

# PCV2 DISEASE DIAGNOSTICS AND VIRUS EVOLUTION:

## Predicting Vaccine Coverage Against Evolving PCV2 Field Strains

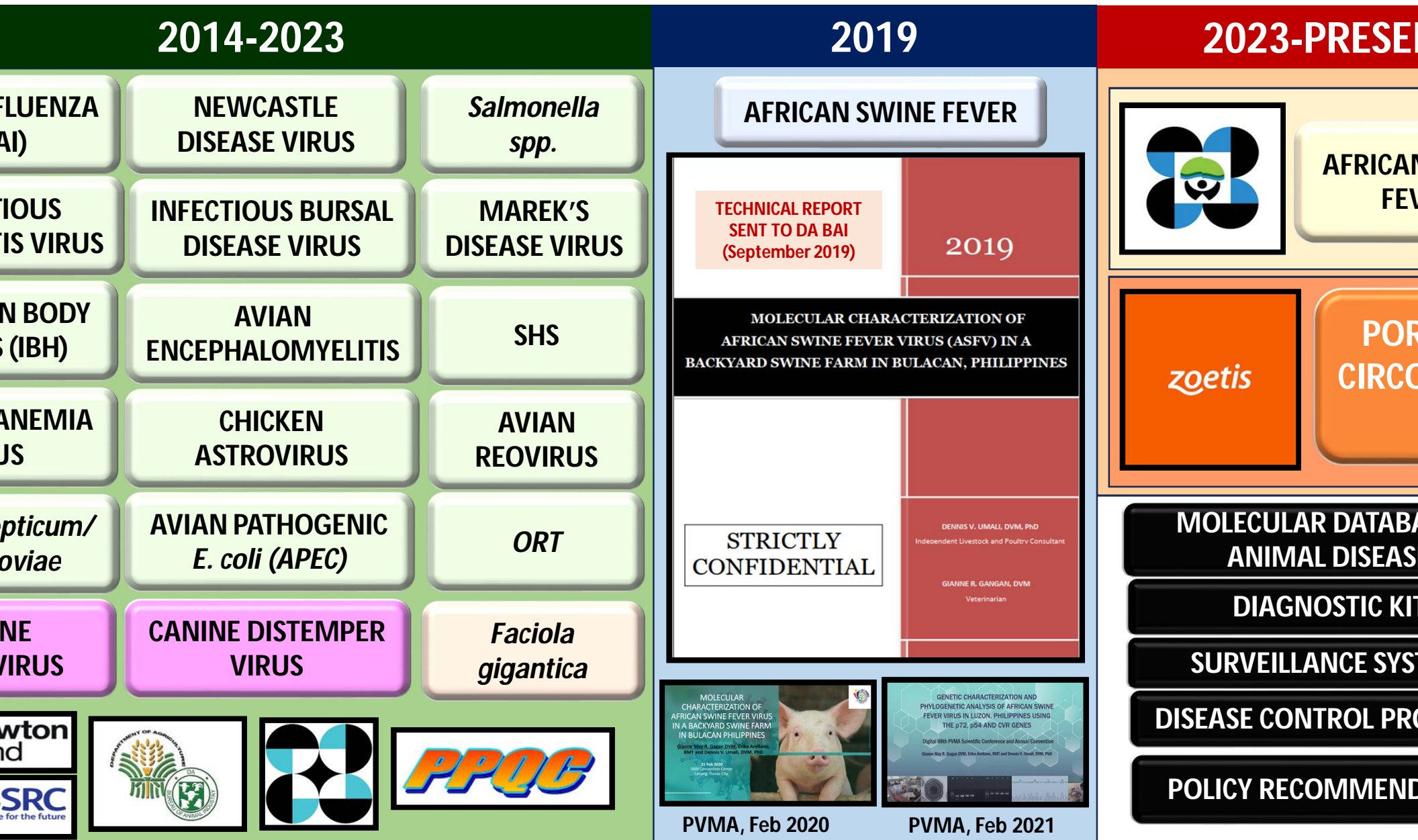
Francis Bonto, DVM<sup>1</sup>, Glorilyn M. Velasco, DVM<sup>1</sup>,  
Marlon Linatoc, DVM and Dennis V. Umali, DVM, PhD<sup>2\*</sup>

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*Center of the study*

# MOLECULAR CHARACTERIZATION OF ECONOMICALLY IMPORTANT VETERINARY PATHOGENS IN THE PHILIPPINES



# OUTLINE OF PRESENTATION

Viral Structure of PCV

PCV2-Associated Diseases

PCV2 Evolution

PCV2 Diagnostic and Monitoring Tools

Clinical Applications

*ptis*

# VIRAL STRUCTURE OF PCV

Family *Circoviridae*, genus *Circovirus*

Icosahedral, non-enveloped, single stranded DNA virus

Single ambisense circular genome (1766 to 1768 bp)

At least 11 Open Reading Frames

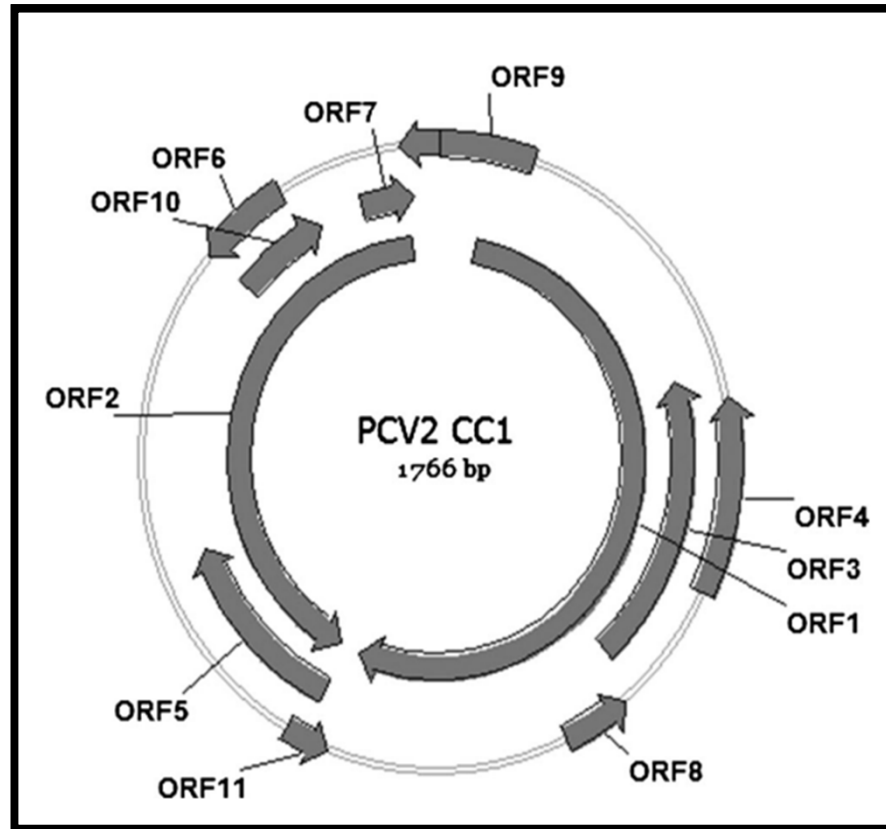
**ORF1 & ORF2:** replicase (Rep and Rep')

ORF3

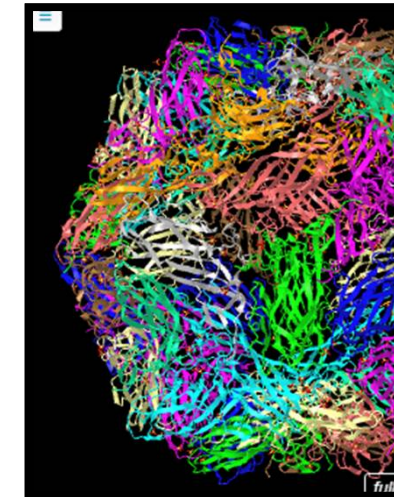
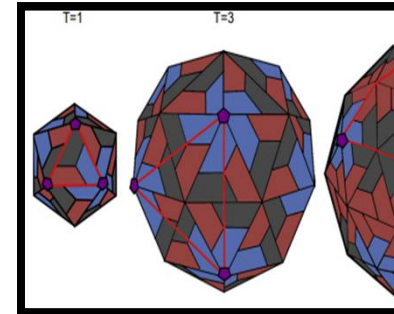
**ORF3:** apoptin

**ORF4:** ORF4 protein

**ORF5:** ORF5 protein



Ren *et al.*, 2016

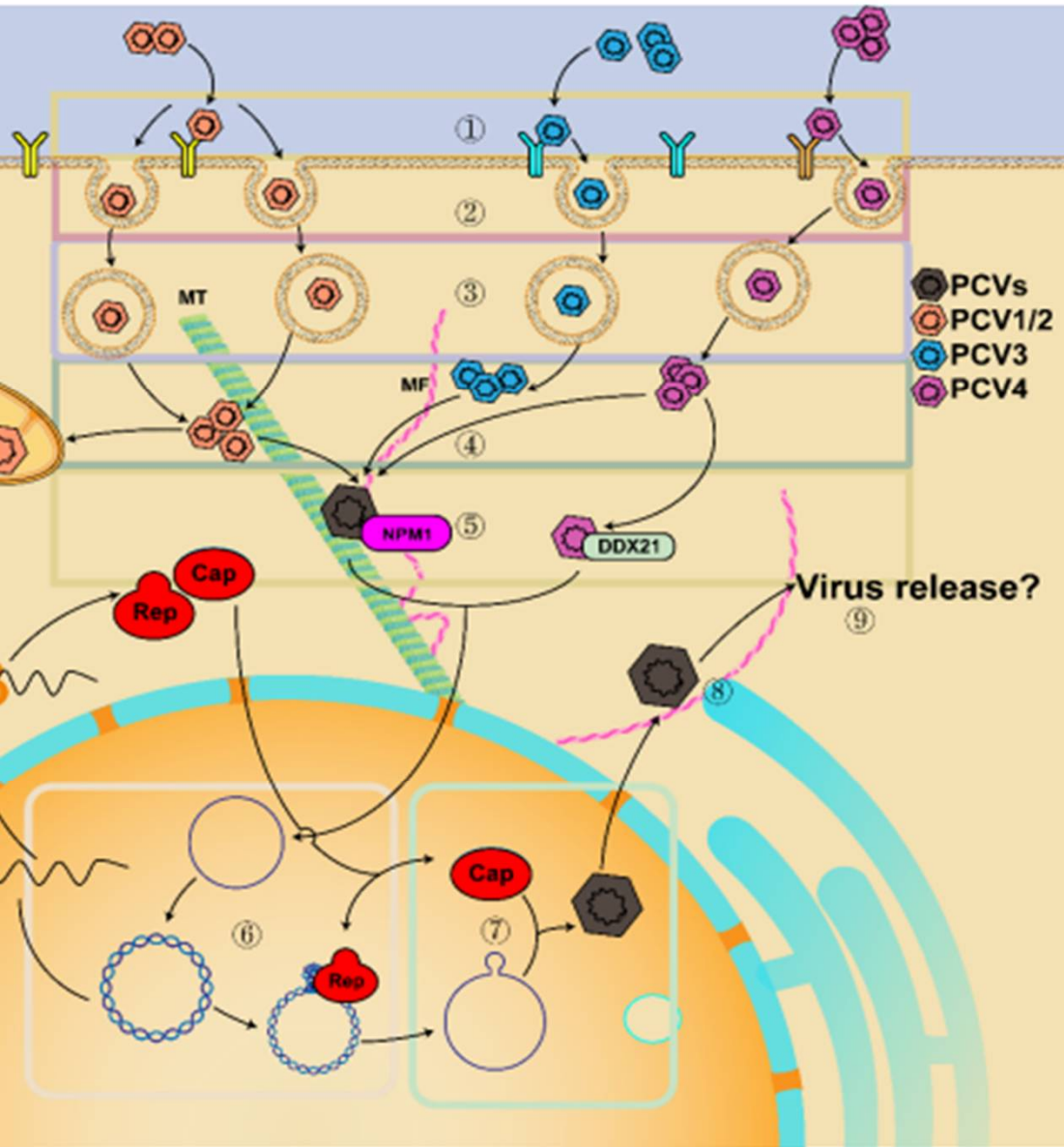


[www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)

