The Updated Epidemic and Controls of Swine Enteric Coronavirus in China

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Content

- ◆Overview of epidemic of SECD in China
- ◆The controls and preventions of porcine viral diarrhea

Overview of Epidemic of SECD in China

Coronavirus Genetic Groups, and Diseases

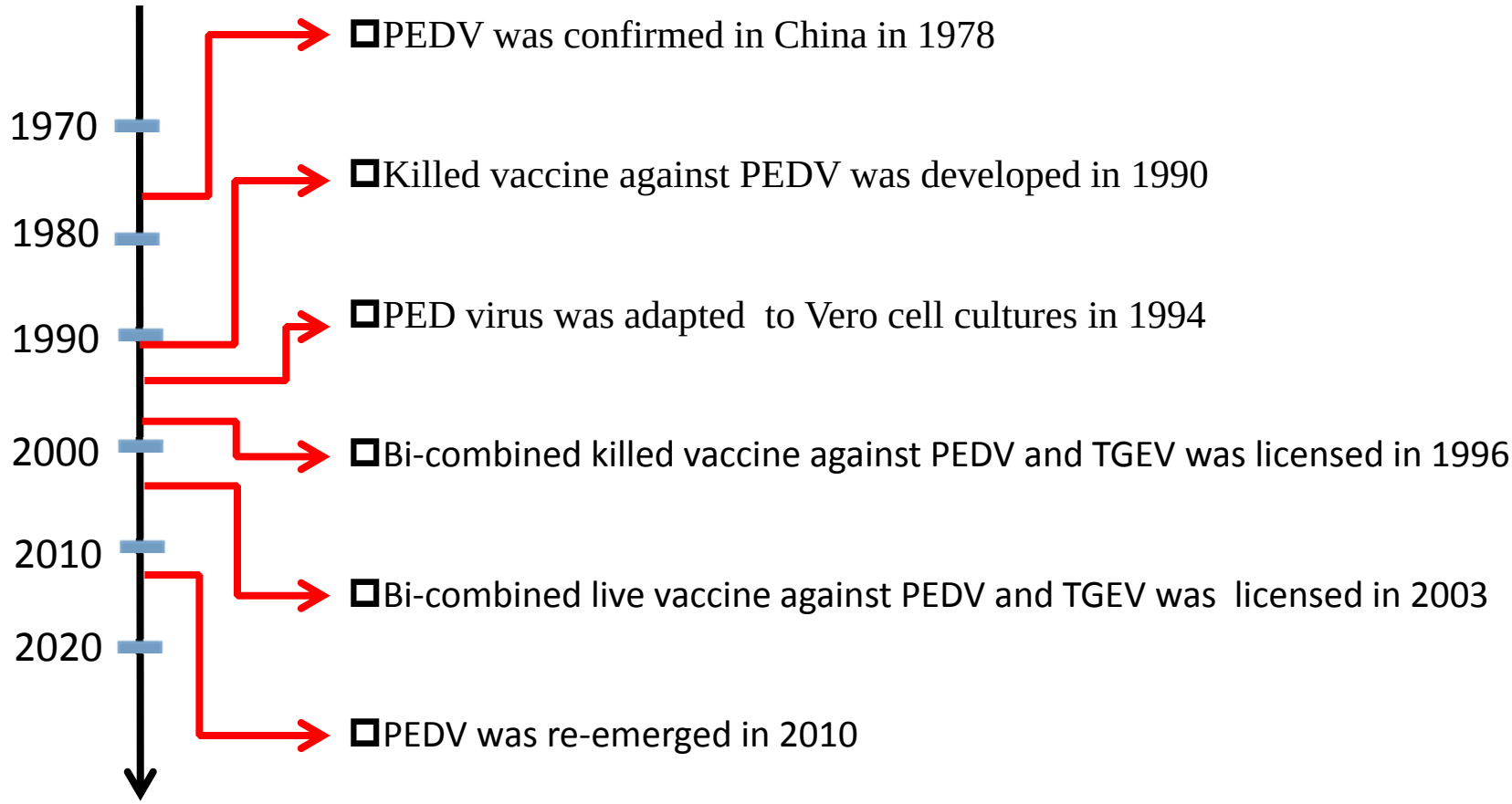
Genetic Groups	VIRUS	HOST	Target Tissues		
			Respiratory	Enteric	Other
Alpha coronavirus	TGEV	swine	(√)	√	
	PRCV	swine	√		
	PEDV	swine		√	
	FIPV	feline	√	√	Systemic
	FCoV	feline		√	
	CCoV	canine		√	
Beta coronavirus	HCoV-OC43	human	√	√	
	MHV	mouse			Liver
	RCoV	rat			Eye, GU
	HEV	swine		√	CNS
	BCoV	bovine		√	
	SARS	human; civet cat; bat	√	√	Kidney, Liver?
Gamma coronavirus	IBV	chicken	√	(√)	kidney
	TCoV	turkey		√	
Delta coronavirus	PDCV	swine		√	

Swine enteric coronavirus disease (SECD)

- PEDV infects the digestive tract and causes the watery diarrhea ,vomiting and dehydration, and high mortality in young pigs
- TGEV, the clinical sign is very similar to the PED
- PDCoV is thought to cause disease similar to PEDV, but to date, no conclusive studies have proved this
- Transmission: The primary mode of transmission is spread by fecal-oral contact with infected swine or contaminated materials

All swine enteric coronavirus diseases are not reportable disease in China.

