

A descriptive study on spatial and temporal distributions of genetic clusters of porcine reproductive and respiratory syndrome virus (PRRSv) in Quebec, Canada, between 2010 and 2019

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Background and objectives

- The huge diversity of PRRSv strains combined with incomplete cross-protection against heterologous challenges complicate disease management.
- The objective of this study was to describe the spatial and temporal distribution of PRRSv genetic clusters in Quebec between 2010 and 2019.

Material and methods

Retrospective surveillance-based study conducted in the province of Quebec, Canada.

Sequence and data collection

- PRRSv ORF5 sequences obtained from pig site samples between January 1, 2010, and December 31, 2019 (Fig. 1).
- Each sequence was matched to pig site data extracted from the Veille Sanitaire Provinciale (VSP) database (Fig. 1).

Genetic analyses

Sequences assigned to genetic cluster according to the following steps:

- Multiple alignment: Clustal Omega
- Maximum-likelihood tree: RAxML
- Clustering according to 2 criteria:
 - ≥ 70% rapid bootstrap branch support value;
 - ≥ 15 sequences.

Statistics

- For each genetic cluster, the number of pig sites according to year and administrative region was computed and displayed using bubble charts in SAS software.
- Each wild-type cluster was pictured using pie chart maps in ArcGIS software using regional county municipality (MRC) and year as geographical and temporal units, respectively. For each cluster, a pie chart was drawn to illustrate the years in which the cluster was identified within each MRC on at least one site.

Results

- 4796 sequences from 1334 pig sites were obtained: 30% vaccine-like, 70% wild-type sequences.
 - Average (min-max) number of sequences : 466 (280-578) per year, 4 (1-27) per site.
- 46 wild-type clusters detected with relative importance varying according to year and region.
- Figure 2 pictures the most prevalent wild-type clusters.

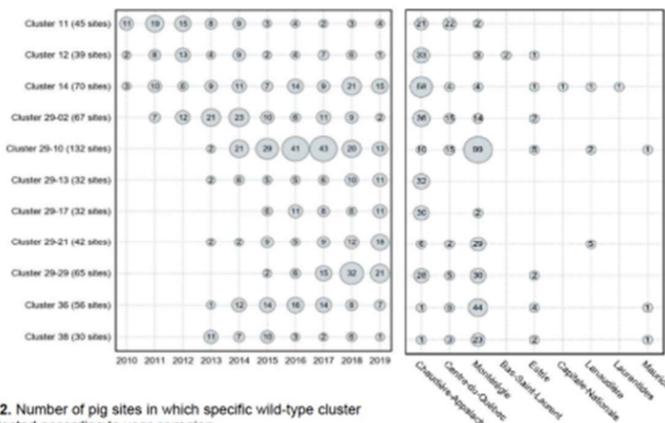


Figure 2. Number of pig sites in which specific wild-type cluster was detected according to year or region. The total number of sites in which a cluster was detected during the study period is shown between parentheses.

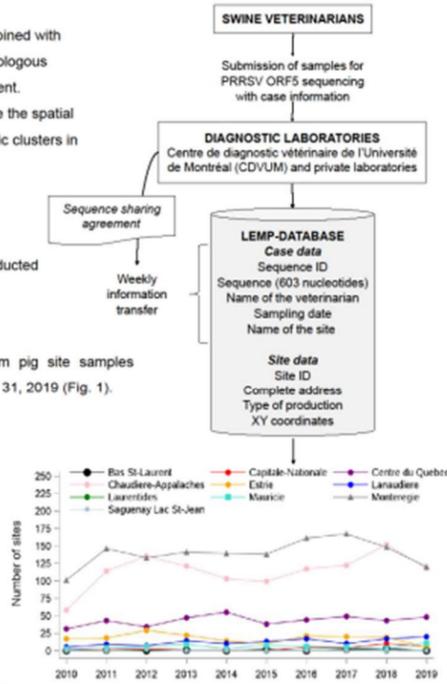


Figure 1. Data collection process and number of pig sites with sequence according to year and administrative region.

Clusters remained localized on a few sites over time (#29-20) or reached many MRC, either slowly (#11) or rapidly (#29-10), and sometimes reached the North Shore on a few MRC (#14, 29-10).

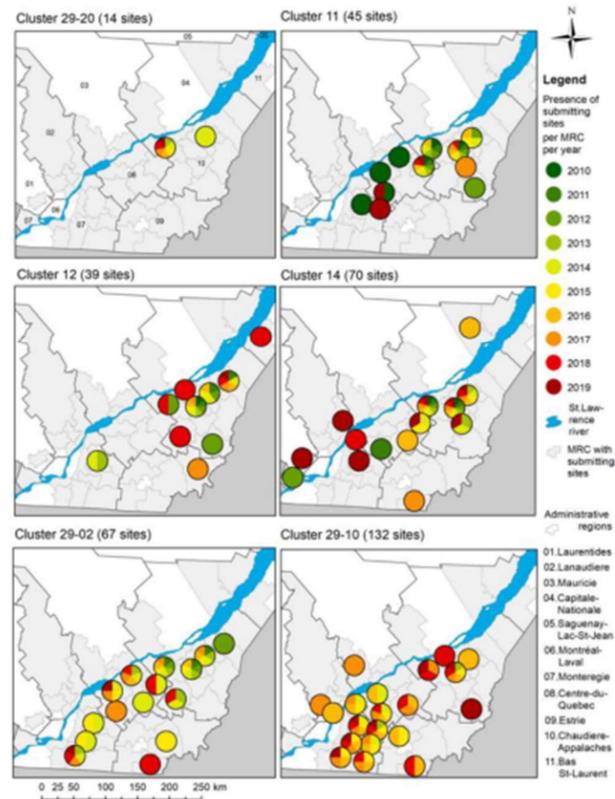


Figure 3. Spatiotemporal distributions of specific wild-type clusters (#11, 12, 14, 29-02, 29-10, 29-20). The total number of sites in which a cluster was detected during the study period is shown between parentheses.

Discussion and conclusion

- The large proportion of vaccine-like strains reflected the widespread use of PRRSV vaccination.
- Most wild-type PRRSV-2 strains in Quebec belong to lineage 1^{1,2}. The 46 wild-type clusters identified revealed the high diversity of strains, and the increased challenges in terms of disease control.
- The newly detected clusters in a region could result from the spreading of PRRSV endemic strains between regions, genetic evolution of local endemic strains, or introductions from outside the province which also support the need of an ongoing surveillance system.
- Some clusters detected in a region where no longer detected in subsequent years, which could be indicative of their successful eradication or the absence of sampling since all herds were not necessarily sampled each year.
- Most pig sites are located in Montérégie, Chaudière-Appalaches or Centre-du-Québec which explains the large numbers of sequences and wild-type clusters observed. These complexify regional disease management. Other regions as Bas St-Laurent might be more amenable to PRRSV regional eradication.
- Several reasons could explain the differences observed in spatiotemporal distribution of clusters, including viral characteristics (e.g. infectiousness, resistance in the environment), or connection networks between pig sites (e.g. pig transportation, visitors). In the future, phylogeographic analysis applied on particular cluster would allow a better evaluation of the dynamics of transmission among sites.

References

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