

# Generation of mAbs to FMDV/A and application in a cELISA for the detection of FMDV/A antibodies

Dr. M. Yang

National Center for Foreign Animal diseases  
/Canadian Food Inspection Agency

# Introduction

Foot-and-mouth disease (FMD) remains one of the world's most widespread epizootic and highly contagious disease.

FMD can cause major economic losses even in previously FMD free countries.

Over 100 countries around world are not considered FMD free by the OIE. FMD is endemic in many areas of Asia, Africa, and South America

FMDV is recognized as 7 serotypes: O, A, C, Asia 1, SAT 1, SAT 2 and SAT 3. O and A are the most wide spread.

FMD is caused by a single-stranded RNA virus belonging to the family *Picornaviridae*.

# FMD is difficult to control and eradicate

because of

1. rapid virus replication
2. high mutation rate
3. high levels of viral excretion
4. small doses required for infection
5. multiple forms of transmission (contact, aerosols)
6. wide geographical distribution
7. broad host range (cattle, buffaloes, pigs, sheep, goats, and ~ 70 wildlife species)
8. ability to establish carrier status (not in pigs)
9. antigenic diversity leading to poor cross immunity among serotypes
10. relatively short duration of immunity

(Longjam et al., 2011; Maree et al, 2011)

# FMDV antibody detection

FMDV specific antibody identification is very useful for:

(1) as an indicator of FMDV infection

(2) the screening of animals for the presence of antibodies before inter-territorial movement,

(3) testing vaccine potency and monitoring the effectiveness of vaccinations

(4) for epidemiological studies of disease in animal populations

(Have and Jensen, 1983)

# Virus neutralization test

VNT is routinely used to detect FMDV antibodies

1. VNT is costly and labour intensive
2. The procedure requires live virus, limiting the test to BL3
3. VNT requires 2-3 days to obtain results.

ELISAs are sensitive, specific, rapid (hours), easy to perform and scale up. cELISA is suitable for the detection of antibodies from different species.

# Objectives

1. To generate and characterize FMDV/A specific mAb
2. To develop a cELISA for serological detection of FMDV-A antibodies
3. To validate the cELISA

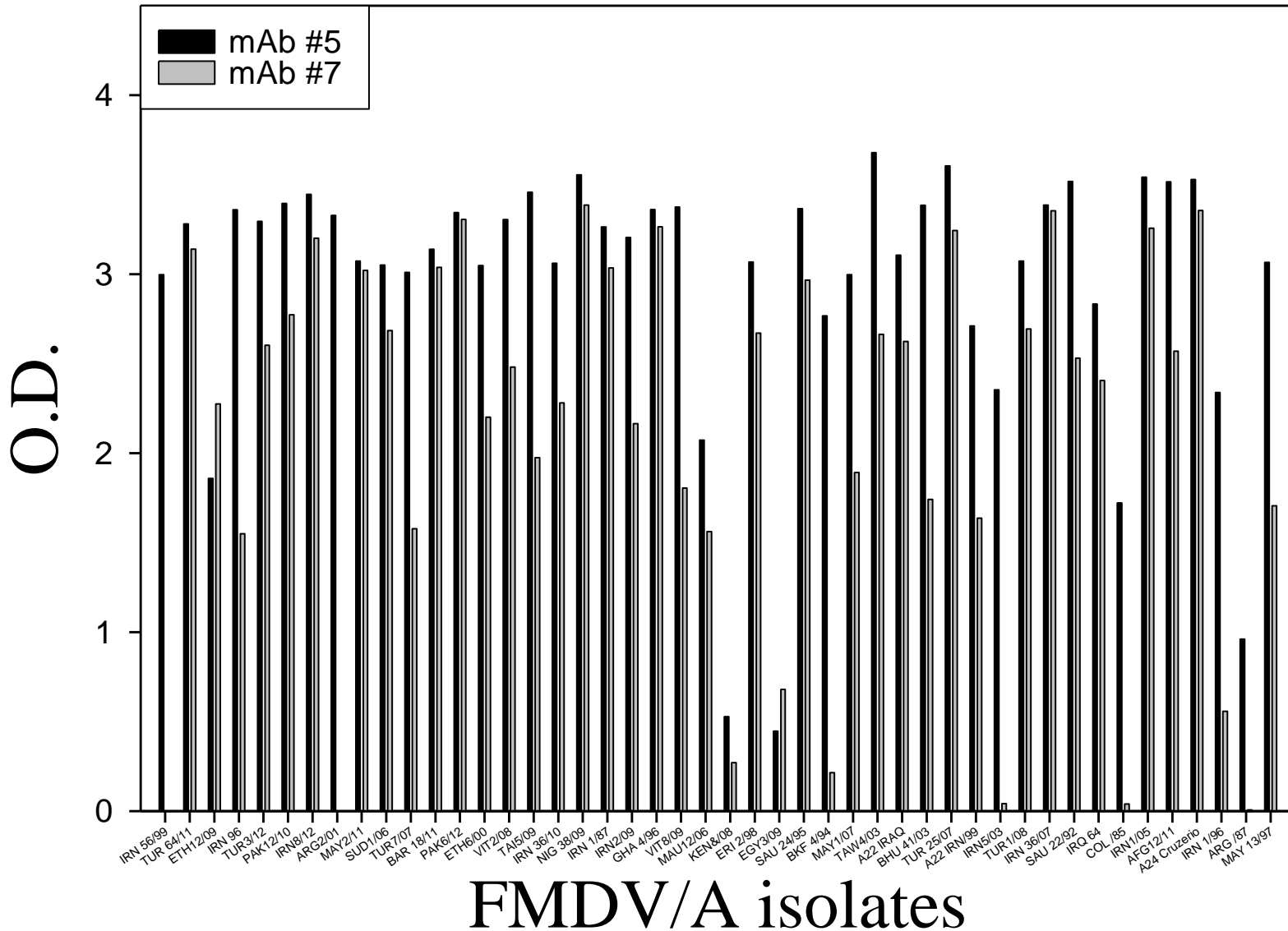
## Advantages using mAbs

low cross-reactivity; easy in standardization;  
and less batch to batch variations

