

PRRSV-1 ORF-5 genetic diversity in Spain (2018-2025) in a multi-site intensive pig company

Paula Rebollo-Igual¹, Celia Martinez-Saz², Daniel Crespo-Piazuelo², Alberto Allepuz¹, Enric Mateu¹

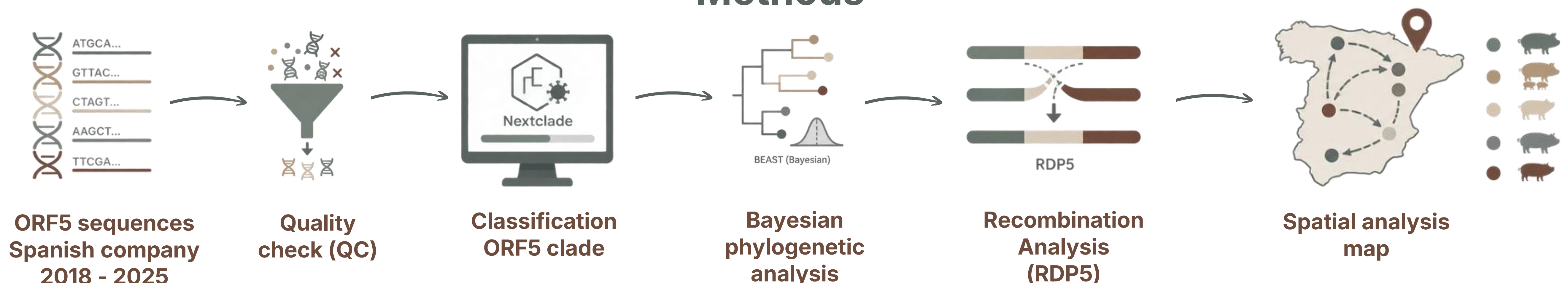
¹ Departament de Sanitat i d'Anatomia Animals, Facultat de Veterinària, Travessera dels Turons s/n, Universitat Autònoma de Barcelona, 08193, Cerdanyola del Vallès, Spain
²R&D Department, Jorge Ganadería, Ctra. de Logroño km 9.2, Grupo Jorge, Monzalbarba, Zaragoza, 50120, Spain

Introduction

PRRS virus is a major cause of economic losses. In 2020, **highly virulent PRRSV-1 "Rosalia"** was introduced. Its spread in large multi-site pig production systems might be facilitated by the highly dense network of connections between farms.

Objective: to describe and analyze the PRRSV-1 genetic diversity and circulation patterns in an intensive, multi-site Spanish pig company.

