Sponsored by People's Republic of China









SEACFMD Laboratory Network Meeting Lanzhou, People's Republic of China 24-25 October 2023

Basic research supports FMD prevention and control

Dr. Zixiang Zhu

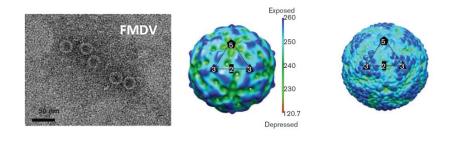
State Key Laboratory for Animal Disease Control and Prevention, National Reference Laboratory for Foot-and-mouth disease, Lanzhou Veterinary Research Institute, Chinese Academy of **Agricultural Sciences, Lanzhou, China**



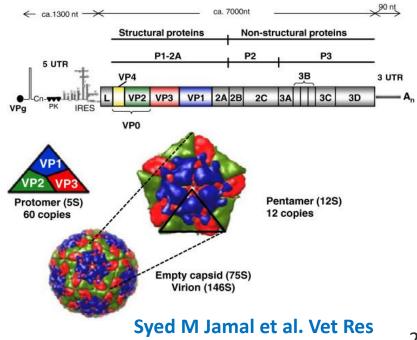
LANZHOU VETERINARY RESEARCH INSTITUTE, CHINESE ACADEMY OF AGRICULTURAL SCIENCES

FMDV: Background

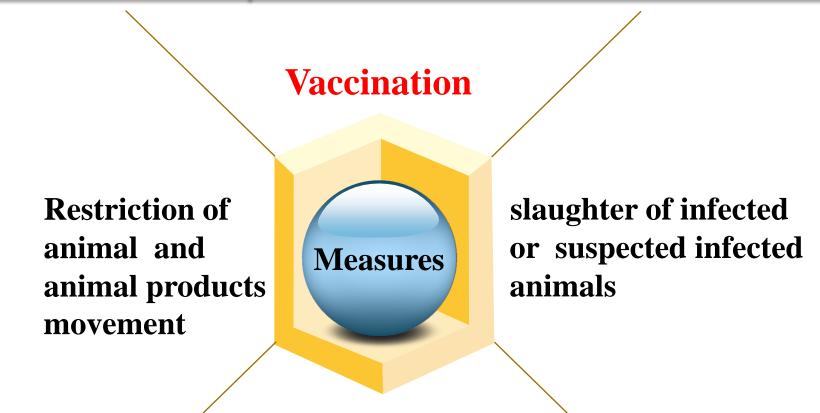
- FMDV is an aphthovirus of the family *Picornaviridae*. It is highly contagious and has a high mutation rate, leading to extensive genetic variation.
- The RNA virus genome of FMDV displays a very high mutation rate because the virus-encoded RNA polymerase lacks a proofreading mechanism.



Maria Gullberg et al. JGV



Outlines of prevention and control of FMD



Serological and etiological surveillance.

Compulsively inoculated with vaccine combined with slaughtering in China

FMD Etiology and Immunity Team

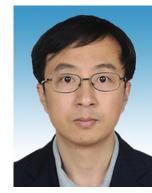
Epidemiology

- FMD virus (FMDV) Isolation
- FMDV evolution and distribution study
- Identifying risk factors for FMD
- Pathogenic mechanism
 - Host tropism of FMDV
 - The virulence and antigenic variation of FMDV
 - The suppressive role of FMDV on host immune system
- Establishment of vaccine development platform
 - Vaccine development
 - Vaccine process development and manufacture

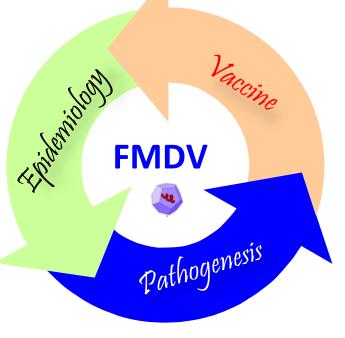
FMD vaccines have been developed:

I. FMD O/May-98 inactivated vaccine II. FMD O-Asia1-A trivalent inactivated vaccine III. FMD DNA vaccine

Two of the developed Vaccines were recommended by WOAH/FAO for FMD control.

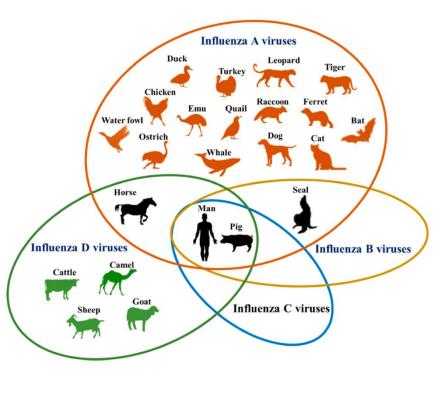


Prof. Dr. Zixiang Zhu Email: zhuzixiang@caas.cn



Changes in host range are central to virus emergence

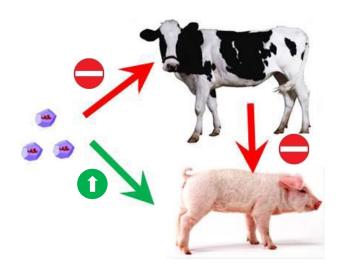
- Tropism of a virus pertains to the types of cells, tissues, and animal species in which it can replicate.
- Because various replication steps of viruses require host proteins, the expression levels of such host proteins in a cell affect tropism.
- This explains why most pathogens are only capable of infecting a limited range of host organisms.



Suresh V. Kuchipudi et al, Vet SCI

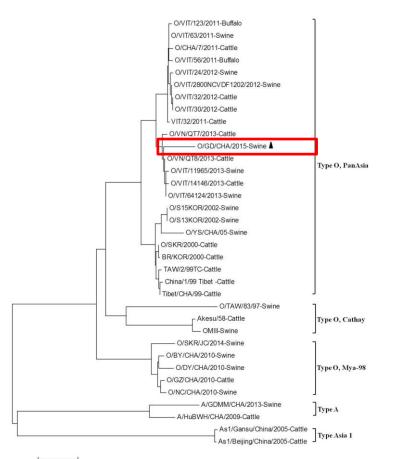
(1) Historical question : Cattle OMII strain, Taiwan 97 Cathay topotype strains (PK region includes a 43- or 86-nt deletion);

(2) Current question: PanAsia lineage FMDV (PK region includes an 86-nt deletion).



3A is a previously reported determinant of altered virulence of FMDV in Taiwan, China. Why all Cathay strains include same PK region deletion?

