similar PRRS virus strain was located more than 9 km away. This demonstrates that long-distance PRRS virus transmission is frequent.

Preliminary analysis also showed that sharing employees between herds occurs frequently, which can increase the risk of PRRS virus transmission. When an employee works with more than one herd, respecting biosecurity rules, particularly the entrance protocol, is crucial in avoiding the transmission of PRRS.

Implications for the swine industry

- The movement of the PRRS virus between farms often occurs via long-distance processes such as vehicle or transport of animals, and hence should be considered when implementing a PRRS regional control program.
- Having employees that work on several herds may increase the risk of PRRS virus transmission. Following biosecurity measures is crucial in reducing this risk.

Collaborators

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