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8TH ANNUAL MEETING OF THE PPR GLOBAL RESEARCH AND EXPERTISE NETWORK (PPR-GREN)

25 – 27 NOVEMBER 2025 QINGDAO, CHINA



中华人民共和国农业农村部

Ministry of Agriculture and Rural Affairs of the People's Republic of China



中国动物卫生与流行病学中心
China Animal Health and Epidemiology Center

A GF-TADS initiative for
PPR control



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GF-TADS
GLOBAL FRAMEWORK FOR THE
PROGRESSIVE CONTROL OF
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Genomic characterization and evolution analysis of peste des petits ruminants virus in China from 2007 to 2024: challenge on PPR eradication in the region

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Outline

1. Distribution of PPR outbreaks in China from 2007 to 2024
2. Genome sequencing of PPRV in China from 2007 to 2024
3. Evolutionary dynamics of PPRV in China from 2007 to 2024
4. Subgroup divergence of PPRV in China from 2013 to 2024
5. Identification of anchor mutations in PPRV genomes collected in China from 2013 to 2024
6. Challenge on PPR eradication in the region



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1. Distribution of PPR outbreaks in China from 2007 to 2024

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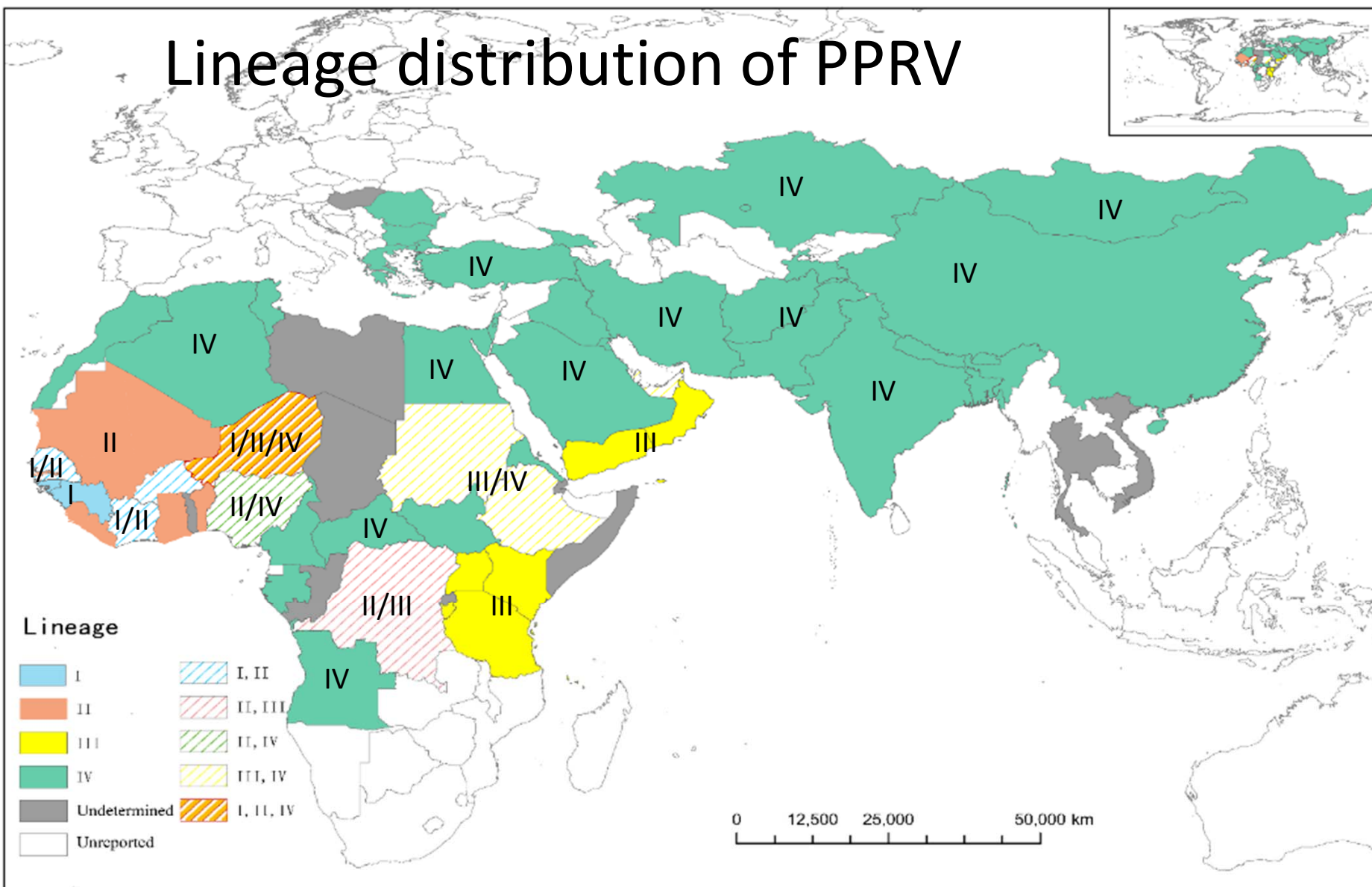
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Lineage distribution of PPRV





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2. Genome sequencing of PPRV in China from 2007 to 2024

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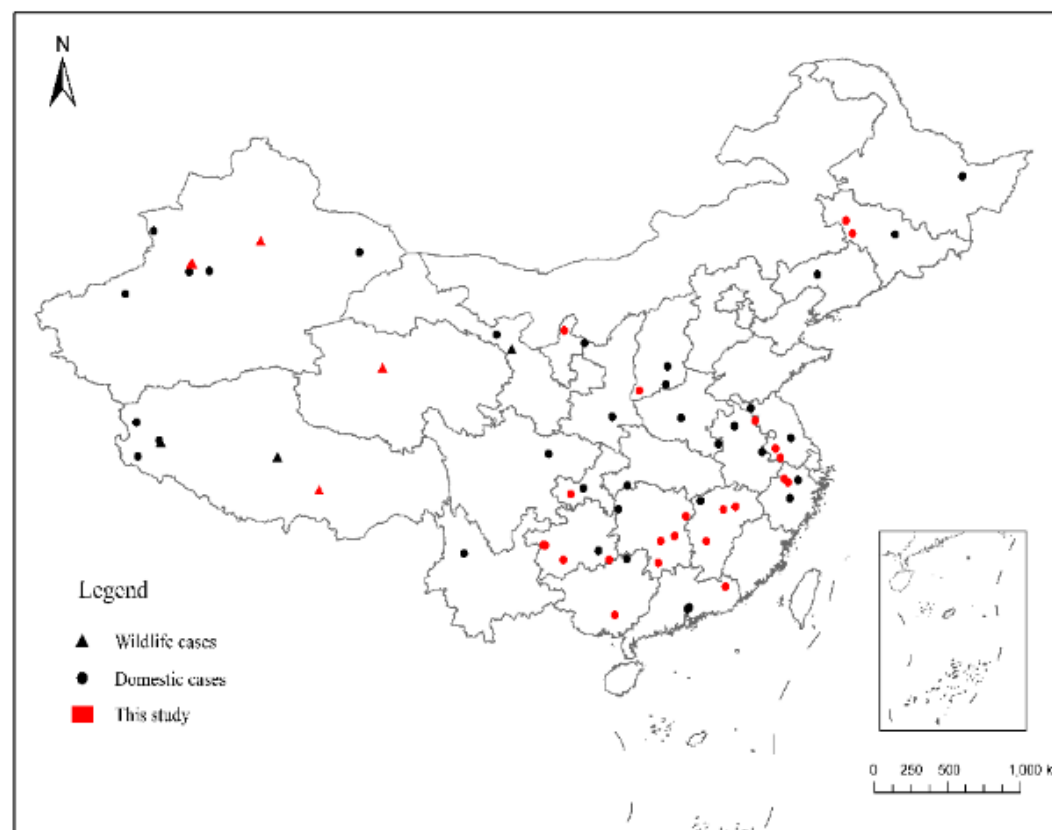


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Genome sequencing of PPRV in China during 2007-2024