A PanAsia lineage FMDV strain O/GD/CHA/2015











0.05	-												
Sequence Name	< Pos = 402												
- Consensus	AAGTTTT	ACCGCCTT	TCCCGGCGT	TAAAGGGAG	GTAACCAC	AAGCTTGCAA	CTGTCTTGCT	CGACGATAAAGG	GCTGTGACC	GCAAGAT GAT	ACCGCCTT	TCCCGGCGTTA	ATTGGA
6 Sequences		410	420	430	440	450	460	470	480	490	500	510	5
O-GD-CHA-2015-PanAsia-Swine.seq	AAGTTTT										GCCGCCTT	TCCCGGCGTTA	AATGGA
O-CHA-7-2011-PanAsia-Cattle.seq	AAGTTTT	FACCGCCTT	TCCCGGCGT	TAAAGGGAG	GCAACCAC	AAGCTTGCAA	CT GT CT T GCT	CGACGATAAAGG	GCT GT GACC	GCAAGAT GAT	ACCGCCTT	TCCCGGCGTTA	ATTGGA
O-YS-CHA-05-PanAsia-Swine.seq	AAGTTTT	FACCGCCTT	TCCCAGCGT	TAAAGGGAG	GT AACCAC	AAGCTTGCGT	CT GT CT T GCT	CGACGATAAAGG	GCT GT GACC	GCAAGAT GAT	ACCGCCTT	TCCCGGCGTTA	ATTGGA
China-1-99-(Tibet)-PanAsia-Cattle.seq	AAGTTTT	ACCGTCGT	TCCCGGCGT	TAAAGGGAG	GTAACCAC	AAGCTTGCAA	CT GT CT T GCT	CGACGATAAAGG	GCT GT GACC	GCAAGAT GAT	ACCGCCTT	TCCCGGCGTTA	ATTGGA
TAW-2-99-TC-PanAsia-Cattle.seq	AAGTTTT	FACCGCCTT	TCCCGGCGT	TAAAGGGAG	GTAACCAC	GAGCTTGCAA	CTGTCTTGCC	CGACGATAAAGG	GYTGTGAYY	GCAAGAT GAT	ACCGCCTT	TCCCGGCGTTA	ATTGGA
Tibet-CHA-99-PanAsia-Cattle.seq	AAGTTTT	TACCGCCTT	TCCCGGCGT	TAAAGGGAG	GTAACCAC	AAGCTTGCAA	CT GT CT T GCT	CGACGATAAAGG	GCTGTGACC	GCAAGAT GAT	ACCGCCTT	TCCCGGCGTTA	ATTGGA