# Characterization of the mAbs against FMDV serotype A

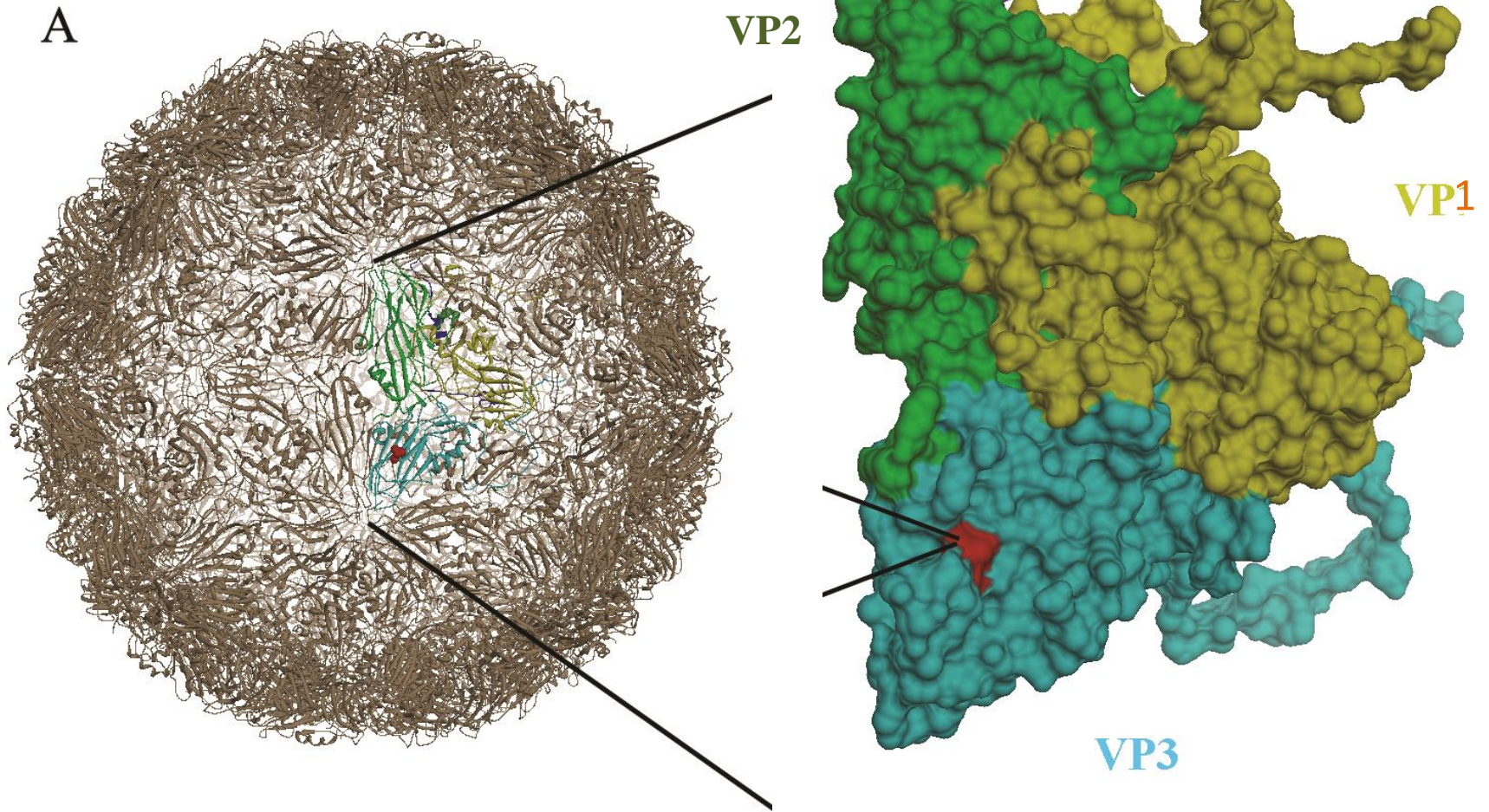
	Name	Isotyping	VNT	Epitope	
#1	F65-2 (F66-2)	IgG2a	>1:16	Con.	
#3	F66-4 (F65-4)	IgG2a	N	Con.	
#4	F66-7	IgG3	N	Con.	
<b>#5</b>	<b>F66-14</b>	<b>IgG2a</b>	<b>&gt;1:16</b>	<b>Con.</b>	<b>cELISA</b>
#6	F67-1	IgG2a	>1:16	Con.	
<b>#7</b>	<b>F67-18</b>	<b>IgG1</b>	<b>&gt;1:16</b>	<b>Con.</b>	<b>cELISA</b>
#8	F67-50	IgG1	N	Con.	
#9	F67-64	IgG1	N	Con.	
#10	F67-92	IgG2a	>1:16	Con.	
#13	F67-25	IgG2a	N	Con.	
#14	F67-30	IgG1	N	Leaner	
#15	F67-49	IgG2a	N	Con.	

