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Protecting animals, preserving our future

Bioinformatics Analysis of PRRSV:
take the RFLP 1-4-4 L1C variant as an example

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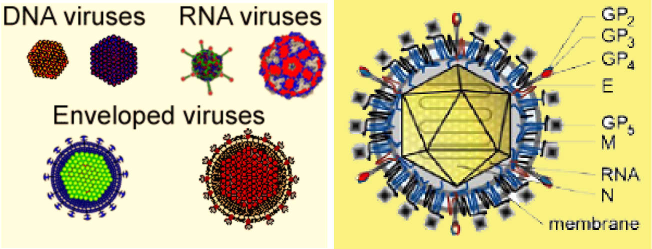
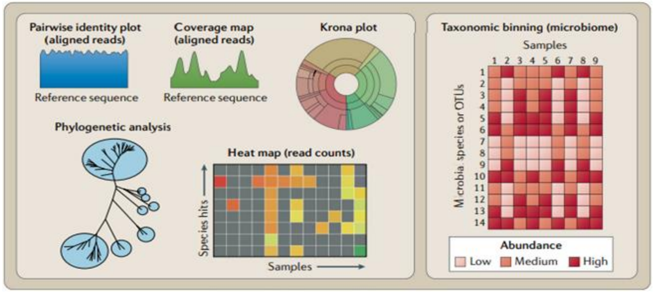
Analysis, including bioinformatics analysis

Increase our understanding of disease

Promote the prevention and control





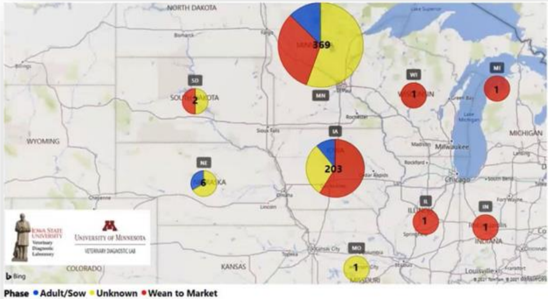
Emergence of PRRSV RFLP 1-4-4 L1C variant

Geological distribution:
-IA and MN (Most frequent)
-Spread to at least other 7 states

Clinical signs:
-Sow mortality
-Increased mummies
-Abortions
-Post-weaning mortality
The mortality rate:17.50%

Vaccine:
-Previous vaccination and virus exposure do not seem to provide immunity to 1-4-4

Sequences available:
-RFLP 1-4-4 lineage 1C variant
(GenBank no: MW887655)
-46/2020
(GenBank no: MZ423535)



So what are they seeing with this strain 1-4-4

- 1-4-4 Pattern
  - Same clinical signs as other PRRS strains
  - Just a LOT WORSE
- **Growing Herd**
  - 15-30% mortality
  - Vaccination not very helpful
  - High fever

Abortions

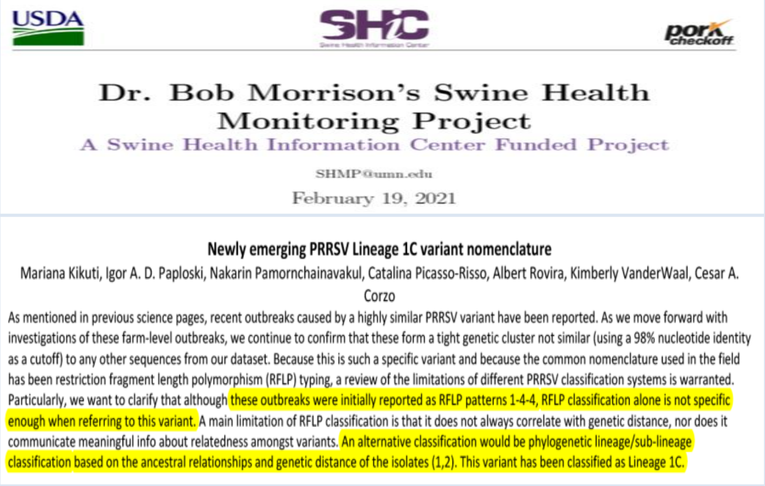
Dead Pigs

Slow Growth

What is different is that this strain **replicates on high levels**:

-easily find Ct on the 10`s.

-occasional cases of below 10.



Dr. Bob Morrison's Swine Health Monitoring Project
A Swine Health Information Center Funded Project
SHMP@umn.edu
February 19, 2021

Newly emerging PRRSV Lineage 1C variant nomenclature

Mariana Kikuti, Igor A. D. Paploski, Nakarin Pamornchainavakul, Catalina Picasso-Risso, Albert Rovira, Kimberly VanderWaal, Cesar A. Corzo

As mentioned in previous science pages, recent outbreaks caused by a highly similar PRRSV variant have been reported. As we move forward with investigations of these farm-level outbreaks, we continue to confirm that these form a tight genetic cluster not similar (using a 98% nucleotide identity as a cutoff) to any other sequences from our dataset. Because this is such a specific variant and because the common nomenclature used in the field has been restriction fragment length polymorphism (RFLP) typing, a review of the limitations of different PRRSV classification systems is warranted. Particularly, we want to clarify that although these outbreaks were initially reported as RFLP patterns 1-4-4, RFLP classification alone is not specific enough when referring to this variant. A main limitation of RFLP classification is that it does not always correlate with genetic distance, nor does it communicate meaningful info about relatedness amongst variants. An alternative classification would be phylogenetic lineage/sub-lineage classification based on the ancestral relationships and genetic distance of the isolates (1,2). This variant has been classified as Lineage 1C.

Emergence of PRRSV RFLP 1-4-4 L1C variant

PRRSV RFLP 1-4-4 L1C variant

RFLP, Restriction Fragment Length Polymorphism based on ORF5 of PRRSV. RFLP classification alone is not specific enough when referring to this variant. A main limitation of RFLP classification is that it does not always correlate with genetic distance, nor does it communicate meaningful info about relatedness amongst variants.

Lineage, Lineage/sub-lineage classification based on the phylogenetic relationships and genetic distance of ORF5 sequences of PRRSV. This variant has been classified as Lineage 1C.

Variant, of all RFLP 1-4-4 Lineage 1C PRRSV, only part of them was the variant associated with the late 2020 outbreaks. Recombination contributes to the variant.

outline

1. Methods for the genetic diversity analysis of PRRSV: RFLP, lineage and recombination
2. Genetic diversity analysis of RFLP 1-4-4 L1C PRRSV
3. Recombination of PRRSV

1

Methods for the genetic diversity analysis of PRRSV: RFLP, lineage and recombination

1. RFLP classification of PRRSV

- ☐ RFLP analysis has been proposed to **distinguish the modified live vaccine RespPRRS/Repro (parent strain VR-2332) from wild-type PRRSVs**.
- ☐ To facilitate the reporting and handling of test data, each isolate is given a numerical code for its ORF5 RFLP pattern with enzymes, ***Mlu* I**, ***Hinc* II**, and ***Sac* II**, in that order.

MluI

5′...A▼CGCGT...3′
3′...TGCGC▲A...5′

HincII

5′...GTY▼RAC...3′
3′...CAR▲YTG...5′

SacII

5′...CCGC▼GG...3′
3′...GG▲CGCC...5′

Differentiation of a porcine reproductive and respiratory syndrome virus vaccine strain from North American field strains by restriction fragment length polymorphism analysis of ORF 5

Ronald D. Wesley, William L. Mengeling, Kelly M. Lager, Deborah F. Clouser, John G. Landgraf, Merwin L. Frey

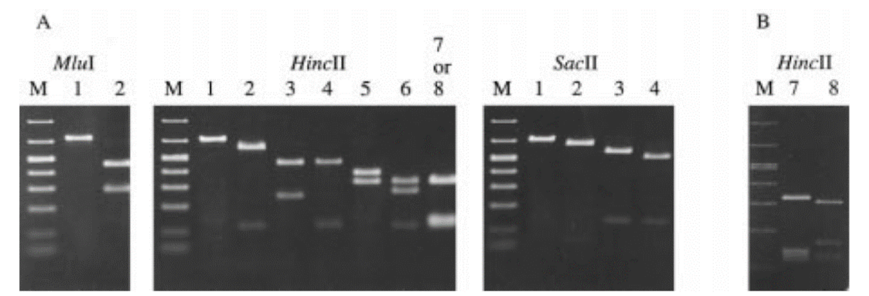
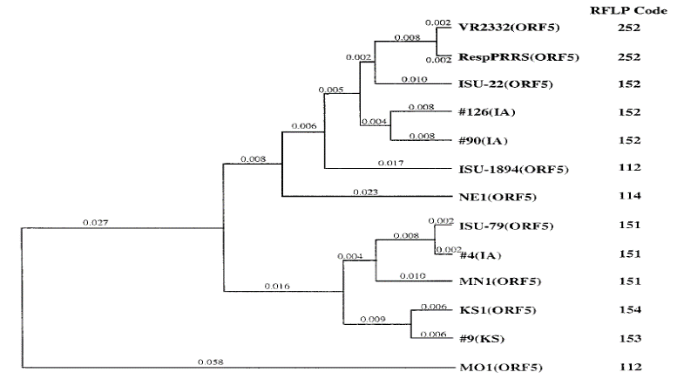


Figure 1. General types of RFLP patterns for PRRSV isolates. PCR products (716 bp) containing ORF 5 were digested with restriction enzymes *Mlu*I, *Hinc*II, and *Sac*II. There are 2 types of RFLP patterns for *Mlu*I, 8 different patterns for *Hinc*II, and 4 different patterns for *Sac*II. A. Restriction enzyme digests were electrophoresed on a 1.8% agarose gel and stained with ethidium bromide. B. A 2% agarose gel with more band migration was used to resolve *Hinc*II patterns 7 and 8. M = marker lane with DNA fragments of known size.



Wesley et al., J Vet Diagn Invest.1998

1. RFLP classification of PRRSV

- ☐ **Wild-type PRRSV:** 41572-2 strain, isolated in 1993, was RFLP 1-4-4 type (Wesley et al., 1998).
- ☐ **modified live vaccine:** Prime Pac PRRS+, was also RFLP 1-4-4 type.

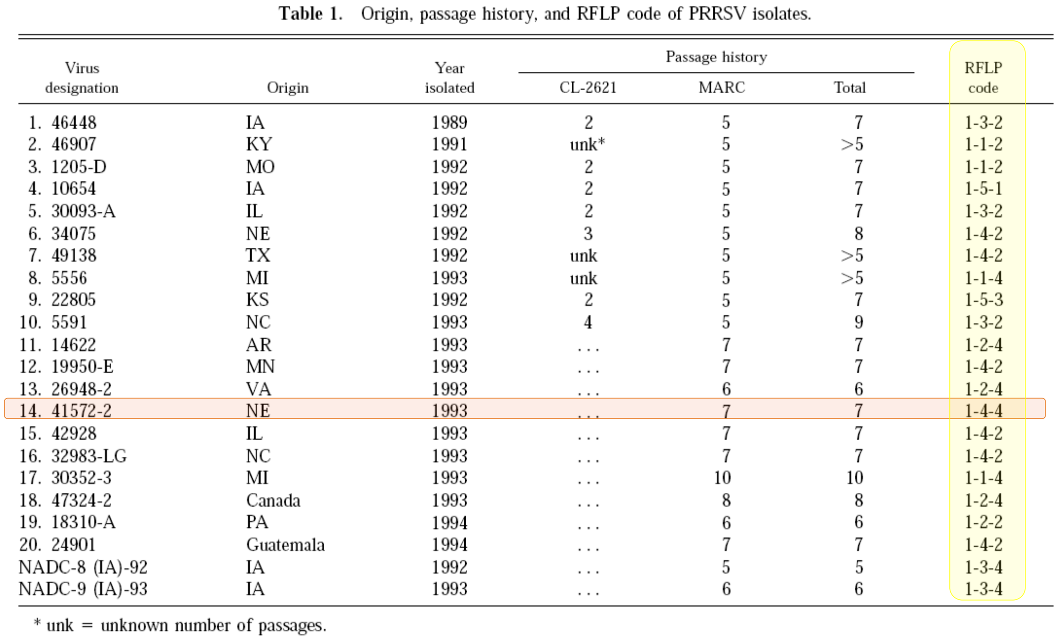


Table 1. Origin, passage history, and RFLP code of PRRSV isolates.