PCV1, PCV2, PCV3 and PCV4

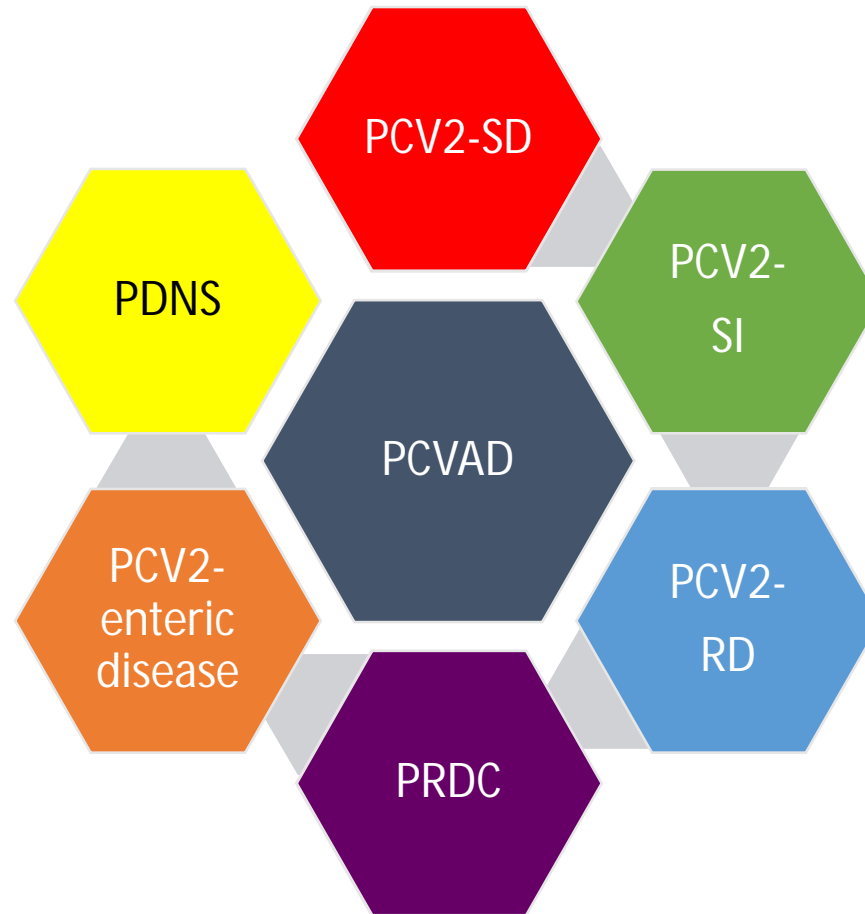


# PCV REPLICATION CYCLE



Niu et al., 2022

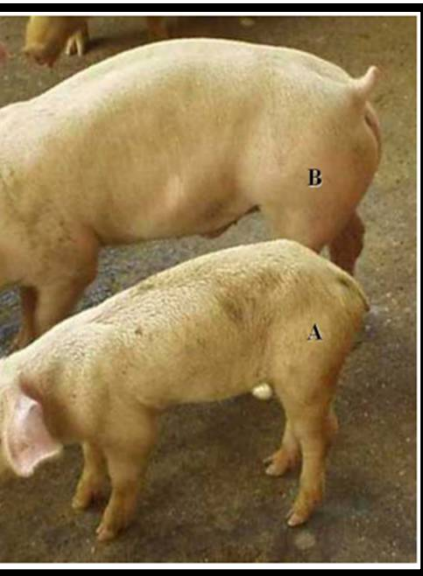
<b>VIRAL RECEPTOR</b> Heparin Sulfate Chondroitin Sulfate B Glycosaminoglycan	Attac
<b>VIRAL LIGAND: Capsid</b>	
<b>Clathrin-mediated Endocytosis</b>	
<b>Macropinocytosis</b>	Vira
<b>Actin and Rho-GTPase dependent manner</b>	Trans
<b>Microtubules/ Microfibers NPM1 and DDX21</b>	
<b>dsDNA conversion &amp; transcription</b>	Rep Trans and T
<b>Rolling Circle Formation (Rep)</b>	
<b>Viral Assembly (Cap)</b>	Ass
<b>Cell Lysis</b>	Vira



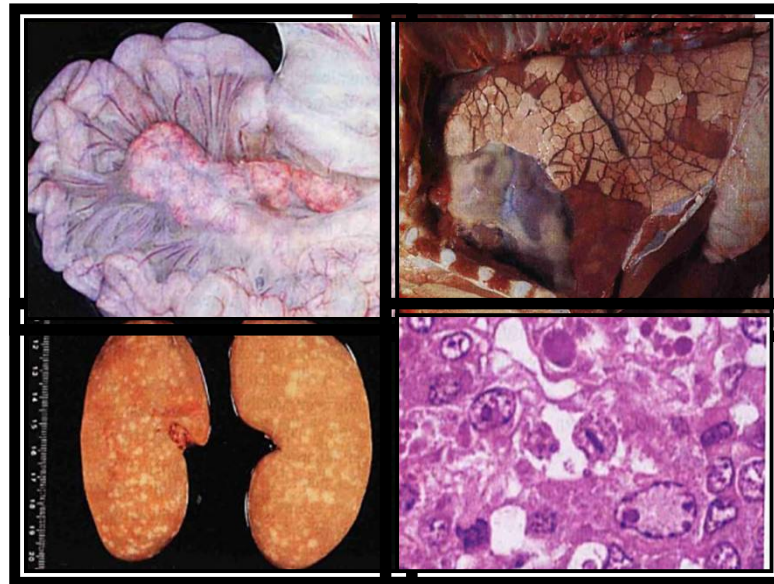
# PCV2-ASSOCIATED DISEASES

*ptis*

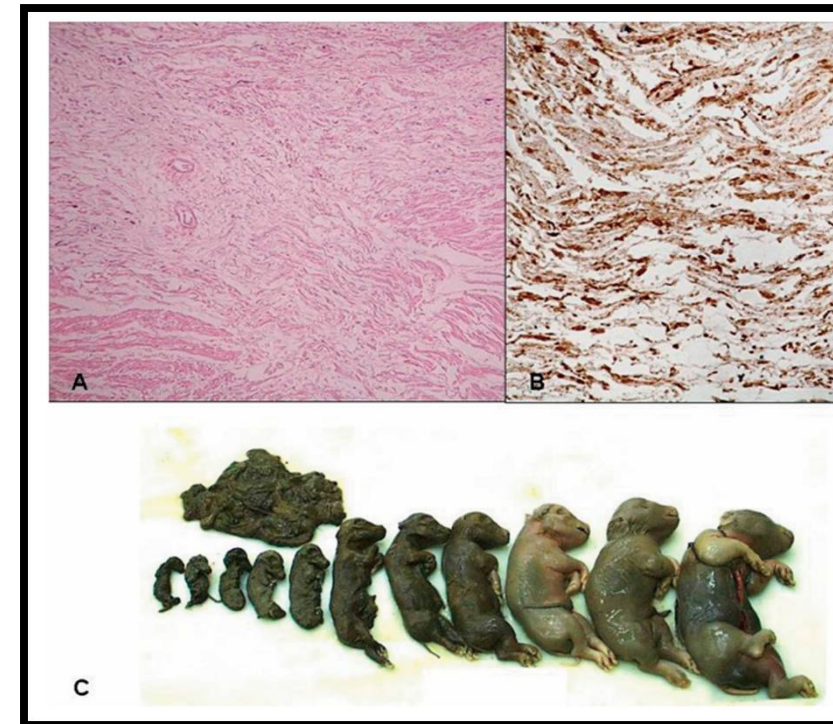
# PCV-2 ASSOCIATED DISEASES (PCVAD)



Rodriguez-Carino, 2010



Segales & Domingo, 2002



Opriessnig *et al.*, 2007

PCV2-systemic disease  
(PCV2-SD) (PMWS)

PCV2-reproductive disease  
(PCV2-RD)

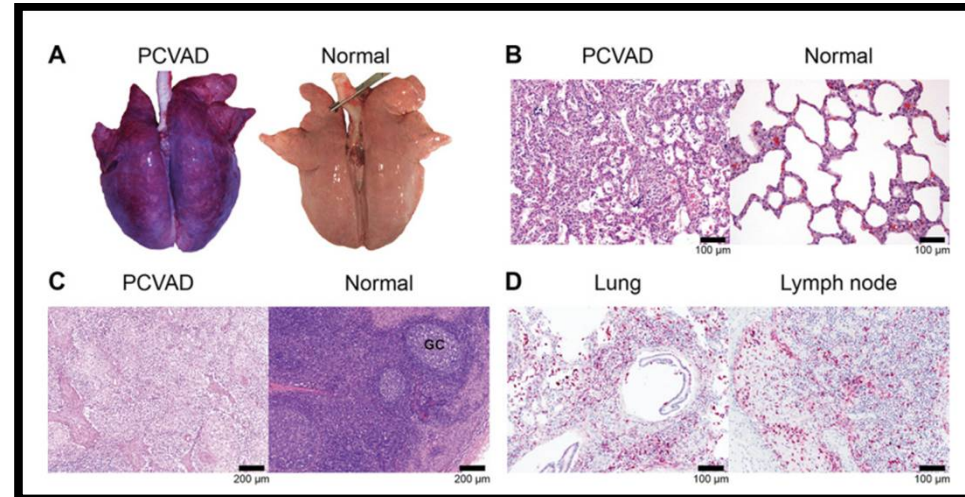
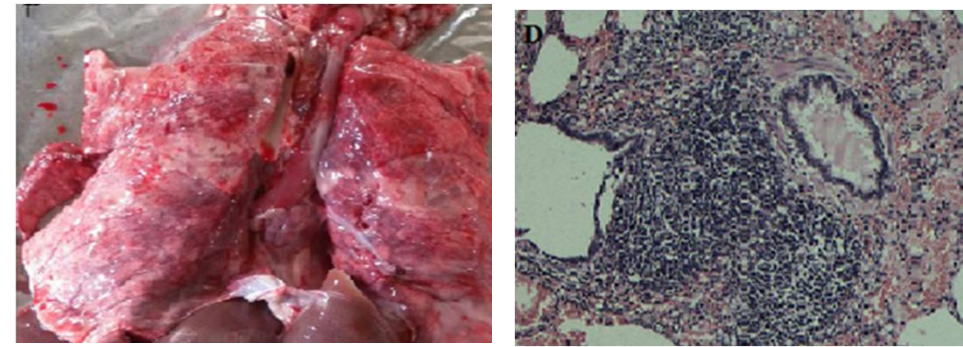
itis



# PCV-2 ASSOCIATED DISEASES (PCVAD)



Opriessnig *et al.*, 2007



Niederwerder *et al.*, 2015/ Li *et al.*, 2016

PCV2-enteric disease

itis

PCV2-respiratory disease  
(Porcine Respiratory Disease Complex) (P

# PCV-2 ASSOCIATED DISEASES (PCVAD)

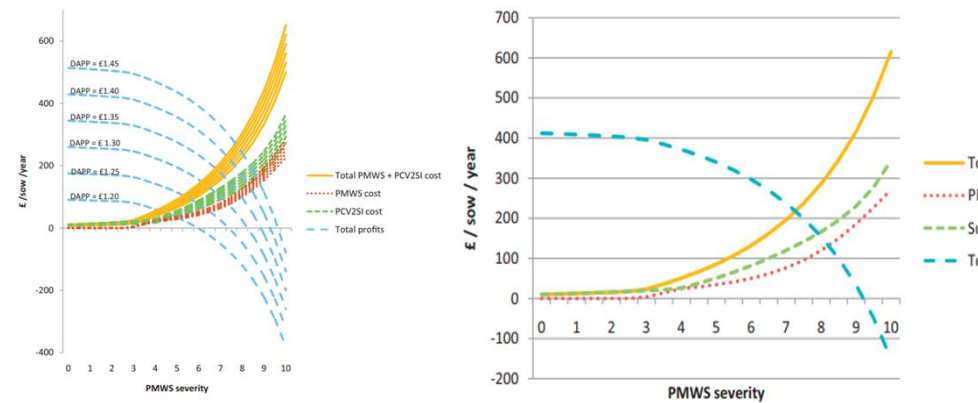


Opriessnig *et al.*, 2007

Segales, 2002



Angulo, 2021



Alarcon *et al.*, 2013

Porcine Dermatitis and Nephropathy Syndrome (PDNS)

