

PRRS in South Korea

(Animal and Plant Quarantine Agency)

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The 6th WOA Regional Training on Swine Disease
Control in Asia and the Pacific

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FARM-LEVEL POSITIVITY

86.2%

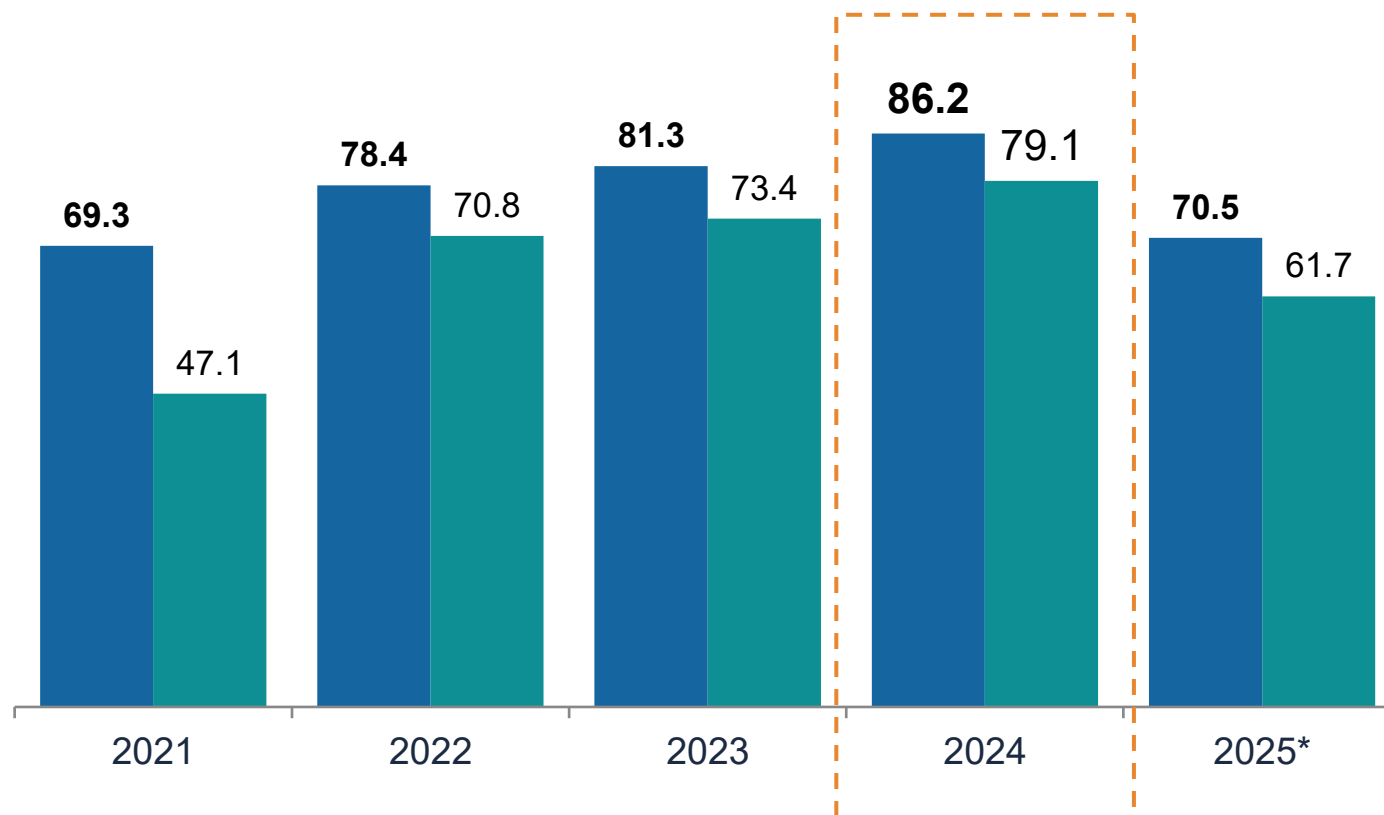
Peak in 2024

SAMPLE-LEVEL POSITIVITY

79.1%

Peak in 2024

Farm-level and sample-level positivity (%)