Virus designation	Origin	Year isolated	Passage history CL-2621	Passage history MARC	Passage history Total	RFLP code
1. 46448	IA	1989	2	5	7	1-3-2
2. 46907	KY	1991	unk*	5	>5	1-1-2
3. 1205-D	MO	1992	2	5	7	1-1-2
4. 10654	IA	1992	2	5	7	1-5-1
5. 30093-A	IL	1992	2	5	7	1-3-2
6. 34075	NE	1992	3	5	8	1-4-2
7. 49138	TX	1992	unk	5	>5	1-4-2
8. 5556	MI	1993	unk	5	>5	1-1-4
9. 22805	KS	1992	2	5	7	1-5-3
10. 5591	NC	1993	4	5	9	1-3-2
11. 14622	AR	1993	. . .	7	7	1-2-4
12. 19950-E	MN	1993	. . .	7	7	1-4-2
13. 26948-2	VA	1993	. . .	6	6	1-2-4
14. 41572-2	NE	1993	. . .	7	7	1-4-4
15. 42928	IL	1993	. . .	7	7	1-4-2
16. 32983-LG	NC	1993	. . .	7	7	1-4-2
17. 30352-3	MI	1993	. . .	10	10	1-1-4
18. 47324-2	Canada	1993	. . .	8	8	1-2-4
19. 18310-A	PA	1994	. . .	6	6	1-2-2
20. 24901	Guatemala	1994	. . .	7	7	1-4-2
NADC-8 (IA)-92	IA	1992	. . .	5	5	1-3-4
NADC-9 (IA)-93	IA	1993	. . .	6	6	1-3-4

* unk = unknown number of passages.

Vaccine strains:

① Ingelvac PRRS MLV, Boehringer Ingelheim; RFLP 2-5-2

② Ingelvac PRRS ATP, Boehringer Ingelheim; RFLP 1-4-2

③ Fostera PRRS, Zoetis; RFLP 1-3-2

④ Prime Pac PRRS+, Merck; RFLP 1-4-4

⑤ Prevacent PRRS, Elanco; RFLP 1-8-4

Wesley et al., J Vet Diagn Invest.1998

How to determine the RFLP pattern of a PRRSV strain?

Mlu I: ACGCGT
Hinc II: GTCGAC
GTCAAC
GTTGAC
GTTAAC
Sac I: CCGCGG

RFLP 1-4-4 L1C variant

```
ATGTTGGGGAAATGCTTGACCGCGGGCTGTTGCTCGCGATTGCTTTCTTTGTGGTGTATCGTGCCGTTCTGGTTTGCTGTGCTCGTCAACGCCAGCAGCAACAGCAGCTCTCATTTTCAGTTGATTTATAACTTGACGCTATGT
GAGCTGAATGGCACAGATTGGCTGGCTAATAAATTTGATTGGGCAGTGGAGAGTTTTGTCATCTTTCCTGTGTTGACTCACATTGTTTCCTATGGTGCACTCACTACTAGCCATTTCCTTGACACAGTCGGTCTGGTTACTGTGT
CCACCGCCGGTTTTTTTCACGGGCGGTATGTCTTGAGCAGCATCTACGCGGTCTGTGCCCTGGCTGCGTTAATTTGCTTTGTCATTAGGCTTGCGAAGAACTGCATGTCCTGGCGCTACTCATGTACCAGATATACCAACTTCC
TTCTGGACACCAAGGGCAGACTCTATCGTTGGCGGTCGCCCGTTATCATAGAGAAAAGGGGTAAGGTTGAGGTCGAAGGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCCGCGGCTACCCCTTTAACCAGAG
TTTCAGCGGAACAATGGGGTCGTCCCTAG
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MN184

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ATGTTGGGGAAATGCTTGACCGCGGGCTATTGCTCGCAATTGCCTTTTTTGTGGTGTATCGTGCCGTTCTGTCTTGCTGCGCTCGTCAACGCCAACAGCAACAGCAGCTCCCATTTACAGTTGATTTATAACTTAACGATATGTG
AGCTGAATGGCACAGACTGGCTGAACAATCATTTTAGTTGGGCAGTGGAGACTTTCGTTATCTTTCCTGTGTTGACTCATATTGTTTCCTACGGCGCCCTCACTACCAGCCACTTCCTTGACACGGTCGGCCTGATCACTGTGT
CCACCGCCGGATACTACCATGAGCGGTATGTCTTGAGYAGCATCTATGCTGCCTGCGCCCTGGCTGCGCTGATTTGYTTCGTCATCAGGTTGACGAAAAATTGTATGTCCTGGCGCTACTCATGTACCAGATATACCAACTTTCTT
CTGGACACCAAGGGCAGACTCTATCGCTGGCGGTCACCCGTCATCATAGAGAAAAGGGGTAAAATTGAGGTTGGAGGTGACCTGATCGACCTCAAGAGAGTTGTGCTTGATGGTTCCGCGGCAACCCCTGTAACCAAAGT
TTCAGCGGAACAATGGGGTCGTCCTTAG
```

