

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

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This research project will take a multidisciplinary approach to develop and apply a new methodology integrating traditional and molecular data to assess various aspects of PRRSv transmission dynamic.

## Summary

### Researchers will:

- evaluate the various algorithms available for classifying PRRSv strains into genetic clusters so as to identify the most likely source of recent herd contamination from sequencing data gathered in the field.
- assess the spatial and temporal dispersal of PRRSv strains based on sequences and compare the results for the areas with and without PRRS control projects.
- develop a methodological approach that is based on sequences and epidemiological data for evaluating the most likely source of virus introduction (e.g. same animal source, sharing of employees, airborne transmission, etc.) into a herd.
- develop an interactive automated mapping system based on the above approaches. This system would integrate sequences and search for epidemiological and spatial connections between infected farms, which can then be applied at the farm level to find the potential source of any new strain introduction.

### Collaborators

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