Alignment of the 5' UTR Sequences

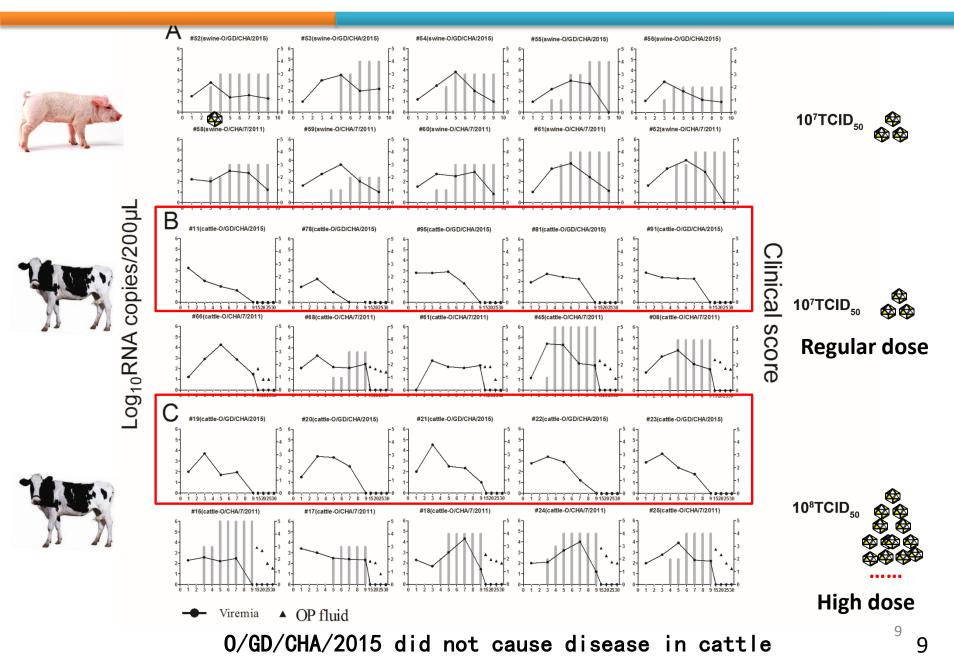
ile Edit Align View Options NetSearch Window Help																		
Sequence Name	< Pos = 417																	
Consensus	AGTTTTTACCG	TCTTTCCCGG	CGTTAAA	GGGGA GGT A	ACCACAAG	CTTGCAAC	CGTCTTG	CCCGACGT	AAAGGGCTG	- TAACCGCAA	GCTT- GTA	CCGCCTTT	- CCCGGCGT	AACGGGAT	GTAACCAC	AGATGAA	CCTTCAC	CCGGAAC
16 Seguences	420	430	440	450	460	47)	480	490	500	510	520	530	1	540	550	560	
Q632769-MAY-7-2001-Cattle.seq		TTCCCGA	CGTTAAAG	GGG- AT GT A	ACCACAAG	CTTAGTAC	CTTCGTG	CCGAAGT	AAAGGACTG	- TAACCACAA	GCTT-AGA	CCGCCTTA	TTCCGGCGT	TAAT GGAAT	GTAACCAC	AGATGGA	CCTTCACO	CGGAAC
Q632770-MAY-1-2004-Cattle.seg	NNNTTT- GCCG	TCGTTCCCG-	ACGTTAAA-	GGGATGAA	ACCACAAG	CTTGGAAC	CGTCTTA	CCCGATGT	AACGGGTTG	- TGACCACAC	GCTT- GTG	CCGCCTTT	- CCCGGCGT	CAATGGGAT	GTAACTAC	AGCTAAA	CCTTCATO	CGGAAC
Q632772-MAY-7-2007-Cattle.seg	NN- TTGCCG	TCGCTCCCAA-	CGTTAAAC	GG- AGGCA	ACCATAAG	CTTTGTGC	CTTCTTG	CCGAAGC	AAAGGACTG	- CAACCGCAA	GCTTTAAA	CCGCCTT-	TCCCGGCGT	CAACGGGAT	GTAACCAC	AGGTAGA	CCTTCGCC	CGGAAG
F112879-TAI-22-2009-Swine.seg	NNNNN G	TCGCTCCCGA	CGTTAAAA	GG- AGGTA	ACCACAAG	ATTTGCGC	CTTCTTG	CCGAAGT	AAAGGACTG	- TAACCGCAA	GCTTTGAA	CCGCCTT-	TCCCGGCGT	AACGGGAT	GTAACCAC	AGATGGA	CCTTCATO	CGGAA
F112880-MYA-5-2009-Cattle.seg	NNNNG	TCGCTCCCGA	CGTTAAAG	GGG- A GGT A	ACCACAAG	ATTTGCAC	CTTCTTG	CCGAAGT	AAAGGACTG	- GAACCGCAA	GCTTTGAA	CCGCCTT-	TCCCGGCGT	AACGGGAT	GTAACCAC	AGATAGA	CCTTCATO	CGGAA
=112881-MOG-7-2010-Cattle.seg	NNTTTGCCG	TCGCTCCCGA	CGTTAAAA	GG- AGGTA	ACCACAAG	CTTTGTGC	CTTCTTG	CCGAAGT	AAAGGACTG	- TAATCGCAA	GCTTTAAA	CCGCCTT-	TCCCAGCGT	AACGGGAT	GTAACCAC	AGATAGA	CCTTCGCC	CGGAA
F112882-MOG-C-10-2010-Cattle.seg	GTACTACCG	TCGCTCCCGA	CGTTAAAC	GGG- A GGT A	ACCACAAG	CTTTGTGC	CTTCTTG	CCGAAGT	AAAGGACTG	- TAACCGCAA	GCTTTAAA	CCGCCTT-	TCCCAGCGT	TAAAGGGAG	GTAACCAC.	AGACAGA	CCTTCGCC	CGGAA
F112885-JPN-1-2010-Cattle.seg	TACTACCG	TCGCTCCCGA	CGTTAAAA	GG- AGGTA	ACCACAAG	ATTTGCGC	CTTCTTG	CCGAAGT	AGAGGGCTG	- TAACCGCAA	ACTTTGAA	CCGCCTT-	TCCCAGCGT	AACGGGAT	GTAATCAC	AGATGGA	CCTTCATO	CGGAA
F112886-SKR-4-2010-Cattle.seg	TACTACCG	TCGCTTCCGA	CGTTAAAG	GG- AGGTA	ACCACAAG	ATTTGCGC	CTTCTTG	CCCGAAGT	AGAGGGCTG	- TAACCGCAA	ACTTTGAA	CCGCCTT-	TCCCGGCGT'	AACGGGAT	GTAACCAC	AGATGGA	CCTTCATO	CGGAA
F112887 -SKR-5-2010-Swine.seq	TACTACCG	TCGCTCCCGA	CGTTAAAA	GG- AGGTA	ACCACAAG	ATTTGCGC	CTTCTTG	CCGAAGT	AGAGGACTO	- TAACCGCAA	ACTTTGAA	CCGCCTT-	TCCCGGCGT	AACGGGAT	GTAATCAC	AGATGGA	CCTTCATO	CGGAA
=112888-DRK-31-2011-Cattle.seg	NNNNN- G	TCGCTCCCGA-	CGTTAAAG	GG- AGGTA	ACCACAAG	ACTTGCGC	CTTCTTG	CCGAAGT	AGAGGGCTG	- TAACCGCAA	ACTTTGAA	CCGCCTT-	TCCCGGCGT	TAACGGGAT	GTAACCAC	AGATGGA	CCTTCATO	CGGAA
112889-HKN15-2010-Swine.seg	NNNNNNN	NN- CTCCCGA-	CGTTAAAG	GG- AGGTA	ACCACAAG	ATTTGCGC	CTTCTTG	CCGAAGT	AGAGGGCTG	- TAACCGCAA	ACTTTGAA	CCGCCTT-	TCCCGGCGT	TAACGGGAT	GTAATCAC	AGATAGA	CCTTCATO	CGGAA
694731-O-S01KOR-2002-Swine.seg	AGTTTTTACCG	CCTTTCCCGG	CGTTAAAG	- GGA GGT A	ACCACAAG	CTTGCGAC	TGTCTTG	CTCGACGA	AAAGGGCTG	- TGACCGCAA	GATG- ACA	CCGCCTTT	- CCCGGCGT	AATTGGAT	GTAACCAC	AGATGAA	CCTTCACO	CGGAA
694732-O-S02KOR-2002-Swine.seg	AGTTTTTACCG	CCTTTCCCGG	CGTTAAAA	- GGA GGT A	ACCACAAG	CTTGCGAC	TGTCTTG	CTCGACGA	AAAGGGCTG	- TGACCGCAA	GATG- ACA	CCGCCTTT	- CCCGGCGT	TAATTGGAT	GTAACCAC	AGATGAA	CCTTCACO	CGGAA

(1) The PKs region of several type O PanAsia FMDV strains and OMII strain includes an 86-nt deletion.

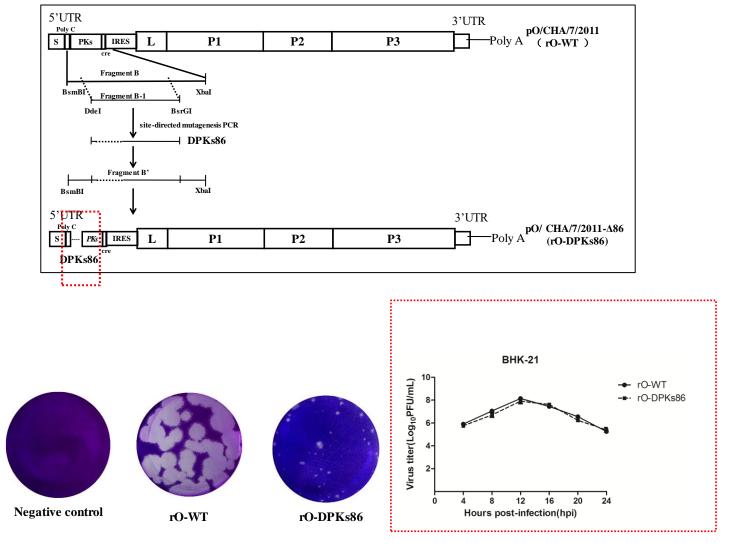
(2) The PKs region of Cathay strains includes 43-nt deletion.