19950-E (MN） 1-4-2

```
ATGTTGGGGAAATGCTTGACCGCGGGCTGTTGCTCGCGATTGCTTTCTTTGTGGTGTATCGTGCCGTTCTGTTTTGCTGTGCTCGTCAACGCCAACAGCAGCAGCAGCTCTCATTTTCAGTTGATTTATAACTTGACGCTATGT
GAGCTGAATGGCACAGATTGGCTGGCTGAGAAATTTGATTGGGCGGTGGAAAGTTTTGTCATTTTTCCCGTGTTGACTCACATTGTTTCCTATGGTGCACTCACTACTAGCCATTTTCTTGACACAGTCGGTCTGGTTACTGTG
TCTACCGCCGGGTTTTGGCACGGGCGGTATGTCTTGAGCAGCATCTACGCGGTCTGTGCCCTGGCTGCGTTAATTTGCTTTGTCATTAGGCTTGCGAAGAACTGCATGTCCTGGCGCTACTCTTGTACCAGATATACTAACTTC
CTTCTAGACACTAAGGGCAGACTCTATCGTTGGCGGTCGCCCGTTATCATAGAGAAAGGGGGTAAGGTTGAGGTCGAAGGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCCGTGGCAACCCCTTTAACCAGA
GTTTCAGCGGAACAATGGGGTCGTCCCTAG
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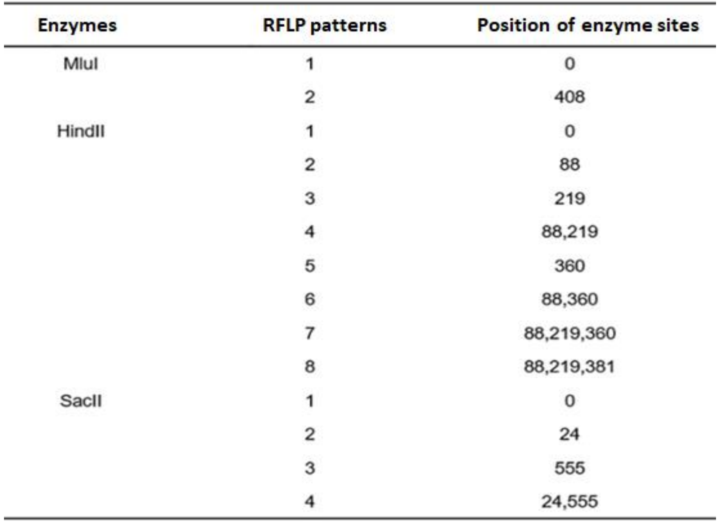


Enzymes	RFLP patterns	Position of enzyme sites
MluI	1	0
	2	408
HindII	1	0
	2	88
	3	219
	4	88,219
	5	360
	6	88,360
	7	88,219,360
	8	88,219,381
SacII	1	0
	2	24
	3	555
	4	24,555

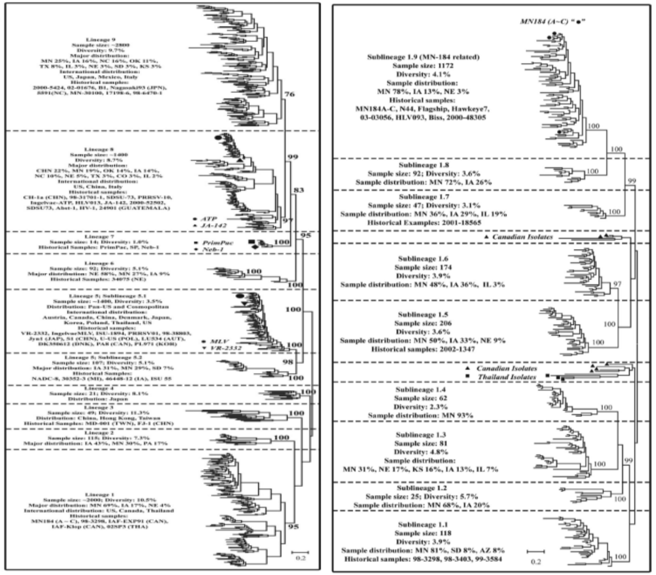
For small number of sequences, the RFLP patterns could be judged by comparing with the reference ORF5 sequences for each RFLP pattern.

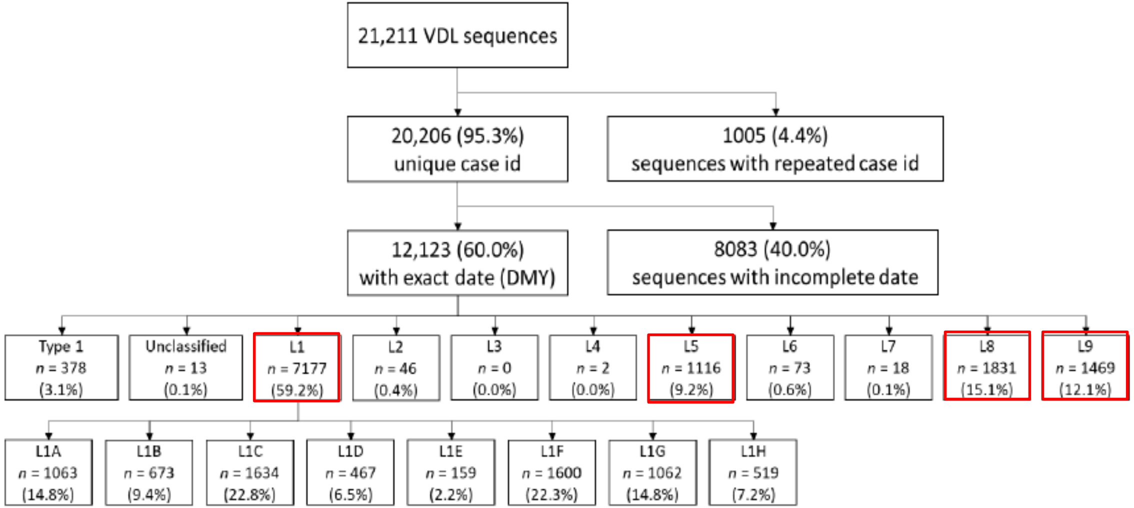
For large number of sequences, it is recommended to use specialized programs or software, such as the RFLP pattern bank information maintained by the University of Minnesota.

Trevisan et al., J Vet Diagn Invest.2021

2. Lineage classification of PRRSV

- ☐ **Lineage:** Systematic classification has led to strains of PRRSV-2 being phylogenetically classified into lineages 1–9. The inter-lineage diversity was at least 11%
- ☐ Lineage 1 has been further categorized into eight sub-lineages, L1A–L1H. The diversity within L1A-L1H was over 7%.





21,211 VDL sequences

20,206 (95.3%) unique case id

1005 (4.4%) sequences with repeated case id

12,123 (60.0%) with exact date (DMY)

8083 (40.0%) sequences with incomplete date

Type 1 *n* = 378 (3.1%)

Unclassified *n* = 13 (0.1%)

L1 *n* = 7177 (59.2%)

L2 *n* = 46 (0.4%)

L3 *n* = 0 (0.0%)

L4 *n* = 2 (0.0%)

L5 *n* = 1116 (9.2%)

L6 *n* = 73 (0.6%)

L7 *n* = 18 (0.1%)

L8 *n* = 1831 (15.1%)

L9 *n* = 1469 (12.1%)

L1A *n* = 1063 (14.8%)

L1B *n* = 673 (9.4%)

L1C *n* = 1634 (22.8%)