PCV2-Subclinical Infection (PCV2-SI)



# PRECISE DEFINITION OF THE DIFFERENT PCVAs

MDPI

## Update of Porcine Circovirus Disease Diagnostic Criteria in the Porcine Circovirus 2 Epidemiological Context

Joaquim Segales<sup>1,2,3,\*</sup> and Marina Sibila<sup>3,4</sup>

**Abstract:** Current knowledge on porcine circovirus diseases (PCVD) caused by *Porcine circovirus 2* (PCV-2) includes the subclinical infection (PCV-2-SI), systemic (PCV-2-SD) and reproductive (PCV-2-RD) diseases, and porcine dermatitis and nephropathy syndrome (PDNS). Criteria to establish the diagnosis of these conditions have not changed over the years; thus, the triad composed by clinical signs, lesions and viral detection in lesions are still the hallmark for PCV-2-SD and PCV-2-RD. In contrast, PCV-2-SI diagnosis is not usually performed since this condition is perceived to be controlled by default through vaccination. PDNS is diagnosed by gross and histopathological findings, and PCV-2 detection is not recognized as a diagnostic criterion. Molecular biology methods as a proxy for PCVD diagnoses have been extensively used in the last decade, although these techniques should be mainly considered as monitoring tools rather than diagnostic ones. What has changed over the years is the epidemiological picture of PCV-2 through the massive use of vaccination, which allowed the decrease in infectious pressure paralleled with a decrease in overall herd immunity. Consequently, the need for establishing the diagnosis of PCVD has increased lately, especially in cases with a PCV-2-SD-like condition despite vaccination. Therefore, the objective of the present review is to update the current knowledge on diagnostic criteria for PCVDs and to contextualize the interest of using molecular biology methods in the overall picture of these diseases within variable epidemiological scenarios of PCV-2 infection.

**Keywords:** *Porcine circovirus 2* (PCV-2); porcine circovirus disease; clinical signs; pathology; diagnosis; epidemiology; vaccination

### 1. Introduction

Ten years ago, a review paper on clinical signs, pathology and laboratory diagnosis in relation to *Porcine circovirus 2* (PCV-2) was published, trying to unify existing criteria to establish a proper herd diagnosis of its infection outcomes [1]. At that time, just few years after starting mass vaccination against PCV-2 all over the world [2], it was discovered that PCV-2-subclinical infection (PCV-2-SI) was not only the most frequent form of this viral infection, but also the costliest one [3]. Since then, more than 10 years of a successful story behind PCV-2 vaccination has been contemplated by the swine industry [4,5], to the point that it is difficult to think of producing pigs without vaccination against this pathogen.

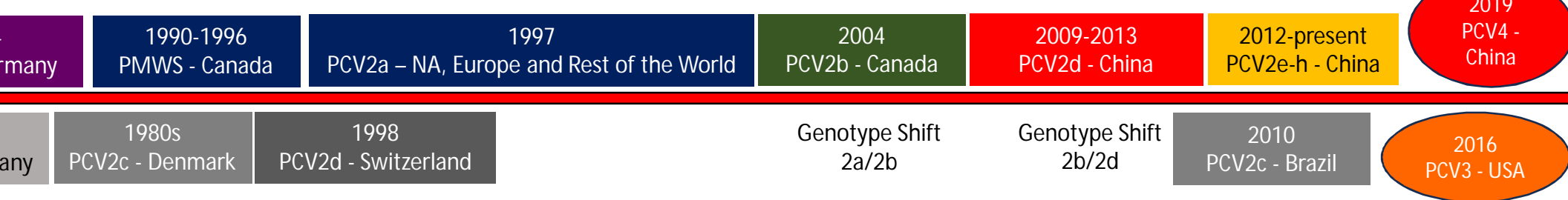
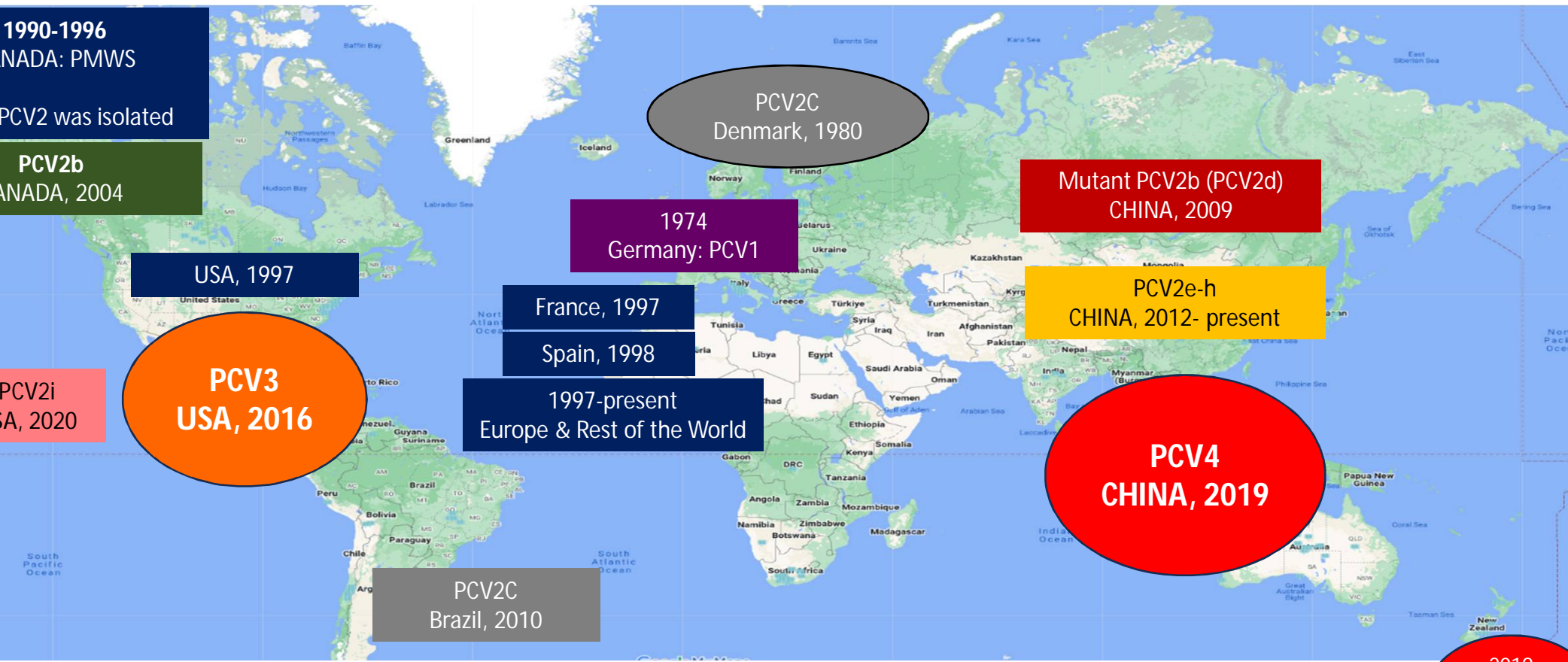
Besides the excellent results given by PCV-2 vaccination of piglets [6–8], the fact of immunizing this age group of animals has implied to change the epidemiology of this viral infection. The systematic vaccination at weaning implied to significantly decrease the overall herd infectious pressure, and some pig batches may reach almost seronegative

PCVD (Acronym)	Major Clinical Signs	Individual Diagnostic Criteria
PCV-2 subclinical infection (PCV-2-SI)	Decreased average daily gain (approx. 10–40 g/day) without any evident clinical sign	<ol style="list-style-type: none"> <li>Lack of overt clinical signs</li> <li>No or minimal histopathological lesions in tissues (lymphoid)</li> <li>Low amount of PCV-2 in few (lymphoid) tissues, u in follicular areas</li> </ol> <p>Criteria 2 and 3 can potentially be substituted by PCV-2 detection techniques such as standard PCR</p>
PCV-2 systemic disease (PCV-2-SD)	Wasting, weight loss, decreased rate of weight gain clinically evident, ill thrift or poor-doing animals, sometimes with respiratory and/or digestive disorders	<ol style="list-style-type: none"> <li>Weight loss and paleness of skin (respiratory and/ digestive clinical signs may be present as well)</li> <li>Moderate to severe lymphocyte depletion with granulomatous inflammation of lymphoid tissues granulomatous inflammation in other tissues)</li> <li>Moderate to high amount of PCV-2 in lymphoid ti (the amount in the rest of affected tissues can be va</li> </ol>
PCV2 reproductive disease (PCV-2-RD)	Abortions or mummifications	<ol style="list-style-type: none"> <li>Reproductive failure at late gestation or SMEDI-like condition *</li> <li>Fibrous to necrotizing myocarditis of fetuses</li> <li>Moderate to high amount of PCV-2 in the heart</li> </ol>
	Regular return-to-estrus	<ol style="list-style-type: none"> <li>Regular return-to-estrus/infertility</li> <li>PCV-2 seroconversion following the return-to-estrus and/or PCV-2 PCR/qPCR positivity around return-to-estrus occurrence</li> </ol>
Porcine dermatitis and nephropathy syndrome (PDNS) **	Dark red papules and macules on skin, mainly in hind limbs and perineal area	<ol style="list-style-type: none"> <li>Hemorrhagic and necrotizing skin lesions and/or s and pale kidneys with generalized cortical petechi</li> <li>Systemic necrotizing vasculitis, and necrotizing an fibrinous glomerulonephritis</li> </ol>