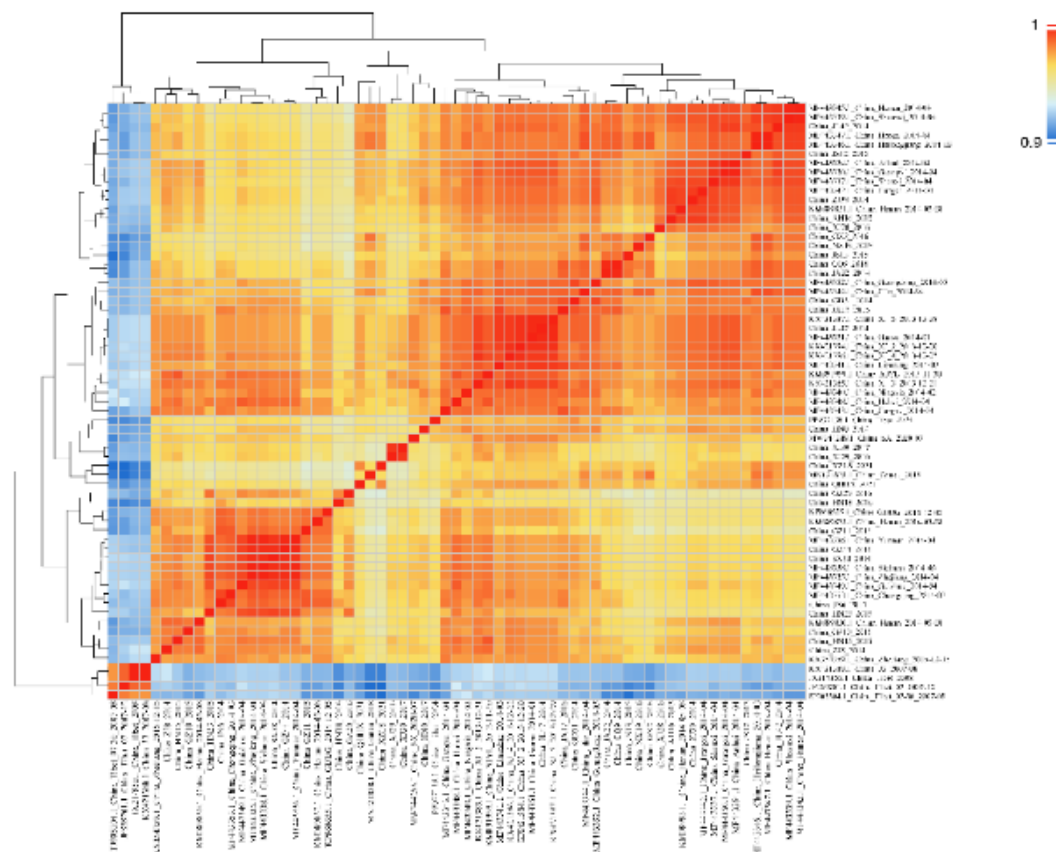
- PPRV positive tissue samples were used for genome sequencing
- Amplification-based Sanger sequencing was used
- 58 genome sequences were determined in CAHEC for PPRV in China during 2007-2024
- 7 PPRV genome sequences published by other laboratories were also included
- A total of 65 PPRV genomes obtained from 65 PPRV outbreaks in 23 provinces in China during 2007 to 2024





The genomic similarity of PPRV in China during 2007-2024

- PPRV 2007-2008 vs PPRV 2013-2024: 96.5–97.3%
- PPRV 2007-2008: 15, 948 nt, 99.8 to 100% similarity
- PPRV 2013-2024: 15, 954 nt, 98.5 to 100% similarity





A curated PPRV genome sequences dataset

Sequences from other countries

142 PPRV genome
sequences

Vaccine strains were not included

36 sequences with low quality trimmed

106 high quality PPRV
genome sequences

8 sequences with signatures of recombination excluded

98 curated high quality
PPRV genome sequences

Sequences from China

65 PPRV genome
sequences

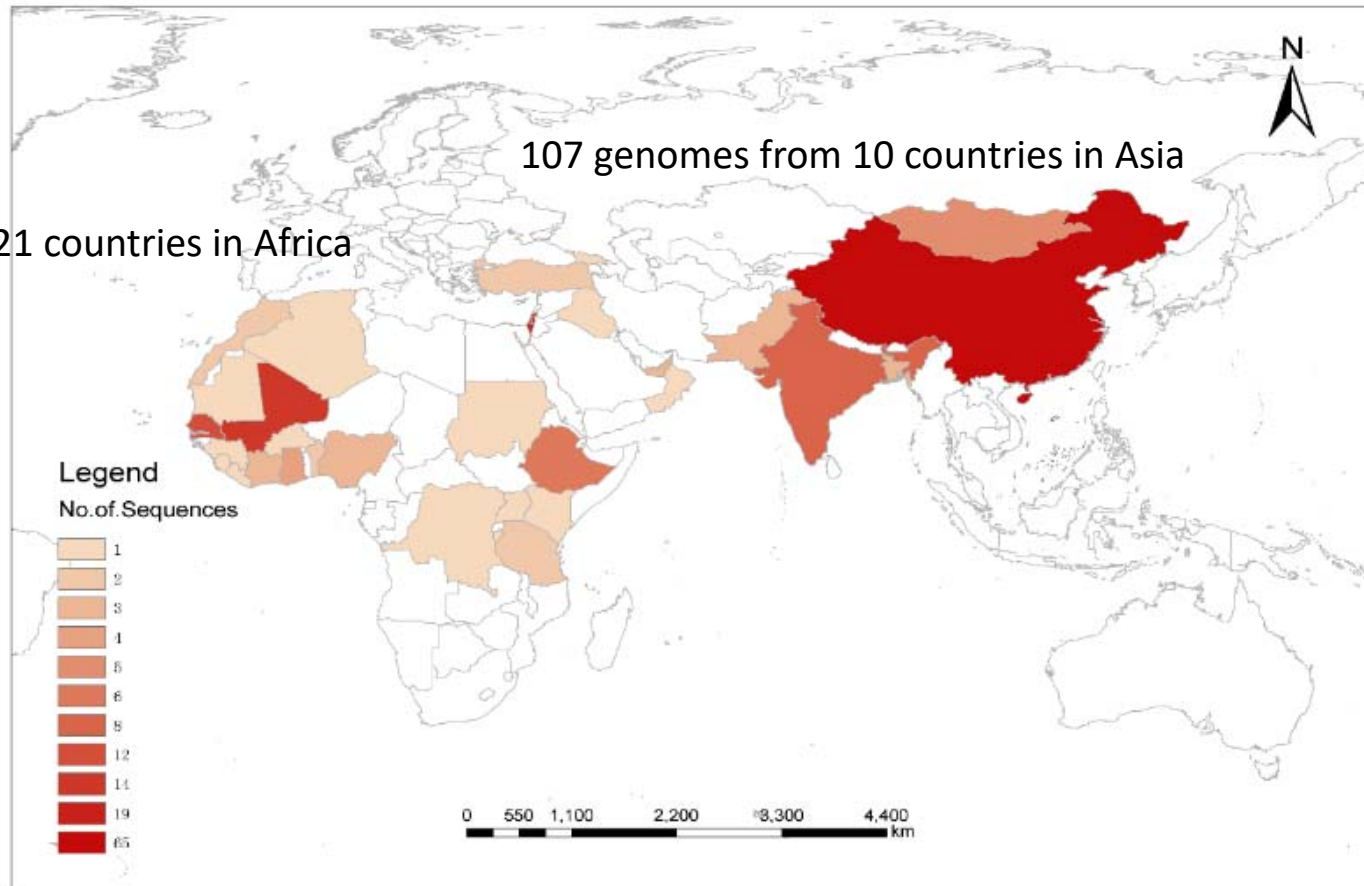
163 curated high quality PPRV genome sequences