The history of PEDV in China



Clinical signs of porcine diarrhea in pig farm

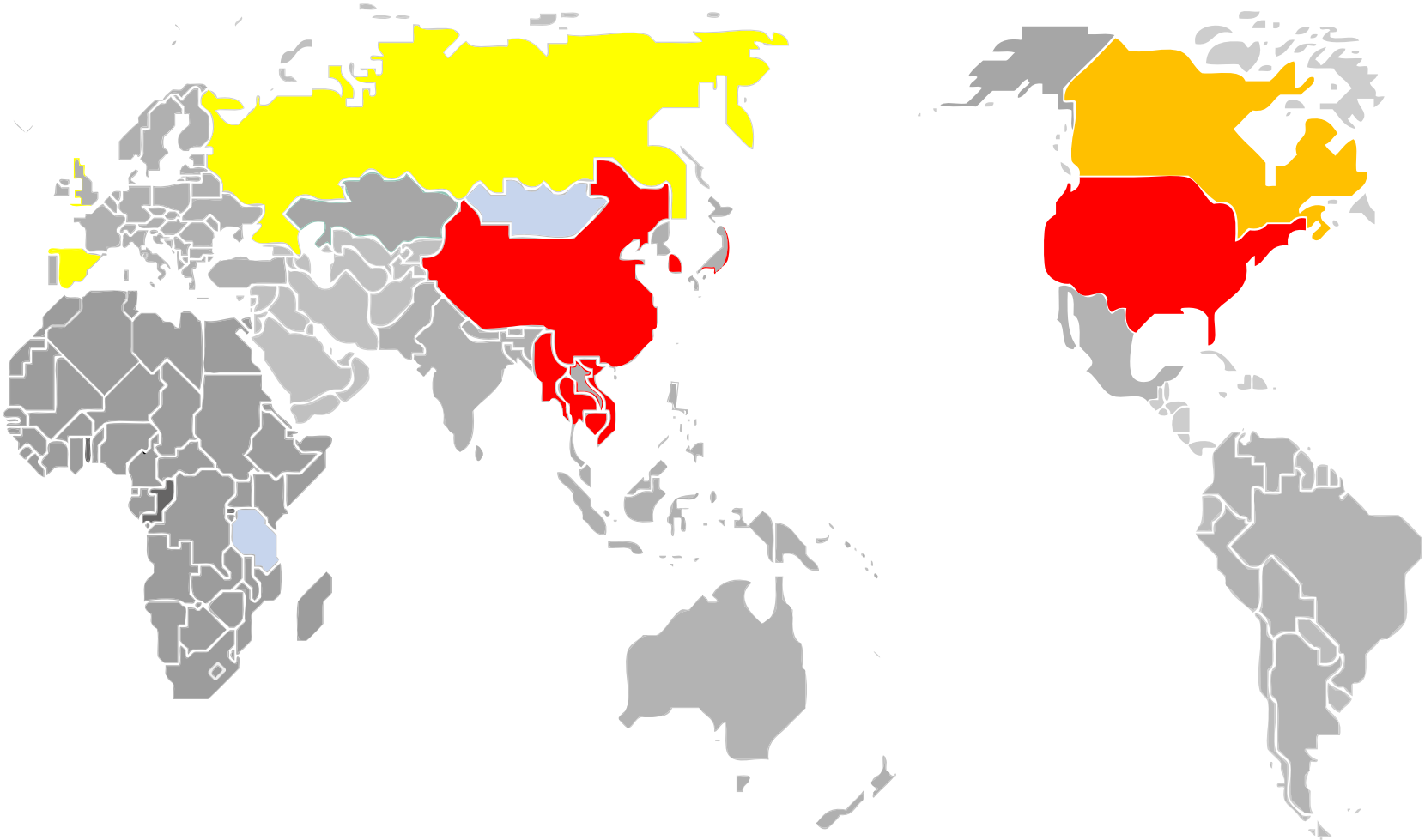
The diarrhea ,vomiting and dehydration, and high mortality in young pigs

Diarrhea of the sows

Clinical signs and epidemic features of porcine diarrhea in pig farms in China

- Clinical signs: Vomiting, watery diarrhea
- Suckling piglets within 1wk old are sick, and with high mortality (10% to 90%)
- Not very good protection after vaccination or back-feeding with virulent viruses in some pig farms
- Recurrence or persistent infection in one pig farm.
- Long-lasting sickness, up to a few months, half a year or one year
- No obvious seasonal character
- Finishing pigs show no symptoms or acute diarrhea.

Global epidemic of PEDV



ASIA: China(1978),South Korea(1992),Japan(1983),Thailand(1995),Vietnam(2005)
EUROPE: U.K.(1971-1999),Belgium(1977),Spain(1995)Russia(2005),Italy(2005-2006)
NORTH AMERICAN: U.S.A ,Canada(2013)

Pathogenic investigation of the diarrhea samples

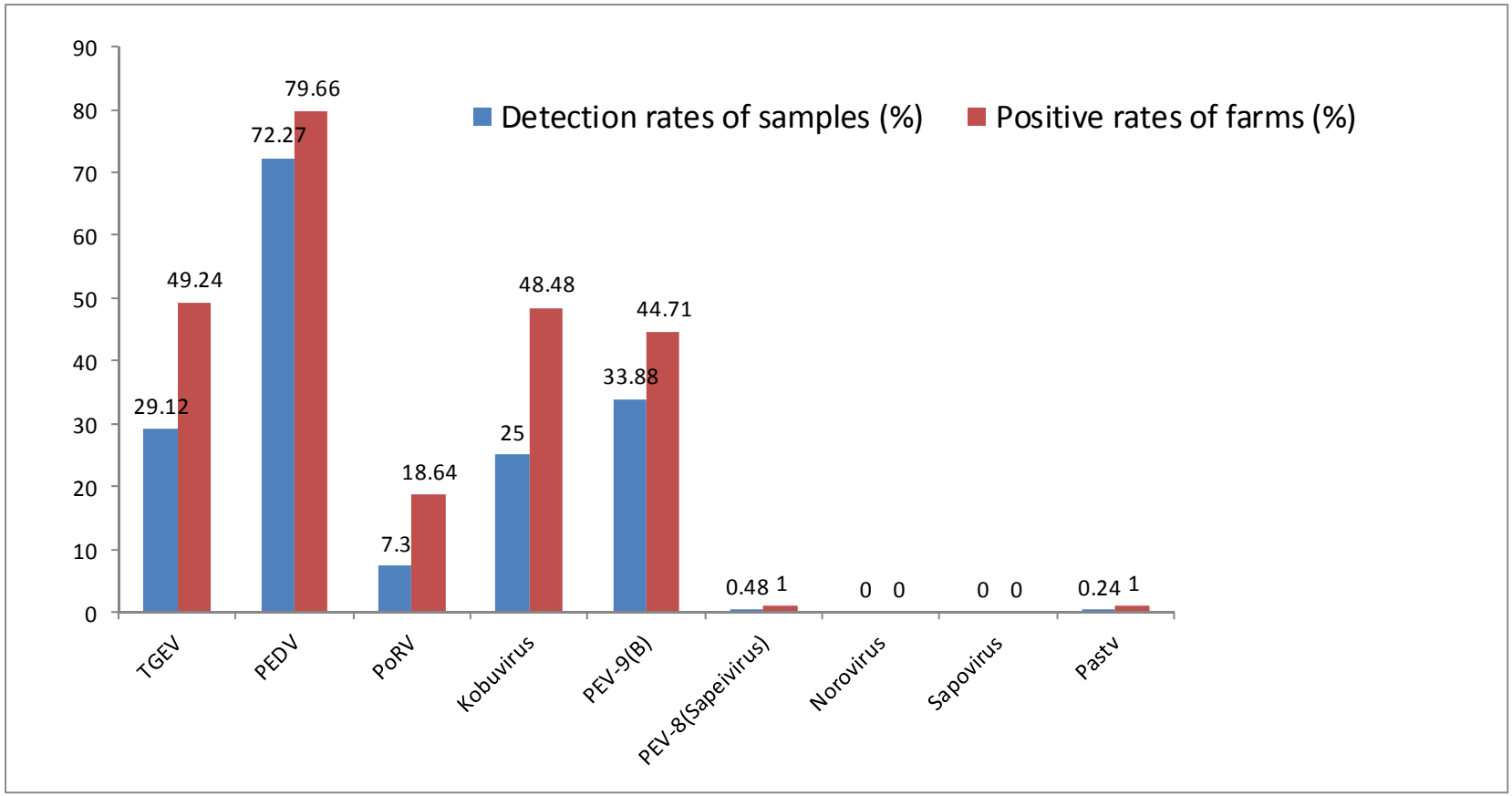
- Time span： 2011.2-2014.03
- Geographical scope： 29 provinces (excluding Tibet, Hainan and Taiwan)
- 276 pig farms（Severe diarrhea pig farms）
- 797 samples were tested（feces and small intestines）
- Methods: RT-PCR, colloidal gold strip, nucleotide sequencing