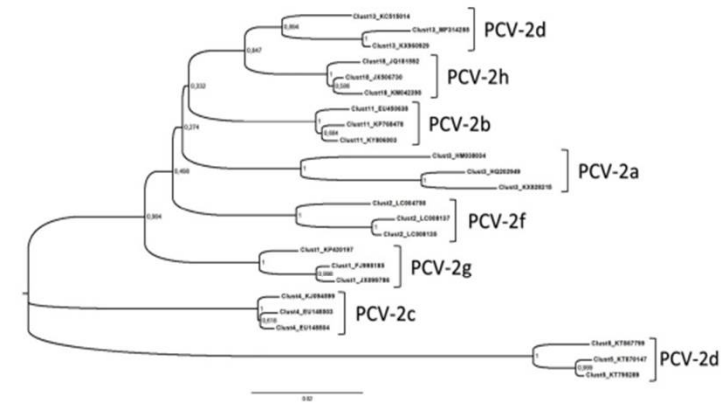
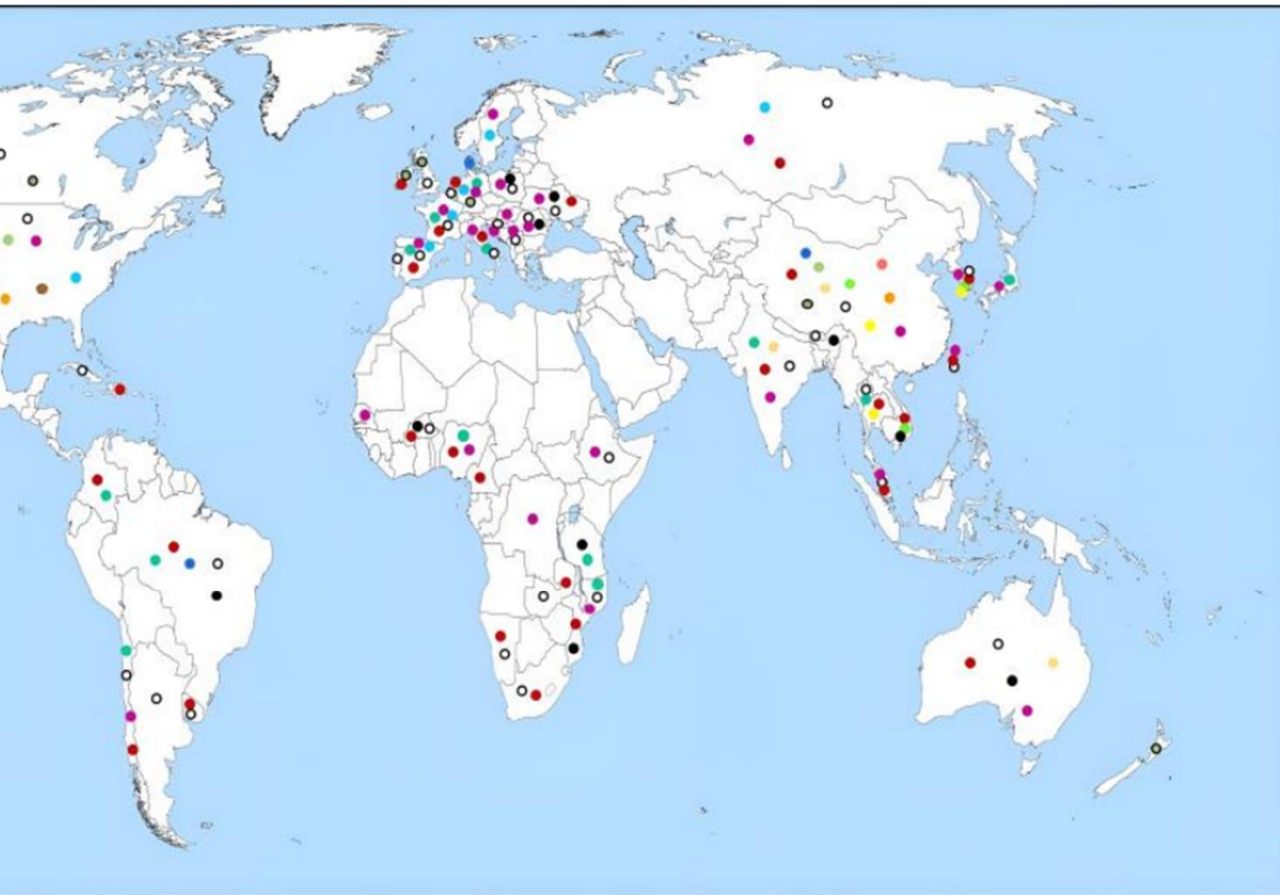
\* SMEDI stands for stillbirth, mummification, embryonic death and infertility; infertility would apply to estrus scenarios. \*\* PCV-2 association with PDNS is still circumstantial, and detection of the virus is not c into its diagnostic case definition.



# EVOLUTION OF PORCINE CIRCOVIRUS



# EVOLUTION OF PORCINE CIRCOVIRUS



Franzo and Segales, 2018

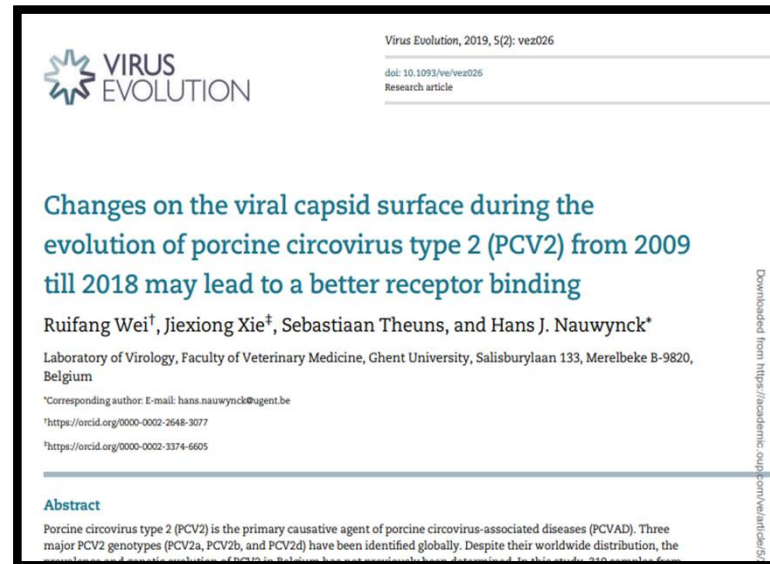
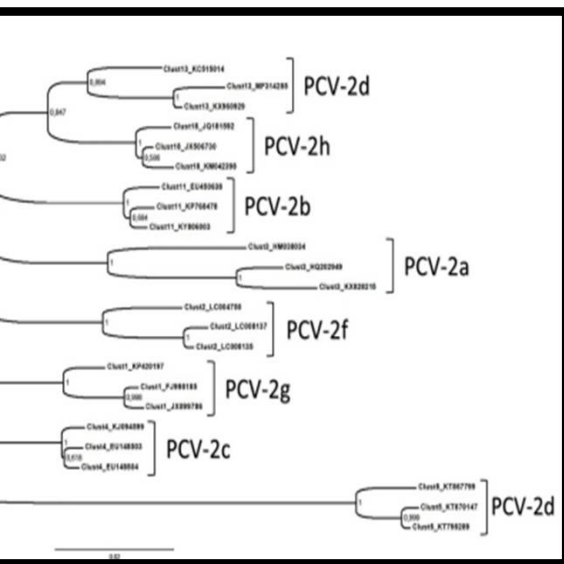
- PCV1
- PCV2h
- PCV2a
- PCV2i
- PCV2b
- PCV3a
- PCV2c
- PCV3b
- PCV2d
- PCV3c
- PCV2e
- PCV4a
- PCV2f
- PCV4b
- PCV2g

**Table 2.** Genomic similarities (%) among porcine circoviruses.

	PCV1-PCV2	PCV1-PCV3	PCV1-PCV4	PCV2-PCV3	PCV2-PCV4	PCV3-PCV4	References
Genome (nt)	68.0–76.0	43.5–44.0	50.3–51.6	42.7–48.0	51.5	42.9–45.0	[12,20–22,26,27]
Capicase (aa)	86.0	45.5–45.9	48.1–50.7	46.3–48.0	16.2–47.2	48.4–49.7	[20,22,24,26,27]
NS2 (aa)	65.0	24.0–25.2	43.1–44.4	25.9–37.0	12.7–45.0	23.2–24.8	[20,22–24,26,27]

# CLINICAL RELEVANCE OF DIFFERENT PCV2 GENOTYPES

## NUMEROUS PCV-2 GENOTYPES BUT ALL BELONG TO ONLY ONE (1) SEROTYPE!



- Some degree of cross-protection across different PCV-2 genotypes
- Vaccination does not produce Sterilizing Immunity
- Changes on the viral capsid lead to a better receptor binding and fitness of certain PCV2 genotypes

# DIAGNOSTIC CRITERIA FOR PCV-2 INFECTIONS

clinical signs and gross pathological lesions (i.e. growth retardation, and wasting)

presence of specific moderate to severe pathological lesions in target tissues of affected

lymphoid tissues for PCV-2-SD, heart for PCV-2-RD and vessels/glomeruli for PDNS; and

presence of a moderate to high amount of PCV-2 in these target tissues.

dermatitis

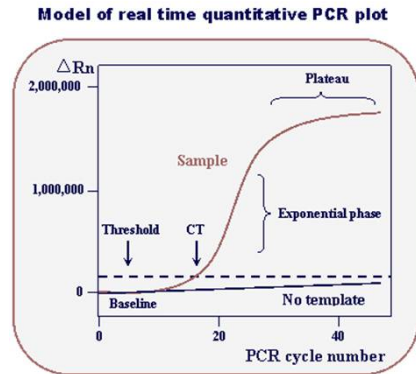
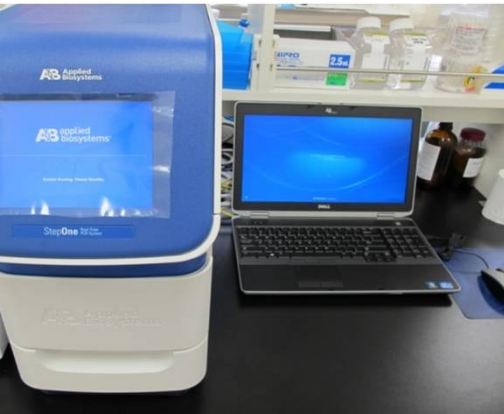
**Table 1**  
Proposed terminology for porcine circovirus diseases (PCVDs) together with their case definition based on clinical and laboratorial findings.

PCVD proposed name (acronym)	Replaced terminology	Main clinical sign	Individual
PCV2 subclinical infection (PCV2-SI)	None	Decreased average daily gain without any evident clinical sign	1. Lack of lesions 2. No obvious lymphoid (lymphoid) Criteria substituting technique
PCV2 systemic disease (PCV2-SD)	Postweaning multisystemic wasting syndrome (PMWS) Porcine circovirus PCV2-associated systemic infection	Wasting, weight loss, decreased rate of weight gain clinically evident, ill thrift or poor-doer	1. Weight (respiratory clinical well) 2. Moderate depletion inflammation (plus gross in a number) 3. Moderate PCV2 infection
PCV2 lung disease (PCV2-LD)	PCV2-associated respiratory disease Proliferative and necrotizing pneumonia (PNP)	Respiratory distress, dyspnea	1. Respiratory 2. Lymphoid granulomatous bronchopneumonia mild-to-moderate ulceration proliferative pneumonia lesions 3. Moderate PCV2 infection Lymphoid display (other microscope)
PCV2 enteric disease (PCV2-ED)	PCV2-associated enteritis	Diarrhea	1. Diarrhea 2. Granulomatous lymphoid Peyer's lymphoid 3. Moderate PCV2 infection patches Lymphoid patches microscopically would PCV2 infection
PCV2 reproductive disease (PCV2-RD)	PCV2-associated reproductive failure	Abortions or mummifications  Regular return-to-estrus	1. Reproductive 2. Fibrotic myocardium 3. Moderate PCV2 infection The use of PCR on sensitivity 1. Regular 2. PCV2 infection the return PCR positive return-
Porcine dermatitis and nephropathy syndrome (PDNS) <sup>a</sup>	None	Dark red papules and macules on skin, mainly in hind limbs and perineal area	1. Hemorrhagic skin lesions pale kidneys cortical 2. Systemic and nephropathy glomerular

<sup>a</sup> PDNS is considered an immune-complex disease of not yet demonstrated etiology; link with PCV2 is still circumstantial, and detection of its diagnostic case definition. Therefore, no novel terminology has been suggested for this particular syndrome.



# PCV-2 MONITORING TOOLS



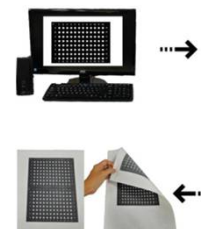
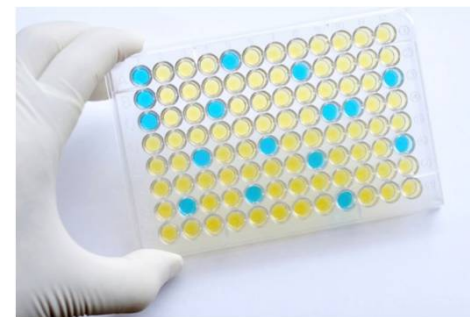
## qPCR THRESHOLDS

Serum	$>10^7$ PCV-2 DNA copies/ml
Swabs or lymph node	2-3 log more than in serum
Formalin fixed and paraffin embedded (FFPE) (e.g. myocardium, spleen and liver)	$>10^9$ PCV-2 DNA copies/g tissue
	none

Segales and Sibila, 2022

etis

qPCR



ELISA

# PCVADs IN VACCINATED PIGS?

Veterinary Microbiology 163 (2013) 177–183

Contents lists available at SciVerse ScienceDirect

Veterinary Microbiology

journal homepage: [www.elsevier.com/locate/vetmic](http://www.elsevier.com/locate/vetmic)



novel mutant PCV2b variant associated with clinical PCVAD in vaccinated pig farms in the U.S. concurrently infected with

Yao-Ting Xiao, Priscilla F. Gerber, Patrick G. Halbur

Department of Clinical and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, IA, USA

## ABSTRACT

Porcine circovirus (PCV) type 2b (PCV2b) emerged in North America in 2005–2006. During May of 2012, PCVAD occurred in 10–18-week-old pigs in two farms within a production system that routinely vaccinated against PCV2. Both farms received replacement gilts from the same multiplier. A mutant PCV2b strain not previously present in North America was identified. The strain was found to be 99.9% identical to a recently described mutant PCV2 isolate reported in China in 2010 and thought to be more virulent than classical PCV2a or PCV2b strains. It is possible that the current PCV2a-based commercial vaccines are not fully protective against this new strain. In addition, emerging porcine parvovirus type 2 (PPV2) was detected in 55% of the serum samples (73/132), perhaps implying that PPV2 could be a cofactor in cases of PCVAD.