Geographical distribution of PPRV genomes

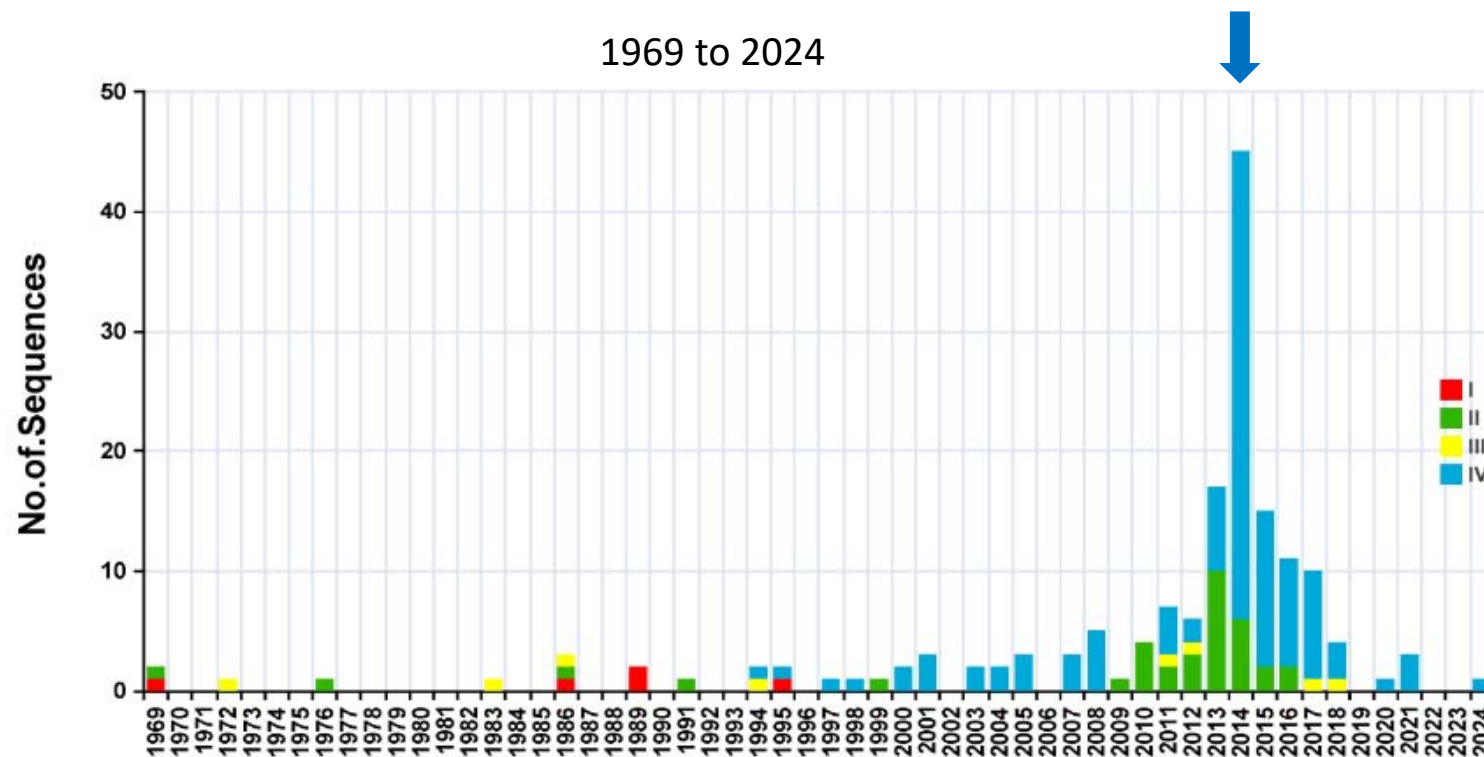
56 genomes from 21 countries in Africa

107 genomes from 10 countries in Asia



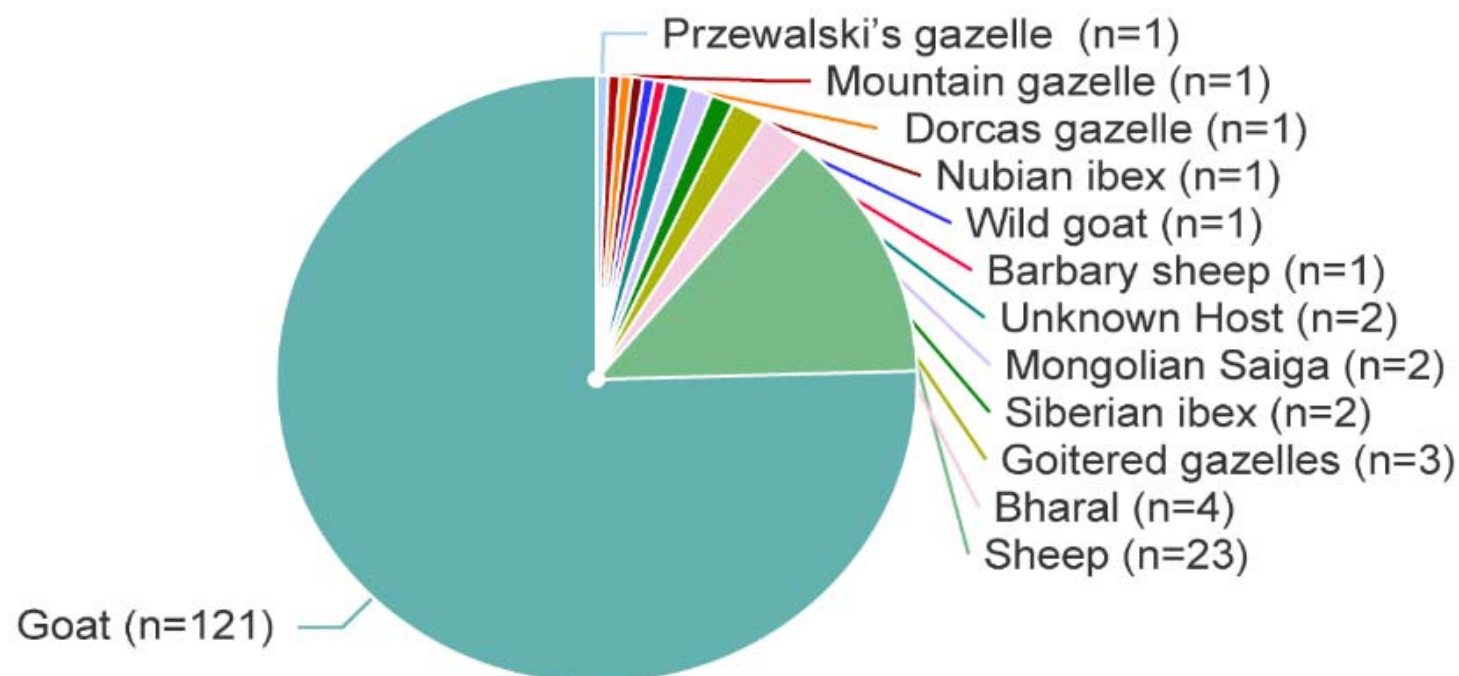


Temporal distribution of PPRV genomes



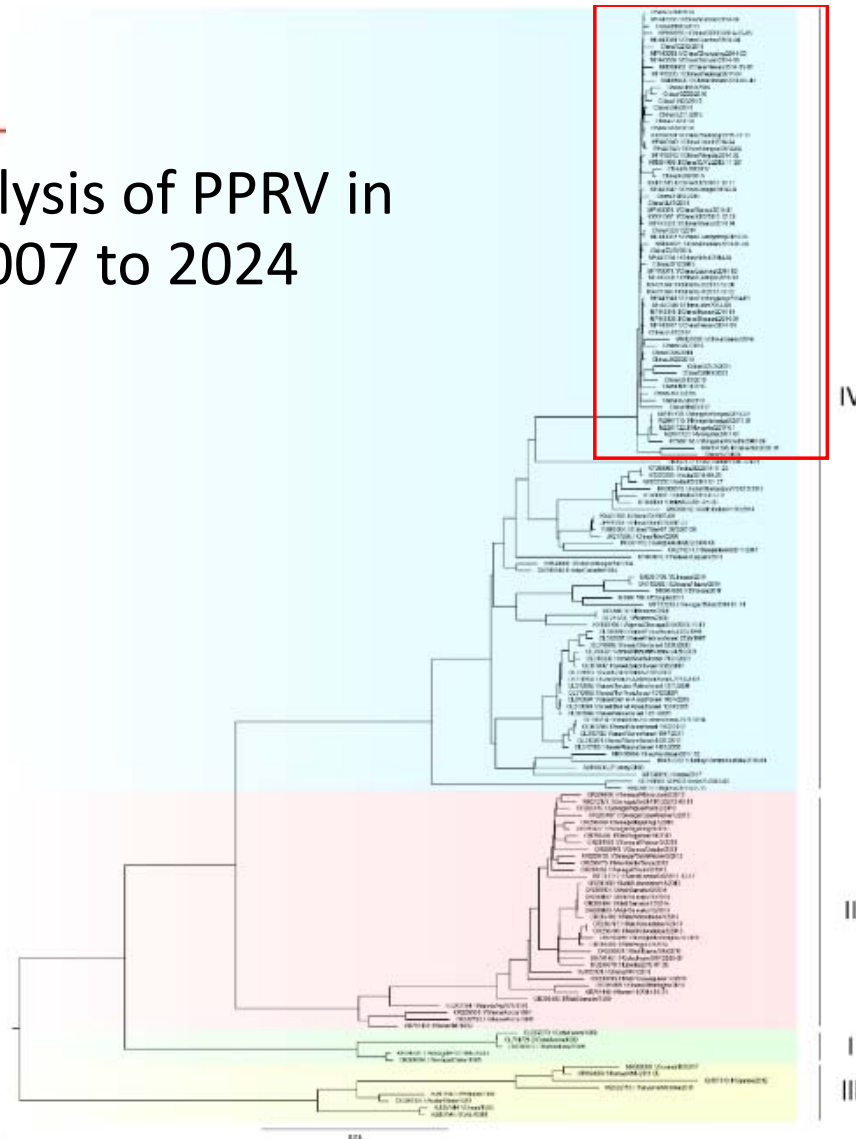


Host distribution of PPRV genomes





Phylogenetic analysis of PPRV in China from 2007 to 2024



IV

115 Lineage IV sequences

II

35 Lineage II sequences

I

5 Lineage I sequences

III

8 Lineage III sequences



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3. Evolutionary dynamics of PPRV in China from 2007 to 2024

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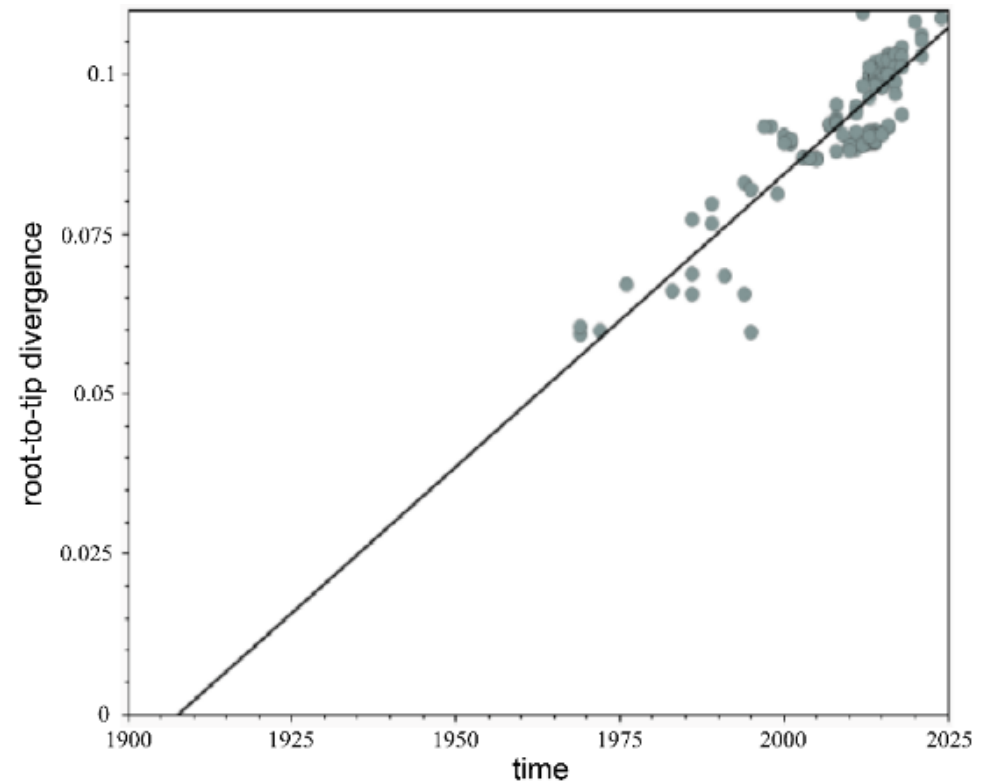
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Temporal signal of PPRV genomes