# Reactivity of mAbs against FMDV/A 46 isolates in DAS ELISA





# 3D structure of FMDV



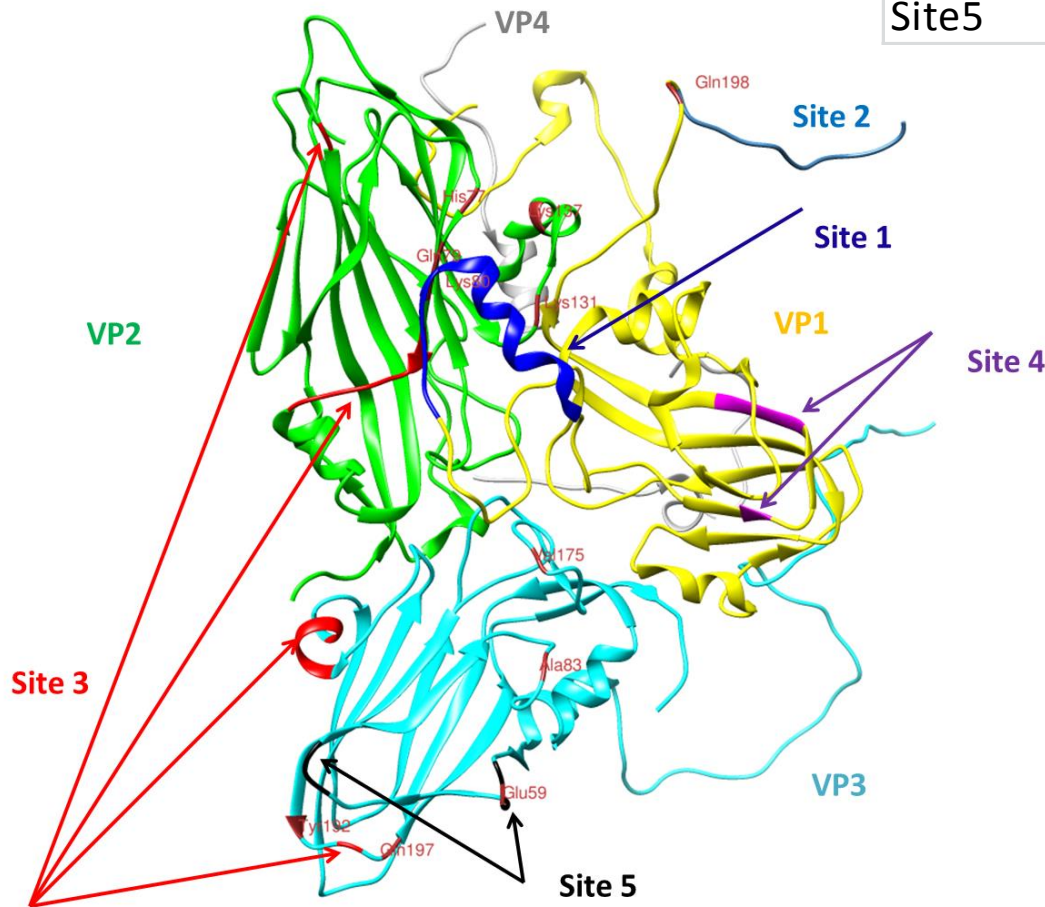
In mature virus particle, 60 copies of the four structural proteins VP1-4 associate to form a capsid which surrounds and protects the genome.

# Localization of FMDV/A antigenic sites in capsid protein

## Serotype A antigenic sites

Site1	VP1 142-157		
Site2	VP1 200-212		
Site3	VP2 82-88, 196	VP3 136-139, 195	
Site4	VP1 169; 175-178		
Site5	VP3 58-61, 69-70		