L1D *n* = 467 (6.5%)

L1E *n* = 159 (2.2%)

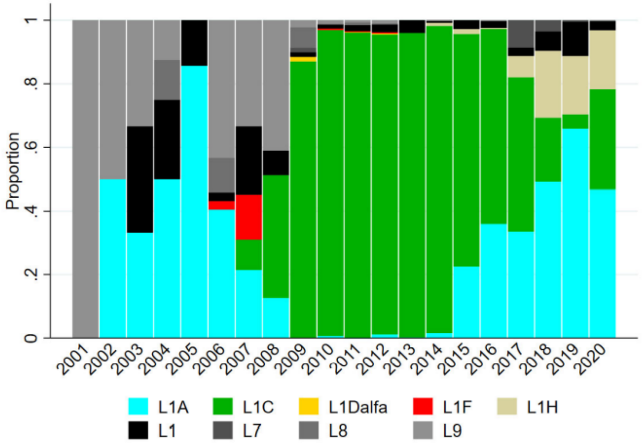
L1F *n* = 1600 (22.3%)

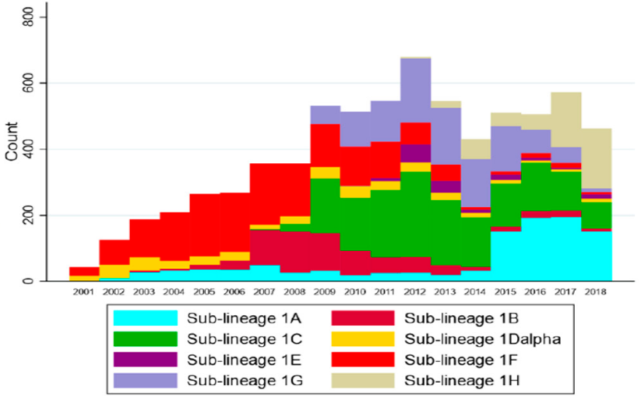
L1G *n* = 1062 (14.8%)

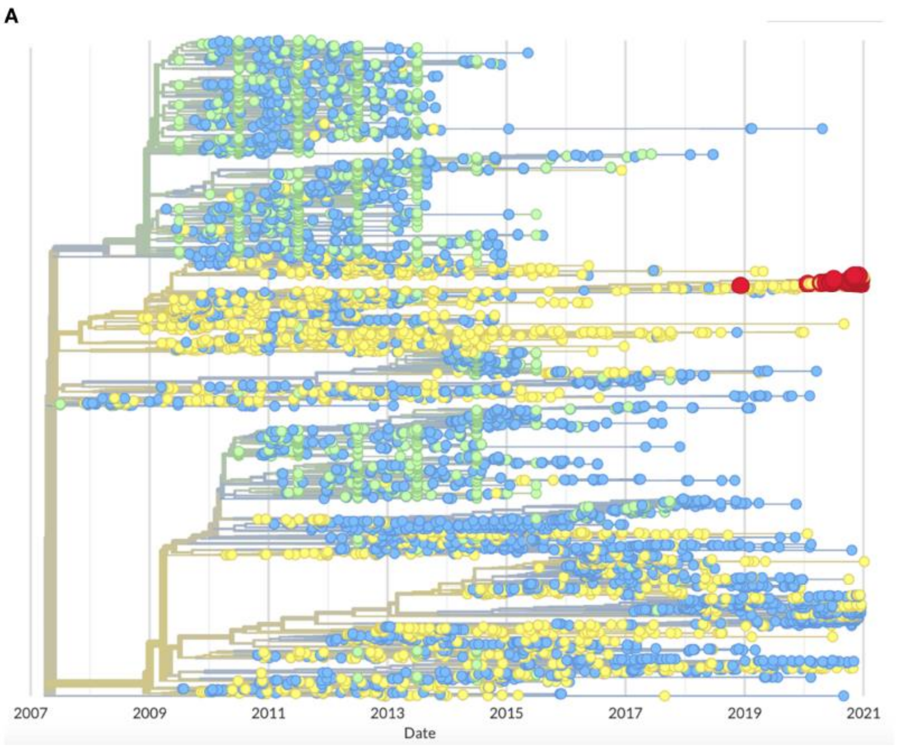
L1H *n* = 519 (7.2%)

Shi et al., J Virol, 2010; Paploski et al., Vaccines, 2021

L1A and L1C were the dominant sublineages in the US







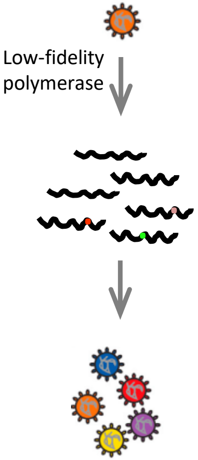
Paploski et al., Vaccines. 2021; Swine Health Monitoring Project, 2021

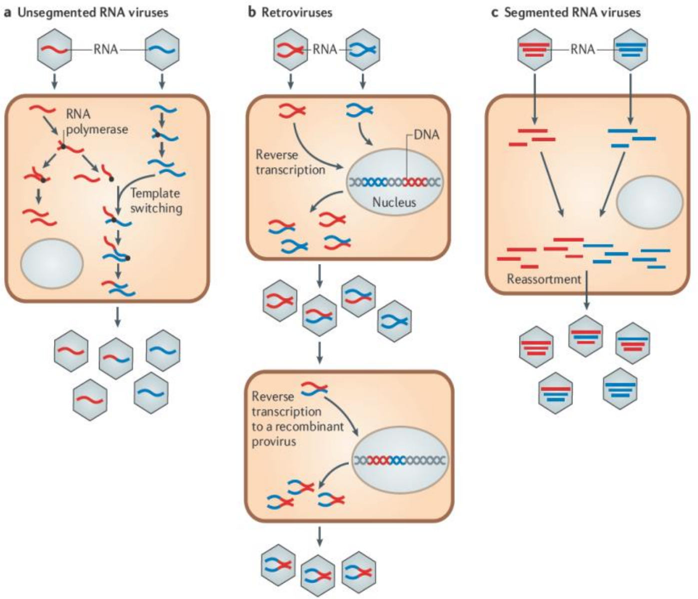
3. Recombination between viruses

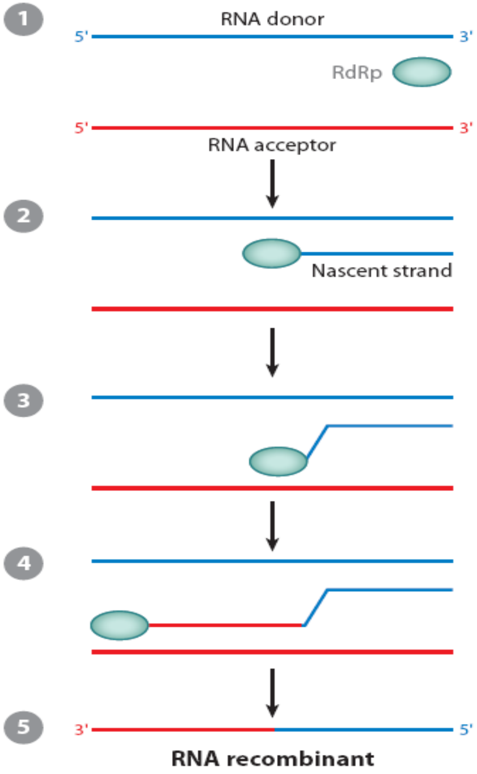
Evolution of Virus

Mutation or Indels

Recombination or Reassortment

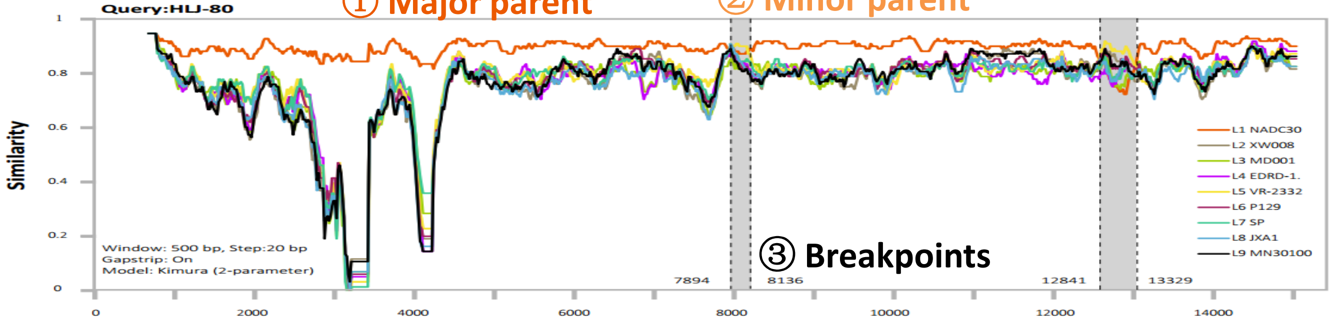






Recombination analysis

Simplot



① Major parent

② Minor parent

③ Breakpoints

RDP

Nucleotide differences

Recombination analysis of PRRSV

Recombination of PRRSVs

Between wild-type PRRSVS

JL580 (China)
NADC30-like PRRSV + HP-PRRSV
Zhao et al., 2015

SC-d (China)
JXA1-like + NADC30-like
Wang et al., 2018

KU-N1202 (Korea)
MN184-like+ VR-2332-like
Kwon et al., 2019

XJzx1-2015 (China)
CH-1a+ QYYZ
Zhang et al., 2019

SDqd1501 (China)
QYYZ+ HP-PRRSV
Zhang et al., 2020

etc.

Between wild-type PRRSVS and MLV strains

TJnh1501 (China)
MLV-like PRRSV + NADC30-like PRRSV
Bian et al., 2017

SCN17 (China)
Resp PRRS MLV +L1
Zhou et al., 2018

GDsg (China)
JXA1-P80 + QYYZ
Dong et al., 2017

IA70388-R (USA)
Fostera+ IA76950-WT
Wang et al., 2019

SDwh1403 (China)
Ingelvac PRRSV + NADC30
Zhang et al., 2020

etc.

Between MLV strains

PRRS-FR-2014-56-11-1 (French)
Unistrain® PRRS + Porcilis® PRRS
Eclercy et al., 2019

Horsens (Denmark)
Amervac + 96V198
Kvisgaard et al., 2020

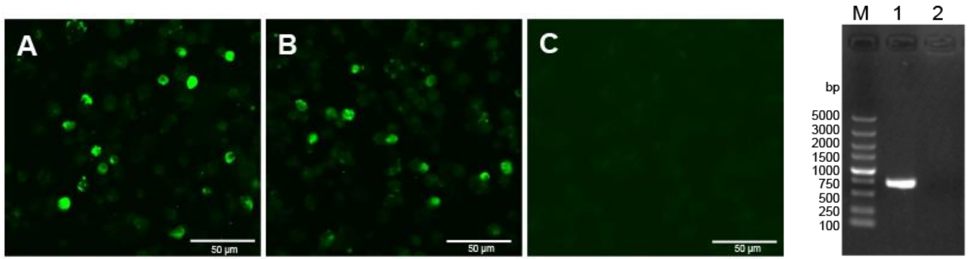
2

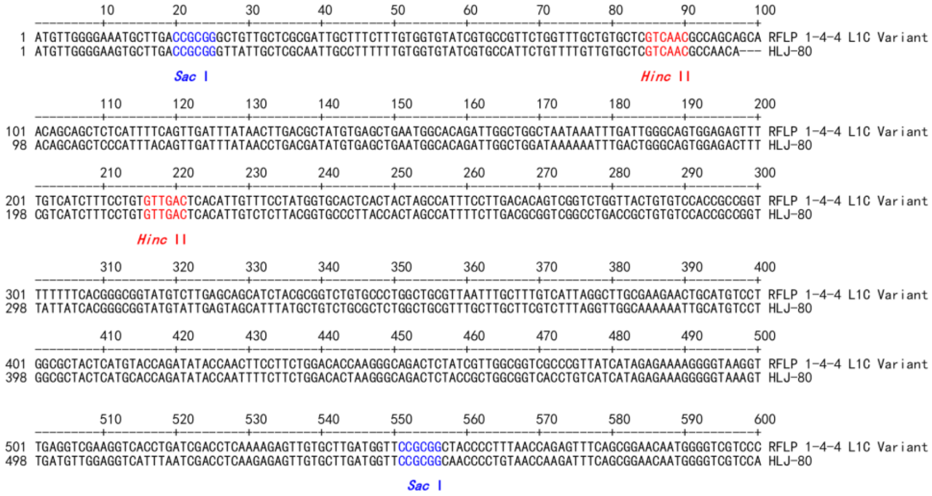
Genetic diversity analysis of RFLP 1-4-4 L1C PRRSV

The RFLP 1-4-4 L1C variant, which newly emerged in the US in late 2020, is spreading rapidly across several states as a recombinant of three PRRSV strains, with the mosaic ORF5 gene contributing to the formation of an independent variant.

Is there any RFLP 1-4-4 L1C PRRSV in other countries?

Isolation of a RFLP 1-4-4 L1C PRRSV, HLJ-80 strain