KX162590-O-SKR-JC-2014-Swine.seg	A GTCCGCCTT-TCCCGGCGTTAACGGGACGTAACCGCAAGATGGACCTTCACCCGGAAGTA
KY234502-O-GD-CHA-2015-PanAsia-Swine.s	
AY359854-OMIII-Cathay-Swine.seq	
AF511039-Akesu-58.seq	
HQ412603-O-YM-YN-2000-Swine.seq	
AY593835-otaiwan97 iso106-112-Swine.seq	
AF308157-Yunlin-Twiwan-1997-Swine.seq	
AY593833-openghu iso108-1999-Swine.seq	
HQ632771-MAY-8-2005-Swine.seq	
KY234501-O-CHA-7-2011-PanAsia-Cattle.se	
JN998085-O-BY-CHA-2010-Swine.seq	AAGTCTTACCGTCATTCCCGA- CGTTAAAGGG- AGGTAACCACAAGATTTGCGCCTTCTTGTCCGAAGTTAGAGGGCTG- TAACCGCAAATTTTGAACCGCCTT- TCCCGGCGTTAACGGGATGTAATCACAAGATGGACCTTCATCCGGAAGTA
AJ539136-TAW-2-99-TC-Cattle.seq	A GTTTTTACCGCCTTTCCCGG- CGTTAAAG- GGAGGTAACCACGAGCTTGCAACTGTCTTGCCCGACGATAAAGGGYTG- TGAYYGCAAGATG- ATACCGCCTTT- CCCGGCGTTAATTGGATACAACCACAAGATGAACCTTCACCCGGAAGTA
AJ539138-Tibet-CHA-99-Cattle.seq	AGTTTTTACCGCCTTTCCCGG- CGTTAAAG- GGAGGTAACCACAAGCTTGCAACTGTCTTGCTCGACGATAAAGGGCTG- TGACCGCAAGATG- ATACCGCCTTT- CCCGGCGTTAATTGGATGCAACCACAAGATGAACCTTCACCCGGAAGTA
LC036265-O-JPN-2010 290-1E-Cattle.seq	AAGTACTACCGTCGCTCCCGA-CGTTAAAGGG-AGGTAACCACAAGATTTGCGCCTTCTTGTCCGAAGTTAGAGGGCTG-TAACCGCAAACTTTGAACCGCCTT-TCCCAGCGTTAACGGGATGTAATCACAAGATGGACCTTCATCCGGAAGTA
AF506822-China-1-99-(Tibet)-Cattle.seq	AGTTTT - ACCGTCGTTCCCCGG- CGTTAAAG- GGAGGTAACCACAAGCTTGCACGACTGTCTTGCTCGACGATAAAGGGCTG- TGACCGCAAGATG- ATACCGCCTTT - CCCGGCGTTAATTGGATGCAACCACAAGATGAACCTTCACCCGGAAGTA
AY593824-o1skr iso85-2000-Swine.seq	AAGTTTTACCGCCTTTCCCGG- CGTTAAAG- GGAGGTAACCACAAGCTTGCAACTGTCTTGCTCGACGATACAGGGCTG- TGACCGCAAGATG- ATACCGCCTTT- CCCGGCGTTAATTGGATGCAACCACAAGATGAACCTTCACCCGGAAGTA
EF614457-O-SKR-14-02-Cattle.seq	A GTTTTTACCGCCTTTCCCGG- CGTTAAAGTGGAGGTAACCACAAGCTTGCG GTCTTGCTCGACGATAAAGGGCTG- TGACCGCAAGATG- ACACCGCCTTT- CCCGGCGTTAATTGGATGTAACCACAAGATGAACCTTCACCCGGAAGTA
HQ009509-China-5-99(Fujian)-Swine.seq	AGTITITACCGTCTTTCCCGG- CGTCAAAG- GGAGGTAACCACAAGCTTGCGTCTGTCTCGCTCGACGATAAAGGGCTG- TGACCGCAAGATG- ATACCGCCTTT- CCCGGCGTTAACTGGATGTAACCACAAGACGAACCTTCACCCGGAAGTA
HM008917-O-YS-CHA-05-Swine.seq	AGTTTTTACCGCCTTTCCCAG- CGTTAAAG- GGAGGTAACCACAAGCTTGCGTCTGCCTCGCCGACGATAAAGGGCTG- TGACCGCAAGATG- ATACCGCCTTT- CCCGGCGTTAATTGGATGTAACCATAAGACGAACCTTCACCCGGAAGTA
HQ632768-MAY-3-2000-Swine.seq	TTCCCGG- CGTTAAAG- GGAGGTAACCACAAGCTTGCAGCTGTCTTGCTCGACGATAAAGGGCTG- TGACCGCAAGATG- ATACCGCCTTT- CCCGGCGTTAATTGGATGTAACCACAAGACGAACCTTCACCCGGAAGTA
JN998086-O-GZ-CHA-2010-Cattle.seq	A GTCTTACCGTCATTCCCGA- CGTTAAAGGG- AGGTAACCACAAGATTTGCGCCTTCTTGTCCGAAGTTAGAGGGCTG- TAACCGCCAAACTTTGAACCGCCTT- TCCCGGCGTTAACGGGATGTAATCACAAGATGGACCTTCATCCGGAAGTA