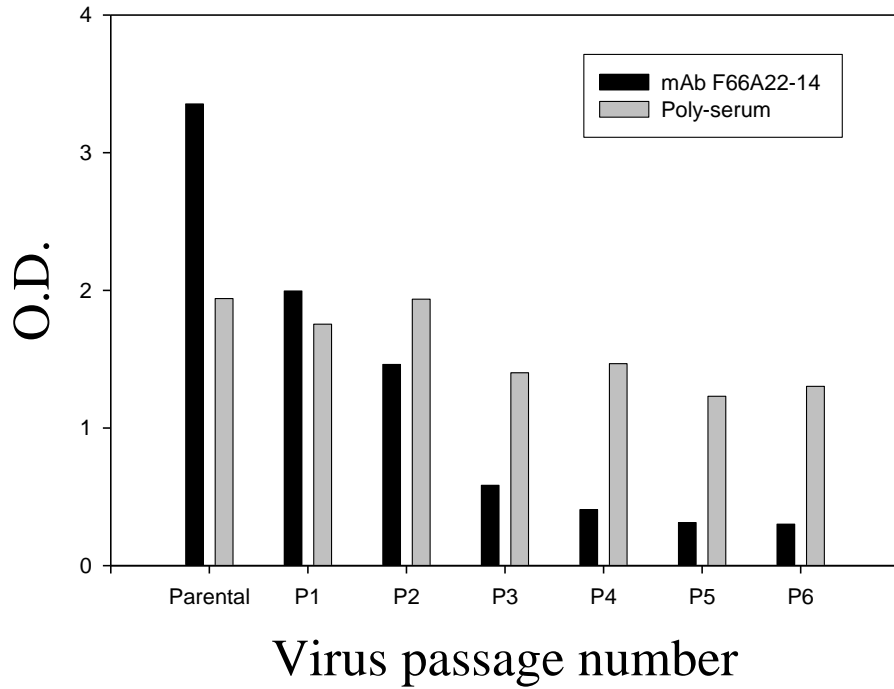
Maree et al, 2011



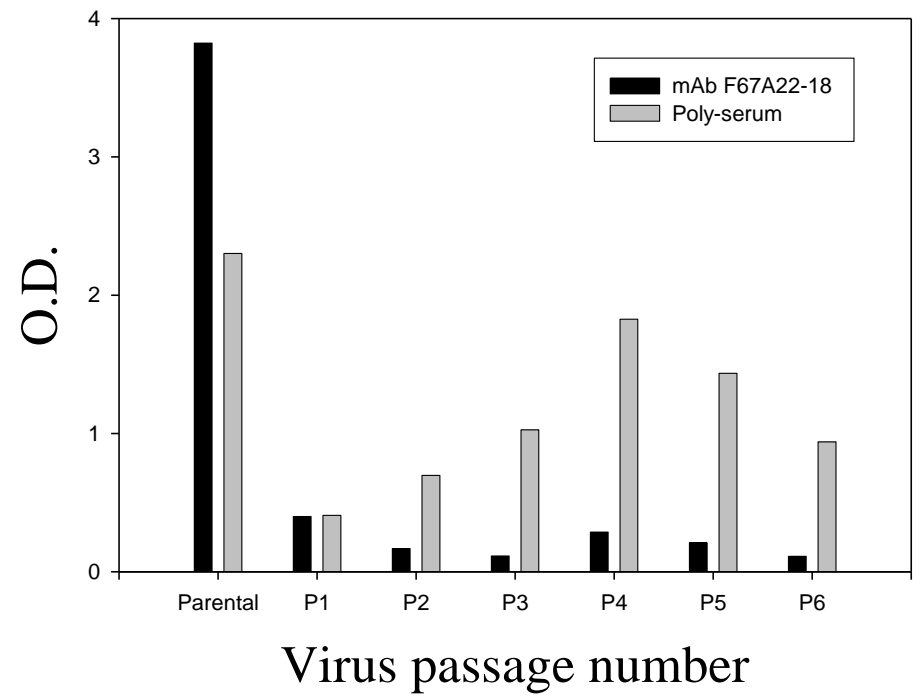
# **mAb resistant mutant selection for conformation epitope identification**

1. FMDV/A22 Iraq and purified mAbs were incubated for 30 min at 37°C.
2. The virus/mAb mixture and controls were inoculated onto MVPK cells.
3. The flasks were incubated until 100% CPE observed and culture supernatants were collected. 1-3 steps were repeated 6 times.
4. The mutants were purified by plaque purification.
5. The selected mutants were sequenced. Pairwise Sequence Alignment is used to identify mutation regions.