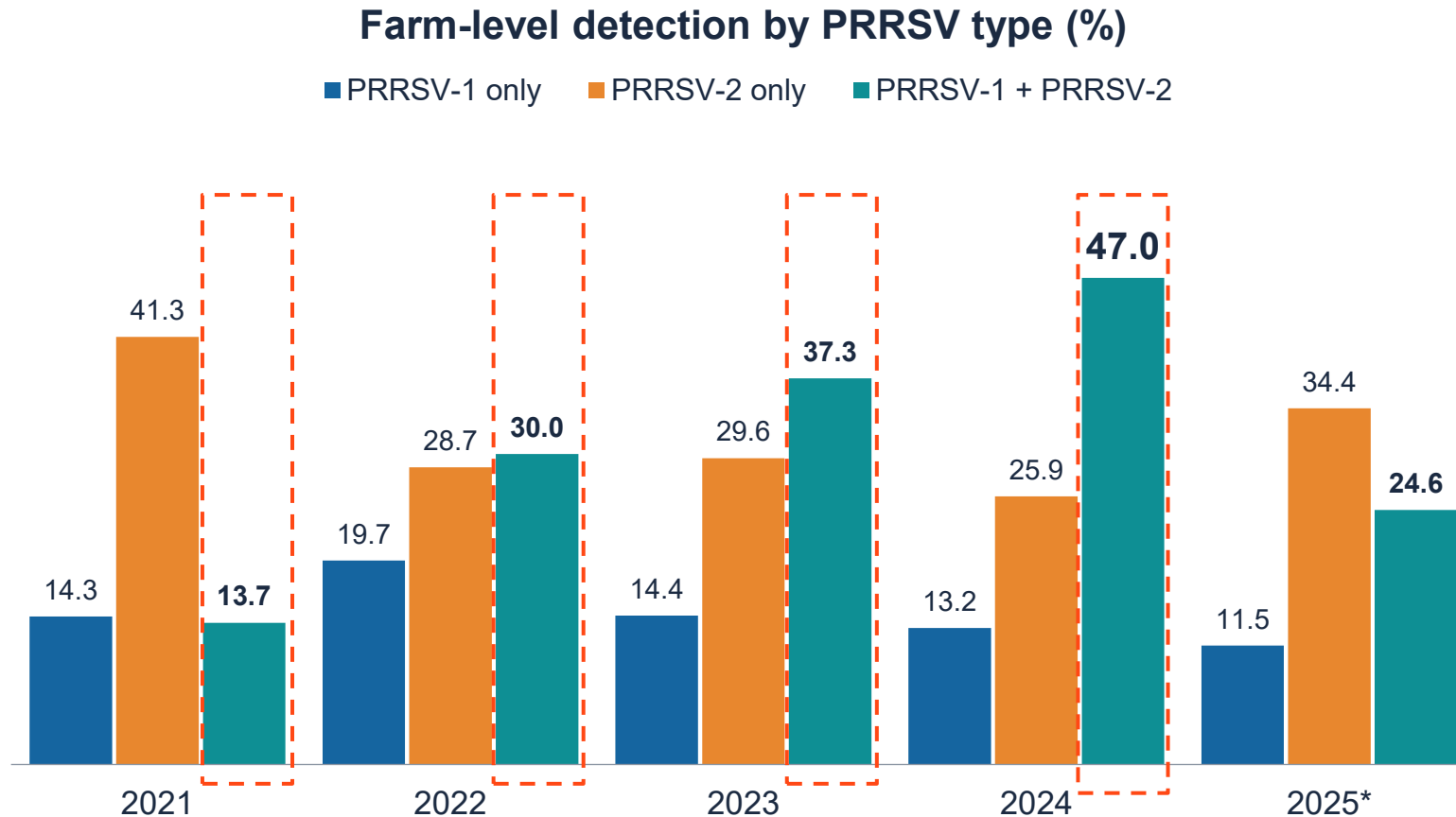


* May 2025 is a partial-year observation.

2024 positivity peaked at 86.2% of farms and 79.1% of samples.