O/GD/CHA/2015 showed a pig-adapted tropism

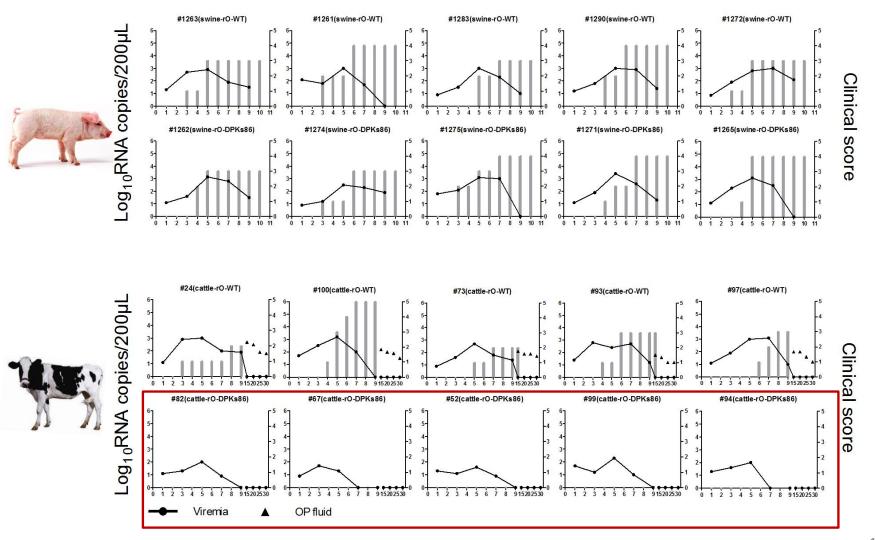


Construction of recombinant FMDV including the 86-nt deletion



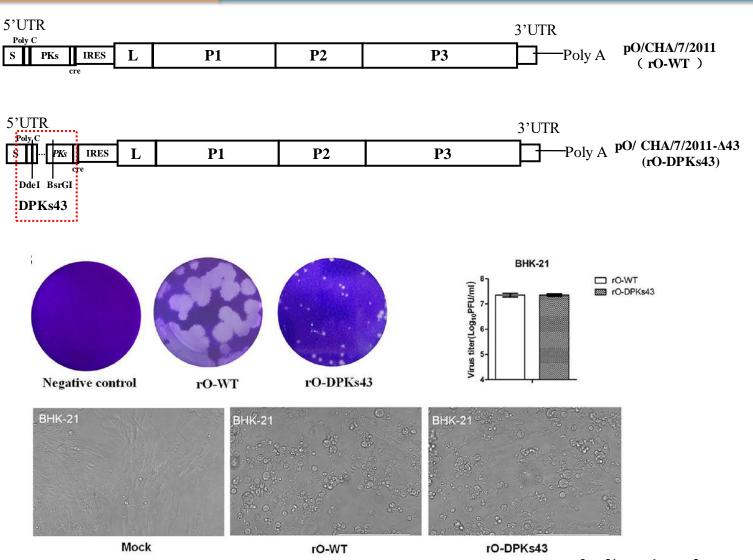
The titers of the recombinant viruses

Deletion of the 86-nt in PKs contributed to the inability of FMDV to cause disease in cattle



¹¹ **11**

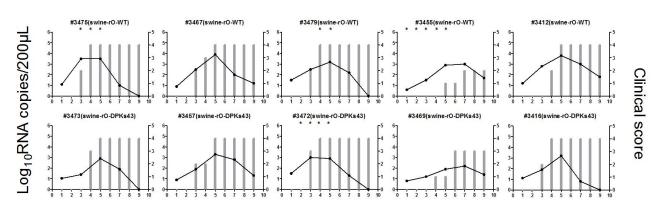
Construction of recombinant FMDV including the 43-nt deletion



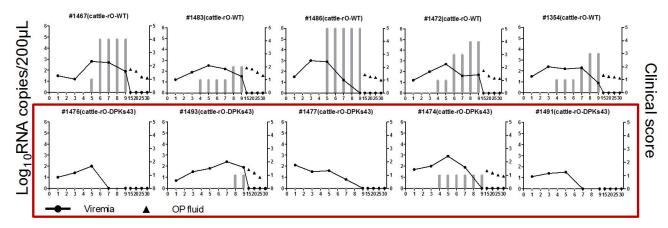
Confirmation of generation of recombinant FMDV ¹²

Deletion of the 43-nt in PKs contributed to the decreased pathogenicity of FMDV in cattle



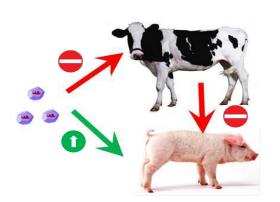






(1) Historical question : Cattle OMII strain and Taiwan 97 Cathay topotype strains showed pig-adapted characteristic that could cause clinical signs in swine but not bovines. PKs deletion is a critical determinant.

(2) Current question: PanAsia lineage FMDV with 86-nt deletion in the PKs region also showed pig-adapted characteristic.





PATHOGENESIS AND IMMUNITY



14

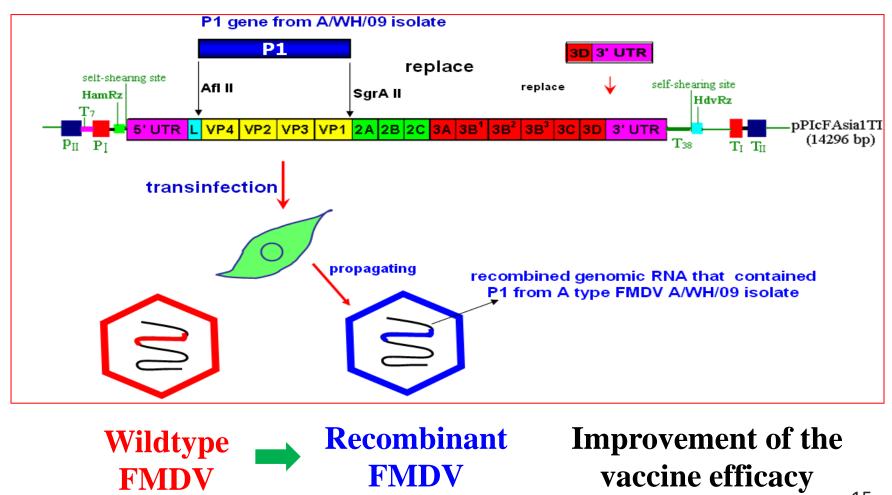
The Pseudoknot Region of the 5' Untranslated Region Is a Determinant of Viral Tropism and Virulence of Foot-and-Mouth Disease Virus

Zixiang Zhu,^a Fan Yang,^a Weijun Cao,^a Huanan Liu,^a Keshan Zhang,^a Hong Tian,^a Wen Dang,^a Jijun He,^a Jianhong Guo,^a Xiangtao Liu,^a Haixue Zheng^a

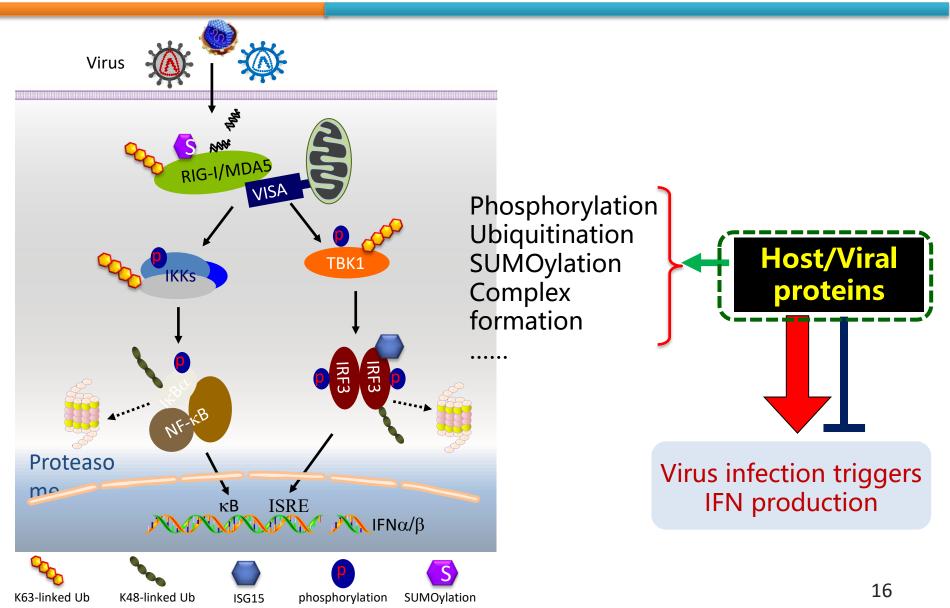
^aState Key Laboratory of Veterinary Etiological Biology, National Foot and Mouth Diseases Reference Laboratory, Key Laboratory of Animal Virology of Ministry of Agriculture, Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Lanzhou, China

These results helped us select appropriate vaccines for controlling of FMD in pigs.