Methods



Results

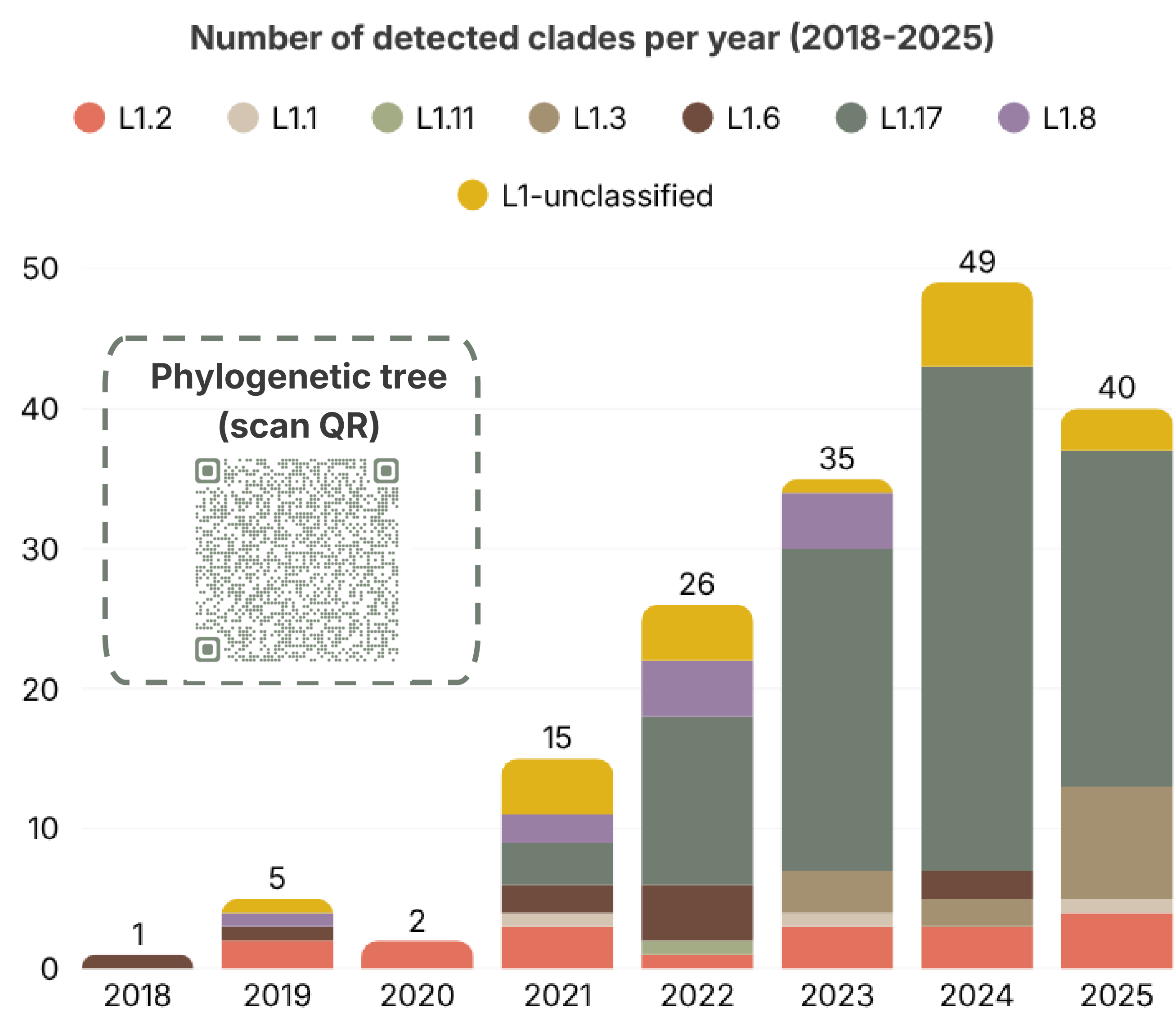


Fig 1. The temporal distribution of clades from 2018 to 2025. The bars show the annual number of PRRSV-1 detections by ORF5 clade, coloured according to their respective clades.

1. After QC, 173 sequences from 82 farms were included and assigned to 8 PRRSV-1 clades (Fig.1).
2. **L1.17 clade** dominated after 2021, with 98 detections probably reflecting the introduction of the so-called "Rosalia" strain.
3. Phylogenetic analysis suggests independent introductions from 2021-2025, with further diversification and spread within the system.
4. Unclassified isolates summed to 11%.
5. Four recombinant strains were detected (n=3 classified as L1.2 and n=1 classified as L1.6).

Farms connected by terminal phylogenetic clusters (posterior probability ≥ 0.95)