PRRSV-1 and PRRSV-2 Detection Patterns, 2021–2025



CO-DETECTION PEAK · 2024

47.0%

of farms positive for both PRRSV-1 and PRRSV-2

PRRSV-2 ONLY · 2025

34.4%

largest detection category in 2025

The three categories sum to farm-level positivity. *2025: partial-year data (through May 2025).

Co-detection rose from 13.7% (2021) to a 47.0% peak (2024), then fell to 24.6% (2025).



PRRSV-1 vs PRRSV-2: Contrasting Epidemiological Patterns

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PRRSV-1

Stable subtype composition

1A

PREDOMINANT FIELD SUBTYPE

83.1–94.0% of PRRSV-1 each year
Subtype 1A remains the predominant field subtype.

1C

MINOR VACCINE-LIKE COMPONENT

6.0–16.9% of PRRSV-1 each year
Vaccine-like subtype 1C persists at low frequency.

PRRSV-2

Rapid lineage turnover

1.5

EMERGING SUBLINEAGE

11.7% → 61.2% of PRRSV-2, 2023–25
NADC34-like strains (sublineage 1.5) are expanding rapidly.

L5/8

DECLINING VACCINE-ASSOCIATED LINEAGES

0.0% of PRRSV-2 in 2025
Lineages 5 and 8 have declined markedly.

PRRSV-1 remains stable with subtype 1A predominance, whereas PRRSV-2 is shifting toward NADC34-like strains.



PRRSV-1: Field Subtype 1A Dominates; Vaccine-like 1C Persists

ORF5-based subtyping of PRRSV-1 (European type): subtype 1A (field virus), 1C (vaccine-like) and near-absent 1B.