Deletion or modification of the immunosuppressive sites or domains in viral proteins is a prominent strategy to develop FMDV vaccine strain

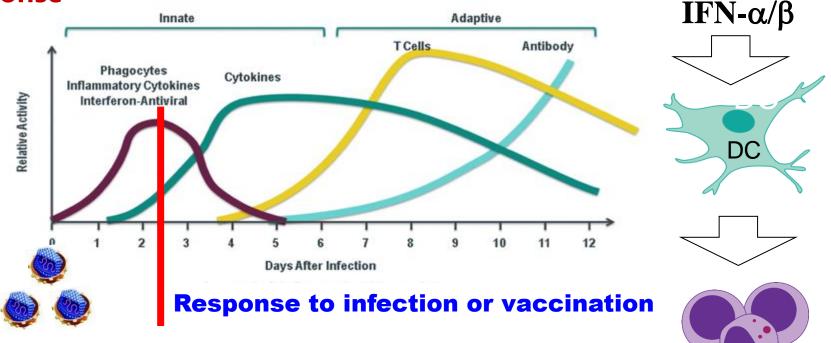


Innate immune pathways are critical for induction of host antiviral response during viral infection



The mechanisms used by FMDV to antagonize host innate immune response are complicated

Innate immune response is critical for initiation of adaptive immune response



Infection of FMDV

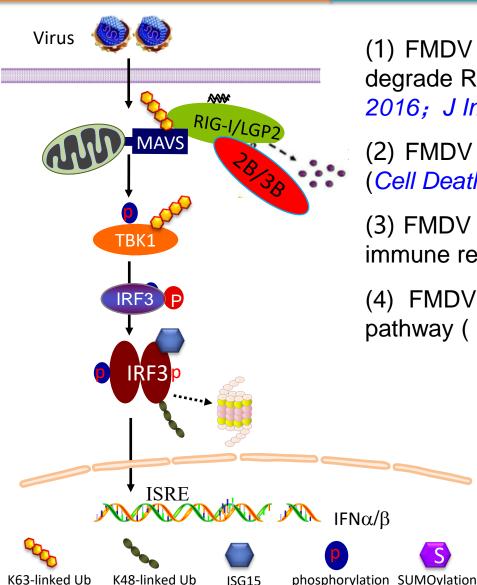
Clarification of the antagonistic mechanisms will provide insights and direction for FMD control

Immune cells

Adaptive immune

response

1. Regulation of pattern-recognition receptors (PRRs) by FMDV

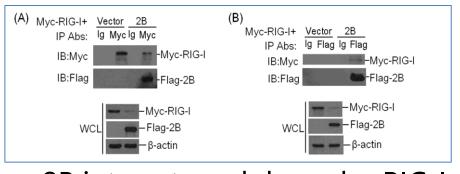


(1) FMDV 2B and 3B proteins interact with RIG-I to degrade RIG-I and promote FMDV replication (*J Virol 2016; J Immunol 2020*).

(2) FMDV 2B interacts with LGP2 to degrade LGP2 (*Cell Death Dis 2017*).

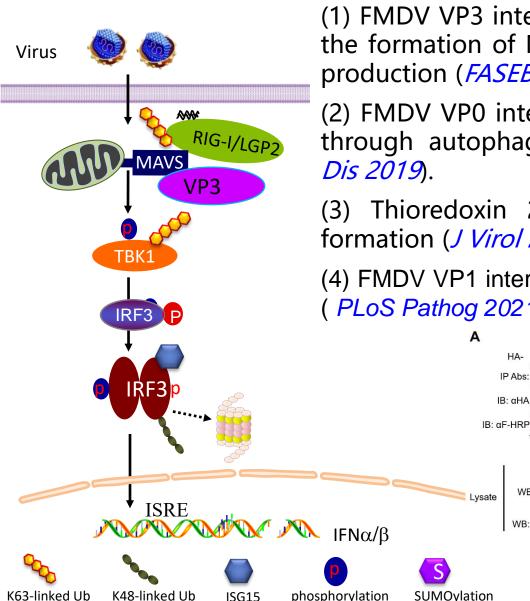
(3) FMDV 2B and 2C degrade NOD2 to block innate immune response (*J Virol 2019*).

(4) FMDV 2C degrades cGAS through autophagy pathway (*PLoS Pathog 2023*)



2B interacts and degrades RIG-I₁₈

2. Regulation of adaptor protein MAVS by FMDV



(1) FMDV VP3 interacts with MAVS and interferes with the formation of MAVS complex, blocking type I IFNs production (FASEB J 2016).

(2) FMDV VP0 interacts with PCBP2 to degrade MAVS through autophagy-dependent pathway (Cell Death

(3) Thioredoxin 2 (TRX2) disrupts MAVS complex formation (J Virol 2020).

(4) FMDV VP1 interacts with IRF3 to block IFNs production (PLoS Pathog 2021)