# ELISA results after mutant selection



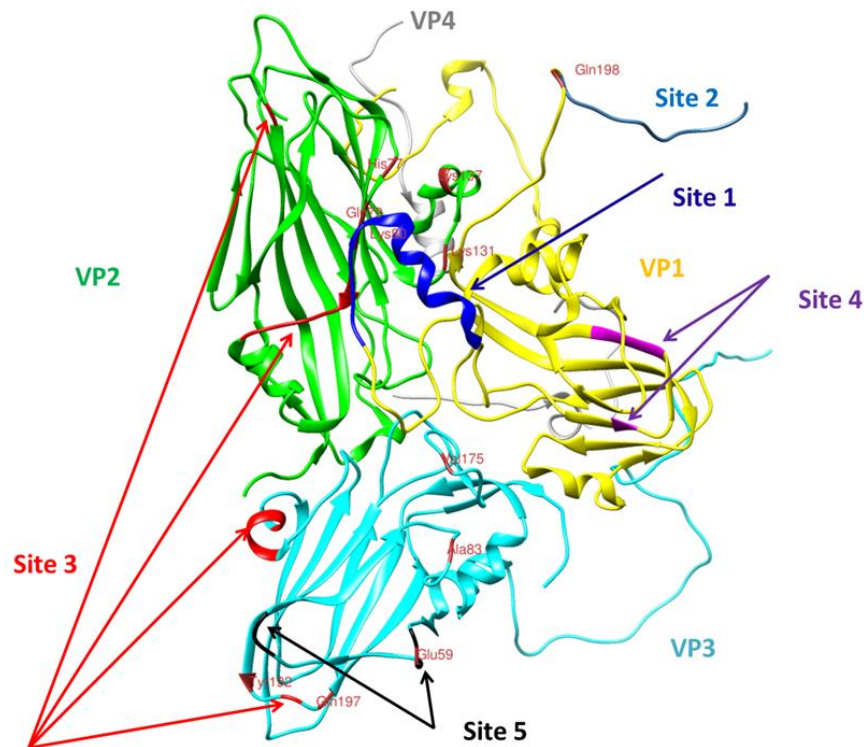
mAb #5



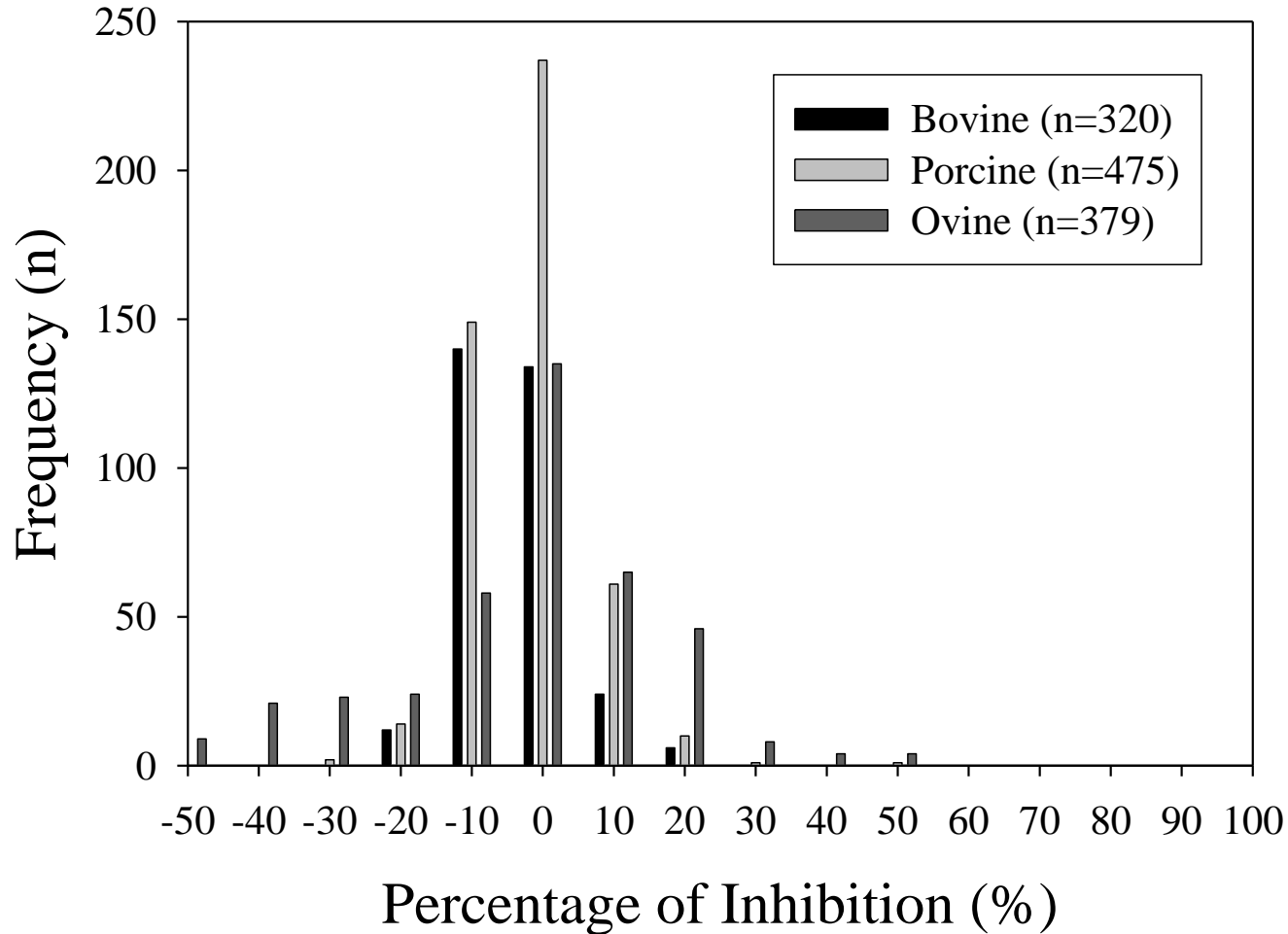
mAb #7

# Identification of neutralization sites of the two mAbs in capsid protein

A22 IRQ mAb mutant	VP2	VP3
F66-14	Gln79→Lys; Lys80→Thr (near site 3); Lys131→Glu	Tyr192→His (near site 3)
F67-18	His77→Arg; Gln79→Glu; Lys80→Thr (near site 3); Lys131→Glu	Tyr192→His (near site 3)