SUBTYPE 1A · FIELD VIRUS

83.1–94.0%

of PRRSV-1 in every year



SUBTYPE 1C · VACCINE-LIKE

6.0–16.9%

of PRRSV-1, persisting every year

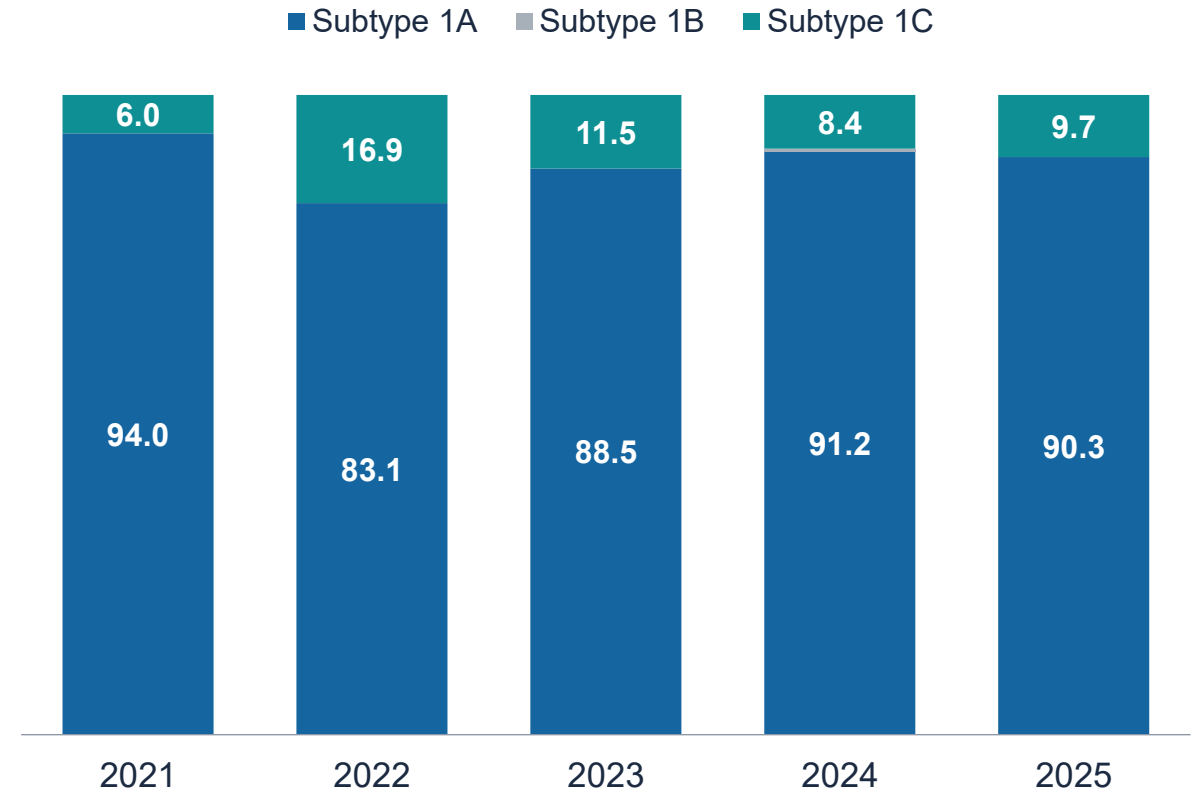


SUBTYPE 1B · NEAR-ABSENT

0.0%

in all years except 0.4% in 2024

Annual PRRSV-1 subtype distribution (%)



Subtype 1A accounted for 83.1–94.0% of PRRSV-1 sequences in every year from 2021 to 2025.



