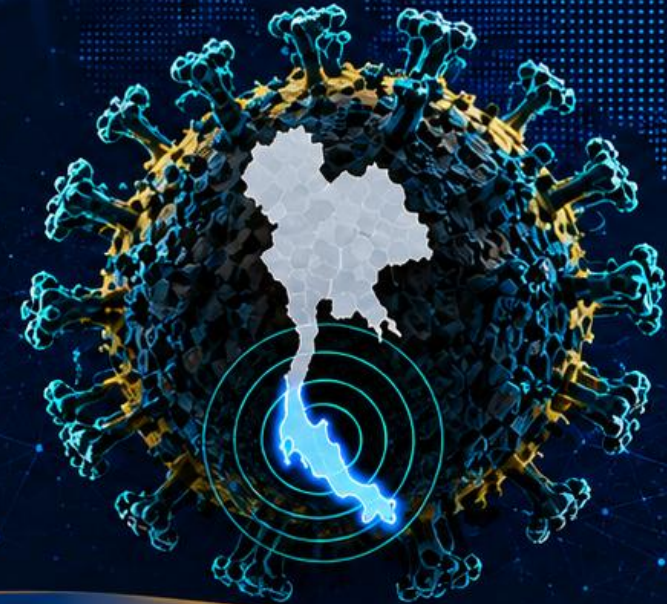


GENETIC DIVERSITY AND EVOLUTION OF **INFECTIOUS BRONCHITIS VIRUS**

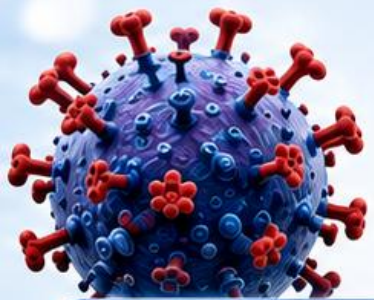
IN SOUTHERN THAILAND (2014–2025)



Pattaramon Suanin * , Sasiwimol Thongmee , Nusara Pathan ,
Wongkae Watjiranon , Khanistar Rattanaburee , Khwansanee Suknao ,
Gamonsiri Bhumibhamon and Wandee Kongkaew



Veterinary Research and Development Center (Upper Southern Region)
Nakhon Si Thammarat, Thailand



Infectious Bronchitis Virus (IBV)