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Opriessnig *et al.*, 2013

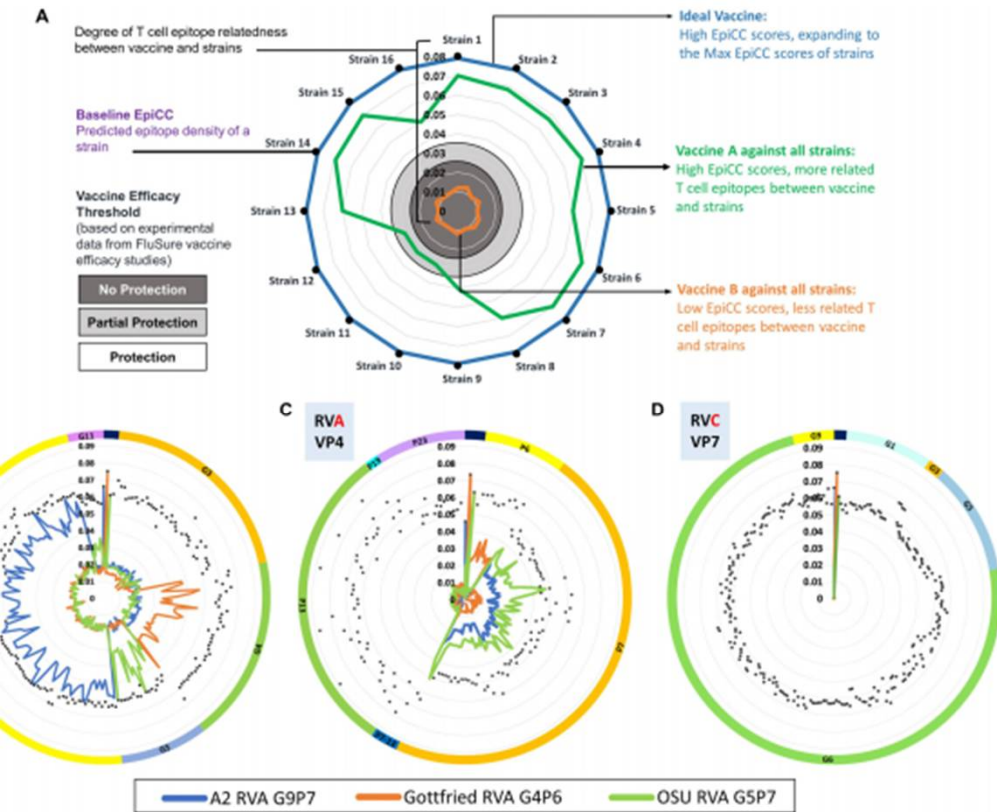
- **OCCURRENCE OF CLINICAL PCVADS IN VACCINATED PIGS?**
  - PCV2d (mutant PCV2b) is currently the most prevalent
  - Most of the commercially available PCV vaccines are prepared from Genotype 2A
- **DIFFERENTIAL EFFICACY of different vaccine platforms when animals are raised in suboptimum conditions?**
  - Non-sterilizing immunity provides opportunity for certain strains to preferentially circulate in “challenging” environment

**MINOR VARIATIONS IN B AND T CELL EPITOPES BETWEEN VACCINES AND FIELD PCV2 HAVE RESULTED TO DIFFERENCES IN IMMUNE RECOGNITION**

Wei *et al.*, 2019



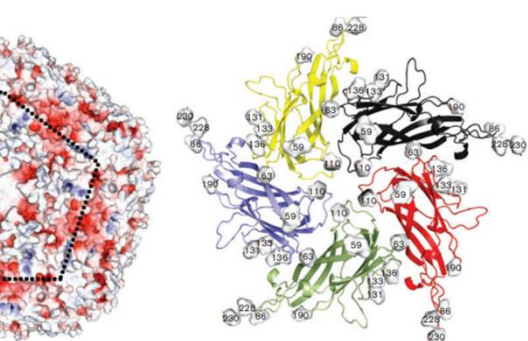
# T-CELL EPITOPE CONTENT COMPARISON (EpiCC)



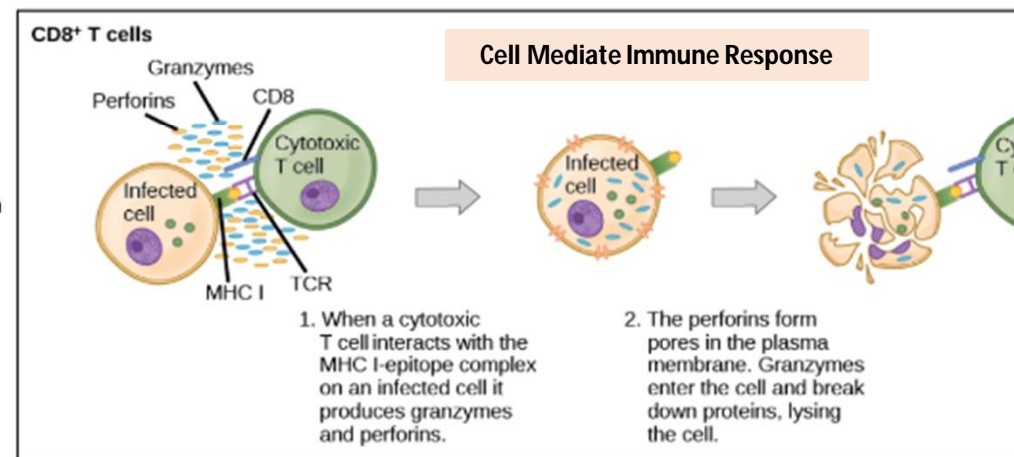
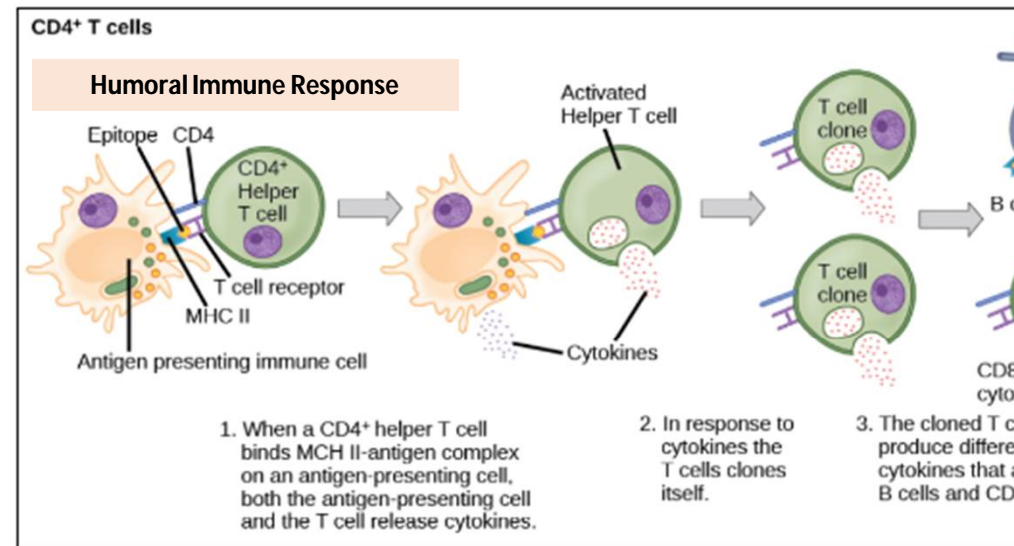
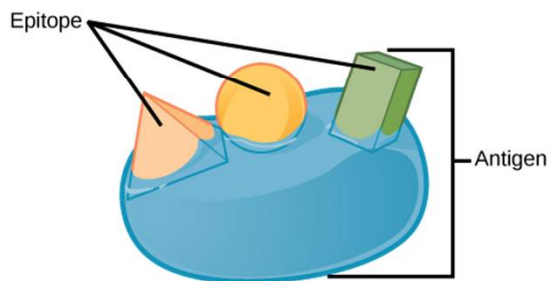
Moise *et al*, 2020

# CELL EPITOPE CONTENT COMPARISON (EpiCO

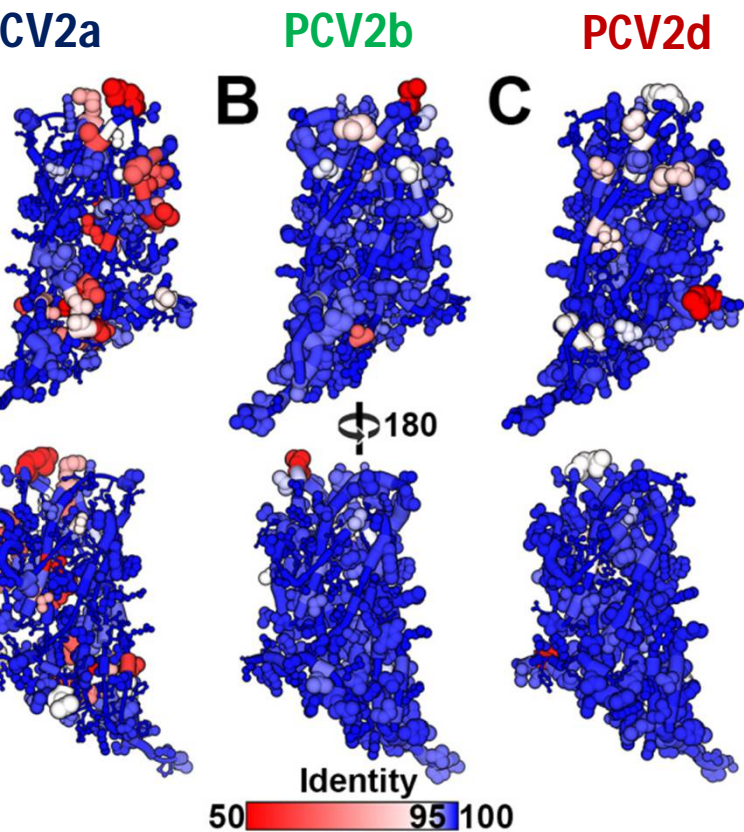
## “AN EMERGING MUNOINFORMATICS TOOL T COMPARES T CELL EPITOPE CONTENT OF PCV2 AND OTHER VIRUSES”



with 60 sub-units of capsid proteins (5x12)  
arranged in canonical viral jelly roll