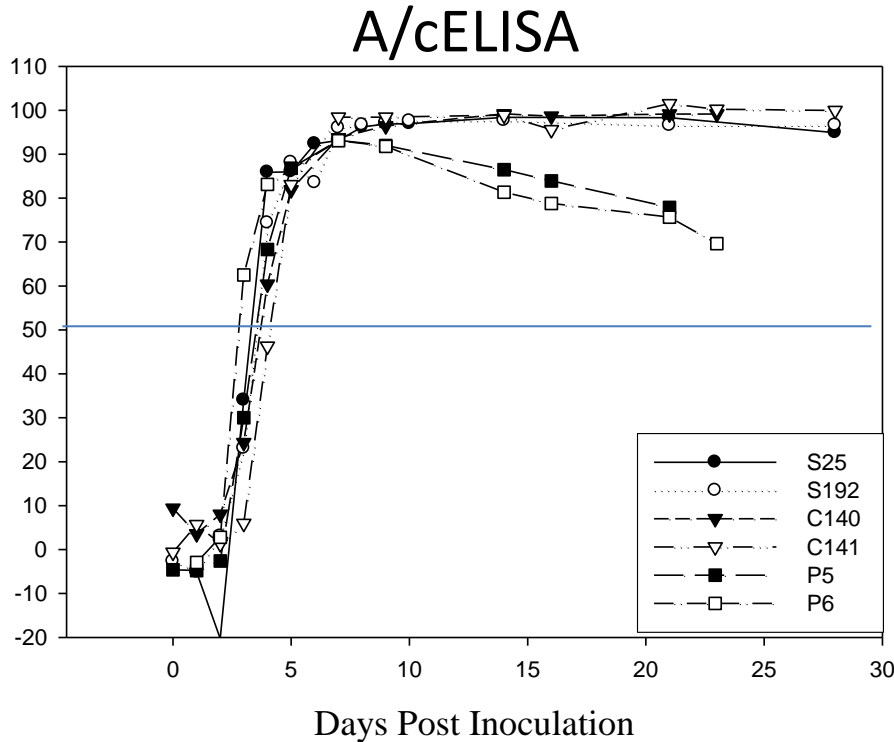


# Frequency distribution of the negative sera in A/cELISA

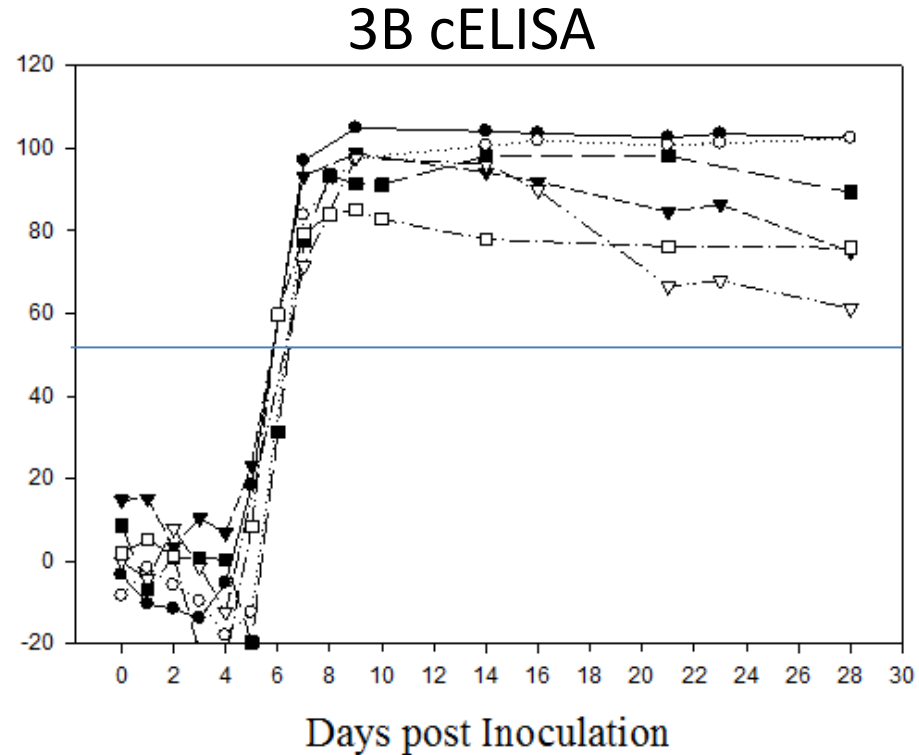


The frequencies of the PI generated from these sera were normal distributed  
Calculated diagnostic specificity is 99.7%

# Detection of FMDV antibodies in animals inoculated with FMDV/A24



100% seroconversion at 5 dpi

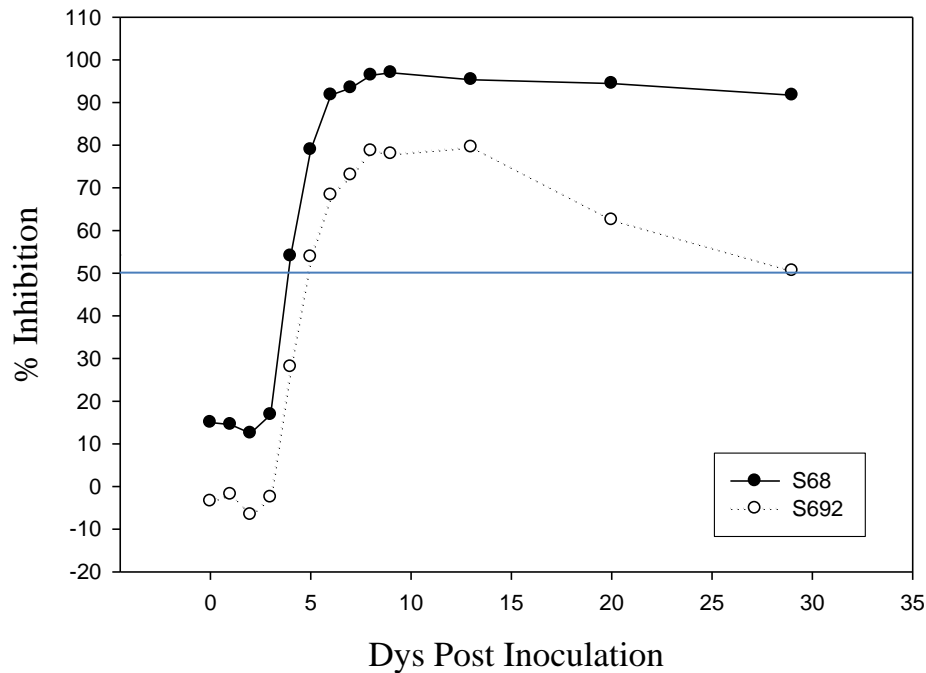


3B cELISA is used for surveillance to monitor FMDV circulation (Chen et al., 2011)