IBV



Coronavirus

- Family : **Coronaviridae**
- Genus : **Gammacoronavirus**
- Genome : **RNA**



Transmission

- Airborne (aerosol droplets)
- Direct contact with contaminated secretions



Multiple IBV genetic lineages are circulating worldwide

IMPACT ON POULTRY HEALTH



Respiratory system



Reproductive system



Renal system

IMPACT ON THE POULTRY INDUSTRY



Reduced Egg Production

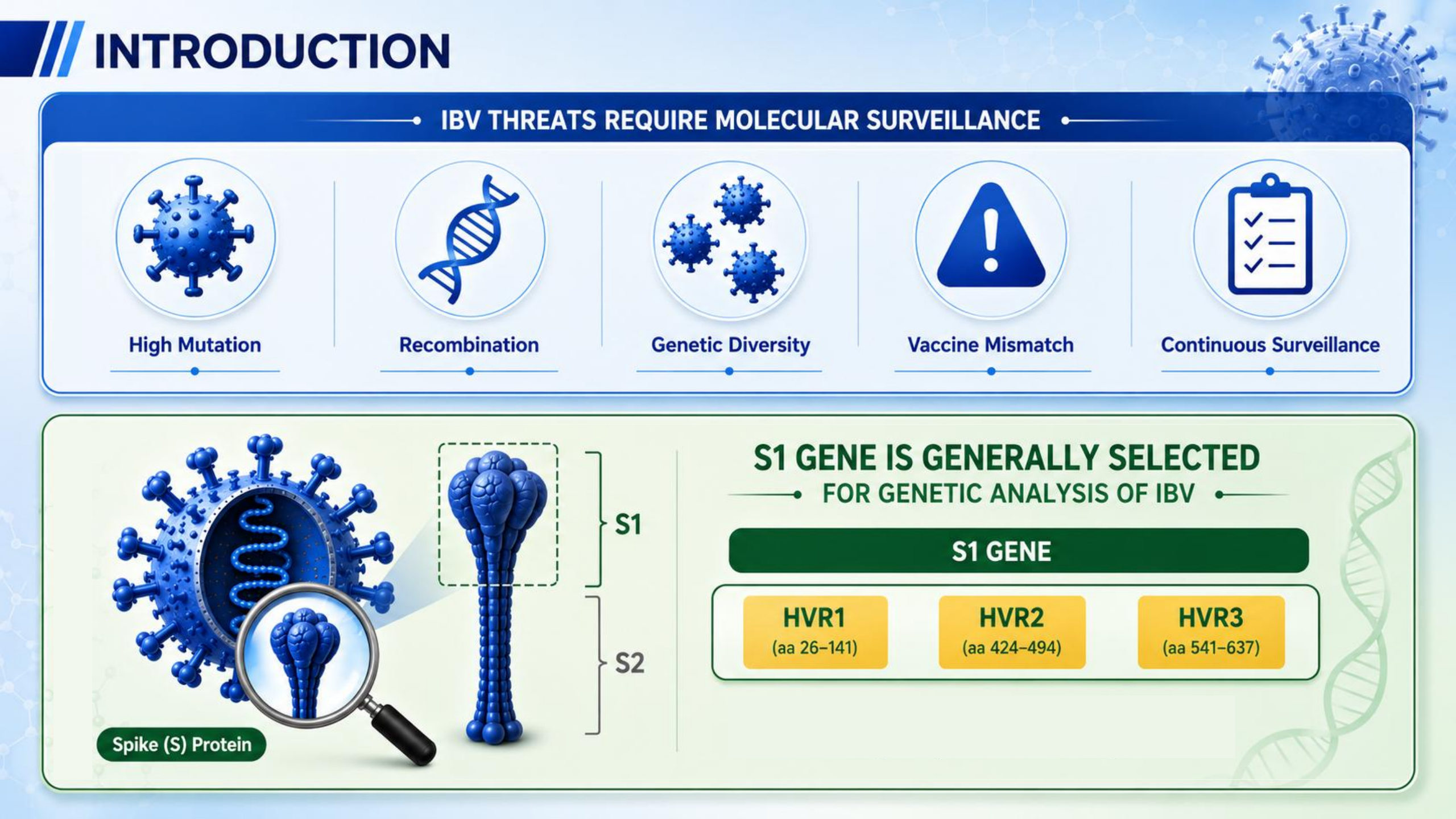


Impaired Growth Performance



Economic Losses





INTRODUCTION



CHONGMAS *et al.*

 14 sample (2007)

Identified 2 IBV groups

- SH3 (GI-7)
- China/LDL/971/97 (GI-13)

VS



TAWATCHAI *et al.*

 15 sample (2008–2009)

Identified 3 IBV groups

- QX-like (GI-19)
- THA001 (GI-7)
- Massachusetts-like (GI-1)
- Recombinant between QX-like (GI-19) and THA001 (GI-7)

NARUEPOL *et al.*

 24 sample (2008–2013)

Identified 4 IBV groups

- QX-like (GI-19)
- 4/91-like (GI-13)
- THA001 (GI-7)
- Massachusetts-like (GI-1)

SIORAT *et al.*

 120 sample (2014–2016)

Identified 4 IBV groups

- QX-like (GI-19)
- 4/91-like (GI-13)
- Massachusetts-like (GI-1)
- Recombinant between QX-like (GI-19) and 4/91-like (GI-13)

OBJECTIVES



Genotype classification
(spatio-temporal distribution)