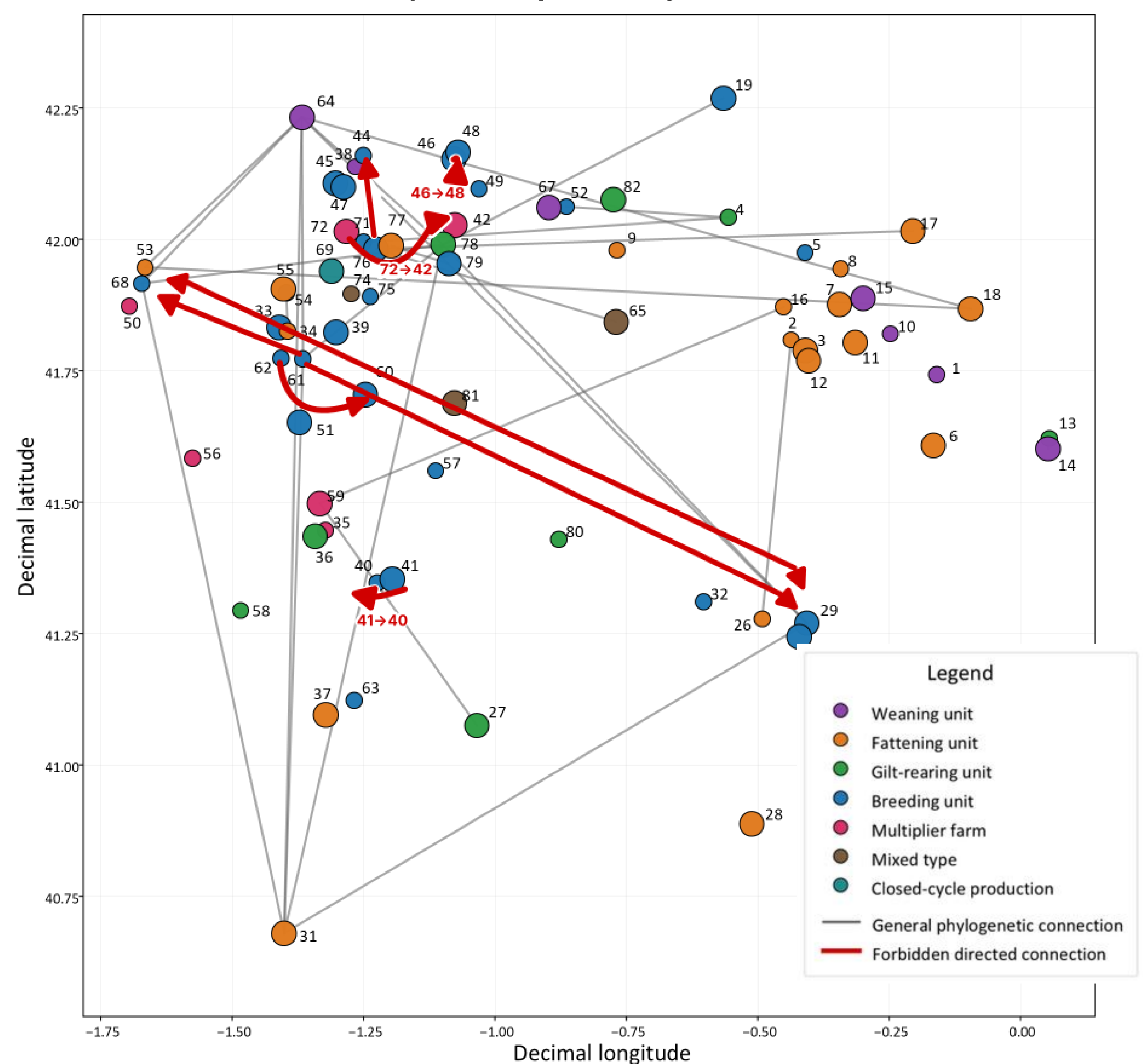


Fig 2. Spatial distribution of the 72 georeferenced farms included in the spatial phylogenetic analysis. Dot is proportional to the number of animals in the farm. Grey and red lines indicate sharing closely related sequences based on the phylogenetic analysis with posterior probability ≥ 0.95 and patristic distance ≤ 0.02 . The red lines with arrows indicate breeding farms and gilt-rearing units that must be unconnected in the pig flow but shared closely similar sequences.

Discussion and Conclusions

This study shows that PRRSV-1 circulation in a large Spanish pyramidal multi-site pig system was genetically diverse and dynamic, with predominance of the L1.17 lineage since 2021, probably indicating the spread of the highly virulent strain "Rosalia". The spread of the virus probably followed the pig flow but also occurred laterally (between farms from the same productive stages). This underscores the need for considering animal movement networks to identify phylodynamic and phylogeographical patterns. It also highlights the need for stricter monitoring of biosecurity.

Contact:
paula.rebollo@uab.cat
PhD student