Etiological Detection

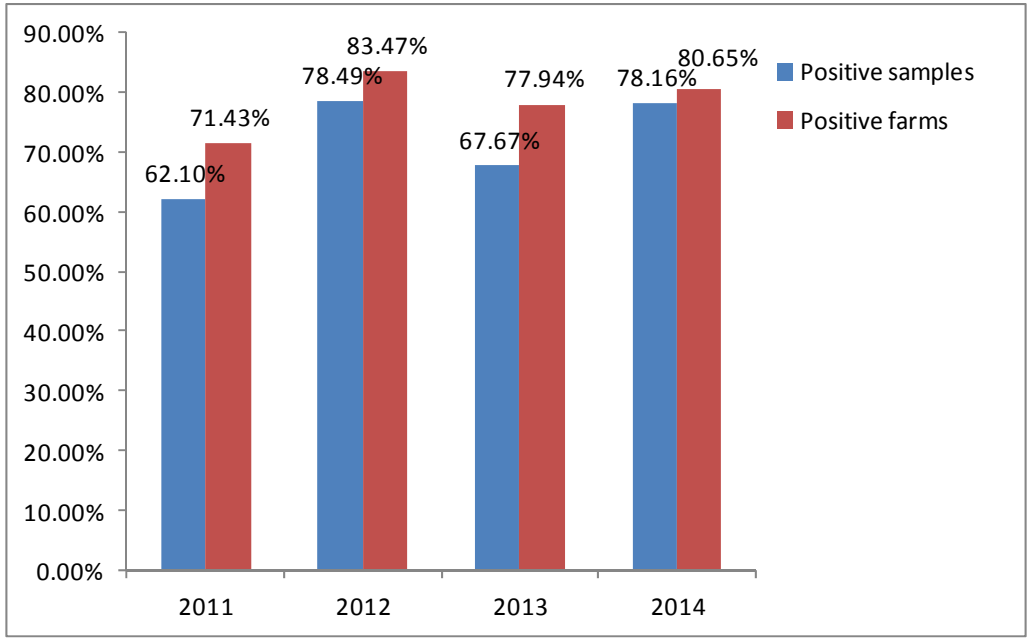
- Transmissible gastroenteritis virus (TGEV) , Coronaviridae
- Porcine epidemic diarrhea virus (PEDV), Coronaviridae
- Porcine rotavirus (PoRV) , Reoviridae
- Porcine delta coronavirus (PDCV), Coronaviridae

- Kobuvirus (KoBV) , Picornaviridae
- Porcine enterovirus (PEV), Picornaviridae
- Porcine techovirus(PTV) , Picornaviridae
- Porcine astrovirus (PAstV), Astroviridae
- Noroviurs, Caliciviridae
- Sapovirus, Caliciviridae

Etiological Detection of diarrhea pig farms in China (2010-2012)