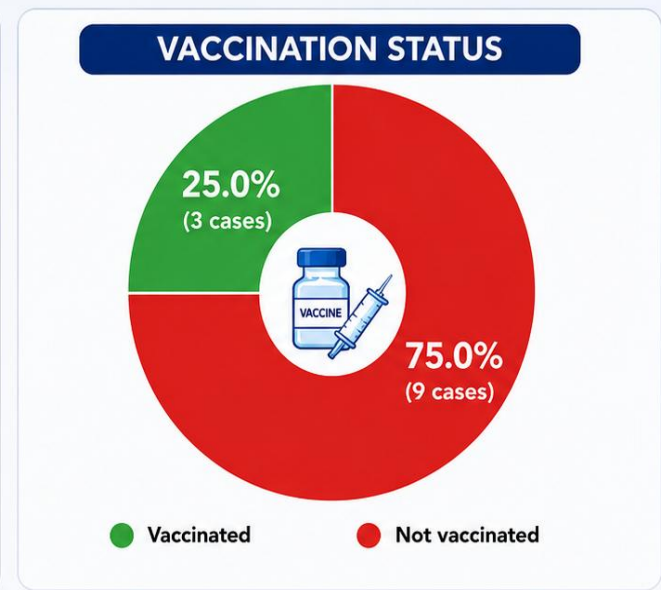
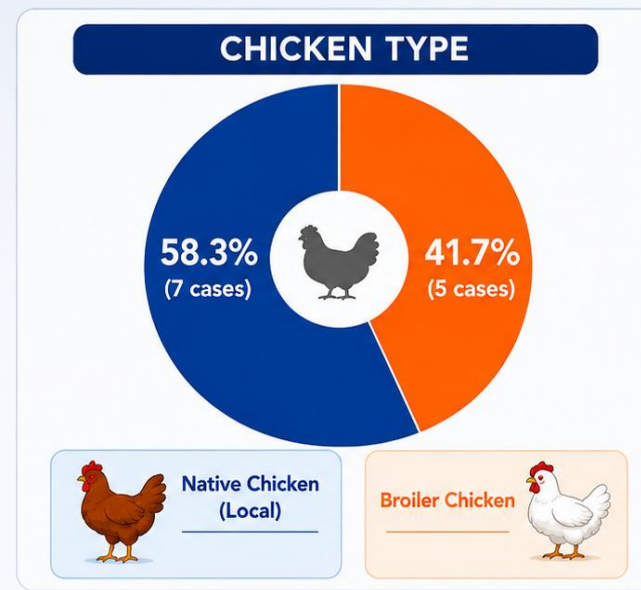
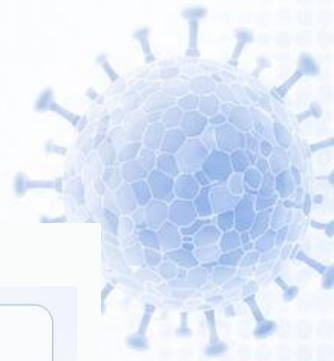