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            10        20        30        40        50        60        70        80        90       100
    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
  1 ATGTTGGGGAAATGCTTGACCGCGGGCTGTTGCTCGCGATTGCTTTCTTTGTGGTGTATCGTGCCGTTCTGGTTTGCTGTGCTCGTCAACGCCAGCAGCA RFLP 1-4-4 L1C Variant
  1 ATGTTGGGGAAGTGCTTGACCGCGGGTTATTGCTCGCAATTGCCTTTTTTGTGGTGTATCGTGCCATTCTGTTTTGTTGTGCTCGTCAACGCCAACA--- HLJ-80

                       Sac I                                                          Hinc II

           110       120       130       140       150       160       170       180       190       200
    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
101 ACAGCAGCTCTCATTTTCAGTTGATTTATAACTTGACGCTATGTGAGCTGAATGGCACAGATTGGCTGGCTAATAAATTTGATTGGGCAGTGGAGAGTTT RFLP 1-4-4 L1C Variant
 98 ACAGCAGCTCCCATTTACAGTTGATTTATAACCTGACGATATGTGAGCTGAATGGCACAGATTGGCTGGATAAAAAATTTGACTGGGCAGTGGAGACTTT HLJ-80

           210       220       230       240       250       260       270       280       290       300
    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
201 TGTCATCTTTCCTGTGTTGACTCACATTGTTTCCTATGGTGCACTCACTACTAGCCATTTCCTTGACACAGTCGGTCTGGTTACTGTGTCCACCGCCGGT RFLP 1-4-4 L1C Variant
198 CGTCATCTTTCCTGTGTTGACTCACATTGTCTCTTACGGTGCCCTTACCACTAGCCATTTTCTTGACGCGGTCGGCCTGACCGCTGTGTCCACCGCCGGT HLJ-80

                 Hinc II

           310       320       330       340       350       360       370       380       390       400
    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
301 TTTTTTCACGGGCGGTATGTCTTGAGCAGCATCTACGCGGTCTGTGCCCTGGCTGCGTTAATTTGCTTTGTCATTAGGCTTGCGAAGAACTGCATGTCCT RFLP 1-4-4 L1C Variant
298 TATTATCACGGGCGGTATGTATTGAGTAGCATTTATGCTGTCTGCGCTCTGGCTGCGTTTGCTTGCTTCGTCTTTAGGTTGGCAAAAAATTGCATGTCCT HLJ-80

           410       420       430       440       450       460       470       480       490       500
    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
401 GGCGCTACTCATGTACCAGATATACCAACTTCCTTCTGGACACCAAGGGCAGACTCTATCGTTGGCGGTCGCCCGTTATCATAGAGAAAAGGGGTAAGGT RFLP 1-4-4 L1C Variant
398 GGCGCTACTCATGCACCAGATATACCAATTTTCTTCTGGACACTAAGGGCAGACTCTACCGCTGGCGGTCACCTGTCATCATAGAGAAAGGGGGTAAAGT HLJ-80