-F-VP3

F-VP3

MDA5

VISA

-VP3

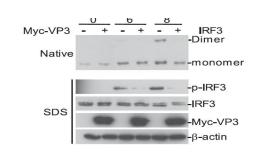
HA-

RIG-I

WB: aHA

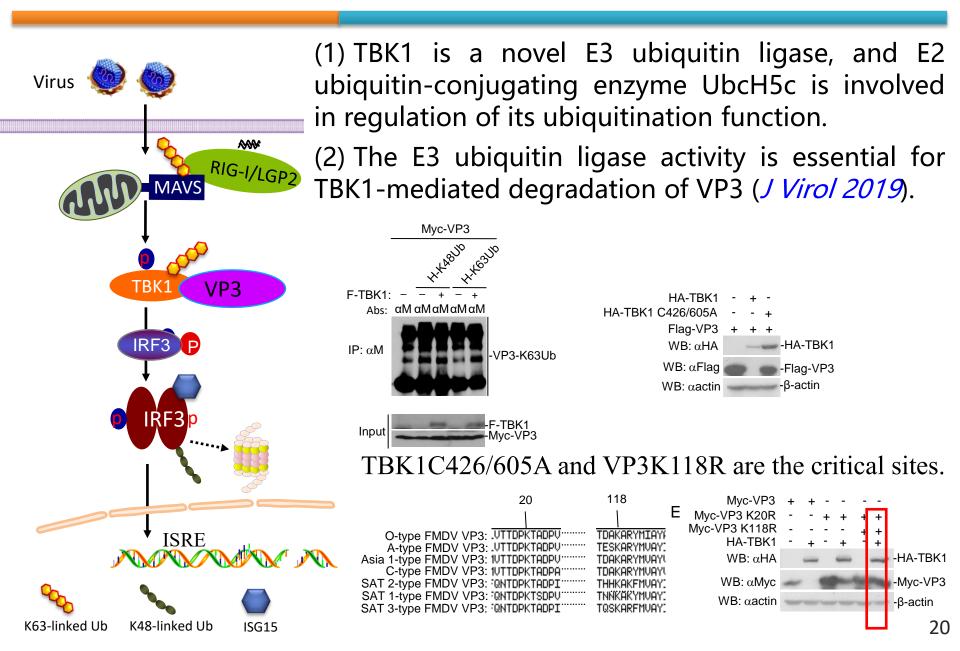
WB: aFlag

IP Abs: Ig aHA Ig aHA Ig aHA

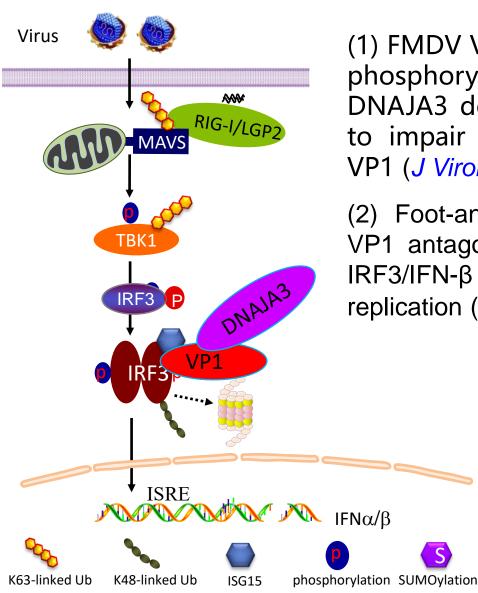


FMDV VP3 interacts with MAVS and blocks IRF3 dimerization.

3. Regulation of adaptor protein TBK1 by FMDV

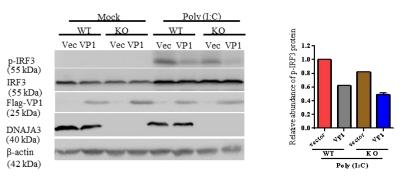


4. Regulation of transcription factor IRF3 by FMDV



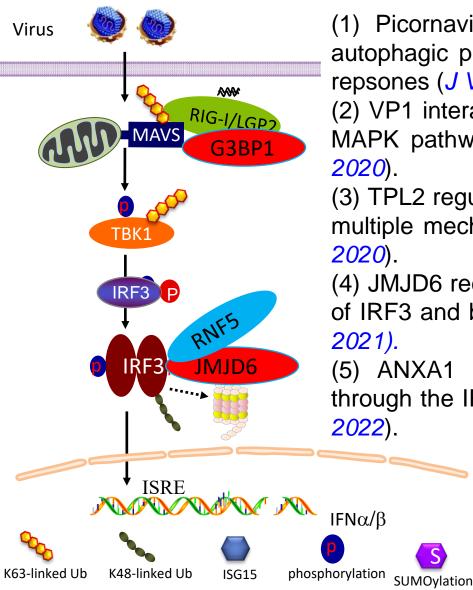
(1) FMDV VP1 interacts with IRF3 and inhibits its phosphorylation and nuclear translocation. Host DNAJA3 degrades VP1 through the autophagy to impair this antagonistic effect induced by VP1 (*J Virol 2019, Cover Story*).

(2) Foot-and-mouth disease virus capsid protein VP1 antagonizes TPL2-mediated activation of the IRF3/IFN- β signaling pathway to facilitate the virus replication (*Frontiers Immunol, 2021*).



Deletion of DNAJA3 enhanced VP1-induced antagonistic effect. 21

5. Regulation of antiviral response by host proteins



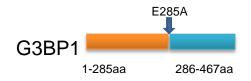
(1) Picornavirus 3A protein degrades G3BP1 through autophagic protein LRRC25 which impairs host antiviral repsones (*J Virol 2020*).

(2) VP1 interacts with RPSA to maintain the activation of MAPK pathway and promote FMDV replication (*J Virol 2020*).

(3) TPL2 regulates host innate immune response through multiple mechanisms (*J Virol, 2020; Frontiers Immunol, 2020*).

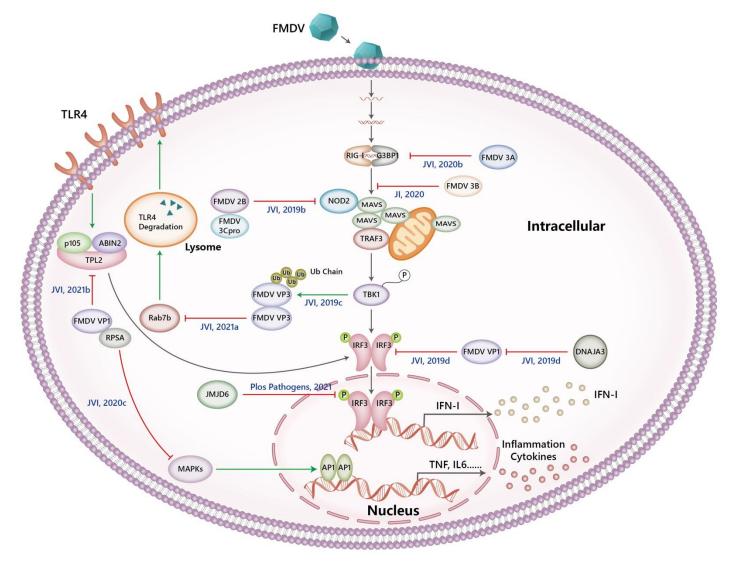
(4) JMJD6 recruits RNF5 to induce the K48 ubiquitination of IRF3 and blocks host antiviral response (*Plos Pathog*, 2021).

(5) ANXA1 promotes FMDV-induced IFNs production through the IRF3 axis at MAVS and TBK1 levels (*J Virol, 2022*).



The 286-467aa of G3BP1 interacts with RIG-I Helicase domain.