Recombinant detection



Identity comparison

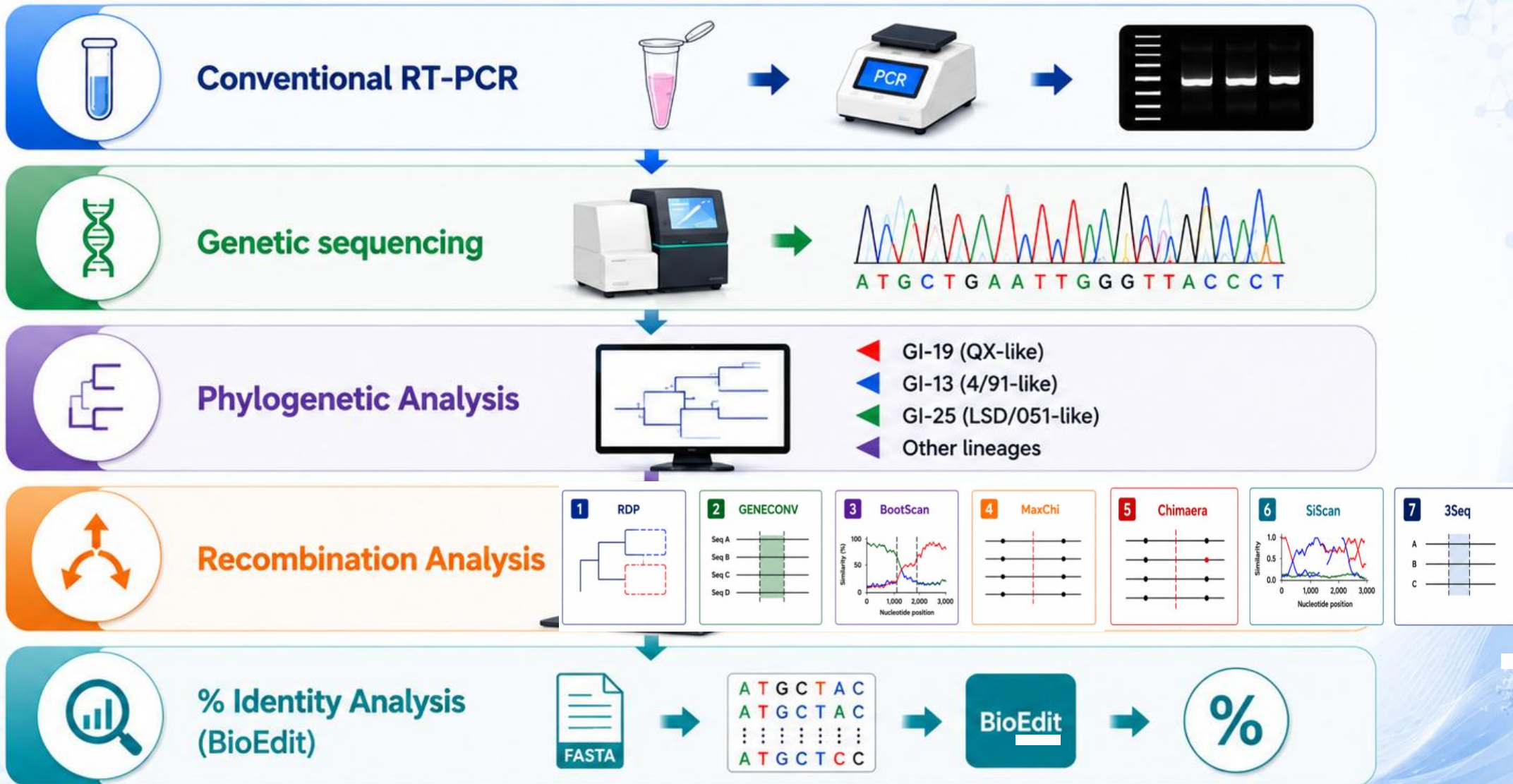
Characteristics of 12 Study Samples



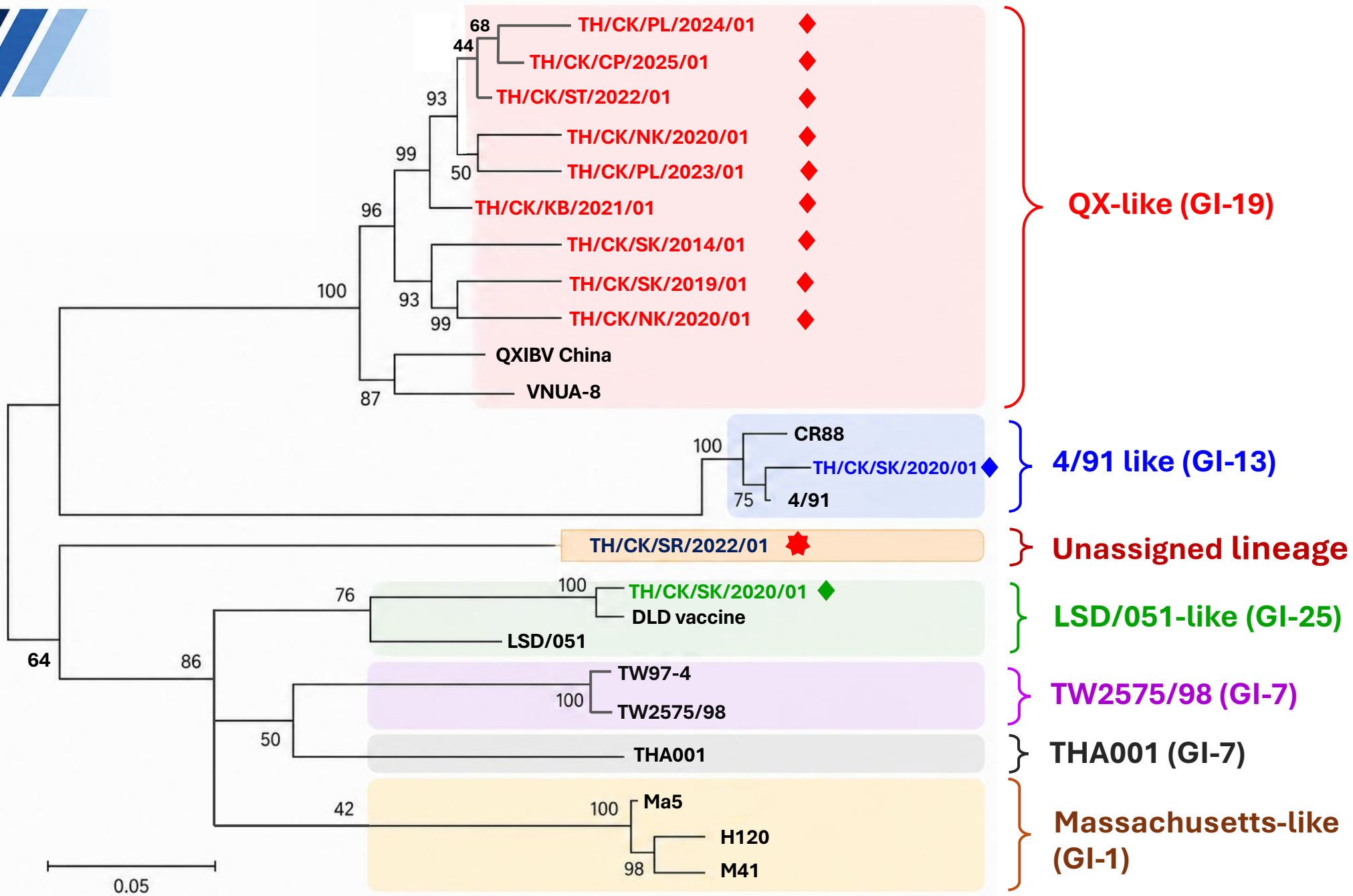
Top 5 most common clinical signs

Rank	Clinical Sign	Number of Cases	Percentage	Bar Chart
1	Depression / Lethargy	7	58.3	
2	Loss of appetite	5	41.7	
3	Respiratory signs	4	33.3	
4	Sudden death	4	33.3	
5	Diarrhea	2	16.7	

MOLECULAR ANALYSIS



RESULTS



RESULTS

Geographic distribution of IBV in Southern Thailand, 2014–2025



*Clustered with the LSD/051 vaccine reference strain; this does not indicate vaccine origin.

RESULTS

RECOMBINATION ANALYSIS

Recombinant strain

TH/CK/SR/2022/01
Recombinant



=

Major Parent (Reference strain)

QXIBV China
(QX-like, GI-19)



+

Minor Parent (Reference strain)

TW97-4
(GI-7)



RDP5 Detection (Seven Methods)

7 of 7 methods detected
significant recombination

Method	Detection	P-value
✓ RDP	✓	8.804×10^{-8}
✓ GENECONV	✓	2.371×10^{-7}
✓ BootScan	✓	7.263×10^{-10}
✓ MaxChi	✓	1.837×10^{-8}
✓ Chimaera	✓	2.808×10^{-6}
✓ SiScan	✓	2.171×10^{-2}
✓ 3Seq	✓	2.182×10^{-6}

Statistical Significance



Statistically Significant

P < 0.05

RESULTS

Identity comparison of Field Isolates with Vaccine Reference Strains



VACCINATED

	Isolate	Chicken Type	Lineage	% Nucleotide Identity with Vaccine Reference Strains			
				DLD	H120	QX	4/91
	TH/CK/SK/2019/01	Native Chicken	QX-like	80.4	78.2	97.3	78.7
	TH/CK/NK/2020/02	Broiler	QX-like	80.0	77.9	95.8	78.4
	TH/CK/PL/2023/01	Broiler	QX-like	79.1	77.5	95.1	77.7