# EPITOPES OF PCV-2



Khayat, *et al.*, 2011/Kekarainen *et al.*, 2014

Evolution Rate of PCV2:  
 $1.2 \times 10^{-3}$  substitution/site/year

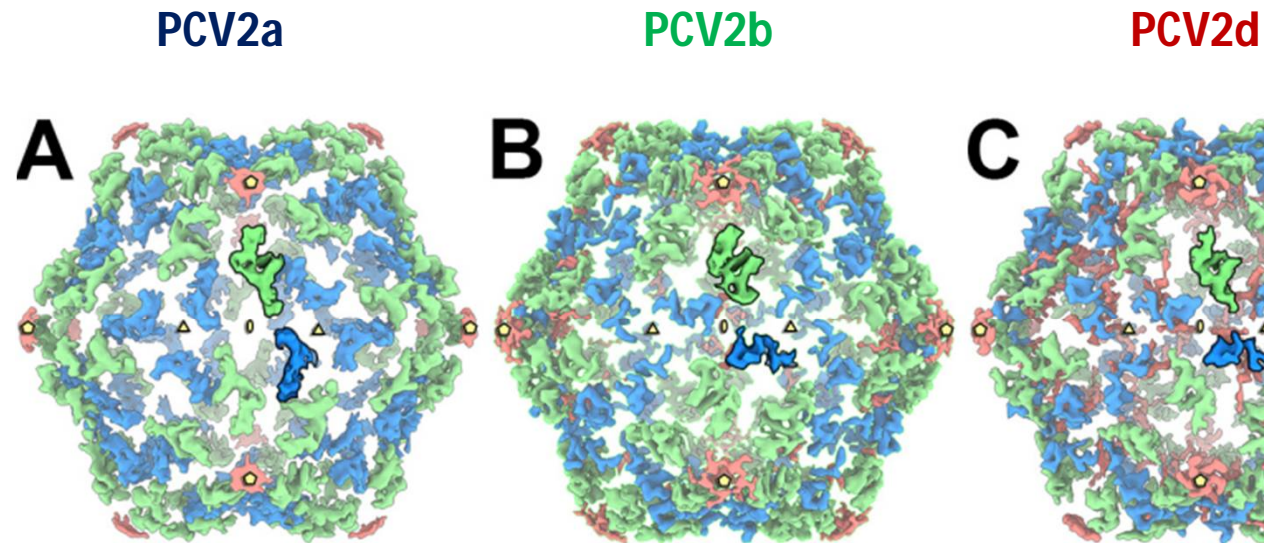


TABLE 1. Epitopes of PCV1 and PCV2

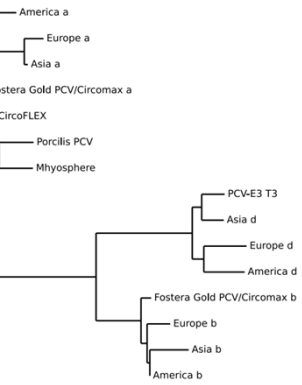
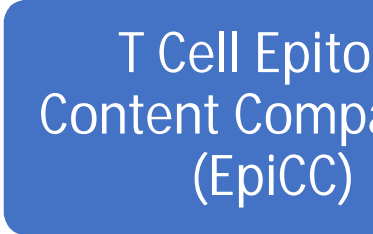
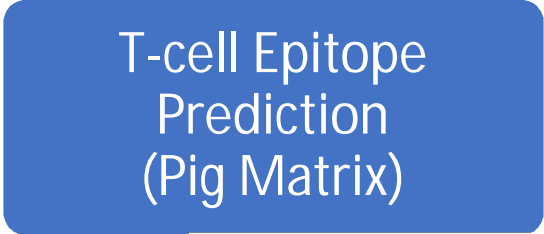
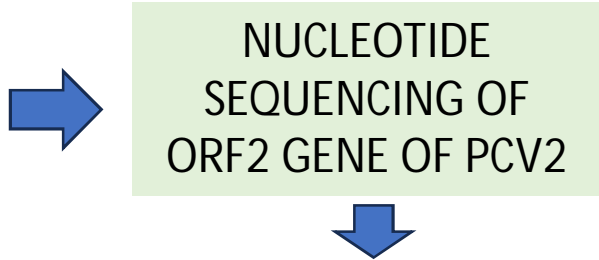
Epitope	Residues <sup>a</sup>	Aligned sequence <sup>b</sup>	MAb binding residue(s)
A	69–83	NVNELRFNIGQFLPP VDMRFNINDFLPPG	Asp70, Met71, Asn77, Asn78
B <sup>d</sup>	113–127	TSNQRGVGS <sup>d</sup> TVVILD QGDRGVGS <sup>d</sup> SAVILDD	Gln113, Asp115
C <sup>d</sup>	117–131	RGVGS <sup>d</sup> TVVILDANFV GVGS <sup>d</sup> SAVILDDNFVT	Asp127
D	169–183	DQ <sup>d</sup> TID <sup>d</sup> WFQPNKRNQ FTID <sup>d</sup> VFQPNKRNQL	Thr170
E	193–207	NVEHTGLGYALQNATT VDHVGLGTAFENSIY	Glu203, Ile206, Tyr207
F	25–39	RRPYLVHPAFRNRYRWR RRPWLVHP--RHRRYRWR	

Khayat, *et al.*, 2019

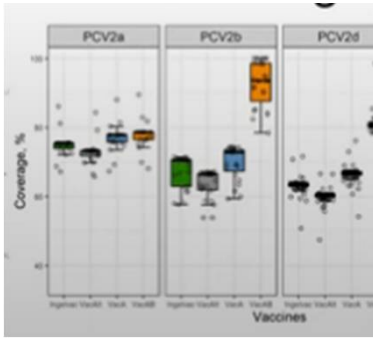
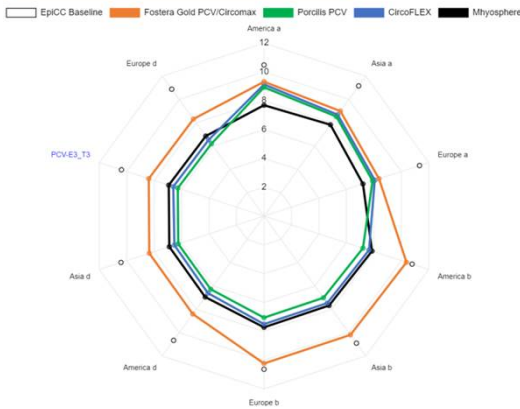


# CELL EPITOPE CONTENT COMPARISON (EpiCC)

LD  
ES OF  
CTED  
/2



Average strain	Average total EpiCC scores				Average T cell epitope coverage (%)			
	Ingevac (PCV2a)	VacAR (PCV2a)	VacA (PCV2a)	VacAB (PCV2a)	Ingevac (PCV2a)	VacAR (PCV2a)	VacA (PCV2a)	VacAB (PCV2a)
10.44	5.92	5.60	7.21	8.52	65.09	62.06	67.90	61.32
10.86	8.14	7.91	8.36	8.45	74.96	72.84	76.96	77.81
10.88	7.29	6.91	7.58	10.07	67.03	63.52	68.65	62.50
10.43	6.60	6.27	6.94	8.39	63.25	60.09	66.53	60.39
12.17	4.96	4.65	4.81	5.91	40.83	36.22	38.53	48.45
10.44	6.12	5.83	6.44	8.16	57.55	54.81	60.49	76.66
10.49	6.65	6.50	7.01	8.48	65.35	60.06	66.78	60.76
10.62	7.05	6.74	7.35	8.71	66.51	63.56	69.15	61.96
10.89	8.06	7.83	8.26	8.34	74.07	71.90	75.92	76.66
10.88	7.30	6.95	7.62	10.30	67.14	63.88	70.07	62.80
10.42	6.59	6.26	6.92	8.36	63.20	60.07	66.29	60.20
10.64	6.12	5.83	6.44	8.16	57.55	54.81	60.49	76.66
10.77	6.76	6.43	7.01	8.48	65.17	60.08	65.54	79.25
10.74	6.47	6.27	6.76	8.90	78.74	76.86	82.39	62.72
10.90	7.27	6.82	7.48	9.99	66.76	62.70	68.71	61.85
10.59	6.57	6.25	6.92	8.36	63.27	60.20	66.63	60.45
12.17	4.96	4.65	4.81	5.91	40.83	36.22	38.53	48.45



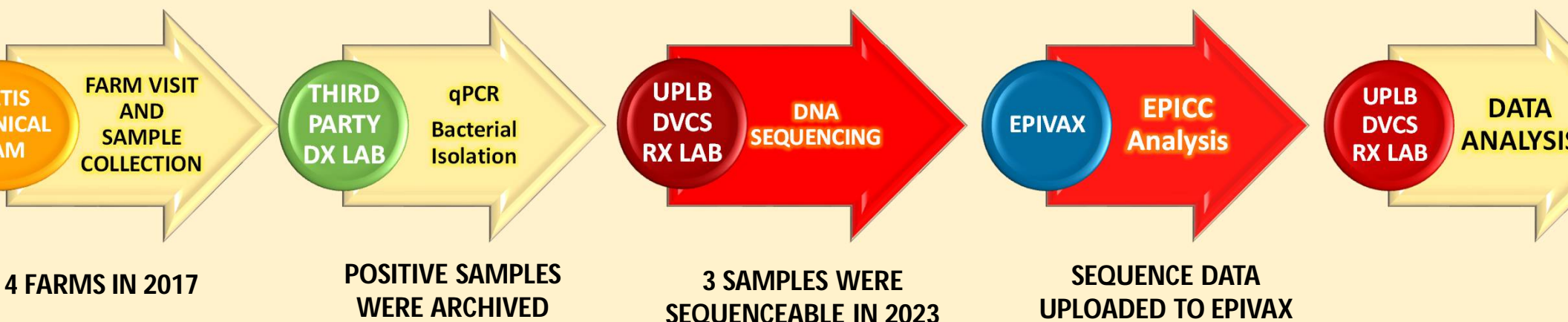
GENETIC ANALYSIS

EpiCC BASELINE

EpiCC SCORES

T-CELL EPITOPE CO

# MOLECULAR CHARACTERIZATION OF PCV-2 IN THE PHILIPPINES: PILOT STUDY



that Xuan Dinh *et al.* 2021. Porcine circovirus genotypes and their copathogens in pigs with respiratory disease in southern provinces of Vietnam. Archives of Virology 166:403-411.  
<https://doi.org/10.1007/s00705-020-04878-y>

# RM 1 (1700 sow level farrow to finish farm, Landrace x Large White x Duroc three-way cross)

## A. Isolate 1 (Module 1)

### Signs:

wasting, thumping, jaundice

elevated mortality (8%) and morbidity (15-20%)

around 6-10 weeks old

### Necropsy signs:

inflamed lymph nodes,

multifocal interstitial nephritis (white spotted kidneys),

edematous lungs.

**Vaccination:** PCV2d whole cell inactivated vaccine at D21, 1mL IM

## LAB RESULTS (from 10-weeks old tissue samples):

PCV2d PCR positive, Ct value of 10,

PRRS North American Strain, Ct value of 15.711

*Pasteurella multocida* positive in bacterial isolation

itis

## B. Isolate 2 (Module 2)

### • PCVAD signs:

- wasting, thumping, jaundice

- elevated mortality 8% and morbidity (15-20%)

- around 6-10 weeks old.

### • Necropsy signs:

- inflamed lymph nodes,

- multifocal interstitial nephritis (white spotted kidneys)

- edematous lungs.

▪ **Vaccination:** PCV2d whole cell inactivated vaccine at D21

## LAB Results (from 10-weeks old tissue samples):

1. PCV2d PCR positive with Ct value of 10

2. PRRS North American Strain, Ct value of 15.711

3. PRRS EU strain with Ct value of 24.632

4. No significant bacteria isolated



# Farm 2 (2200 sow level farrow to finish farm, drace x Large White x Duroc three-way cross)

## AD signs

astating, thumping, jaundice  
evated mortality (8%) and morbidity (40%)  
ound 9-10 weeks old.

## opsy signs

flamed lymph nodes,  
ultifocal interstitial nephritis (white spotted kidneys),  
dematous lungs,  
thrititis of the hind limbs.