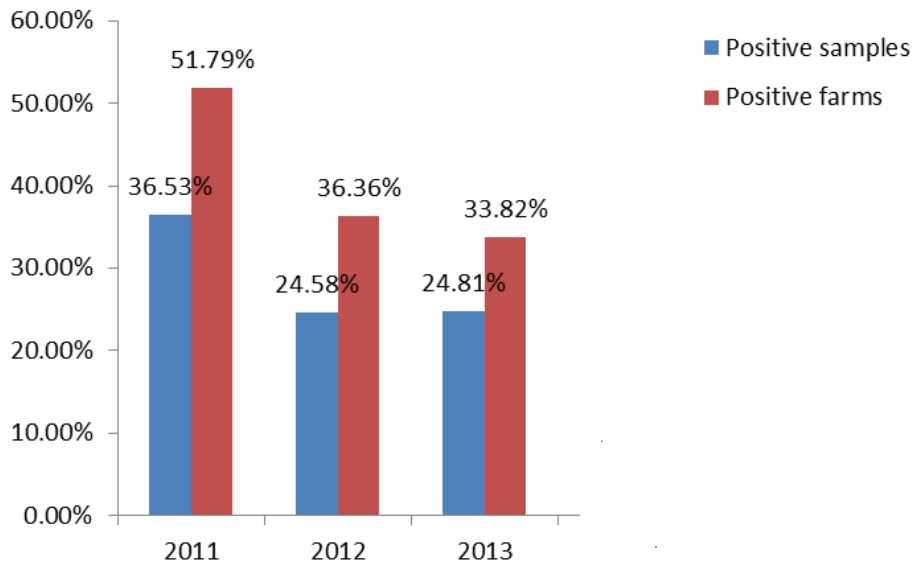


Circulation of PEDV in China



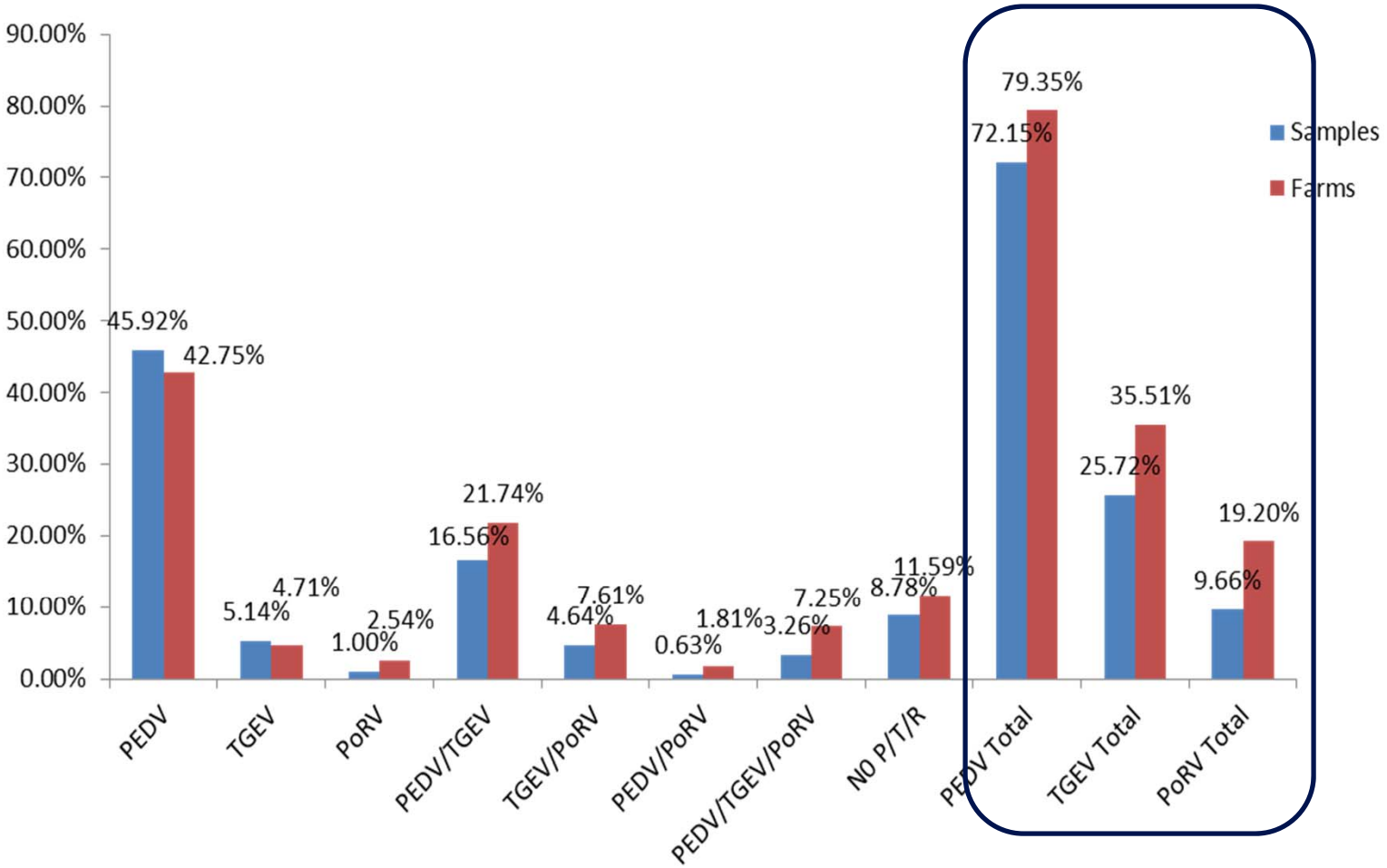
PEDV is circulating in at least 29 provinces. The positive rate of samples varies from 62.10% to 78.49% ; the positive rate of pig farms varies from 71.43% to 83.47%.

Circulation of TGEV in China



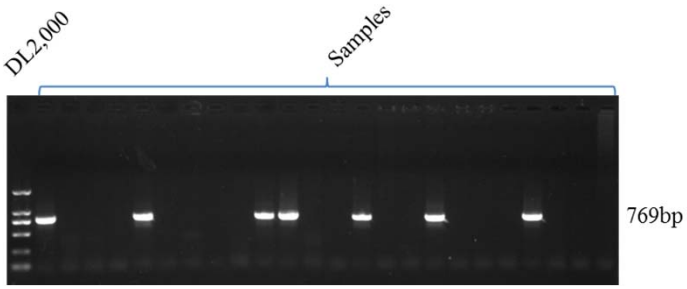
TGEV is circulating more than 22 provinces. The positive rate of samples is up to 36.53% ; the positive rate of pig farms is up to to 51.79%.

Epidemic study results of samples and farms with positive PEDV,TGEV, or PoRV（2011-2014）