- Root-to-tip regression analysis
- Strong association between genetic distance and sampling date





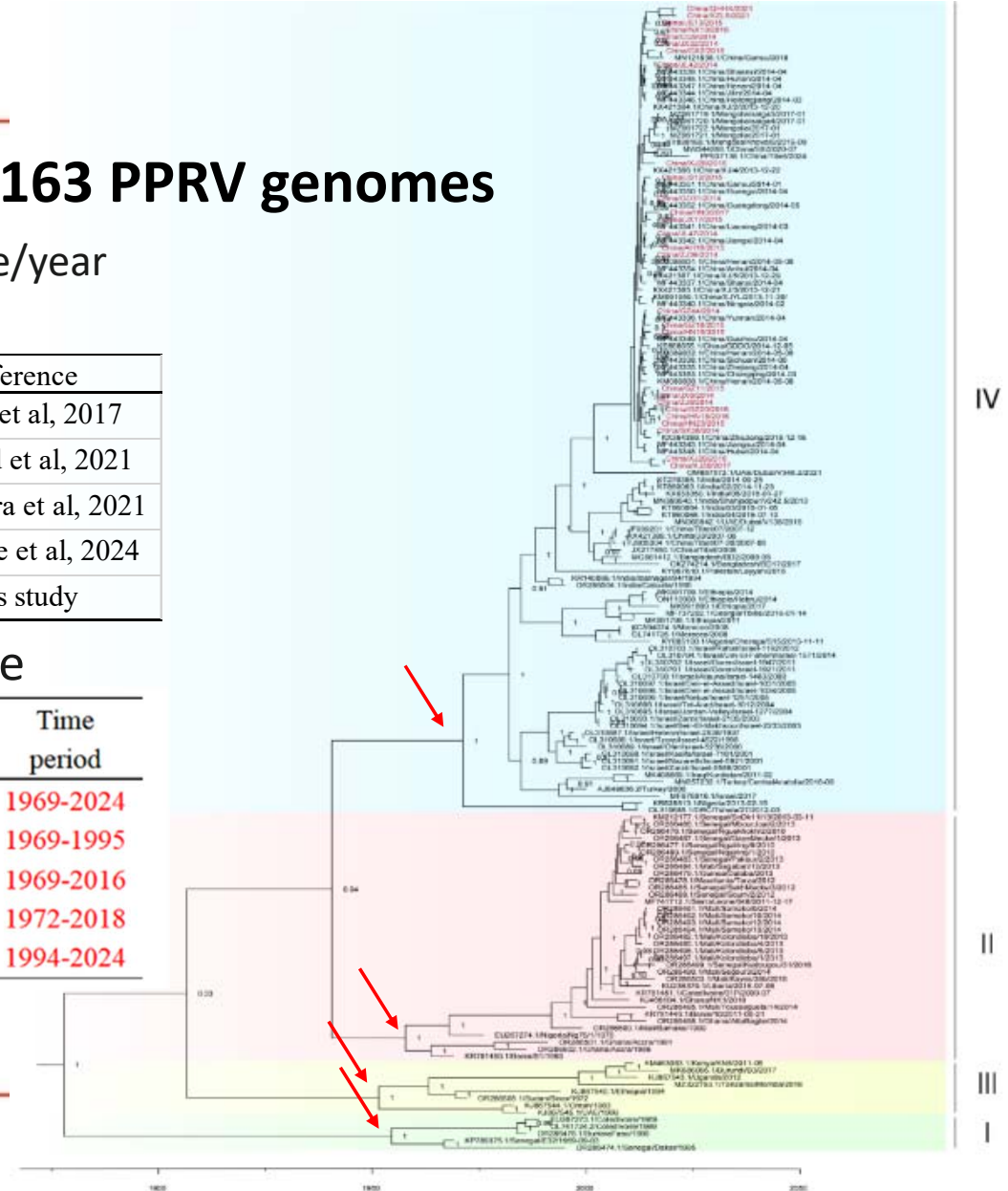
Time resolved Phylogenetic analysis of 163 PPRV genomes

The evolutionary rate was 6.70×10^{-4} nt substitutions/site/year equivalent to previous estimates

Data set	Time Period	Mean Evolutionary rate	95% HPD Interval	Reference
39	1969-2015	9.22×10^{-4}	6.21×10^{-4} - 1.26×10^{-3}	Clarke et al, 2017
81	1969-2018	9.22×10^{-4}	6.78×10^{-4} - 1.17×10^{-3}	Benfield et al, 2021
103	1969-2018	8.098×10^{-4}	5.867×10^{-4} - 9.056×10^{-4}	Mahapatra et al, 2021
136	1969-2021	6.04×10^{-4}	4.68×10^{-4} - 7.53×10^{-4}	Courcelle et al, 2024
163	1969-2024	6.70×10^{-4}	5.63×10^{-4} - 7.87×10^{-4}	This study

Lineage IV is the most recently diverged lineage

Set description	TMRCA	95% HPD Interval	Number of sequences	Time period
root	October 1877	June 1813-November 1927	163	1969-2024
Lineage I	May 1954	April 1922-April 1966	5	1969-1995
Lineage II	September 1957	August 1944-June 1965	35	1969-2016
Lineage III	June 1951	June 1930-October 1965	8	1972-2018
Lineage IV	February 1971	January 1956-June 1982	115	1994-2024

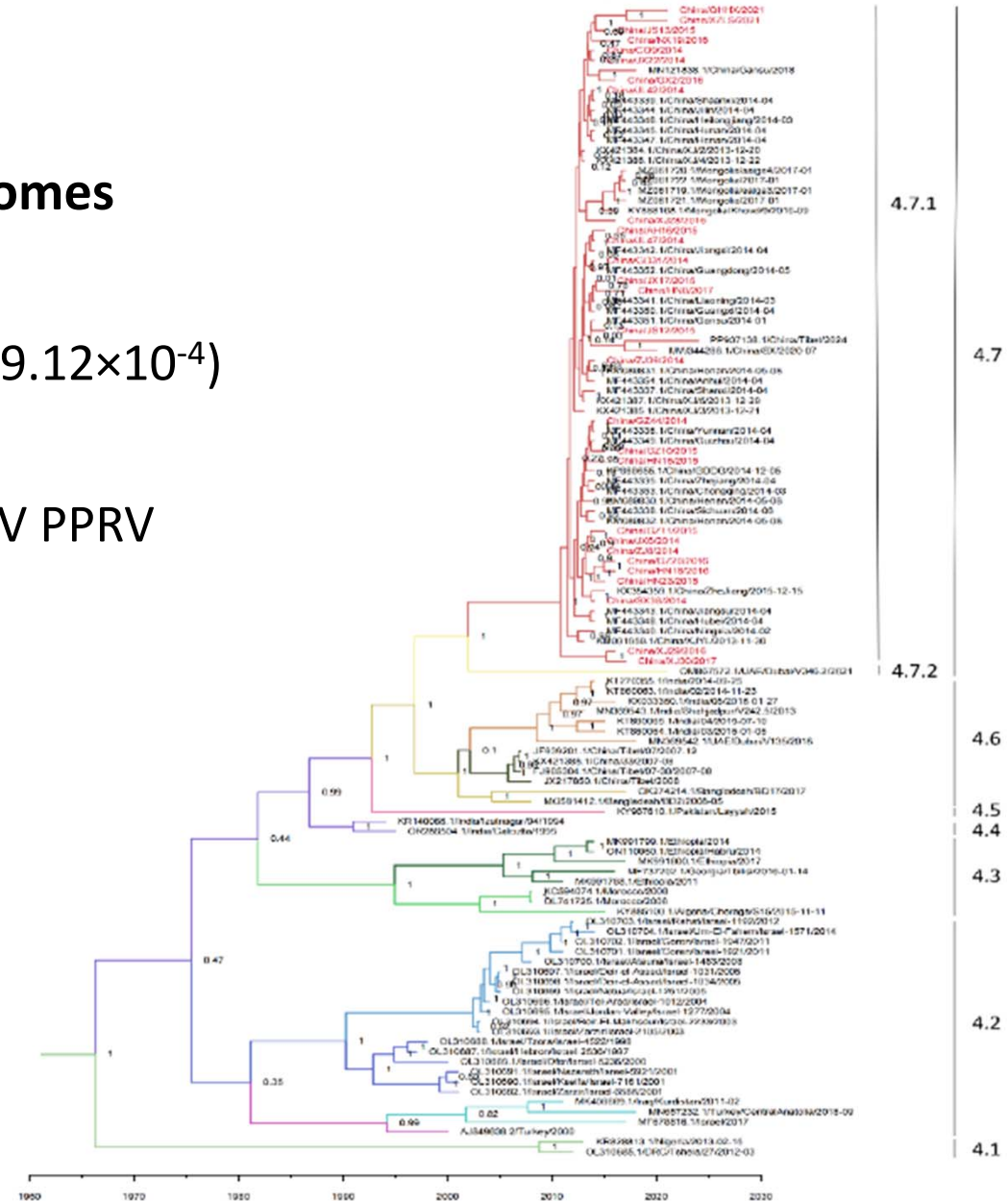




Phylogenetic analysis of 115 PPRV LIV genomes

- Mean evolutionary rate 7.54×10^{-4} nt substitutions/site/year ([95% HPD], 5.98×10^{-4} ; 9.12×10^{-4})
- PPRV LIV strains clustered into 7 clades
- The TMRCA of the different clades of lineage IV PPRV ranged from April 1982 to April 2008