## ination:

aculovirus expressed PCV2a vaccine, 1mL IM.

ptis

## LAB Results (from 10-weeks old tissue samples):

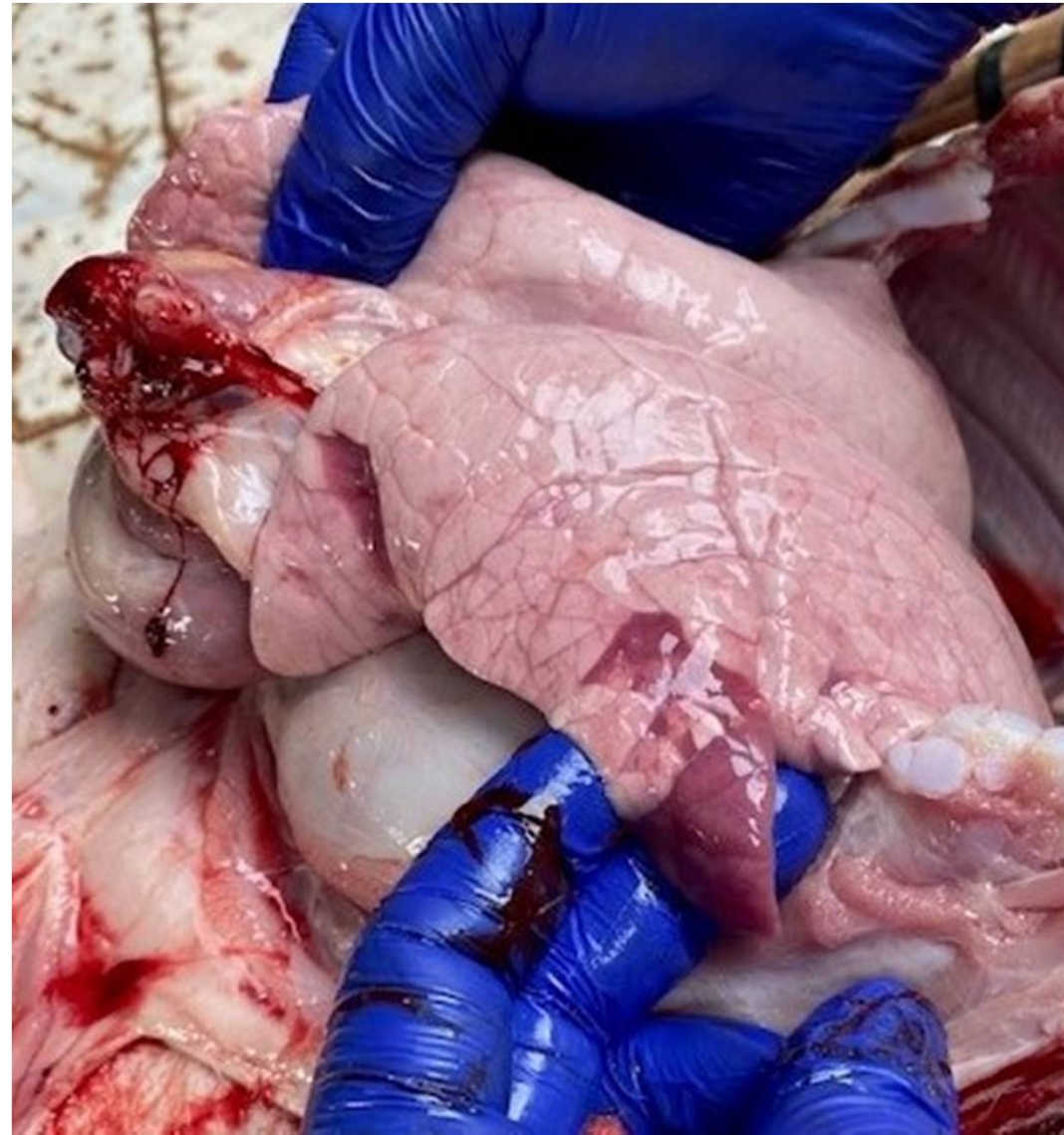
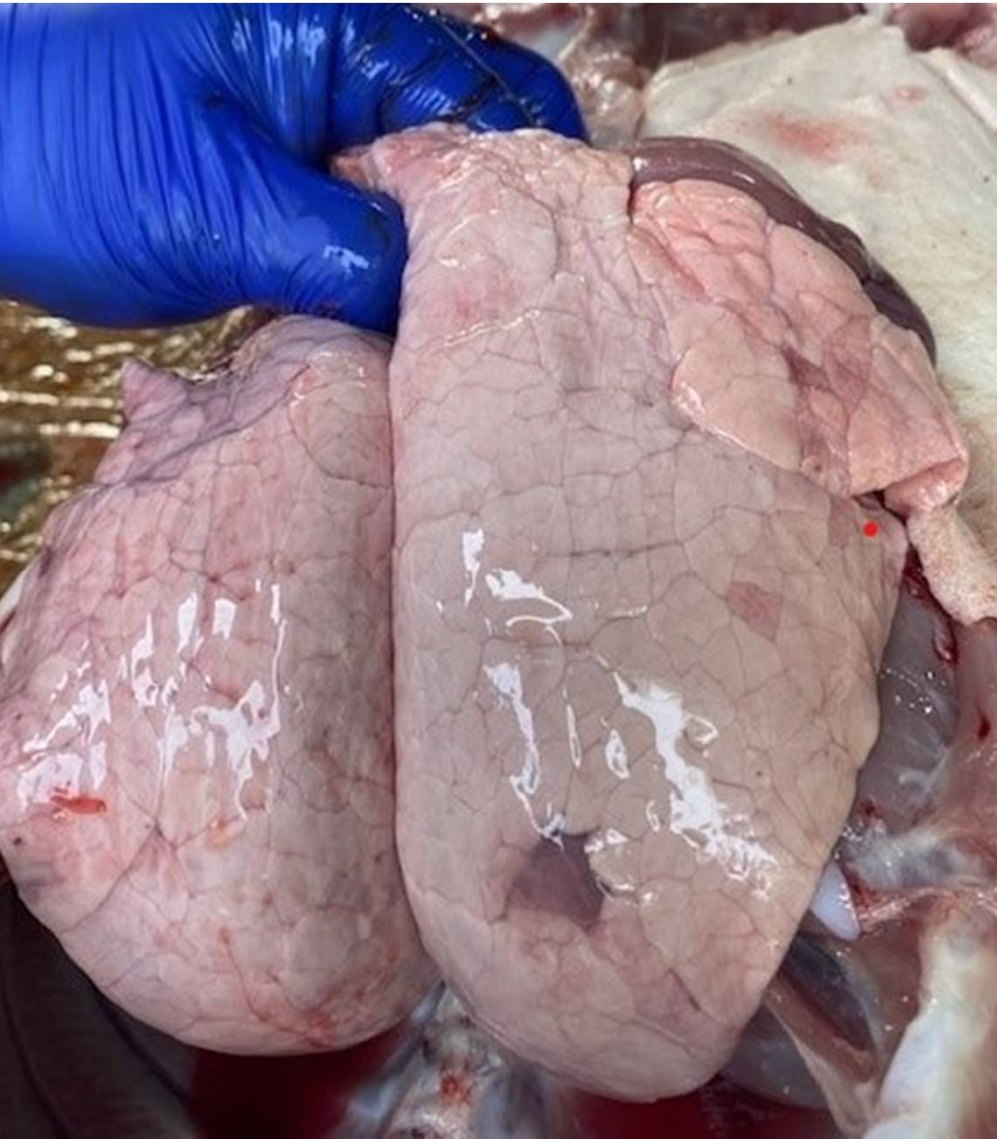
1. PCV2d PCR positive with Ct value of 5.
2. PRRS North American Strain, Ct value 13.338
3. *Hemophilus parasuis* serovar 6 and 14 positive in bacterial isolation and serotyping

# GROSS MORPHOLOGICAL LESIONS





# GROSS MORPHOLOGICAL LESIONS





# GROSS MORPHOLOGICAL LESIONS





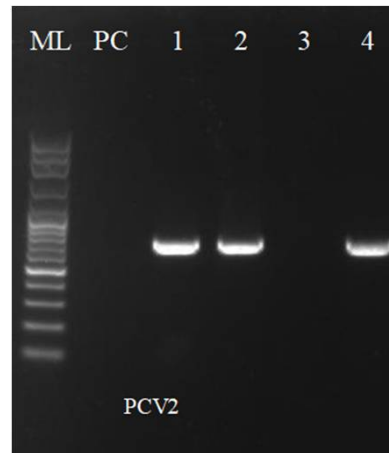
# GROSS MORPHOLOGICAL LESIONS



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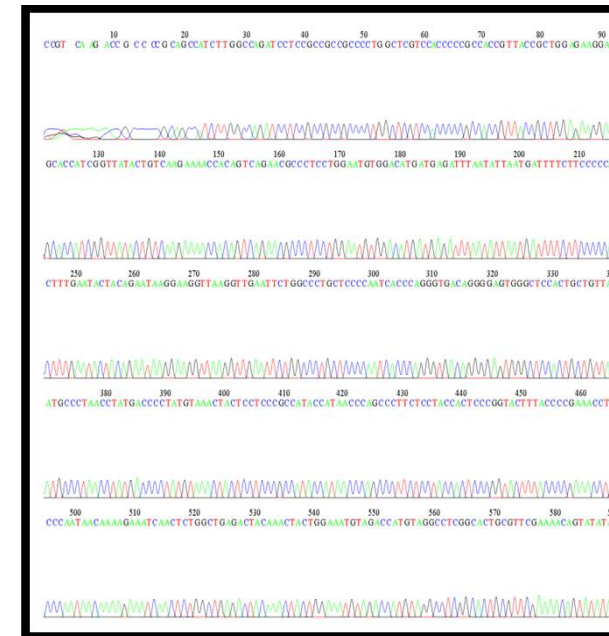
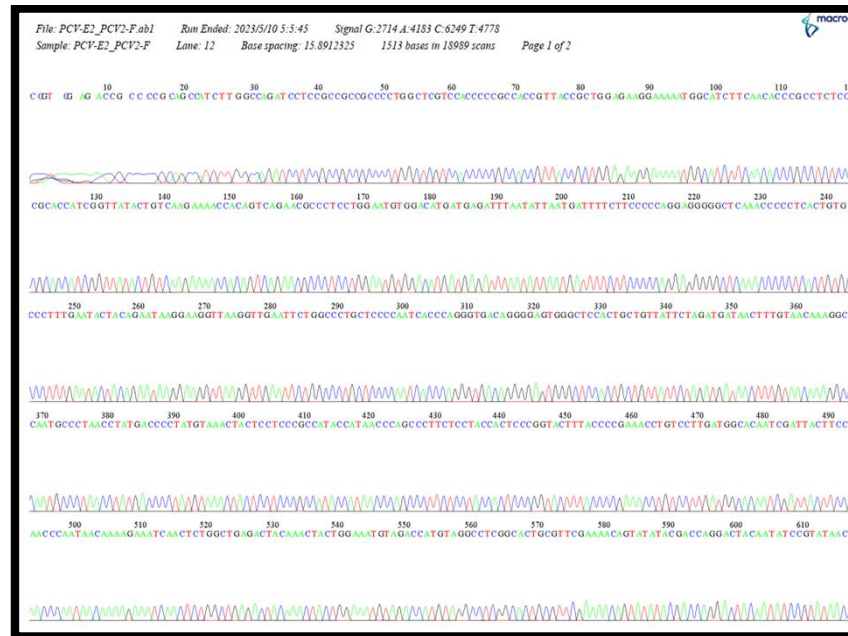
# NUCLEOTIDE SEQUENCING OF ORF2 OF PCV-2 FIELD SAMPLES

SAMPLE NAME	SAMPLE TYPE	RESULTS
Farm 1A	DNA extract	PCV-2 DNA Detected
Farm 1A	Tissue samples	PCV-2 DNA Detected
Farm 1B	DNA extract	PCV-2 DNA Detected
Farm 1B	Tissue samples	PCV-2 DNA Detected
Farm 3	DNA extract	PCV-2 DNA Not Detected
Farm 3	Tissue samples	PCV-2 DNA Not Detected
Farm 2	DNA extract	PCV-2 DNA Detected
Farm 2	Tissue samples	PCV-2 DNA Detected



**NUCLEOTIDE SEQUENCING**  
**674bp ORF2 gene**  
**224 amino acid sequence**

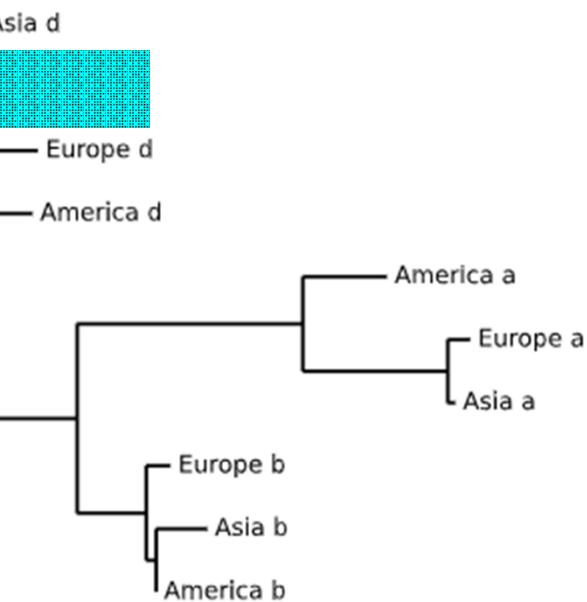
*Length of ORF2 of PCV2: 705bp*  
*Total Amino Acid Sequence: 223-234 aa*