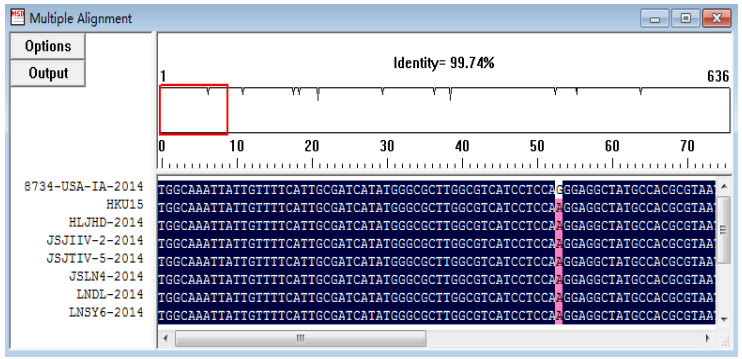


Postive rates in samples and pig farms

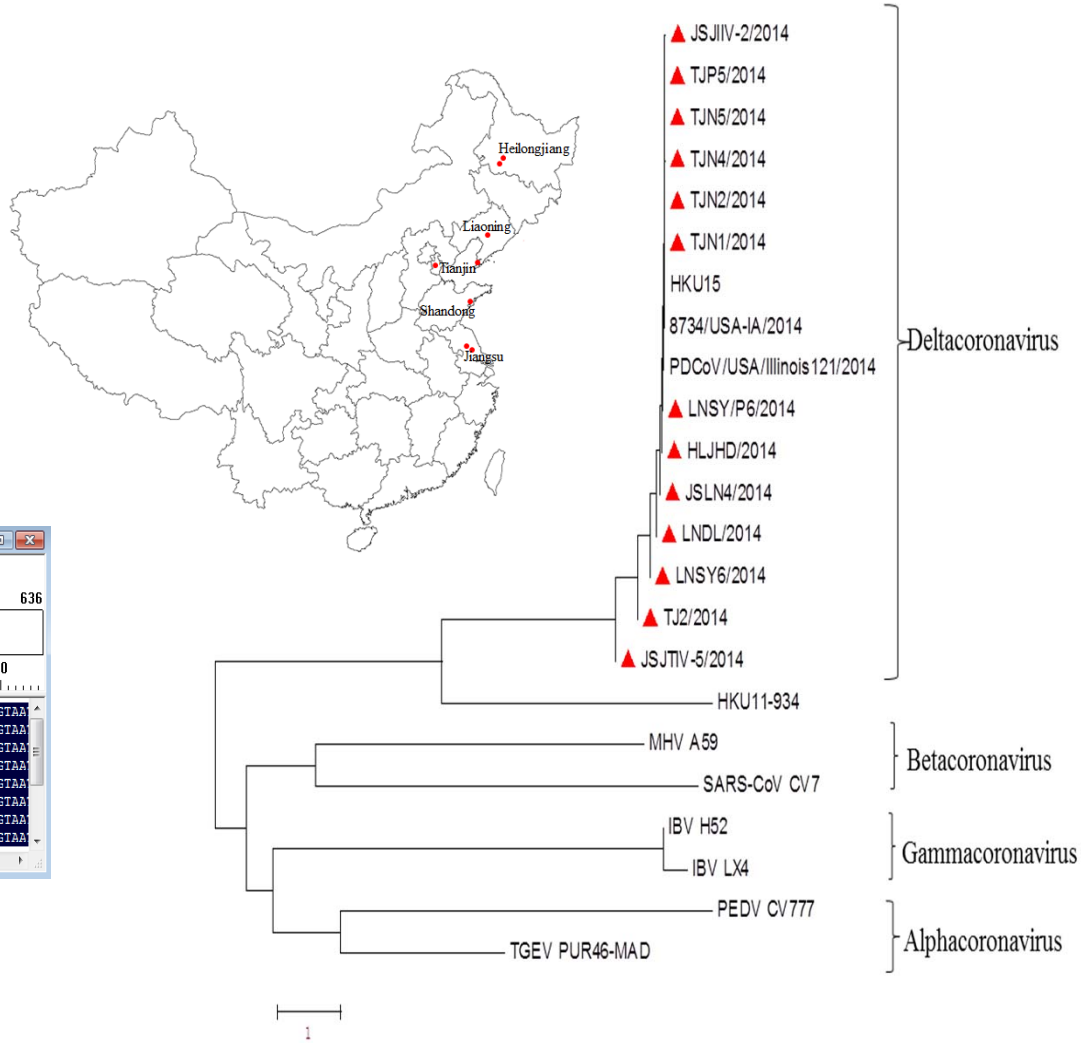
The detection of Porcine delta coronavirus in China