PRRSV-2: Rapid Expansion of NADC34-like Strains

NADC34-LIKE (SUBLINEAGE 1.5) · 2025

61.2%

of PRRSV-2 sequences

SHARE OF ALL SEQUENCED PRRSV · 2025

37.5%

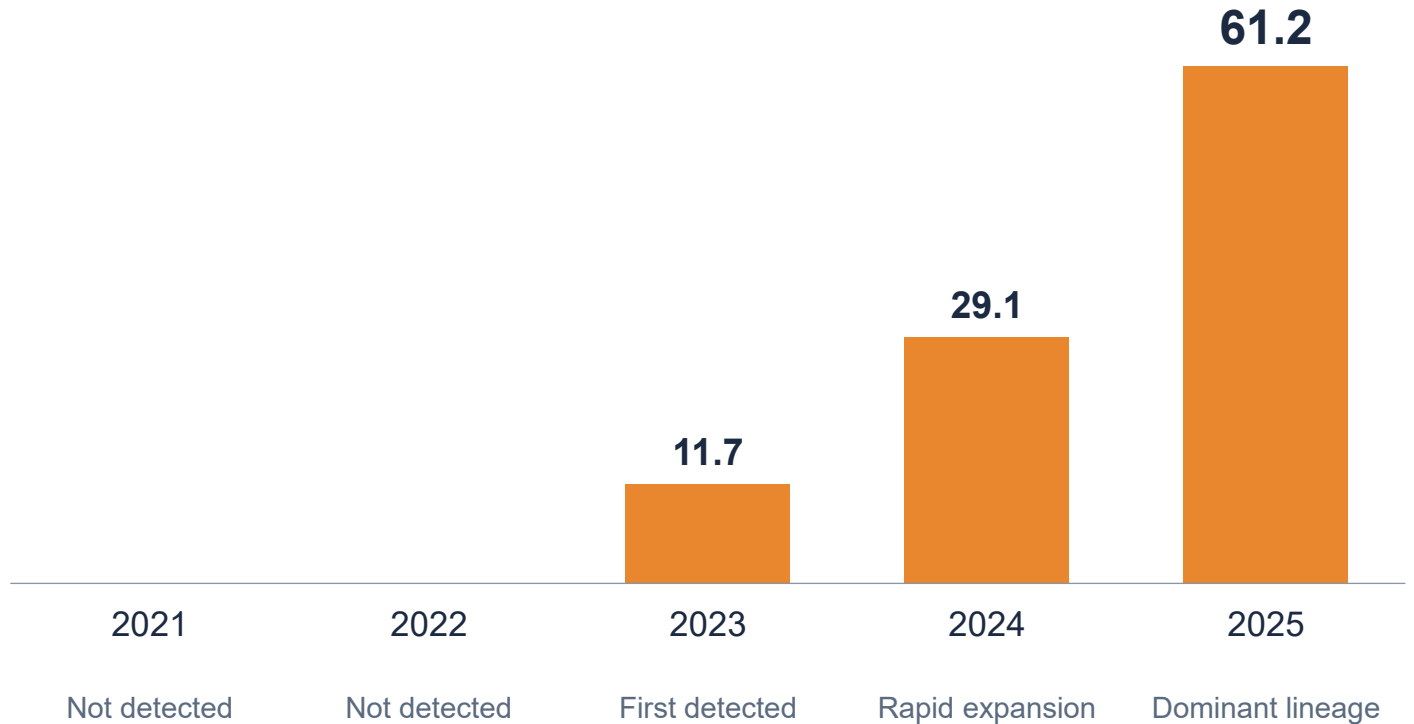
of all PRRSV detections

LINEAGES 5 AND 8 · 2025

0.0%

vaccine-associated lineages, down from substantial shares in 2021

NADC34-like share of PRRSV-2 sequences (%)



NADC34-like strains rose from 11.7% of PRRSV-2 in 2023 to 61.2% in 2025; lineages 5 and 8 fell to 0.0%.