Set description	TMRCA	95% HPD Interval	Number of sequences	Time period
Lineage IV	December 1966	March 1937-May 1984	115	1994-2024
Clade 4.1	April 2008	May 2023-April 2001	2	2012-2013
Clade 4.2	April 1982	January 1972-February 1990	22	1997-2018
Clade 4.3	December 1993	February 1982-February 2002	8	2008-2017
Clade 4.4	June 1990	March 1993- May 1986	2	1994-1995
Clade 4.5	/	/	1	2015
Clade 4.6	April 2001	April 1997-May 2004	13	2007-2018
Clade 4.7	June 2002	June 1996 - March 2008	67	2013-2024





Phylogeographic analysis

- PPRV LIV strains clustered into 7 clades showing spatial correlation
- PPRV strains from 2007 to 2008 in Tibet, China were grouped into clade 4.6, sharing a single origin
- PPRV strains from 2013 to 2024 in China were grouped into clade 4.7, sharing a single origin
- The country of origin for clade 4.7 was inferred UAE with high support





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4. Subgroup divergence of PPRV in China from 2013 to 2024

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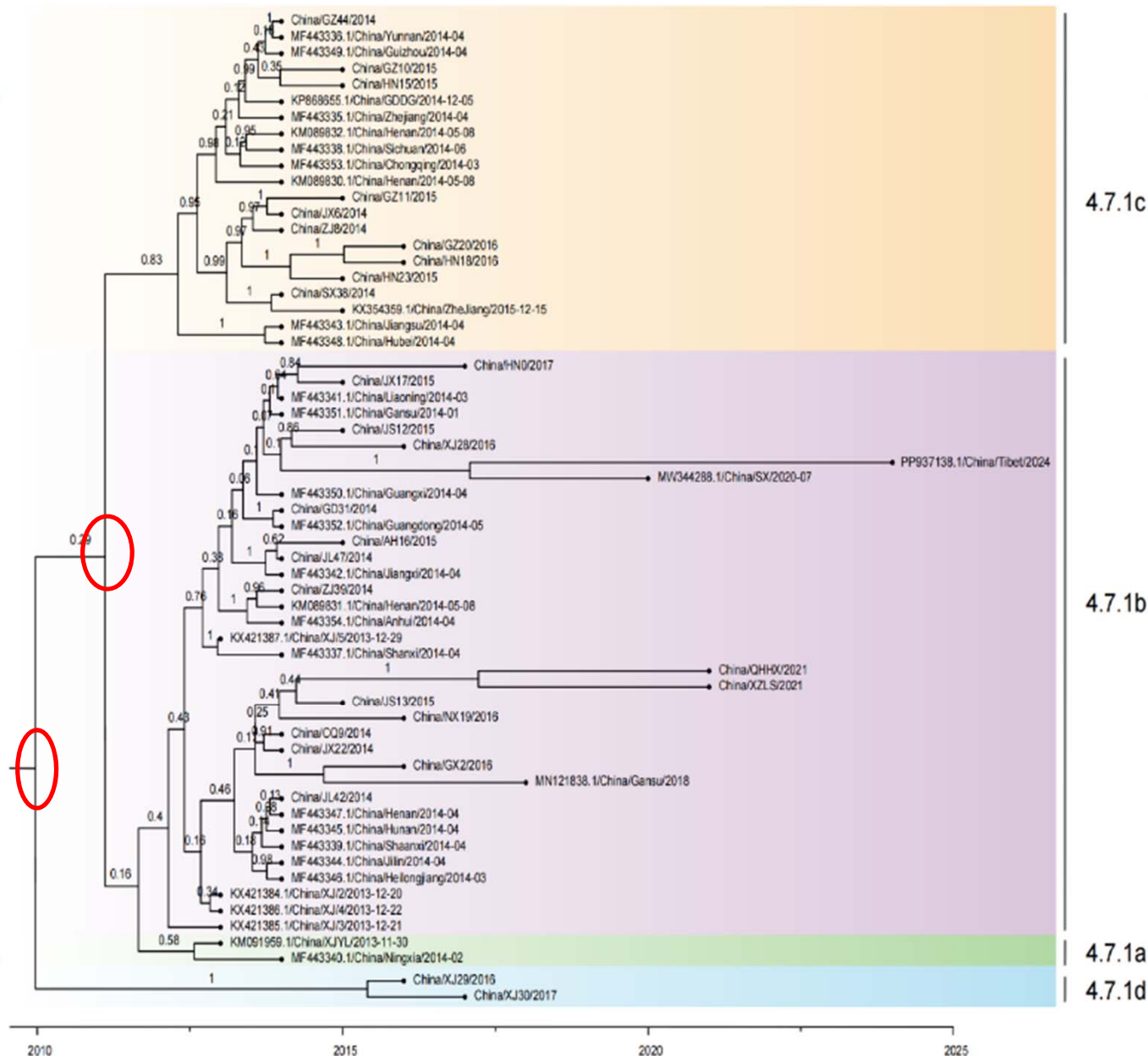
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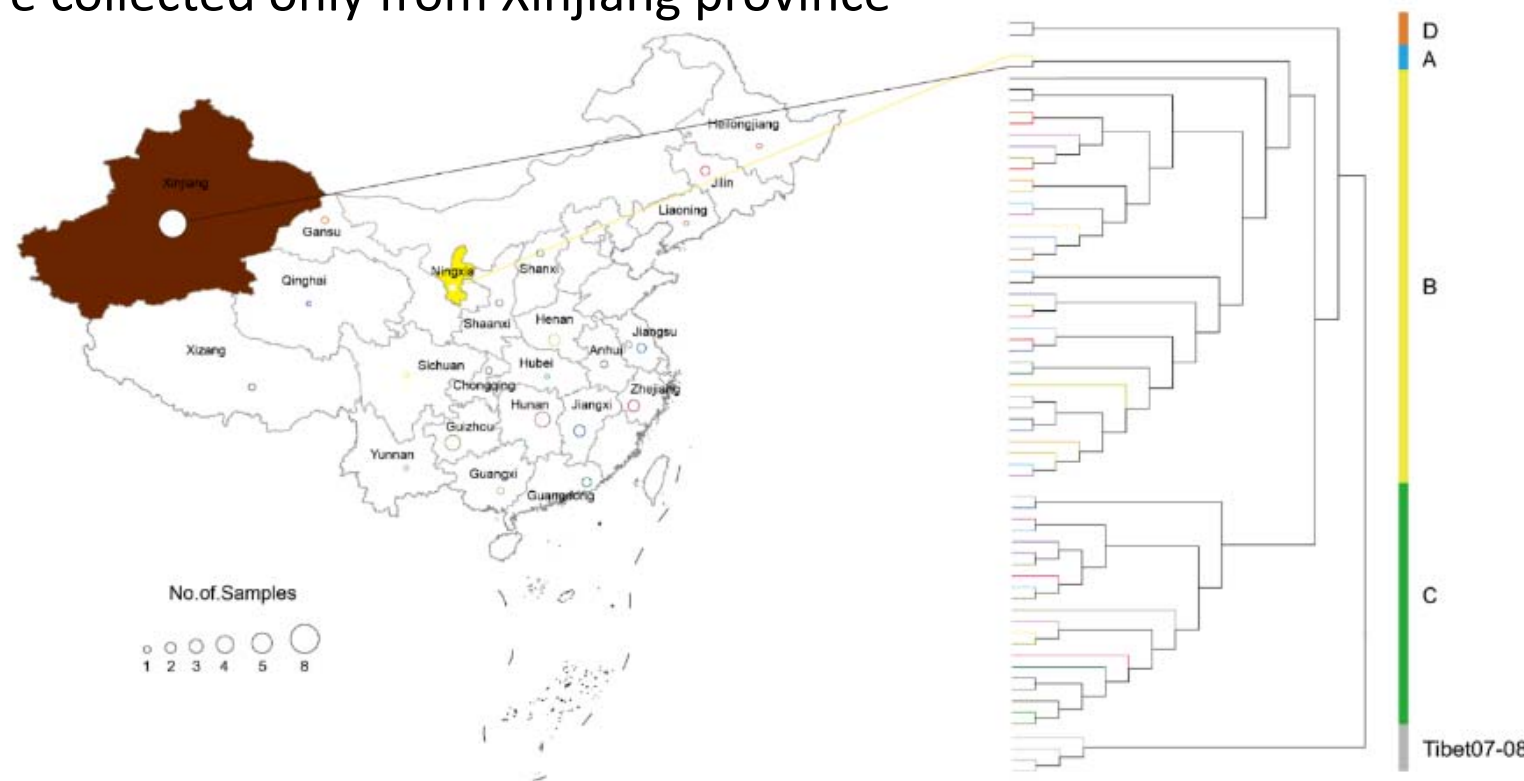
- PPRV in China from 2013 to 2024 were divided into 4 distinct clusters
- Cluster 4.7.1a, 4.7.1b, and 4.7.1c shared a single origin
- Cluster 4.7.1d formed a monophyletic cluster
- Cluster 4.7.1d diverged 13 months earlier than the common ancestor of clusters 4.7.1a, 4.7.1b, and 4.7.1c