           510       520       530       540       550       560       570       580       590       600
    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
501 TGAGGTCGAAGGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCCGCGGCTACCCCTTTAACCAGAGTTTCAGCGGAACAATGGGGTCGTCCC RFLP 1-4-4 L1C Variant
498 TGATGTTGGAGGTCATTTAATCGACCTCAAGAGAGTTGTGCTTGATGGTTCCGCGGCAACCCCTGTAACCAAGATTTCAGCGGAACAATGGGGTCGTCCA HLJ-80

                                                      Sac I
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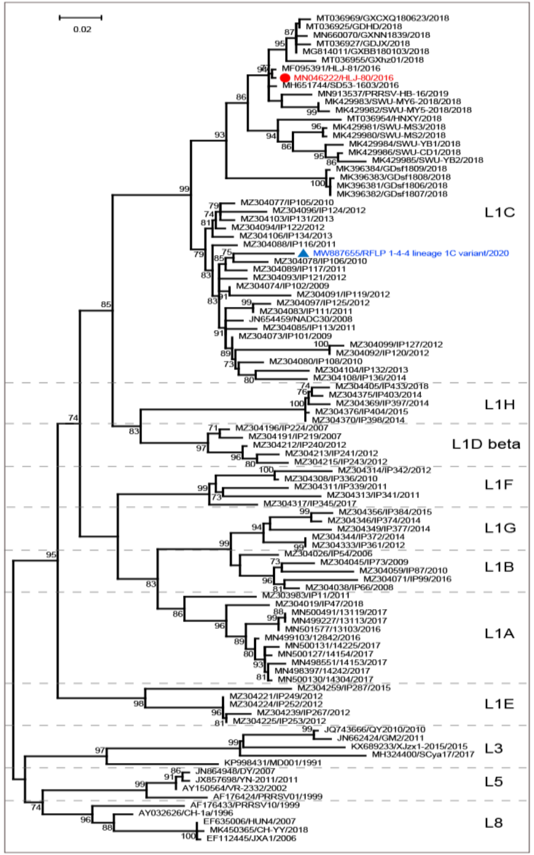
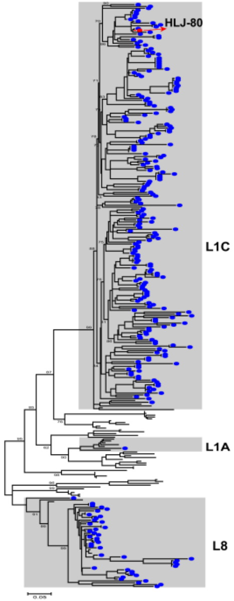
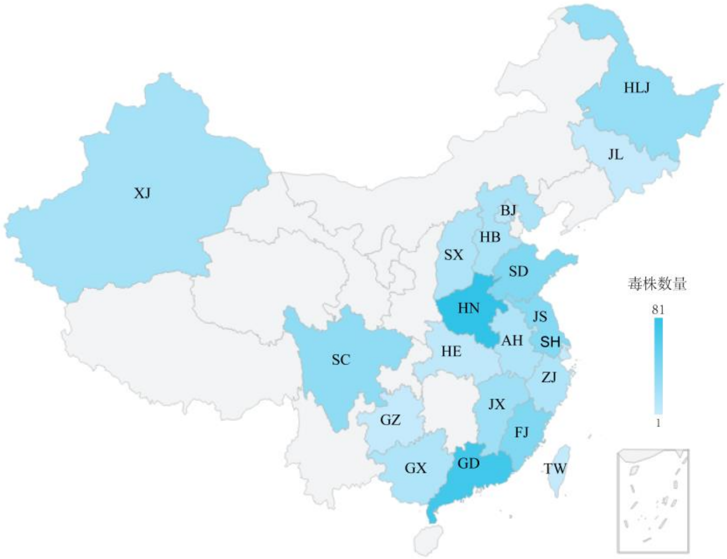


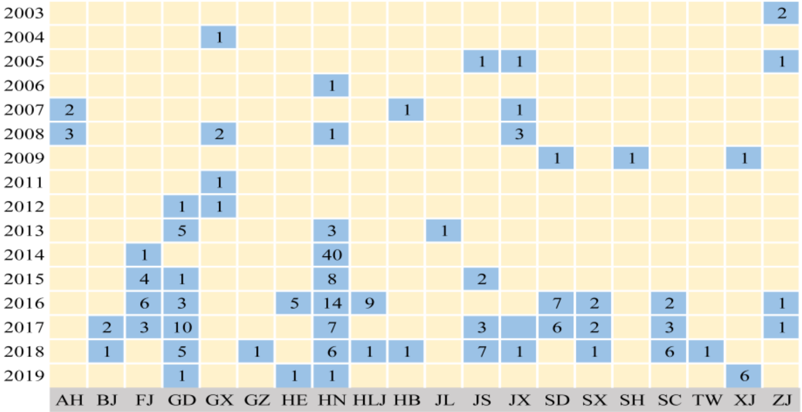
In press

Distribution of RFLP 1-4-4 PRRSVs in China

- ☐ **Geographical distribution**: the RFLP 1-4-4 PRRSV was distributed in more than 10 provinces, and mainly distributed in Henan, Guangdong and Shandong provinces, accounting for 31.15%, 10% and 5.38%, respectively.
- ☐ **Temporal distribution**: The RFLP 1-4-4 virus was dated back to 2003.





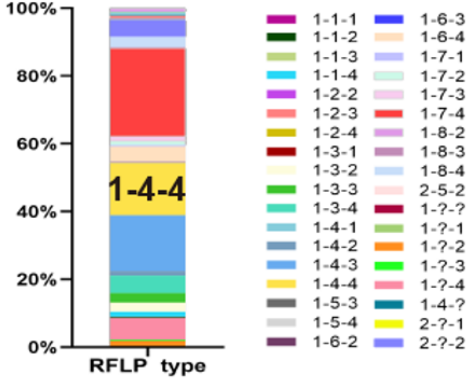


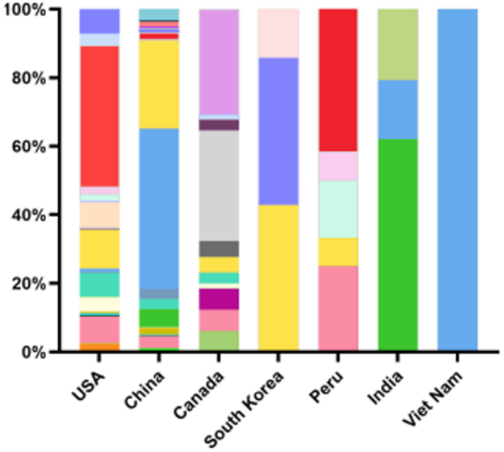
	AH	BJ	FJ	GD	GX	GZ	HE	HN	HLJ	HB	JL	JS	JX	SD	SX	SH	SC	TW	XJ	ZJ
2003																				2
2004					1															
2005												1	1							1
2006								1												
2007	2									1			1							
2008	3				2			1					3							
2009														1		1			1	
2011					1															
2012				1	1															
2013				5				3			1									
2014			1					40												
2015			4	1				8				2								
2016			6	3			5	14	9					7	2		2			1
2017		2	3	10				7				3		6	2		3			1
2018		1		5		1		6	1	1		7	1		1		6	1		
2019				1			1	1											6	

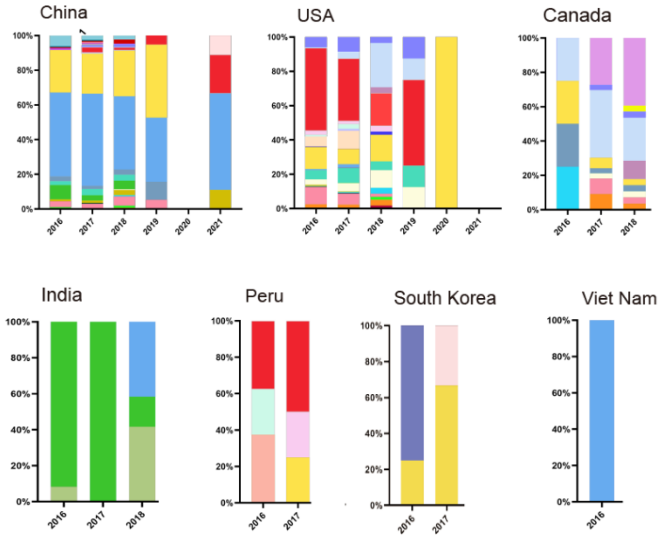
In press

RFLP Patterns of PRRSV-2 in GenBank, 2016-2021

- ☐ The PRRSV-2 ORF5 sequences in GenBank from 2016-2021, including PRRSVs from the US (n=1 167), China (n=635), Canada (n=65), India (n=29), Peru (n=12), South Korea (n=7) and Vietnam (n=3)
- ☐ RFLP classification revealed there are 36 RFLP patterns. RFLP 1-7-4, 1-4-3 and 1-4-4 are main patterns.
- ☐ The RFLP patterns of PRRSVs in the US (28 types) and China (23 types) show high diverse.







In press