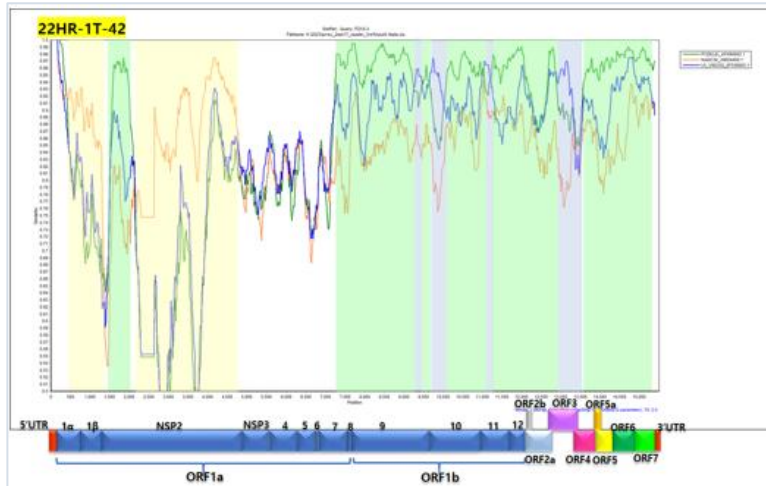


Mosaic Recombination: ORF5 vs Whole-Genome Classification

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1T-42

NADC30 (L1) + L8 + L5



BY ORF5

L8

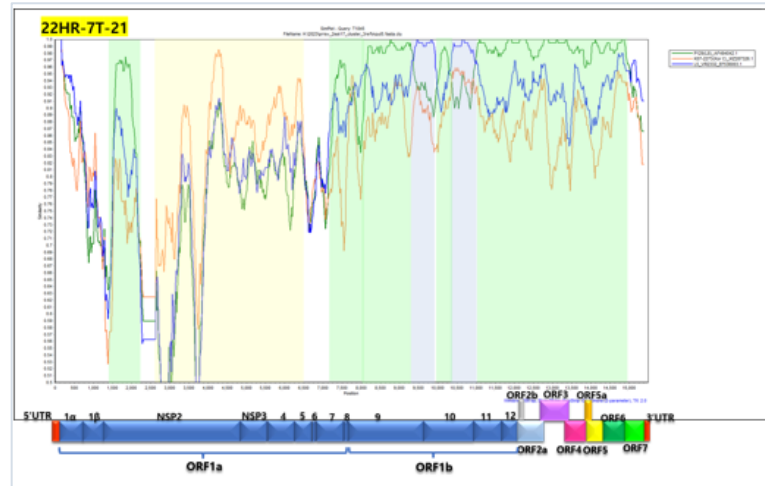


BY WHOLE GENOME

Lineage 1

7T-21

LKC + L8 + L5



BY ORF5

L8

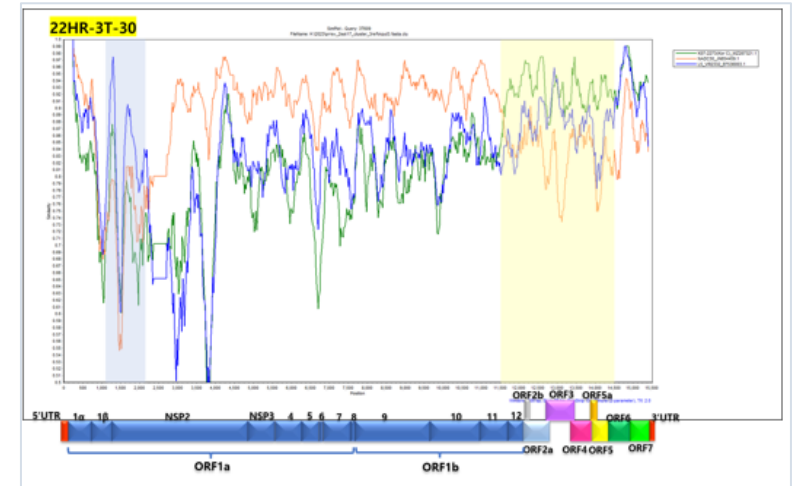


BY WHOLE GENOME

LKC

3T-30

NADC30 (L1) + LKB + L5



BY ORF5

LKB



BY WHOLE GENOME

Lineage 1

Same isolate, different answers: ORF5 assigns each isolate to one lineage, the whole genome to another.

Whole-genome analysis reveals mosaic ancestry that ORF5-only lineage assignment can miss.

ORF5 IDENTITY TO IA_2014_NADC34 (%) · RANGE BY YEAR

Sequence identity	2023 (<i>n</i> = 21)	2024 (<i>n</i> = 133)	2025 (<i>n</i> = 30)
Nucleotide	95.7–96.5	94.5–96.7	94.7–96.5
Amino acid	95.5–97.5	94.5–98.0	93.5–97.5

ORF5 VS WHOLE GENOME · IDENTITY TO IA_2014_NADC34 (%)

1T-N22

96.5% → 90.8%

ORF5

WHOLE GENOME

Whole-genome identity 5.7 points below ORF5

Carries the 100-aa NSP2 deletion

1T-N20

90.6% → 89.1%

ORF5

WHOLE GENOME

Recombinant: 5' NADC34-like + 3' NADC30-like

Carries the 100-aa NSP2 deletion

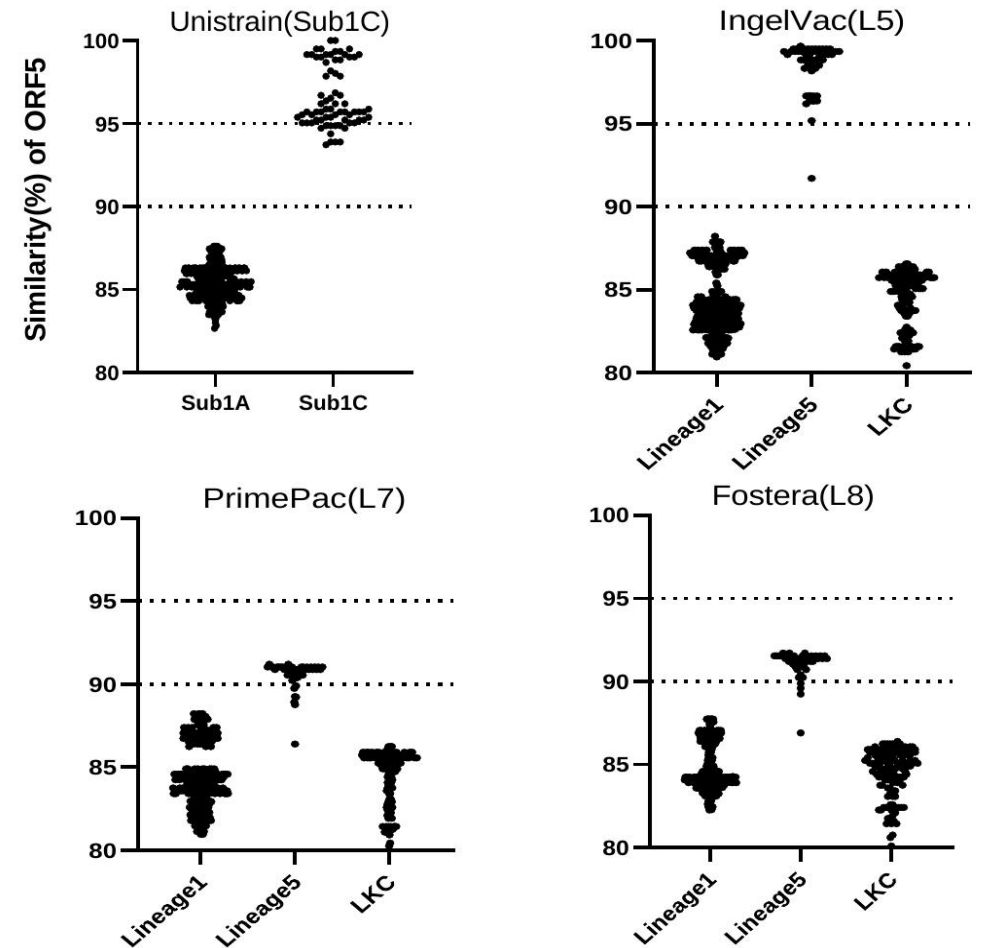
NADC34-like strains continue to diverge, driving a shift from ORF5 to whole-genome surveillance.