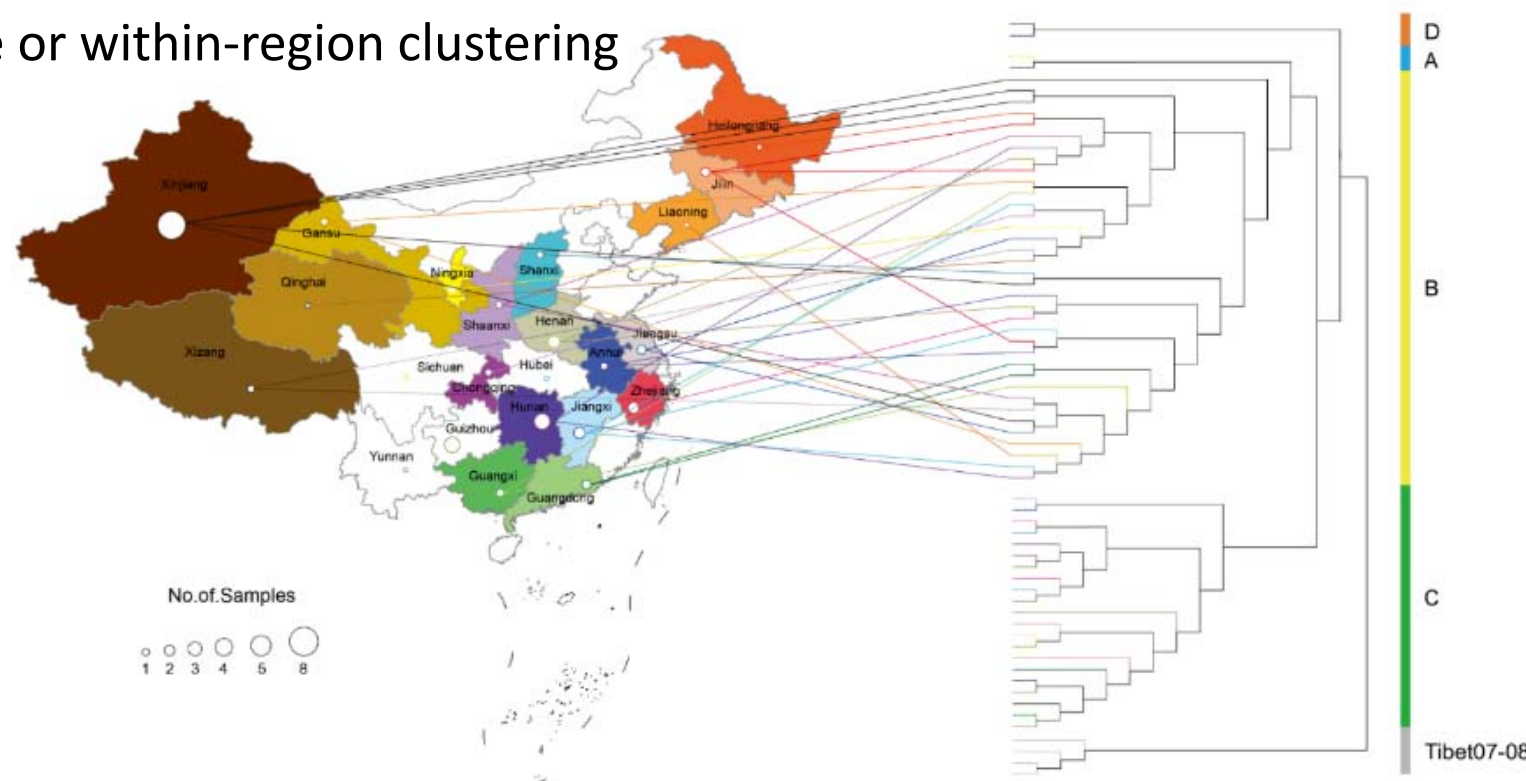
Geographical distribution

- Clusters 4.7.1a strains were collected only from Xinjiang province



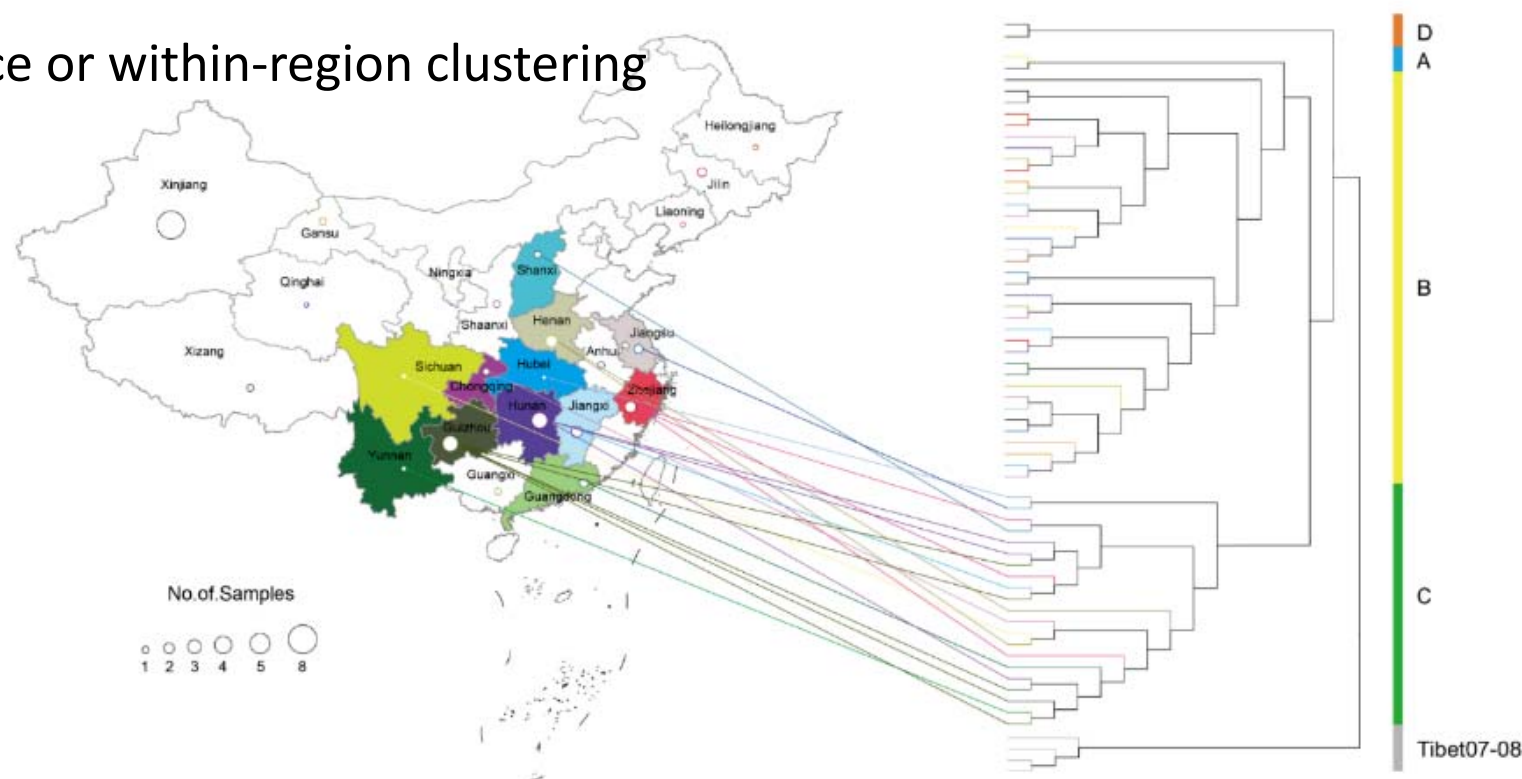


- Cluster 4.7.1b strains were widely distributed across 19 provinces, covering all 7 geographic regions in China
- No sign of within-province or within-region clustering