PDCV PCR



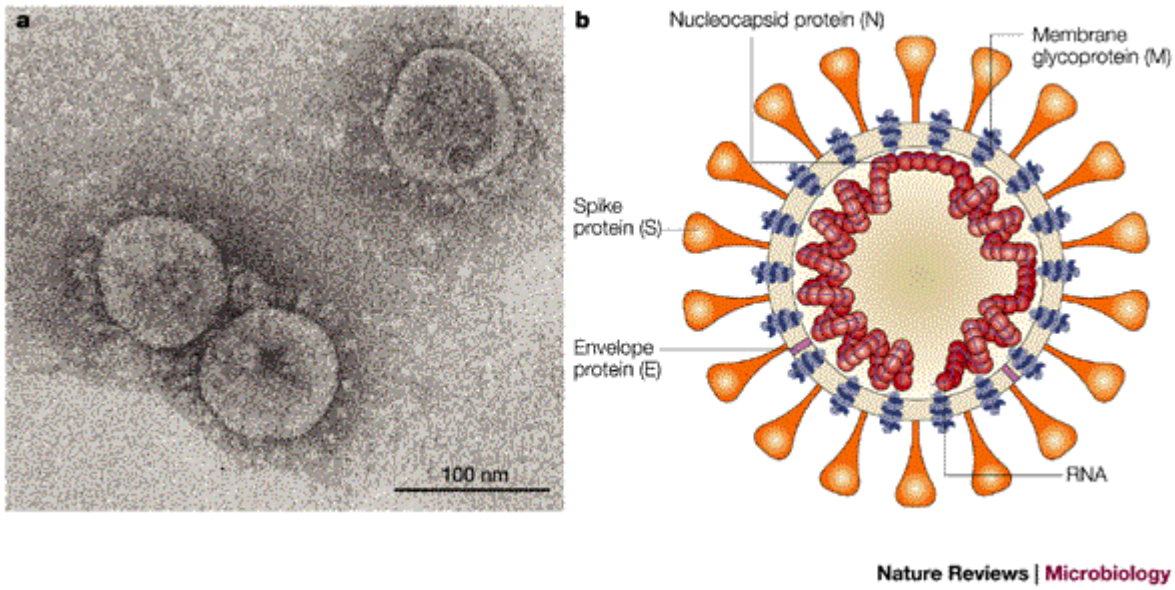
Alignment of M genes

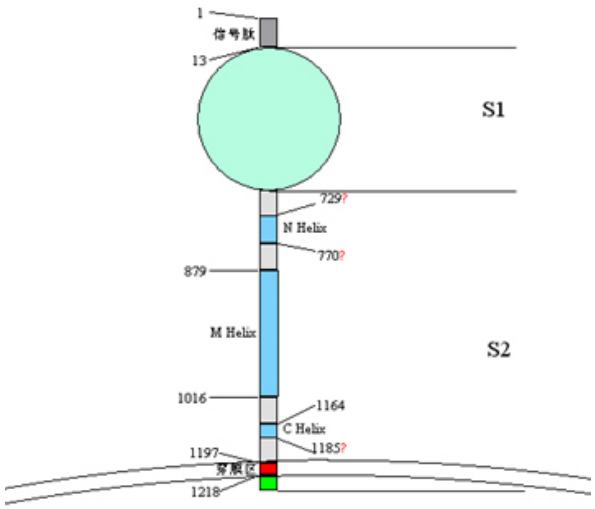


Porcine delta coronavirus is detected in 5 provinces in China, the positive rate of PDCV is about13.99% (20/143).

What's the genetic diversity of the circulating PEDV strains in China?

Spike protein of coronaviruses

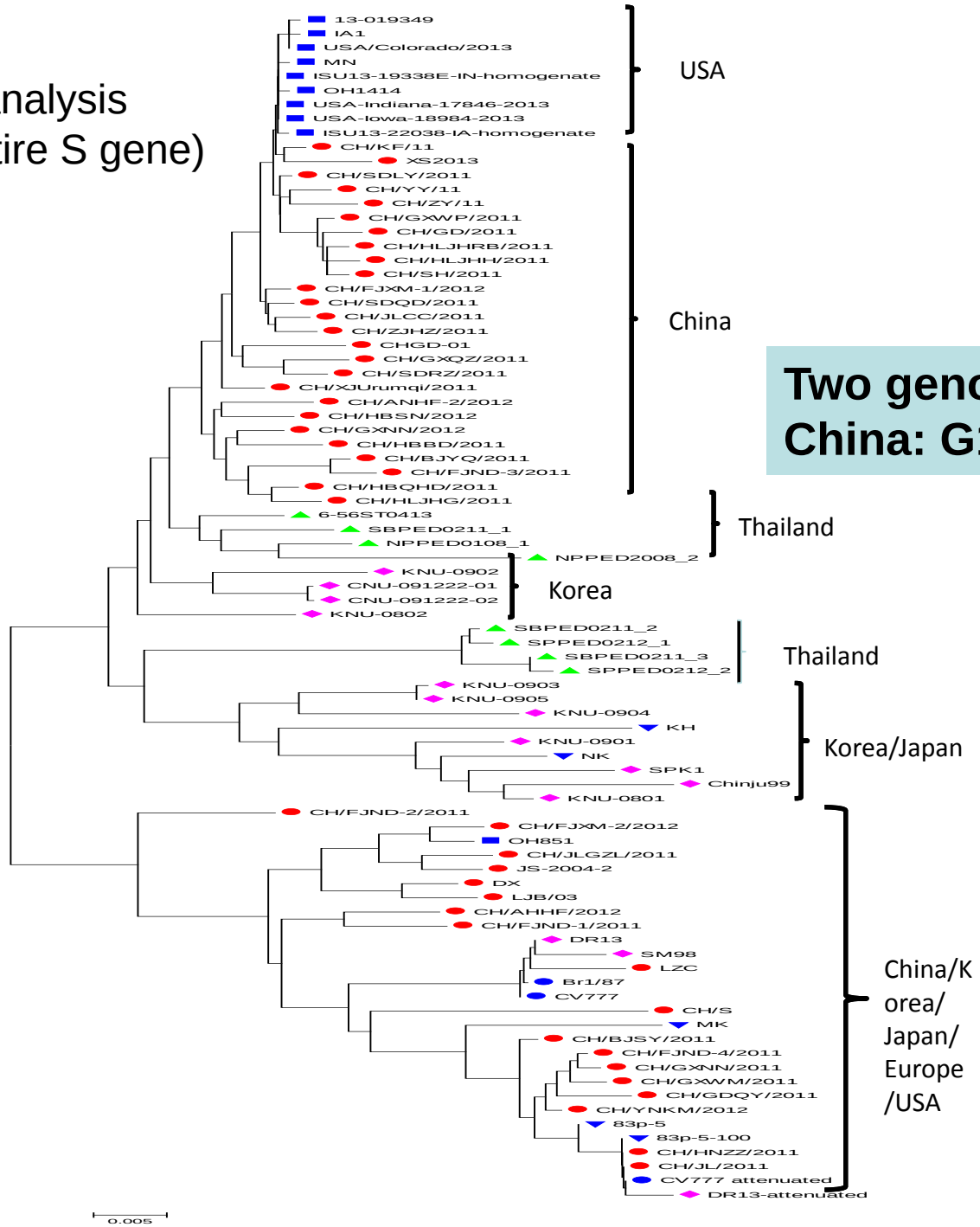




Roles of Spike protein

- Inducing neutralizing antibodies
- Determining tissue tropism of the virus
- Binding to the viral receptor, and infecting host cells
- Determining the virulence of the virus
- ……

Phylogenetic analysis
(Based on the entire S gene)