6. Schematic representation of the antagonistic mechanisms used by FMDV



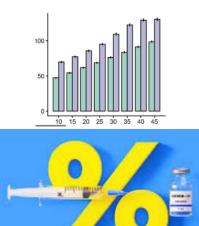
The multiple mechanisms of immune suppression used by FMDV.

Application

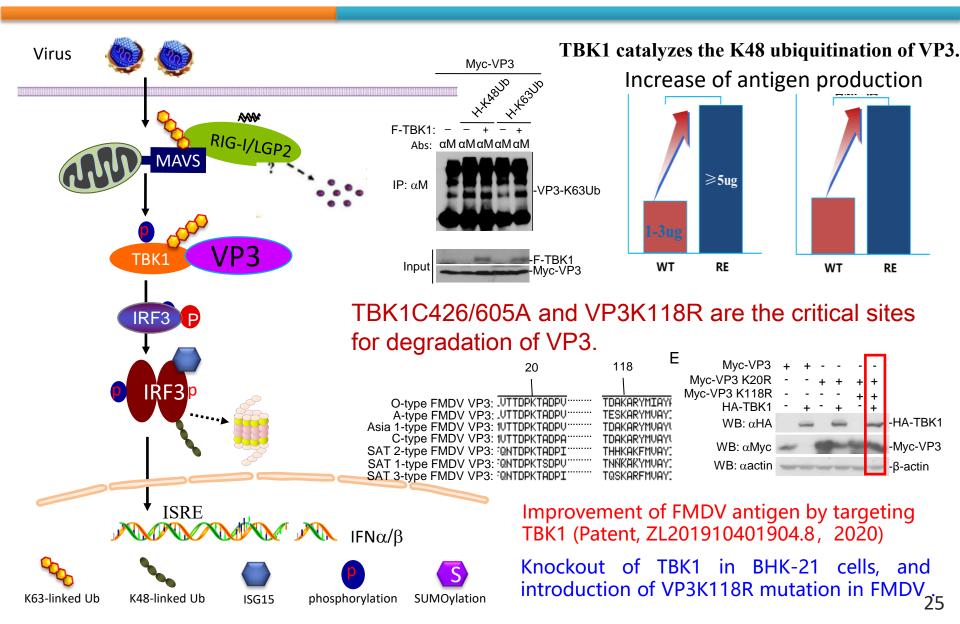
Improvement of vaccine production, safety and efficacy



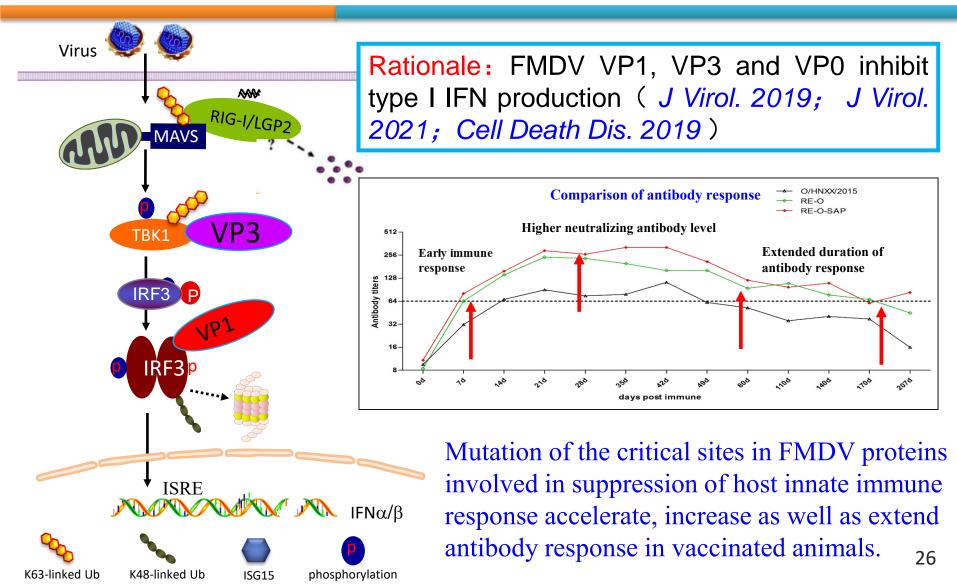




1. TBK1 degrades VP3 which decreases the antigen level during vaccine production

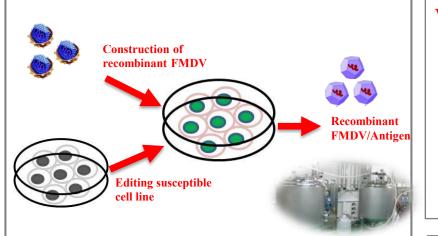


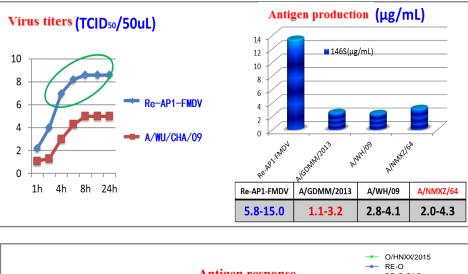
2. Deletion or modification of the immunosuppressive sites in structural proteins to improve the efficacy of FMDV vaccine



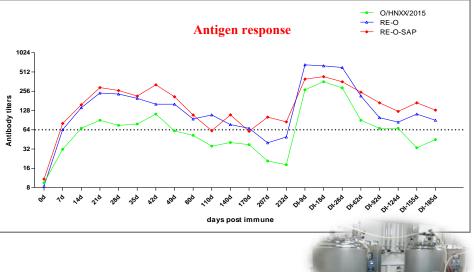
3. Improvement of vaccine performance based on the mechanisms used by FMDV

Producing high-quality vaccines with the performance of high production rates, increased immune efficacy, and improved safety. (Editing virus and cells)





performance	Wildtype vaccine	Modified vaccine
Antigen production	1-3µg/mL	3.89~15.0µg/mL
Start of immune		
response	5-7 d	2-3d
Protection duration	4-6 month	8-12 month
Stability	4℃	√ improved
Cross-protection	Νο	√ improved
Immunosuppressive		
activity	Yes	√ improved
Marker	+/-	√ included



ACKNOWLEDGEMENTS

Haixue Zheng (General Director of LVRI) Xiangtao Liu (Director of NRL-FMD, LVRI)

Jijun He (LVRI)

Jianhong Guo (LVRI)

Donald P King (Pirbright)

Andrew E Shaw (Pirbright)

Dan Li (LVRI)

Yang Fan (LVRI)

Wen Dang (LVRI)

Weijun Cao (LVRI)

Ye Jin (LVRI)

Yanmin Li (SMU)



Thanks for your attention!



Lanzhou Veterinary Research Institute