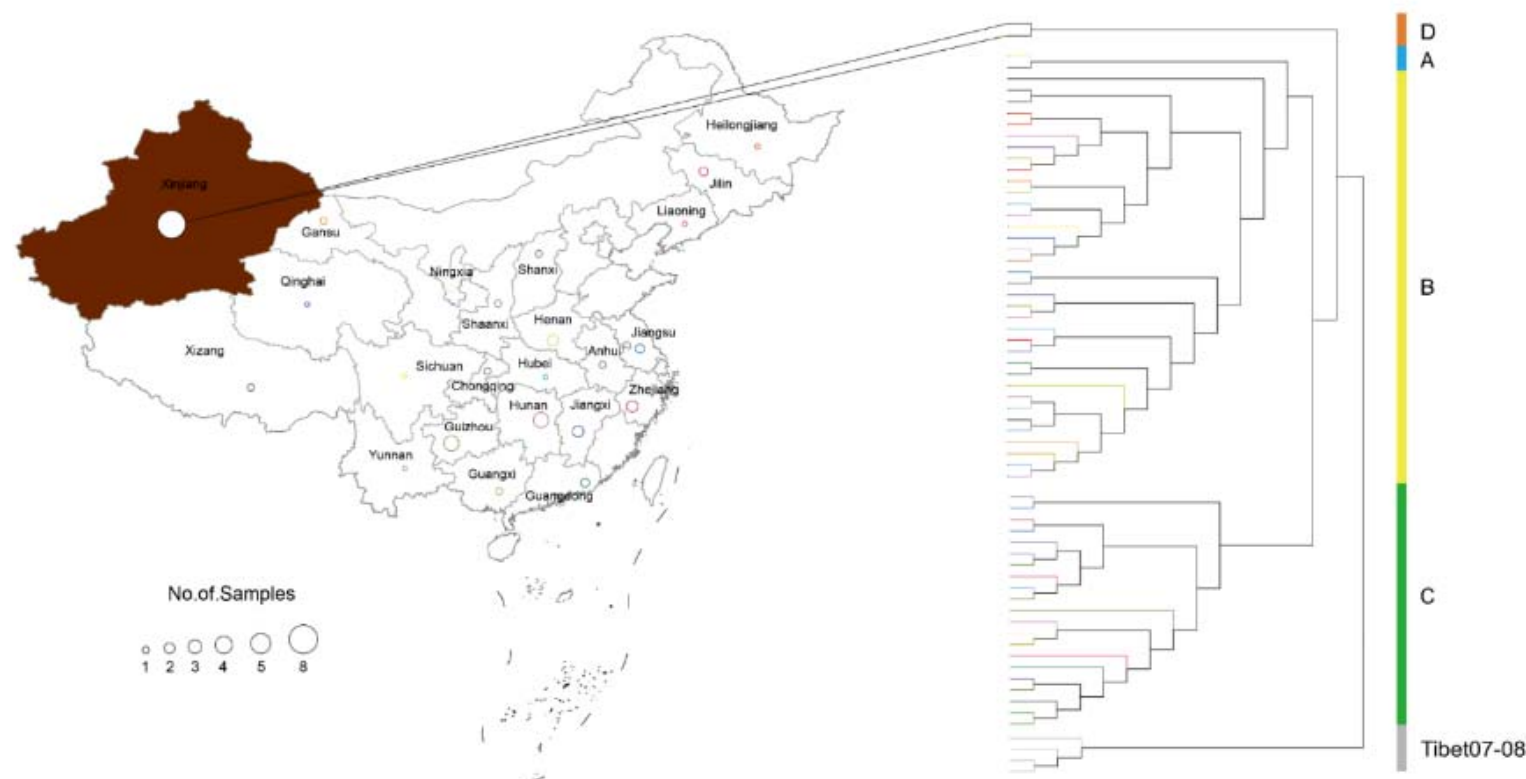


- Cluster 4.7.1c strains were collected from 12 provinces across 5 geographic regions
- No sample from Northeast China or Northwest China
- No sign of within-province or within-region clustering



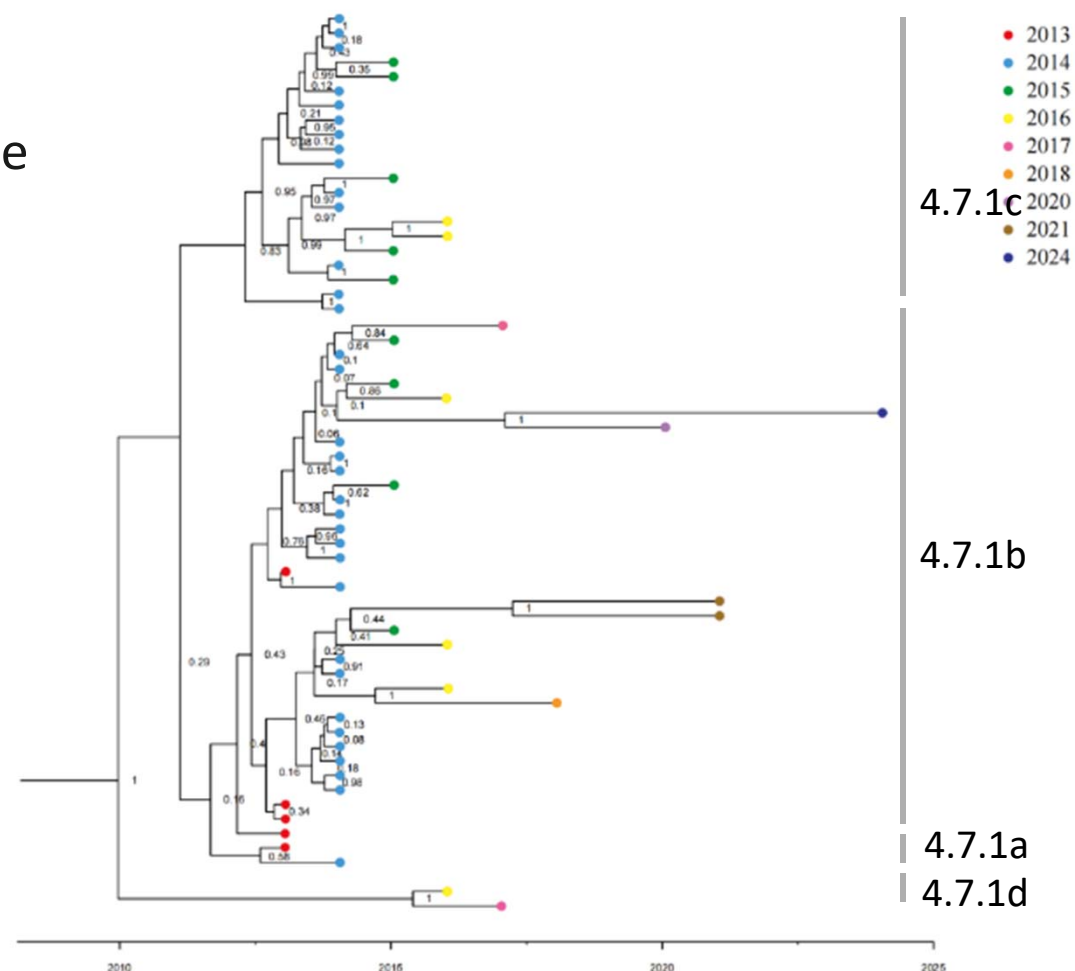


- Clusters 4.7.1d strains were collected only from Xinjiang province





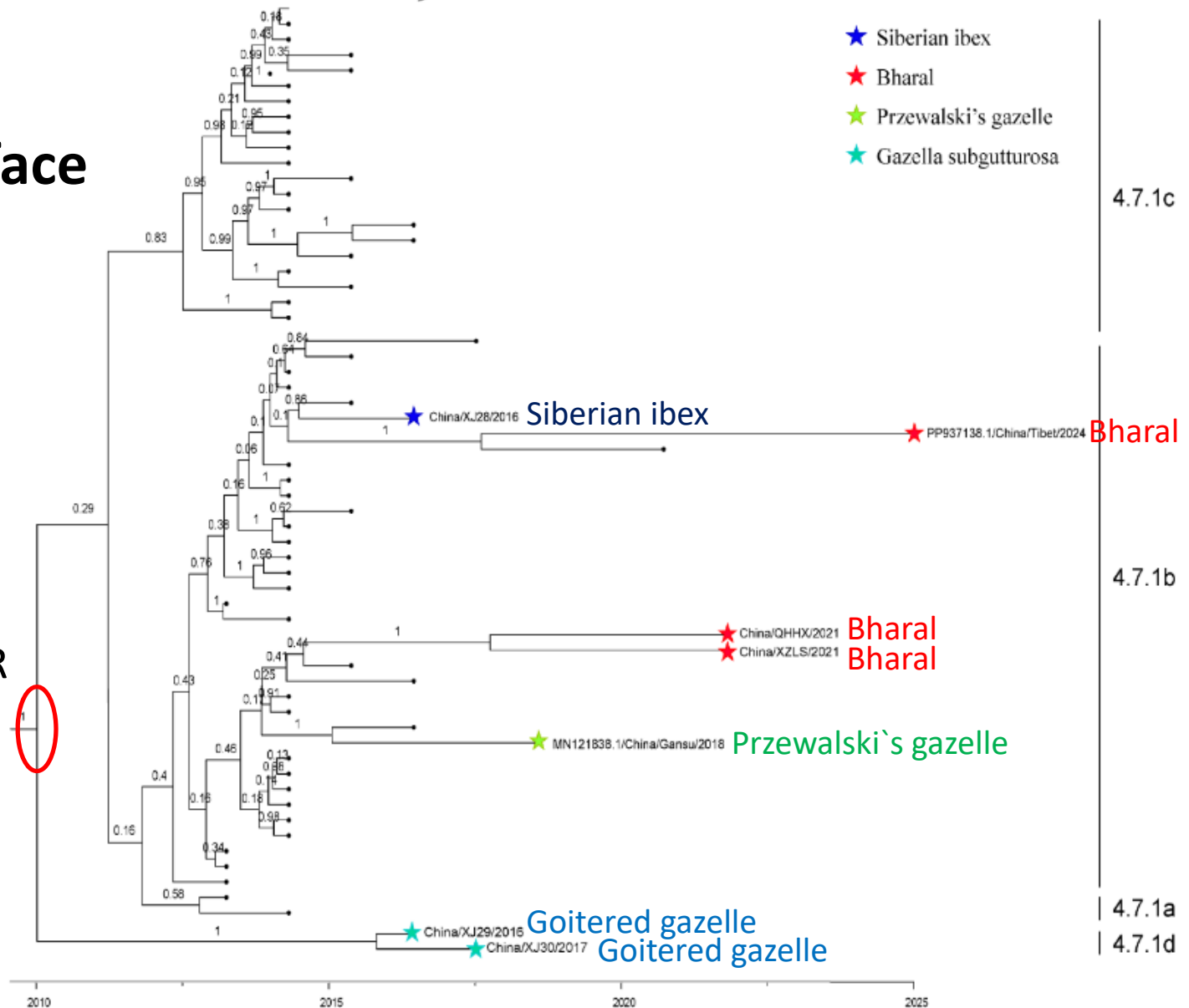
- No distinct temporal correlation among the strains in each cluster
- PPRV cluster 4.7.1b has been the temporally dominant cluster in China.





Livestock-wildlife interface distribution

- PPRV from wildlife were interspersed with those from sheep or goats.
- Two goitered gazelle strains from Xinjiang grouped into a distinct cluster of 4.7.1d.
- It suggested an separated PPR incursion through wildlife transboundary migration from neighboring countries.