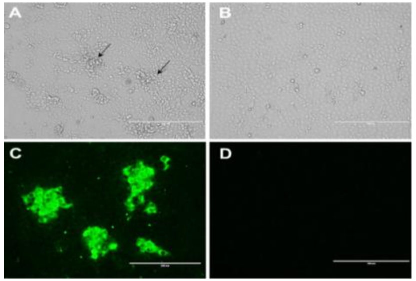
3

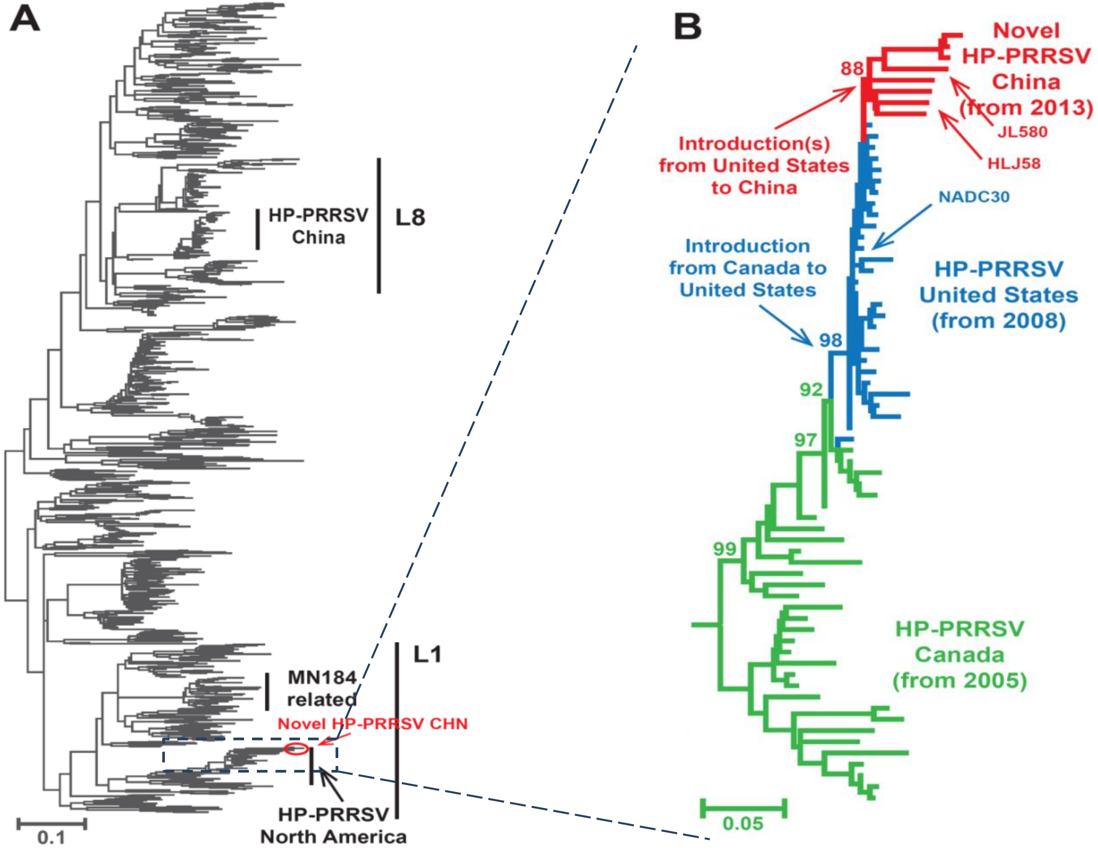
Recombination analysis of PRRSV

Importation and recombination of NADC30-like PRRSV

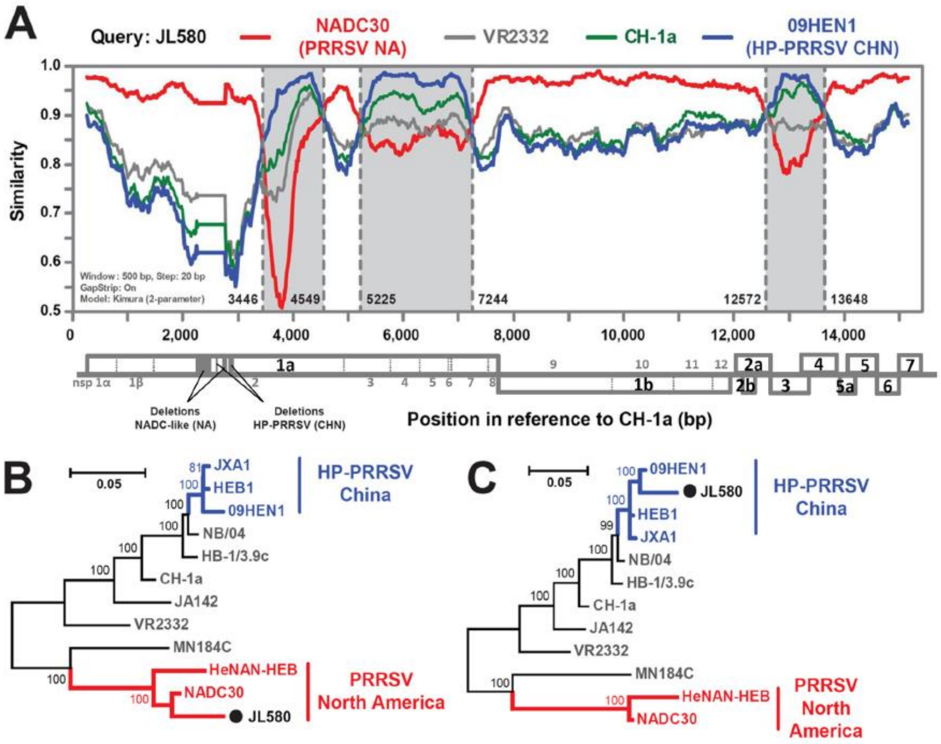
Clinical symptoms:

- high fever
- morbidity (100%)
- mortality (77%, 230/300)



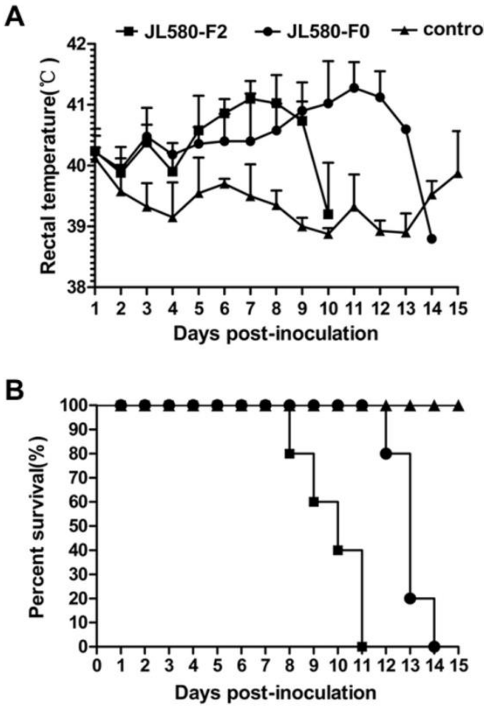


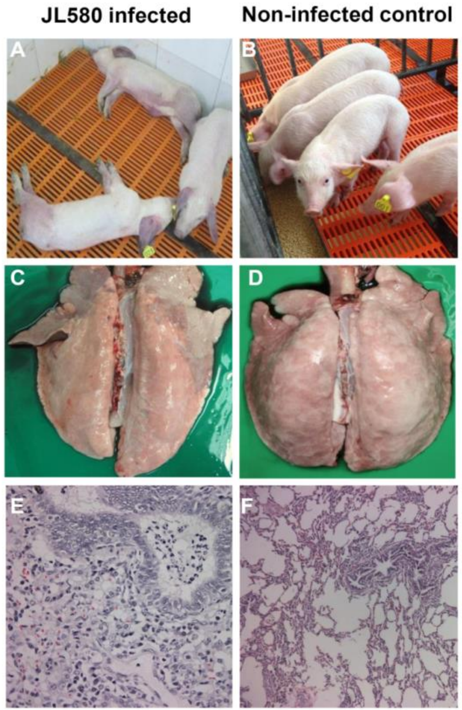
Recombination analysis of NADC30-like PRRSV JL580 strain



A. Homologous recombination analysis
B. The phylogenetic tree of non-combination regions
C. The phylogenetic tree of combination regions

Pathogenicity of NADC30-like PRRSV JL580 strain

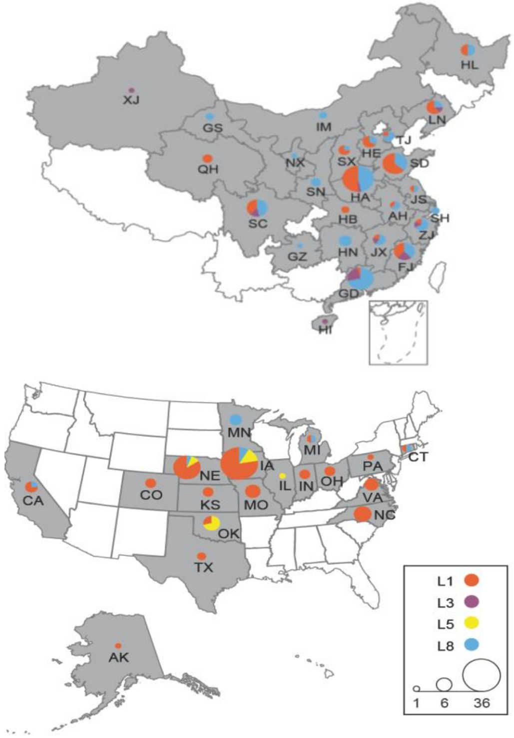




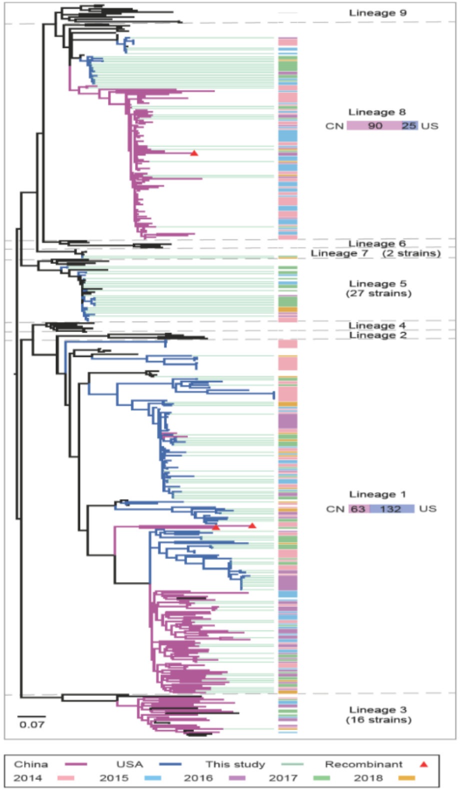
The recombinant virus has high pathogenicity and a mixed genetic background, which makes it complex to control the disease.

Zhao K, , , An TQ*, J Virol, 2015

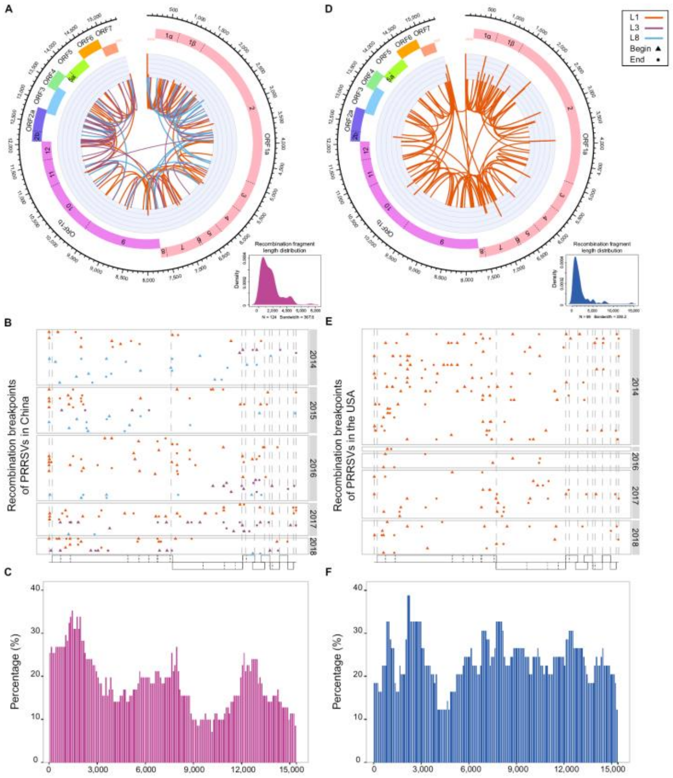
Recombination of PRRSV in China and the US in 2014–2018



NA-type PRRSVs , n=713
Sequenced in this study, n=138 (36 + 102)
From GenBank , n=575 (217 + 358)



Lineage classification



Intra-lineage recombination

Inter-lineage recombination of PRRSV in China，1991-2018

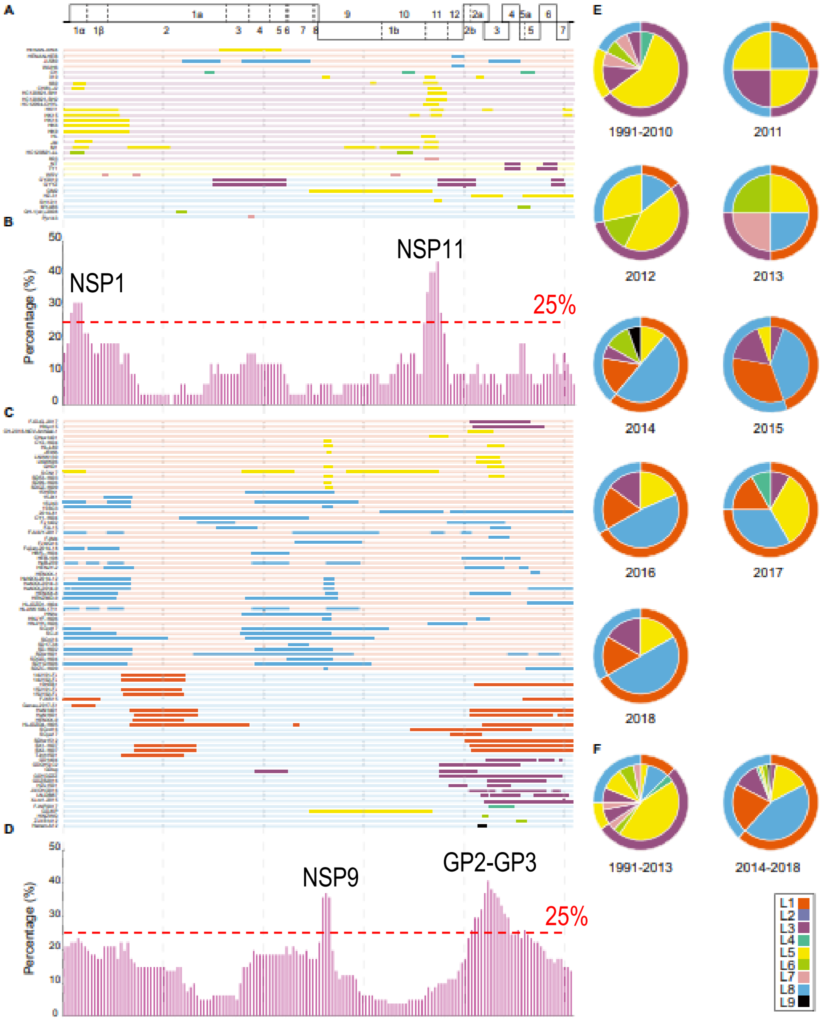
Recombination hot spots:

NSP1 and NSP11 coding regions from 1991-2013.

NSP9,GP2-GP3 coding regions from 2014-2018.

Recombination patterns:

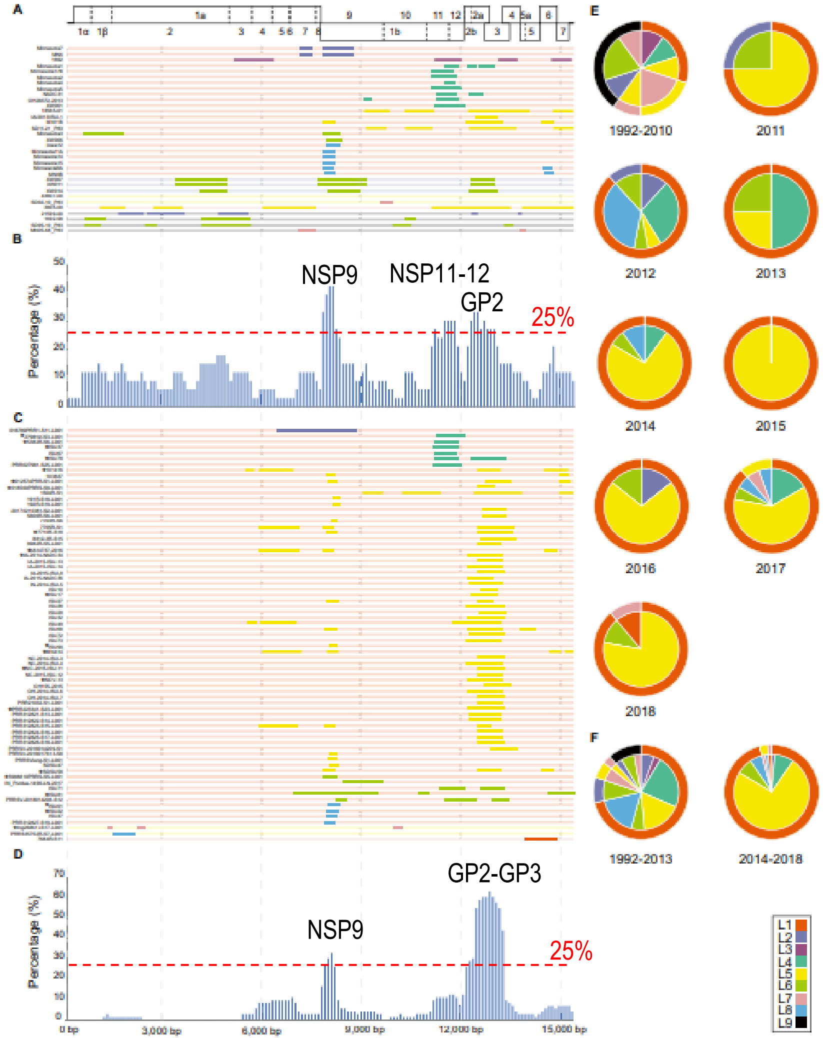
During 2014 –2018, the major inter-lineage recombination patterns observed were L1 and L8 PRRSVs.



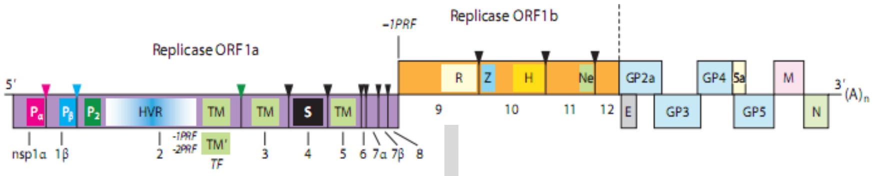
Yu F, , , An TQ*, J Virol, 2020

Inter-lineage recombination of PRRSV in the US，1992-2018

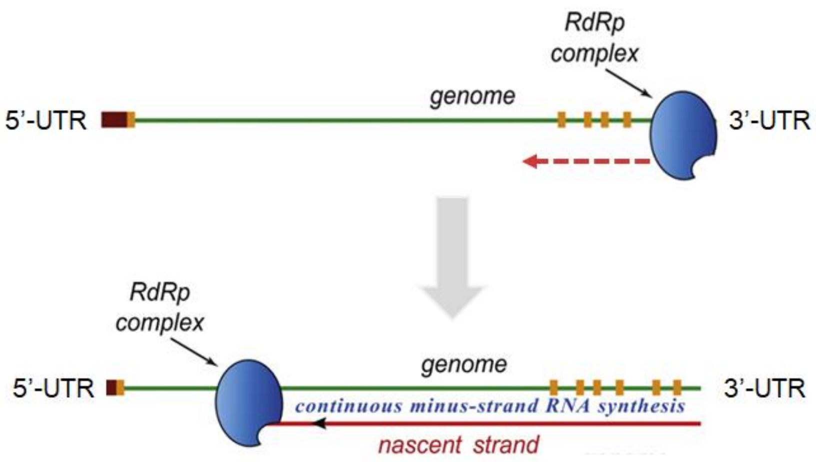
- Recombination hot spots: NSP9,GP2 and GP3 coding regions from 2014-2018.
- Recombinants evolved from a complex pattern of L1+L4, L1+L5, and L1+L8 during 1991–2013, into a singular pattern dominated by L1+L5 during 2014–2018.

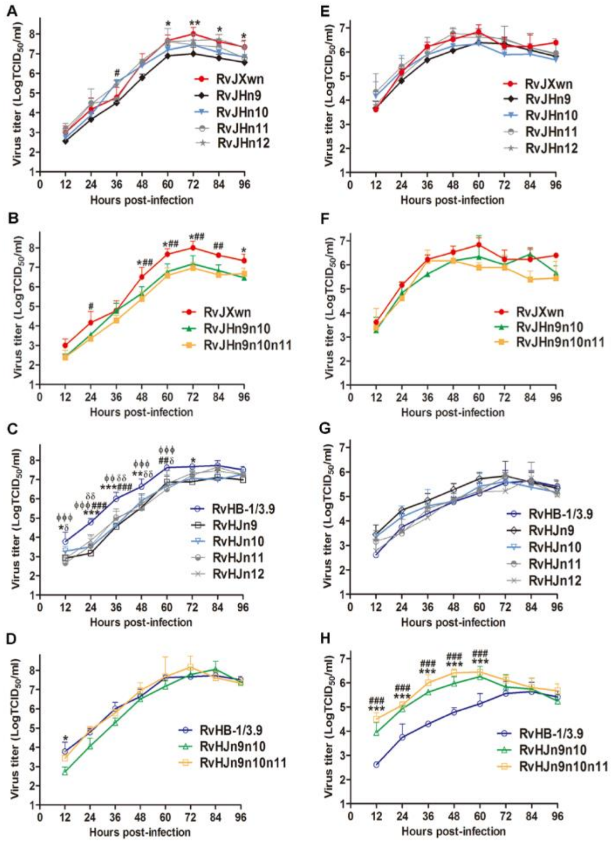


NSP9 (RdRp) contributes to the replication of PRRSV



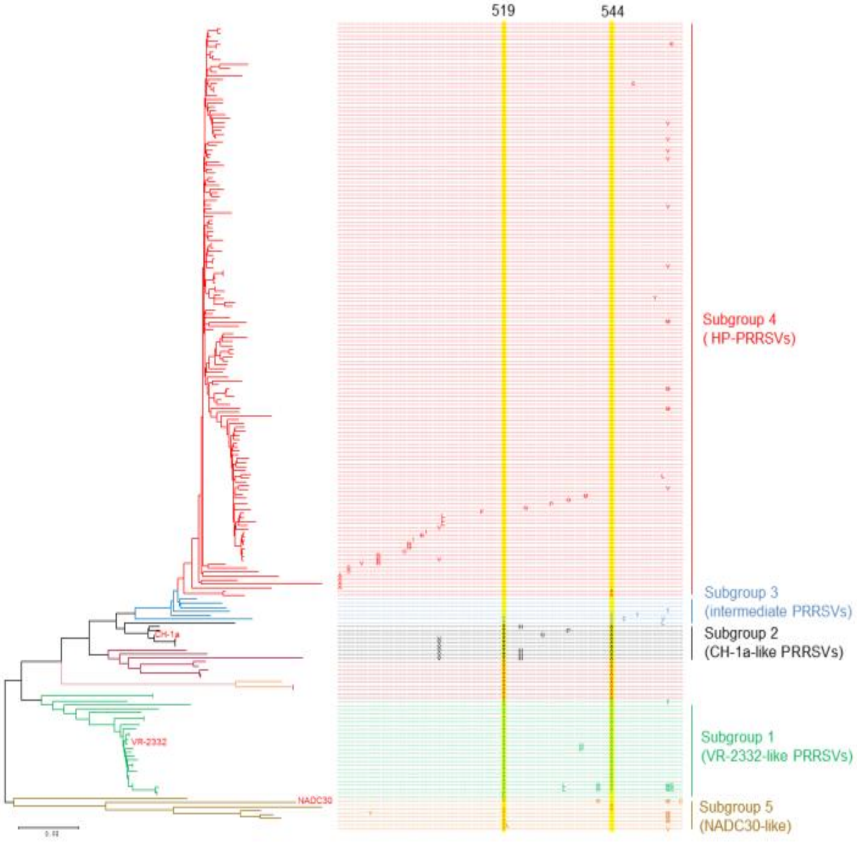
RdRp




Nsp9 and Nsp10 Contribute to HP-PRRSV Virulence

Li et al., Plos Pathogens, 2014

NSP9 (RdRp) contributes to the replication of PRRSV