0% positive at 5 dpi

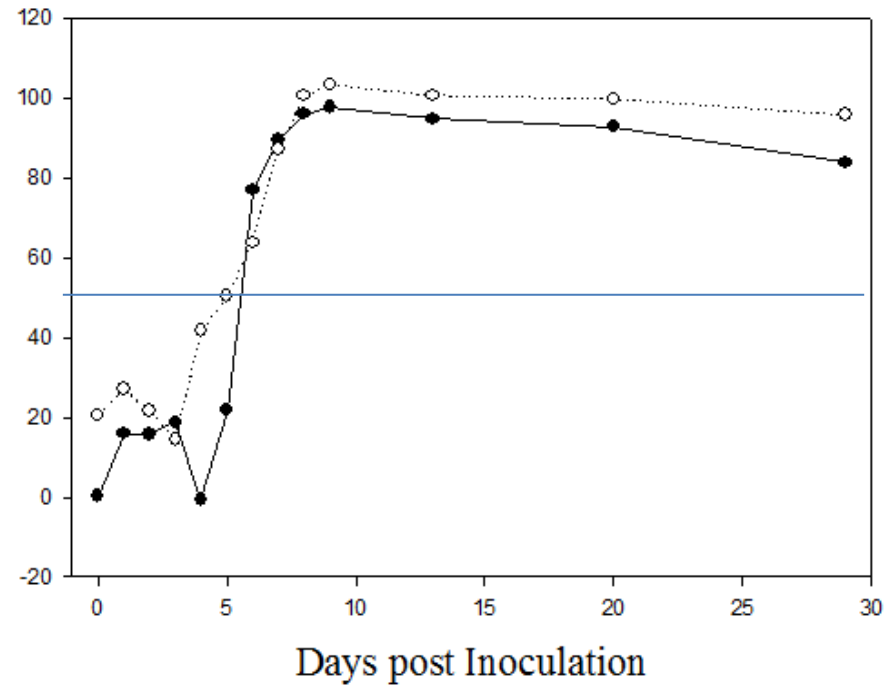
83% seroconversion at 7 dpi

# Detection of FMDV antibodies in animals inoculated with FMDV/A22 Iraq



A/cELISA

Both were seropositive at 5 dpi



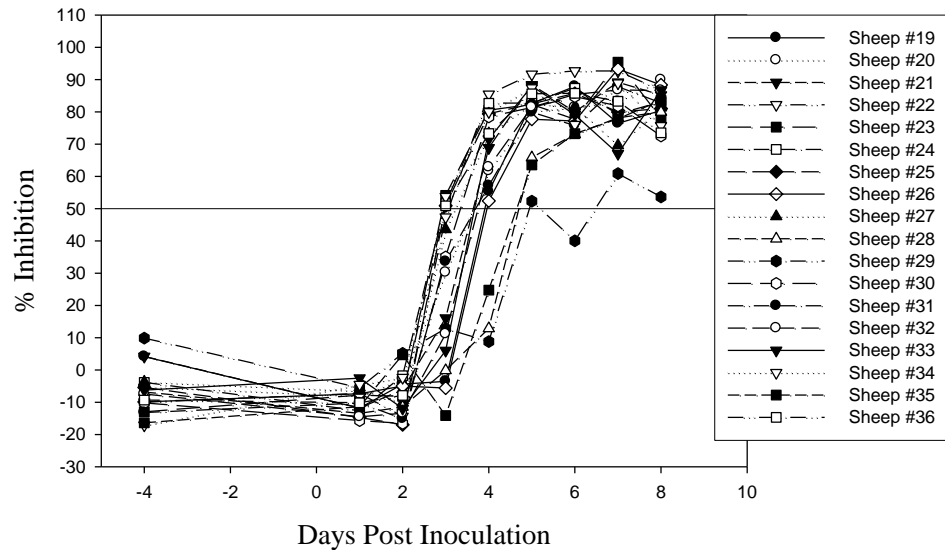
3B cELISA

Both were positive at 6 dpi



# Detection of FMDV antibodies in sheep inoculated with FMDV/A Vietnam/13

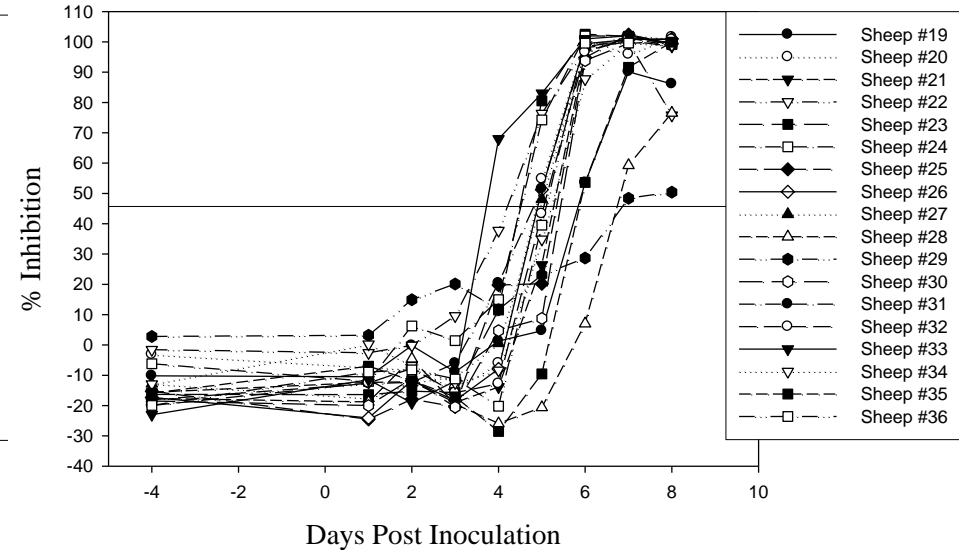
#19-28 coronary band inoculated and #29-36 contact infected by Jacquelyn Horsington