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5. Identification of anchor mutations in PPRV genomes collected in China from 2013 to 2024

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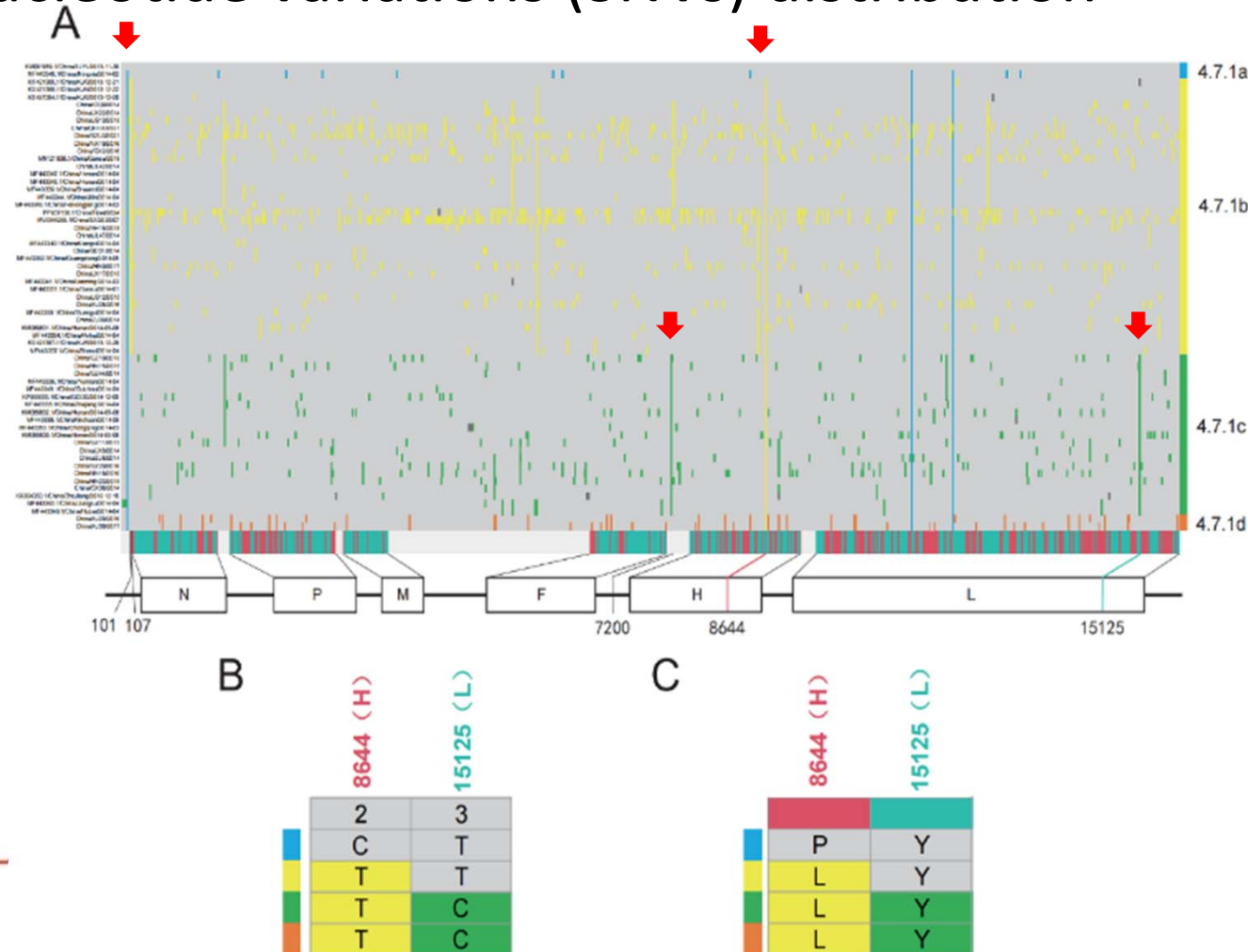
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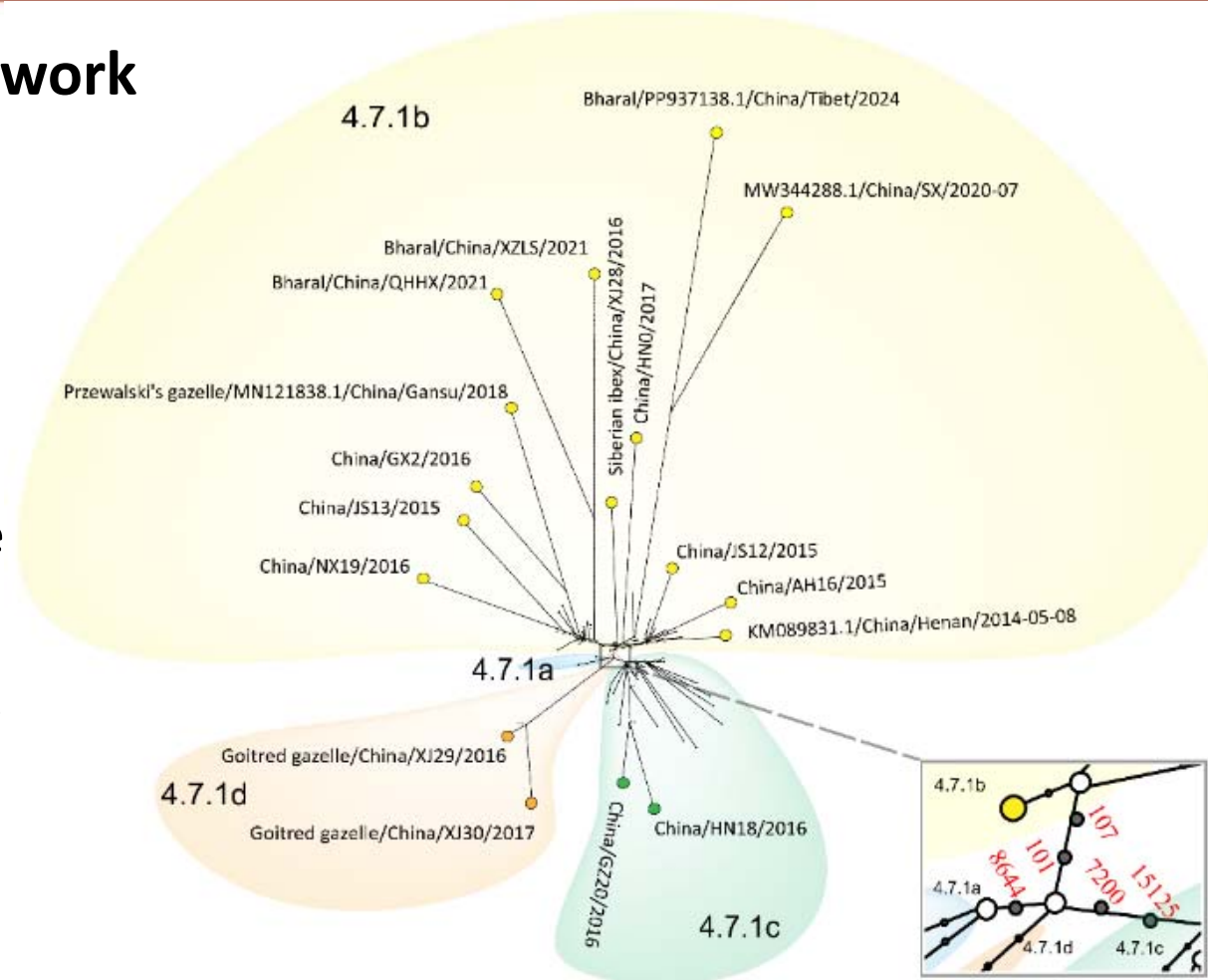
Pattern of PPRV single nucleotide variations (SNVs) distribution

- A total of 997 SNVs were identified and listed in a matrix
- Five SNVs were identified as anchor mutations
- cluster 4.7.1a
 - C8644T: Pro438Leu in H gene
- cluster 4.7.1b
 - T101C and T107C in the 3' leader region
- Cluster 4.7.1c
 - T15125C in the L gene (Tyr1944)
 - A7200G in the 5' UTR-F gene



Median-joining phylogenetic network

- Four clusters were identified mutationally branching from a single common node through 5 anchor mutations
- Mutational branches in clusters 4.7.1b and 4.7.1c formed star-like radiation topology, indicating a single origin and the expansion of strains in the cluster
- Expansion of long branches in cluster 4.7.1b suggested that it was the dominant circulating cluster in China in recent years





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6. Challenge on PPR eradication in the region

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- The reservoir core population of the episystem in China need to be identified.
- Strategy should be taken to focus vaccination across all reservoir populations to stop the virus circulating.
- The evolutionary rate of **lineage IV PPRV** genomes was slightly faster than other lineages, maybe due to factors like widespread circulation, mass vaccination, large sheep/goat populations, and inadequate biosecurity in Asia.
- The effects of the anchor mutations on the viral antigenicity, transmissibility, and pathogenicity of PPRV need to be further investigated.
- The transmission route of PPRV clade 4.7 from UAE to China remains unclear because of the lack of PPRV genome sequence in the Middle East and Central Asia. Knowledge of genome sequences of PPRV strains from Central Asia will improve our understanding of the transmission patterns of PPRV in the region.
- Goitered gazelles, which were widely distributed in the Middle East, Central Asia, western China, and western Mongolia, might play an important role in the transboundary transmission of PPR in the region. Intensified surveillance for PPR in wildlife in border regions is essential for early detection of a PPR outbreak.



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Thank You for your attention!

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