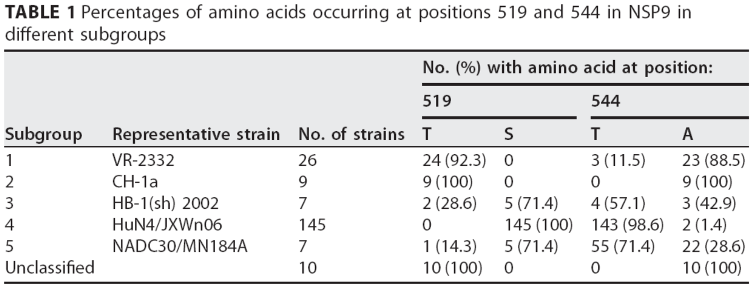
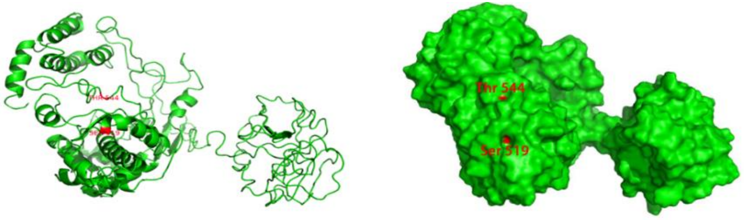
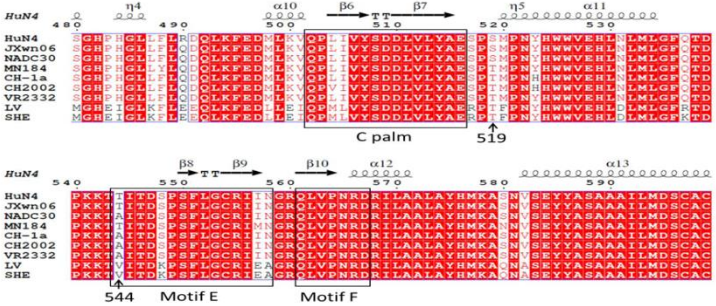


TABLE 1 Percentages of amino acids occurring at positions 519 and 544 in NSP9 in different subgroups

Subgroup	Representative strain	No. of strains	No. (%) with amino acid at position:			
			519		544	
			T	S	T	A
1	VR-2332	26	24 (92.3)	0	3 (11.5)	23 (88.5)
2	CH-1a	9	9 (100)	0	0	9 (100)
3	HB-1(sh) 2002	7	2 (28.6)	5 (71.4)	4 (57.1)	3 (42.9)
4	HuN4/JXWn06	145	0	145 (100)	143 (98.6)	2 (1.4)
5	NADC30/MN184A	7	1 (14.3)	5 (71.4)	55 (71.4)	22 (28.6)
Unclassified		10	10 (100)	0	0	10 (100)



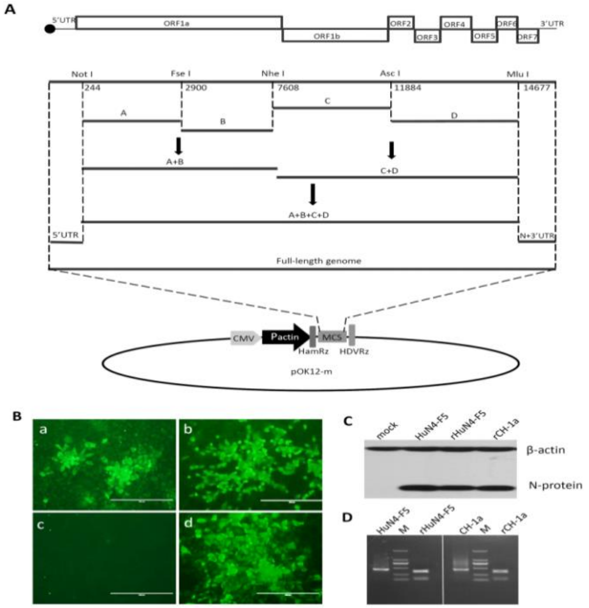


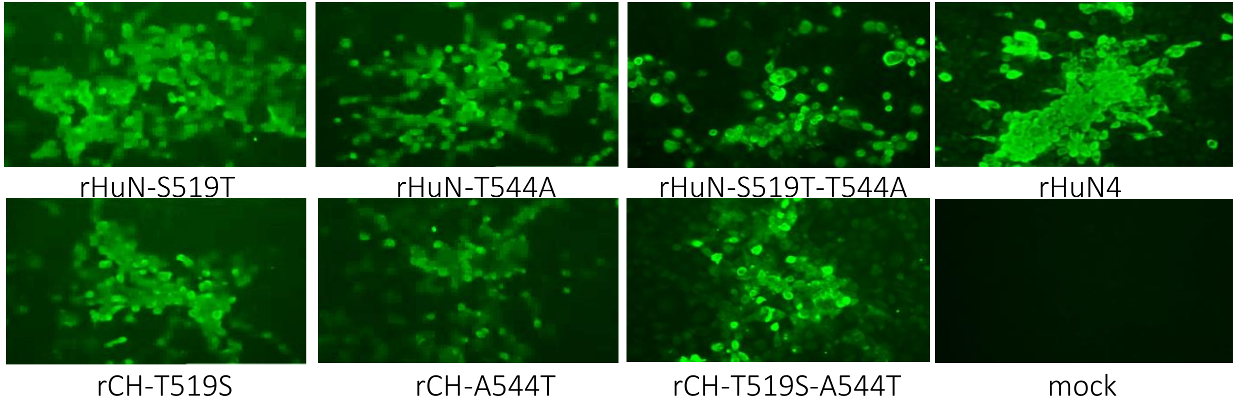
NSP9 (RdRp) contributes to the replication of PRRSV

Infectious clones:

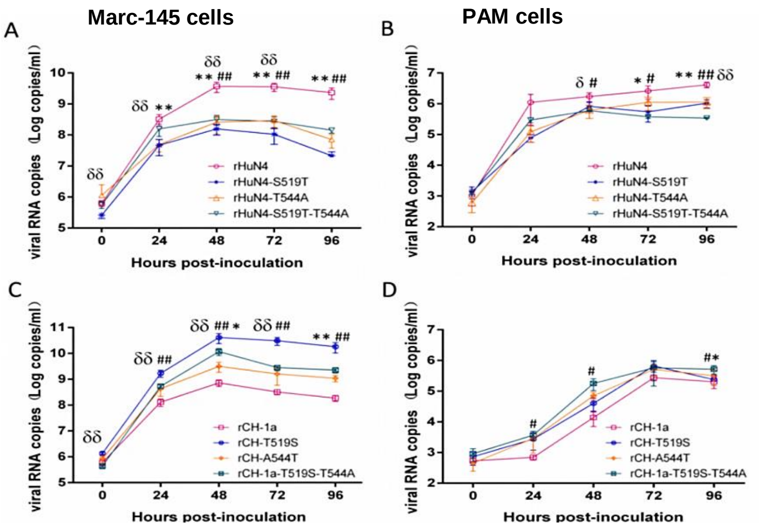
HP-PRRSV: HuN4 strain

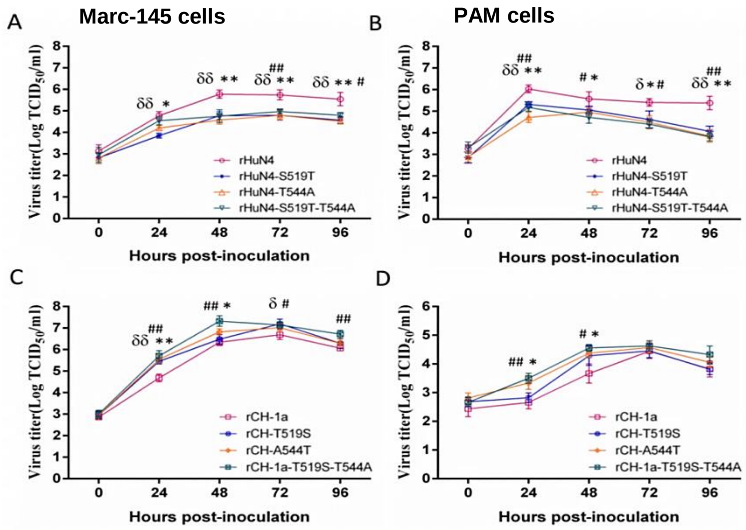
Classical PRRSV: CH-1a strain

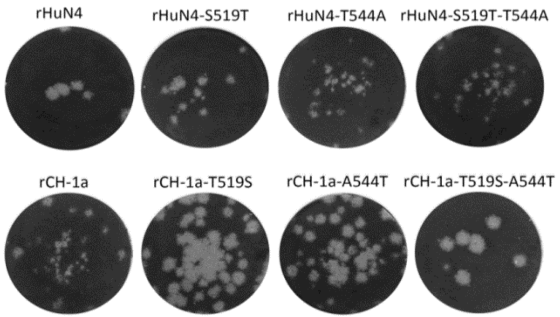


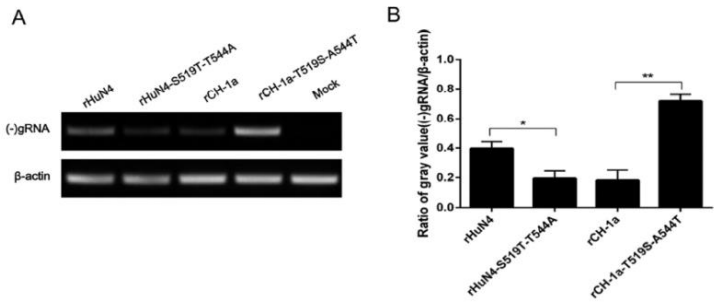


NSP9 (RdRp) contributes to the replication of PRRSV

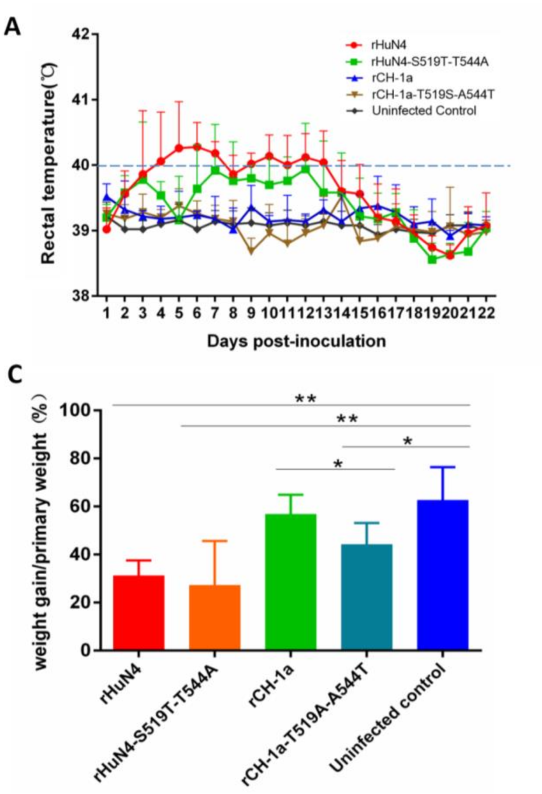


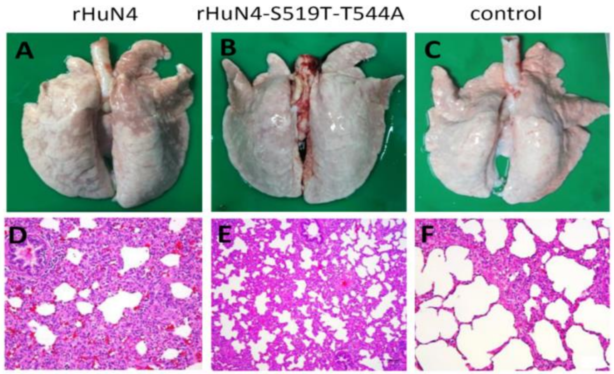


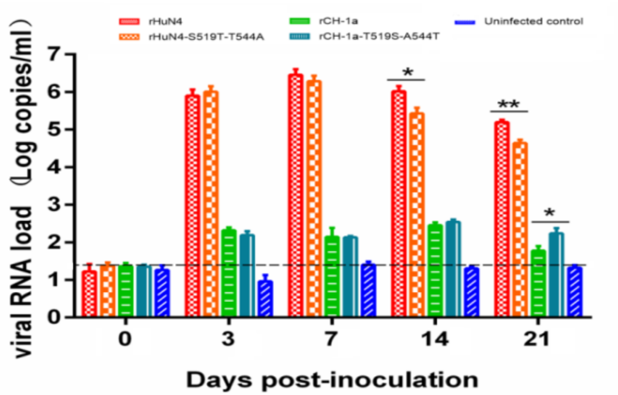




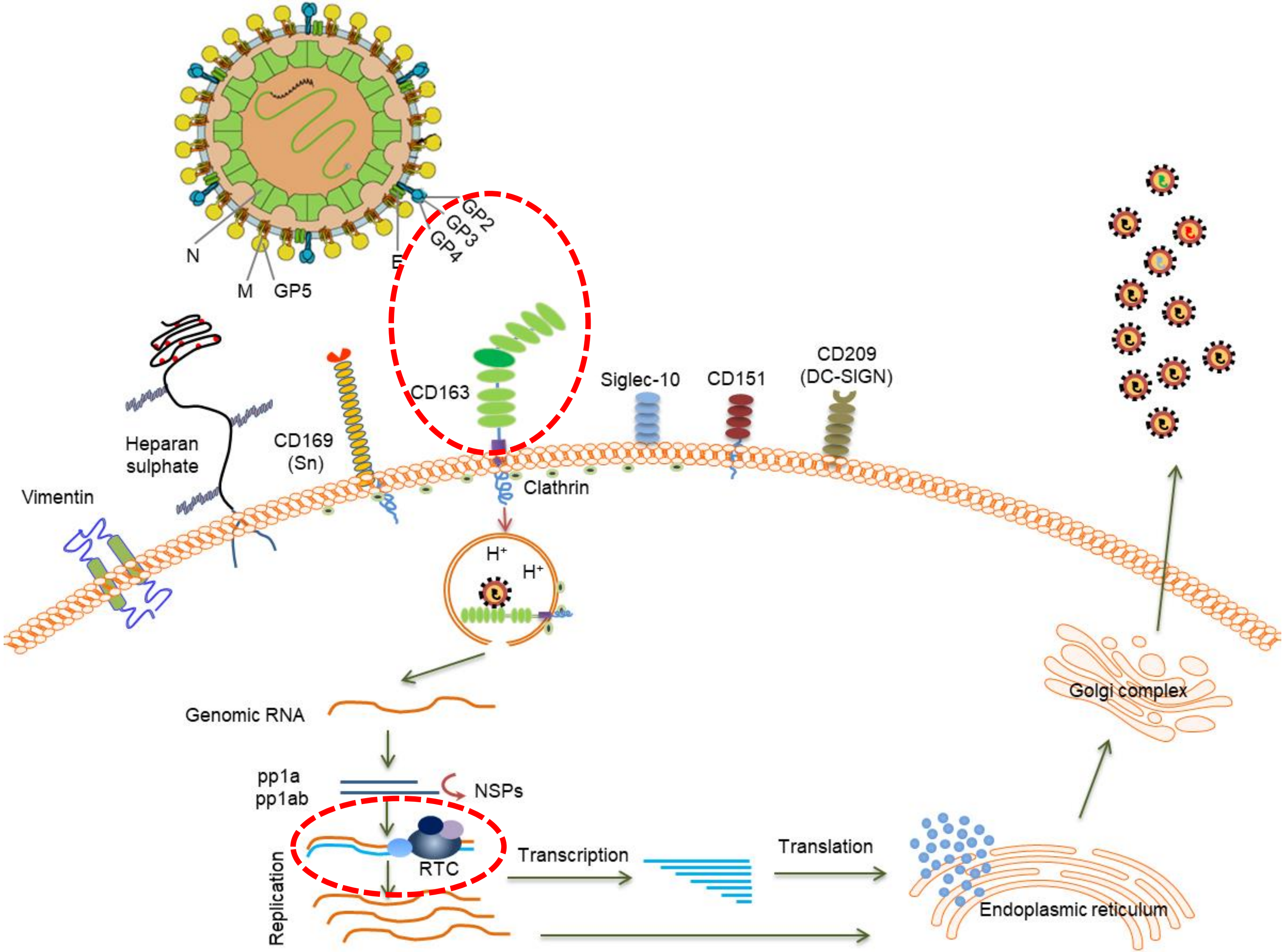
NSP9 (RdRp) contributes to the replication of PRRSV







Zhao K, , ,An TQ*, J Virol, 2018


GP2
GP3
GP4
N
M
GP5
E
Heparan sulphate
Vimentin
CD169 (Sn)
CD163
Clathrin
Siglec-10
CD151
CD209 (DC-SIGN)
H+
H+
Genomic RNA
pp1a
pp1ab
NSPs
RTC
Replication
Transcription
Translation
Endoplasmic reticulum
Golgi complex

Take Home Message

1. Intra-lineage recombination is responsible for the emergence of RFLP 1-4-4 lineage 1C variants in the US.

2. RFLP 1-4-4 L1C PRRSVs are dominant in China and the US.

3. Recombination is frequent in PRRSV. Recombination hotspots were located in the NSP9 and in the GP2-GP3 region.

Acknowledgements

Harbin Veterinary Research Institute

Xing-Yang Cui

Xiao-Xiao Tian

Dr. Kuan Zhao

Dr. Fang Yu

Dr. Xue-Hui Cai

China Animal CDC

Dr. Zhi Zhou

Sun Yat-sen University

Dr. Mang Shi

Iowa State University

Dr. Giovani Trevisan

Dr. Jianqiang Zhang

Dr. Ganwu Li

University of Minnesota

Dr. Kimberly VanderWaal

Thank you for your attention!