A/cELISA

100% seroconversion at 7 dpc

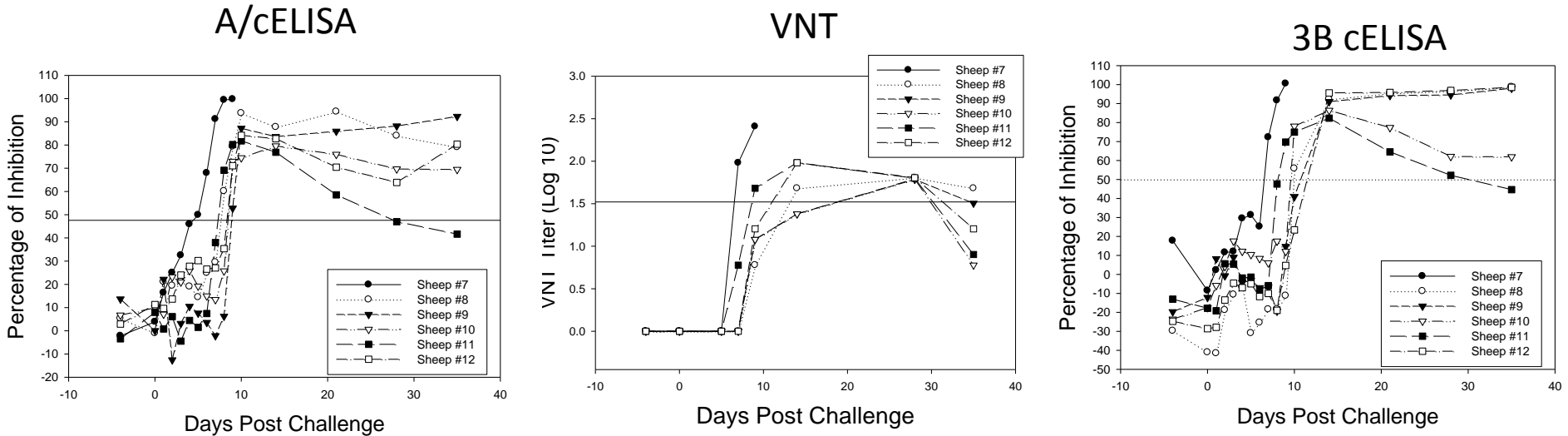
VNT 100% at 9 dpc



3B cELISA

38.9% seroconversion at 7dpc  
100% at 10 dpc

# Detection of FMDV antibodies in vaccinated and challenged-sheep

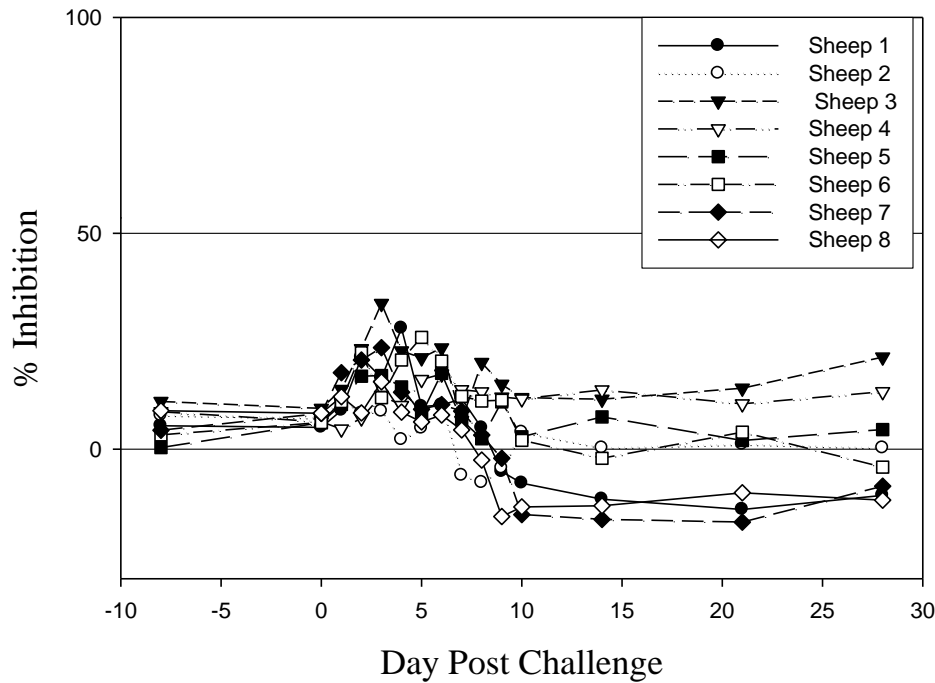


Sheep were vaccinated with A22 Iraq and challenged with A Vietnam/13 after 4 days vaccination

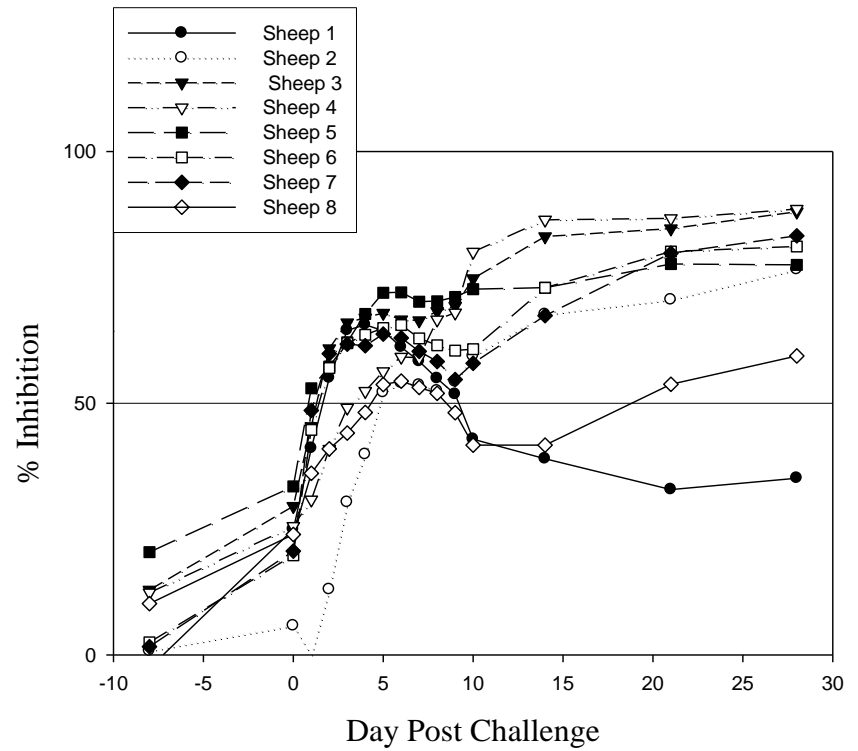
## Seroconversion

	A/cELISA	VNT	3B cELISA
8 dpc	50%	17%	17%
9dpc	100%	33%	33%

# A/cELISA specificity using sera from sheep vaccinated with O1 Manisa and challenged with O/SKR/10



A/cELISA



O/cELISA  
(Jacquelyn Horsington et al., 2014)

## Summary

1. A panel of FMDV/A specific mAbs were generated. The binding epitopes of the two mAb used in this A/cELISA were well characterized.
2. One of the mAbs' binding sites is conserved among all the tested isolates of FMDV/A.
3. The FMD A/cELISA that was developed using two mAbs and BEI inactivated FMDV/A antigen.
4. The A/cELISA exhibited comparable performance to the VNT and 3B cELISA, but more sensitive than the VNT and 3B cELISA
5. The cELISA is a simple and rapid test for the detection of FMDV/A-specific Abs.

# **Acknowledgements**

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