USA strains

China strains

Thailand strains

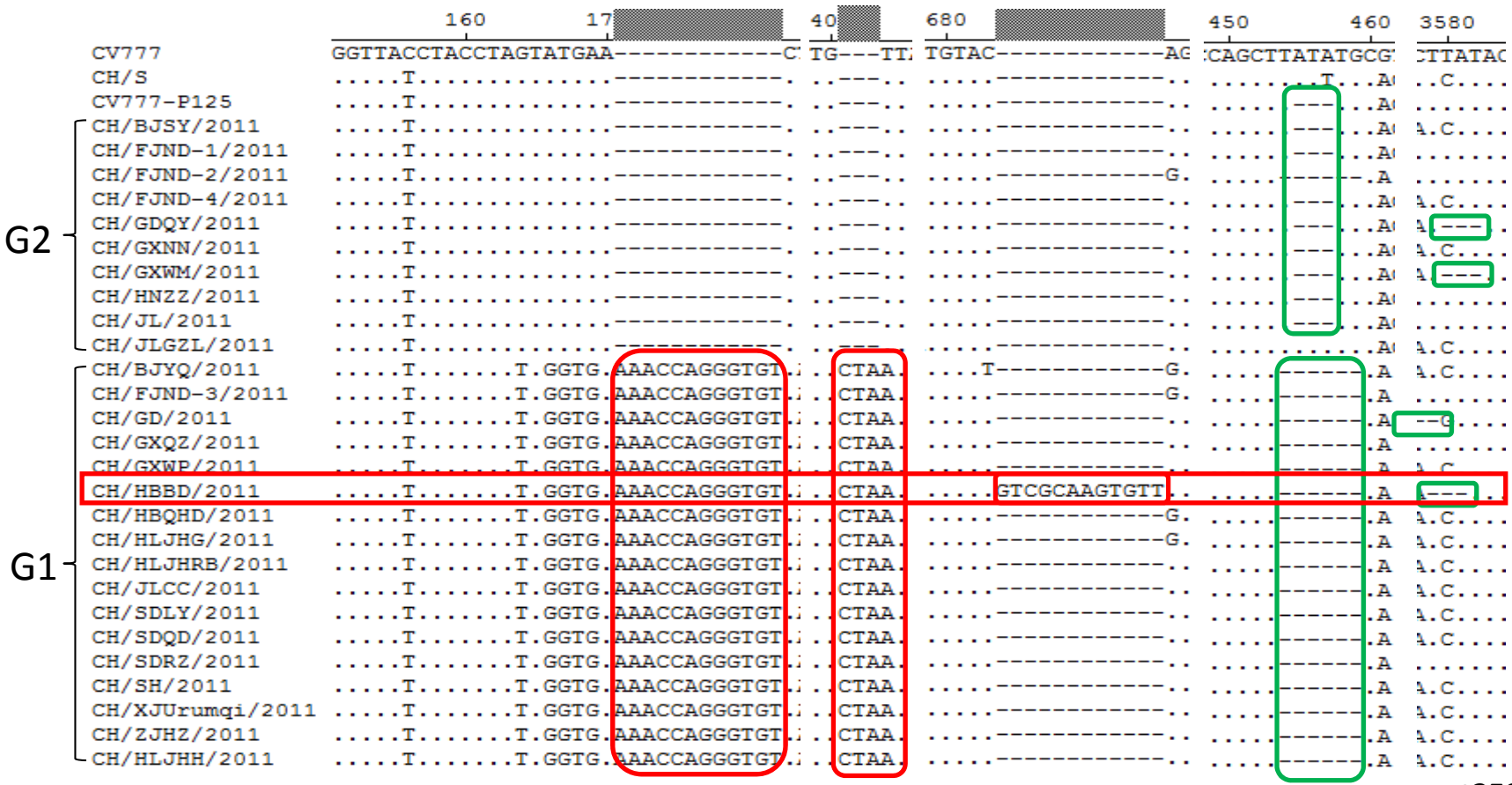
Korea strains

Japan strains

Europe strains

Two genotypes in China: G1 and G2

Nucleotide insertion and deletion seen in S genes of G1 PEDV compared to G2 PEDV in China