NOT VACCINATED

	Lineage Group	Isolate	Chicken Type	Lineage	% Nucleotide Identity with Vaccine Reference Strains			
					DLD	H120	QX	4/91
	QX-like	TH/CK/SK/2014/01	Native Chicken	QX-like	80.3	78.0	97.3	78.5
		TH/CK/NK/2020/01	Broiler	QX-like	80.2	77.6	97.1	78.5
		TH/CK/KB/2021/01	Native Chicken	QX-like	80.5	78.2	97.1	78.5
		TH/CK/ST/2022/01	Native Chicken	QX-like	80.0	77.8	96.0	78.2
		TH/CK/PL/2024/01	Broiler	QX-like	79.6	77.6	95.3	78.1
		TH/CK/CP/2025/01	Native Chicken	QX-like	80.2	78.2	96.0	78.1
	4/91	TH/CK/SK/2020/01	Native Chicken	4/91	75.2	75.9	78.2	95.5
	LSD/051	TH/CK/ST/2021/01	Native Chicken	LSD/051	98.6	80.8	80.9	76.6
	Recombinant	TH/CK/SR/2022/01	Broiler	Recombinant	80.6	78.3	80.1	75.7

DISCUSSION

Dominance of QX-like circulation strain

Previous studies (Tawatchai, Naruepol, Siorat)



QX-like
(GI-19)



China/LDL/971/97,
4/91-like
(GI-13)



Massachusetts-like
(GI-1)



THA001, SH3
(GI-7)



This study



QX-like
(GI-19)



4/91-like
(GI-13)



Massachusetts-like
(GI-1)



THA001, SH3
(GI-7)



LSD/051-like
(GI-25)



Emergence of GI-19/GI-7 recombinant

Recombinant strain



Previous studies

Tawatchai



QX-like
(GI-19)

+



THA001
(GI-7)



Recombinant

Sirorat et al.



QX-like
(GI-19)

+



4/91-like
(GI-13)



Recombinant

Guo



QX-like
(GI-19)

+



TW2575/98
(GI-7)



Recombinant



This study



QX-like
(GI-19)

+



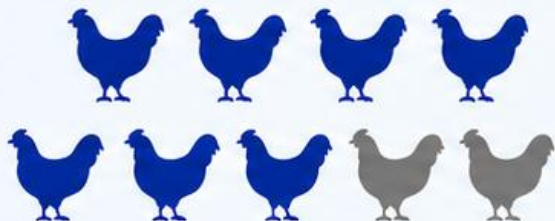
TW97-4
(GI-7)



GI-19/GI-7 recombinant

DISCUSSION

1



n = 11 isolates
(vaccinated and unvaccinated)

11 vaccinated and unvaccinated IBV isolates



95–98.6% Complete S1 nucleotide identity
with the corresponding vaccine reference strain.

2



n = 1 isolate
(recombinant)

Recombinant isolate



75–80% Complete S1 nucleotide identity
to all four vaccine reference strains
(LSD/051, QX, 4/91, and Massachusetts).

3



Consistent with Chongmas *et al.* (2008)

- ✓ **95.6–100%** S1 nucleotide identity within the same genotype.
- ✓ **76.7–79.8%** S1 nucleotide identity between different genotypes.

Conclusion

1



QX-like (GI-19)

Co-circulation of 3 Genotypes



4/91-like (GI-13)



LSD/051-like (GI-25)



2



Predominance of QX-like (GI-19)

Major circulating lineage
in Southern Thailand
(2014–2025)



3



Recombinant

Between QX-like (GI-19) and TW97-4 (GI-7)