LICENSED PRRS VACCINES

Type	Company	Vaccine name	Lineage / subtype	Approval
MLV (attenuated)	Boehringer Ingelheim	Ingelvac PRRS	L5	1995
	MSD	Prime Pac PRRS	L7	2013
	Zoetis	Fostera PRRS	L8	2013
	Hipra	Unistrain PRRS	Subtype 1C	2013
	Biopoa	PoaVac PRRS	L5	2021
	MSD	Porcilis PRRS	Subtype 1C	2022
	Woogene B&G	Immunis PRRS-NA	L1	2023
	Elanco	Prevacent PRRS	L1	2024
Inactivated	Ceva	Progressis	Subtype 1A	2022

* Shaded rows : PRRSV-1 vaccines; Unshaded : PRRSV-2 vaccines.

ORF5 SIMILARITY TO VACCINE STRAINS (%)



Select vaccines on evidence of protection against circulating strains, not genetic labels alone.

APQA Vaccine Initiatives

A

PATHWAY A

Live Attenuated Vaccines

1

CPD platform

Establish a codon-pair deoptimization (CPD) attenuation platform.

2

SAVE candidates

Develop NADC34-like PRRSV vaccine candidates using Synthetic Attenuated Virus Engineering (SAVE).

B

PATHWAY B

Advanced Inactivated Vaccines

1

Gene-edited cell lines

Develop gene-edited cell lines permissive to PRRSV.

2

Suspension culture

Optimize suspension culture to increase virus yield.

3

adjuvants

Evaluate novel adjuvants to improve immunogenicity.

NADC34-like vaccine through CPD/SAVE attenuation and improved cell culture and adjuvants for inactivated vaccines.



1 Contrasting genotype dynamics

83.1–94.0%

Subtype 1A share of PRRSV-1, every year 2021–2025

61.2%

NADC34-like share of PRRSV-2 in 2025 (from 11.7% in 2023)

PRRSV-1 is stable; PRRSV-2 is turning over rapidly.

2 Loss of vaccine-associated lineages

28.1 → 0.0%

Lineage 5, 2021 → 2025

0.0%

Lineage 8 in 2025 (peak 4.2% in 2023)

Non-detection does not demonstrate elimination.

3 Mosaic recombination

3 isolates

Lineage differs between ORF5 and whole-genome analysis

–5.7 pts

1T-N22 identity to NADC34: whole genome 90.8% vs ORF5 96.5%

ORF5-only typing can misclassify recombinant strains.

4 Strategic priorities

Surveillance Move routine typing from ORF5 to whole-genome sequencing.

Vaccines NADC34-like SAVE candidates and PRRSV-permissive gene-edited cell lines.

Keep PRRSV control aligned with shifting lineages through whole-genome surveillance and adaptable vaccines.

Thank you for your attention

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