nt170-171
12 nt insertion

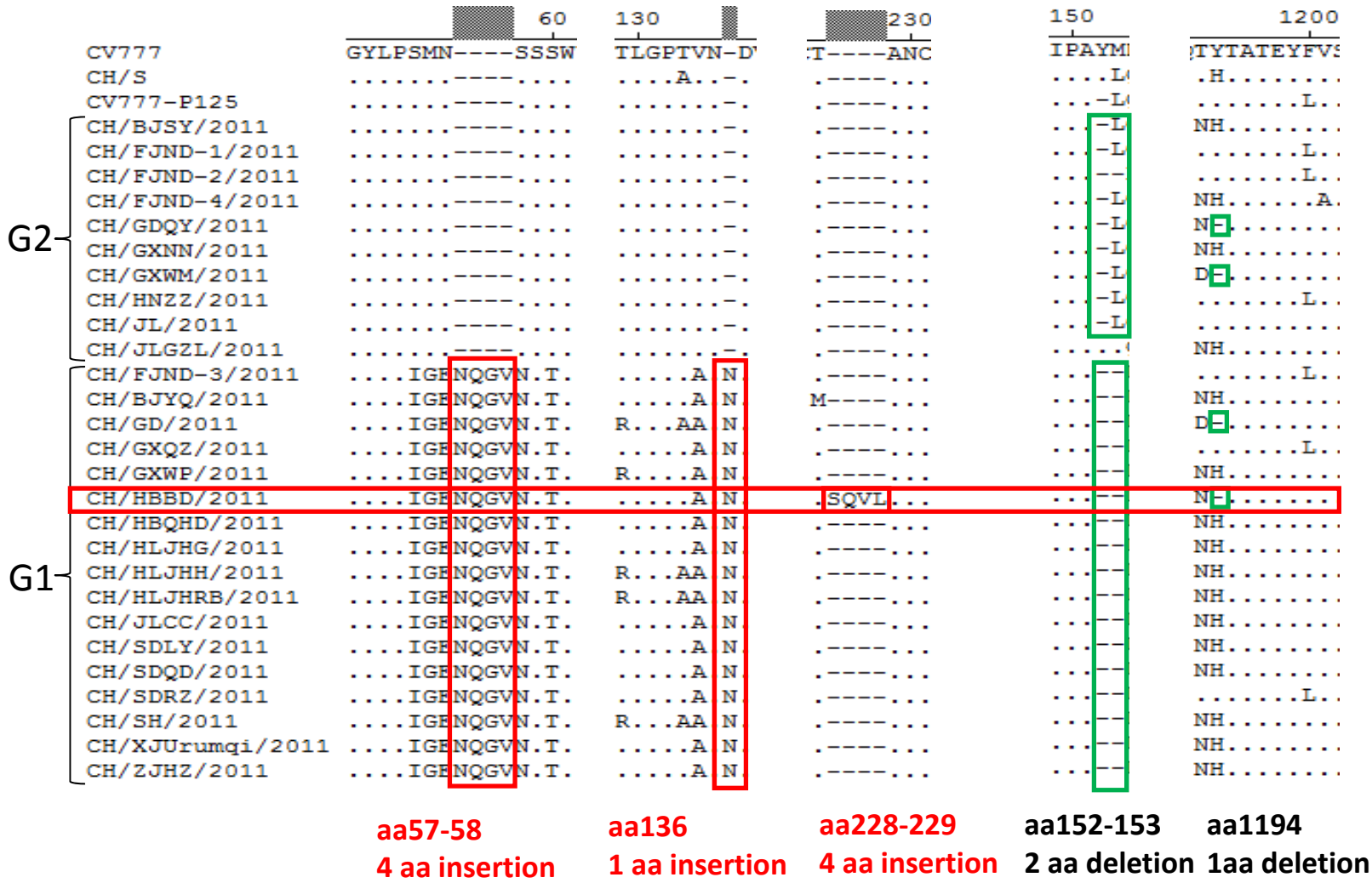
nt401-402
3 nt insertion

nt683-684
12 nt insertion

nt454-459
6 nt deletion,
nt455-457
3 nt deletion

nt3580-3582
3 nt deletion,
nt3578-3580
3 nt deletion

Amino acid mutations present in S protein of G1 PEDV compared to G2 PEDV in China



aa57-58
4 aa insertion

aa136
1 aa insertion

aa228-229
4 aa insertion

aa152-153
2 aa deletion

aa1194
1aa deletion

Analysis of amino acid sequences in COE(aa499-638) domains of PEDV S protein

Strains	Amino acids in COE of CV777-P125																			Ratios
	500S	505I	509T	520N	526A	530H	543N	546S	558T	572K	576S	603G	610F	614E	615F	617S	618G	629T	632E	
BJSY, FJND-4, GDQY, GXNN, HNZZ, JL																				0/140
GXWM																		A		1/140
JLGZL					S				S			S								3/140
FJND-1/-2					S	P			S			S				G				5/140
GXQZ		T							S	N		S								4/140
JLCC		T							S	N		S								4/140
SDLY			A		S				S			S								4/140
BJYQ					S	P			S			S				G				5/140
SDRZ		T	I						S	N		S								5/140
XJUrumqi		T			S	R			S			S								5/140
ZJHZ		T							S	N		S						I		5/140
GXWP					S				S		T	S		D	Y					6/140
HBBD		T						G	S			S	L				A			6/140
HBQHD		T				R			S	N		S				G				6/140
SDQD		T			S	L			S			S		D						6/140
GD				I	S				S		T	S		D	Y					7/140
HLJHG		T				R	S		S	N		S				G				7/140
HLJHH/HRB				I	S				S		T	S		D	Y					7/140
FJND-3	G				S	P		R	S		G	S				G				8/140
SH				I	S				S		T	S		D	Y				G	8/140

COE (aa499-638) domain firstly reported by **Chang S H, et al.2002, Mol. Cells 14:295–299. Chen et al., 2013**

Comparison of the antigen epitopes of S proteins of field strains and reference strains

SS2 (^{748}YSNIGVCK^{755}) **SS6** (^{764}LQDGQVKI^{771}) ^{1368}GPRLQPY^{1374} against 2C10

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CV777-attenuated TEPVLVYSNIGVCKSGSIGYVPLQDGQVKIAPMVTGNISIPTNFSMSI RGPRLQPYEAFEKVHVQ
CV777            ..........................S.Y.......T................ ........................
CH/S             ..........................S.S........................ ........................
CH/BJSY/2011     ..........................S.S.......T................ .........V.......
CH/FJND-4/2011   .......................................................... .........V.......
CH/GDQY/2011     ..........................S.S.......T................ ........................
CH/GXNN/2011     .......................................................... .........V.......
CH/GXWM/2011     .......................................................... ........................
CH/HNZZ/2011     .......................................................... ........................
CH/JL/2011       .......................................................... ........................
CH/YNKM/2012     ..........................S.S.......T................ .........V.......
CH/FJND-1/2011   ..........................S.S.......T................ ........................
CH/FJND-2/2011   ..........................S.S.......T................ ........................
CH/JLGZL/2011    ..........................S.S........................ ........................
CH/AHHF/2012     ..........................S.S........................ ........................
CH/FJXM-2/2012   ..........................S.S.......T................ .........V.......
CH/BJYQ/2011     ..........................S.S.......T................ .........V.......
CH/FJND-3/2011   ..........................S.S.......T................ ........................
CH/GD/2011       ..........................S.S.......T................ ........................
CH/GXQZ/2011     ..........................S.S.......T................ ........................
CH/GXWP/2011     ..........................S.S.......T................ ........................
CH/HBBD/2011     ........................SS.S.......T................ .........V.......
CH/HBQHD/2011    ..........................S.S....V..T................ ........................
CH/HLJHG/2011    ......C...................S.S.......T................ .........V.......
CH/HLJHH/2011    ..........................S.S.......T................ .........V.......
CH/HLJHRB/2011   ..........................S.S.......T................ .........V.......
CH/JLCC/2011     ..........................S.S....V..T................ ........................
CH/SDLY/2011     ..........................S.S.......T................ .........V.......
CH/SDQD/2011     ..........................S.S........................ .........V.......
CH/SDRZ/2011     ..........................S.S.......T................ ........................
CH/SH/2011       ..........................S.S.......T................ .........V.......
CH/XJUrumqi/2011 ..........................S.S.......T................ .........V.......
CH/ZJHZ/2011     ..........................S.S.......T................ .........V.......
CH/AHHF-2/2012   ..........................S.S........................ ........................
CH/FJXM-1/2012   ..........................S.S.......T................ .........V.......
CH/GXNN/2012     ..........................S.S.......T................ ........................
CH/HBSN/2012     ..........................S.S.......T................ .........V.......
CHGD-1           ........................RS.S.......T................ ........................
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(Chen J et al., 2013, Viruses)

Summary

- PEDV is the main pathogen causing the pig diarrhea. More than 80% pig farms are positive of PEDV. And PED are presented in at least 29 provinces in China.
- Although the hogs show similar clinical signs, but there are big different agents or situation in diarrheal pig farms, about 40% pig farms are positive of TGEV in China, and PoRV presented in China, and co-infection (TGEV,PEDV,PoRV) is serious, too.
- 2 genotypes of PEDV are present in China, and genetic variation (insertion or deletion) is present in the genome of different PEDV strains(group2), point mutations of amino acids are present in the antigenic region and epitopes.

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