4



11 Vaccinated & Not Vaccinated

QX vaccine, 4/91 vaccine, DLD vaccine > 95%

1 Recombinant

DLD vaccine, QX vaccine, 4/91 vaccine ≤ 75-80



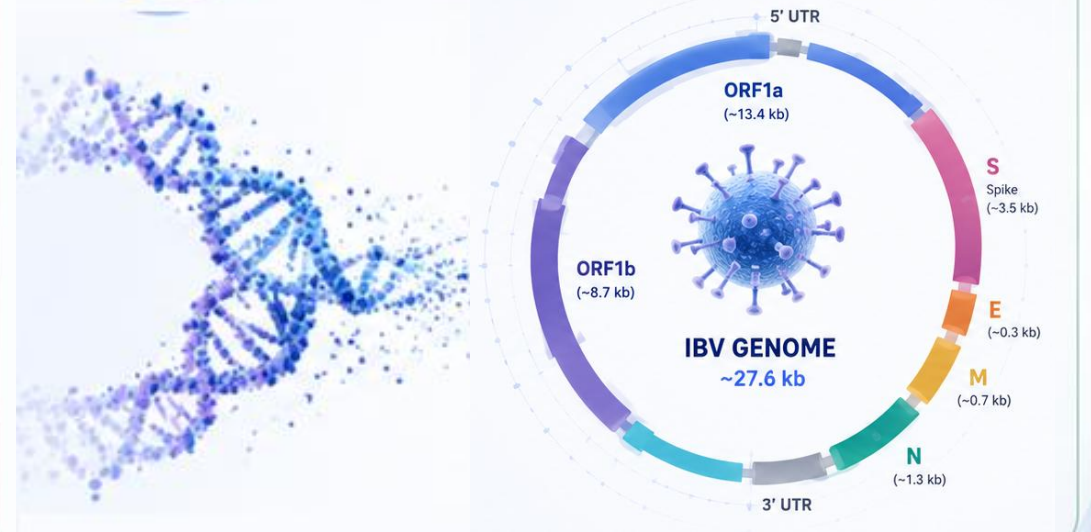
Recommendation



Animal History



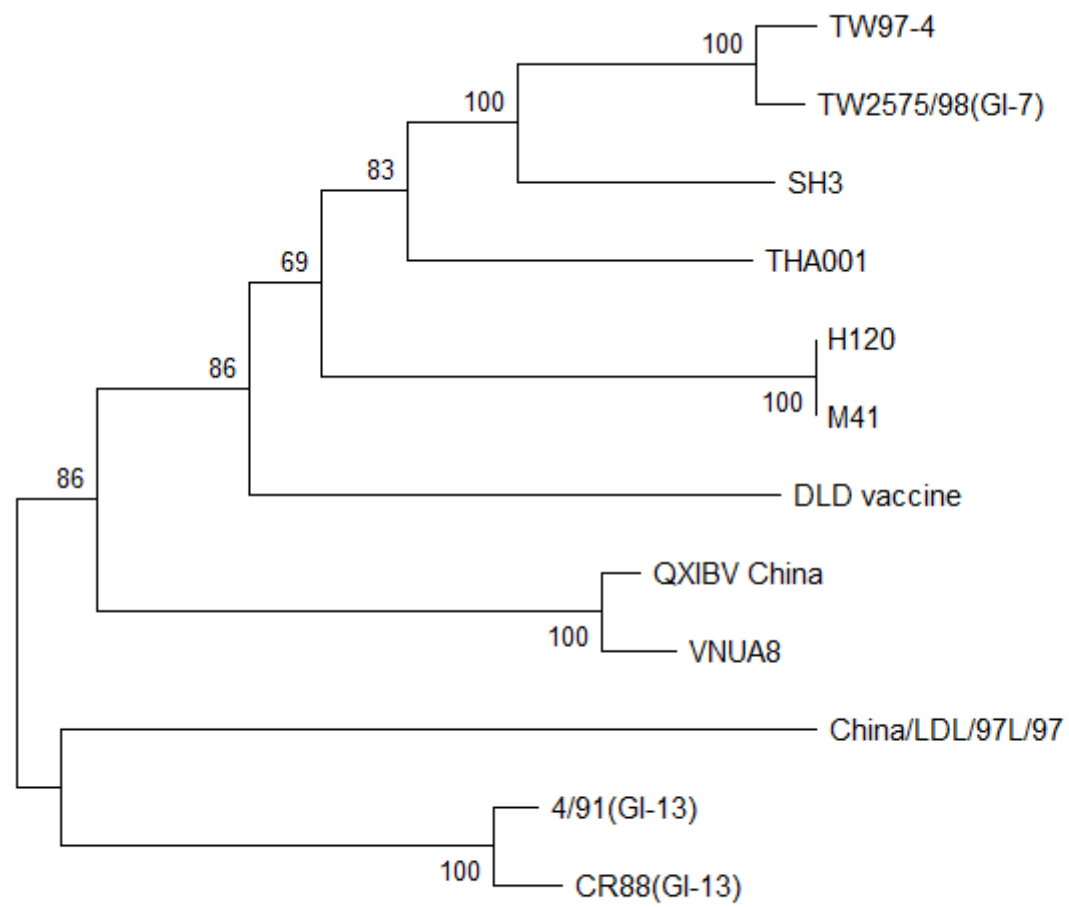
Whole-Genome Sequencing





Thank You

• Q & A •



0.05