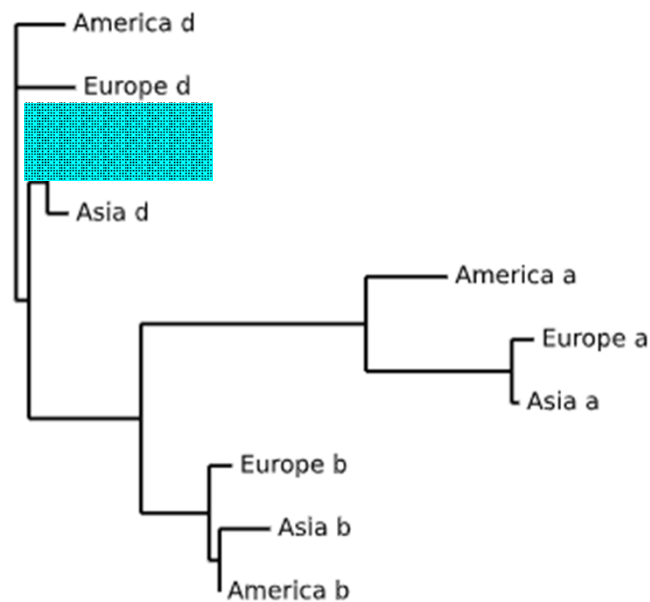


# ANALYSIS 1. GENOTYPING AND PHYLOGENETIC ANALYSES OF FIELD PCV2 SAMPLES

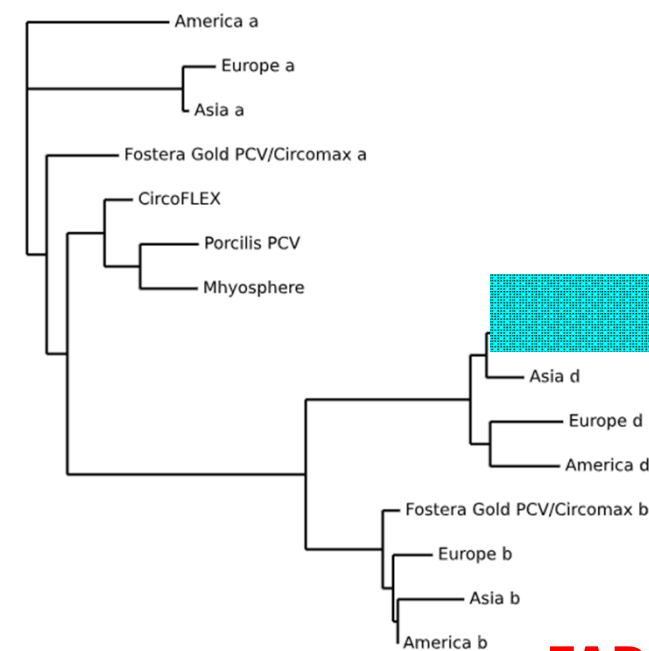
ID	Submission ID	Country	Genotype	Farm Name	Collection Date	Veterinarian Name	Sample Type	PCR Ct Values	PCR Vir
	ZTS-EpiVax-2023-51.1	Philippines	PCV2d	08222022 Farm 5	08/22/2022	Marlon Linatoc	Tissues (lungs+LN)	10 Ct	
	ZTS-EpiVax-2023-53.1	Philippines	PCV2d	08222022 Farm 5	08/22/2022	Marlon Linatoc	Tissues (lungs+LN)	10 Ct	
	ZTS-EpiVax-2023-46.1	Philippines	PCV2d	Farm 5 M3 020723	02/07/2023	Marlon Linatoc	Tissues (lungs+LN)	5.552 ct	



**FARM 1A**



**FARM 1B**

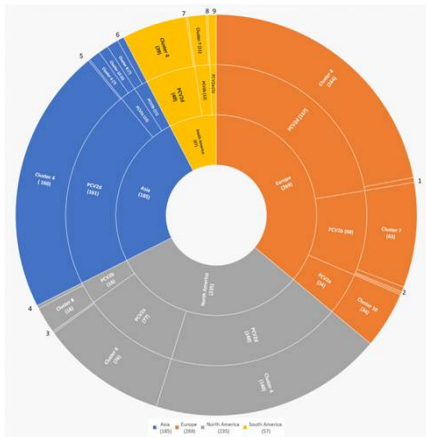


**FARM 1C**

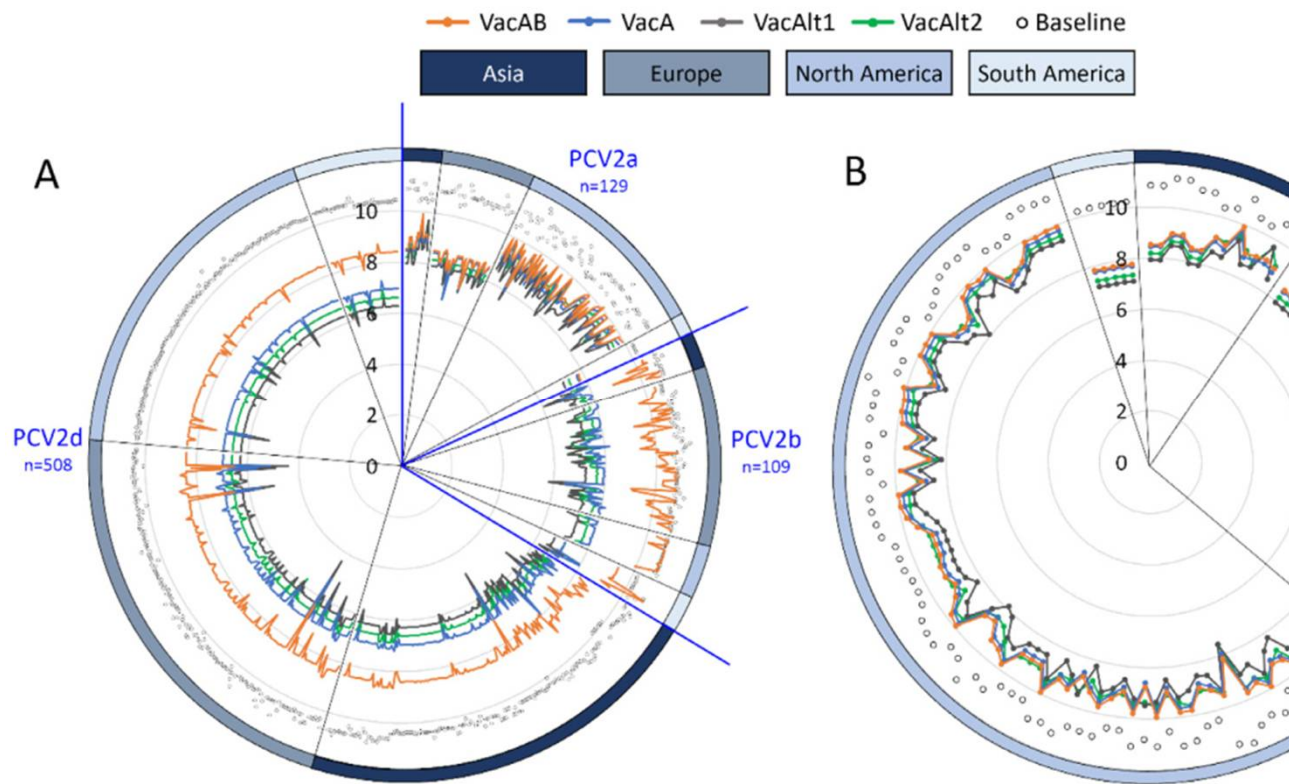
# EPICC BASELINE SCORES AND RADAR PLOT FOR PCV2 (GLOBAL STANDARDS)

Field isolate genotype	America N=292; a=82, b=30, d=180 Average (min-max)	Asia N=185; a=13, b=11, d=161 Average (min-max)	Europe N=269; a=34, b=68, d=167 Average (min-max)
PCV2a	9.33 (7.80-10.10)	8.96 (8.54-9.93)	8.37 (7.34-8.65)
PCV2b	10.23 (9.00-10.87)	10.19 (8.90-10.76)	10.23 (9.10-10.87)
PCV2d	8.37 (7.37-8.74)	8.32 (7.02-8.91)	8.31 (6.34-8.78)
PCV2a	8.75 (7.13-9.48)	8.51 (7.94-9.71)	7.87 (7.16-8.18)
PCV2b	6.98 (6.21-7.41)	7.00 (6.06-7.40)	7.06 (5.80-7.48)
PCV2d	6.26 (5.25-6.63)	6.22 (4.90-6.94)	6.21 (4.37-6.67)
PCV2a	9.14 (7.38-9.71)	8.82 (8.19-9.66)	8.08 (7.19-8.34)
PCV2b	7.41 (6.65-7.69)	7.39 (6.50-7.69)	7.38 (6.25-7.76)
PCV2d	6.58 (5.58-6.95)	6.55 (5.23-7.47)	6.54 (4.73-6.95)
PCV2a	7.79 (6.43-8.49)	7.65 (7.24-8.46)	7.21 (6.59-7.97)
PCV2b	7.65 (6.87-7.95)	7.61 (6.76-7.95)	7.64 (6.51-8.18)
PCV2d	6.92 (5.91-7.56)	6.86 (5.56-7.60)	6.86 (5.03-7.33)

Minimum and Maximum EpiCC Scores of PCV isolates globally

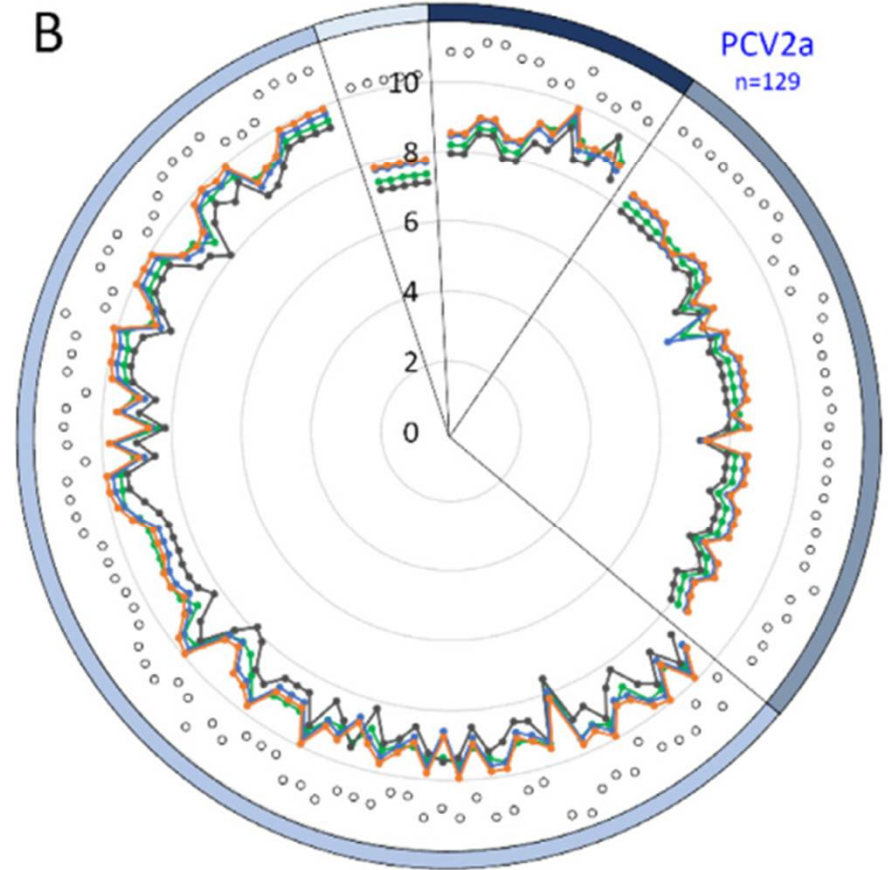
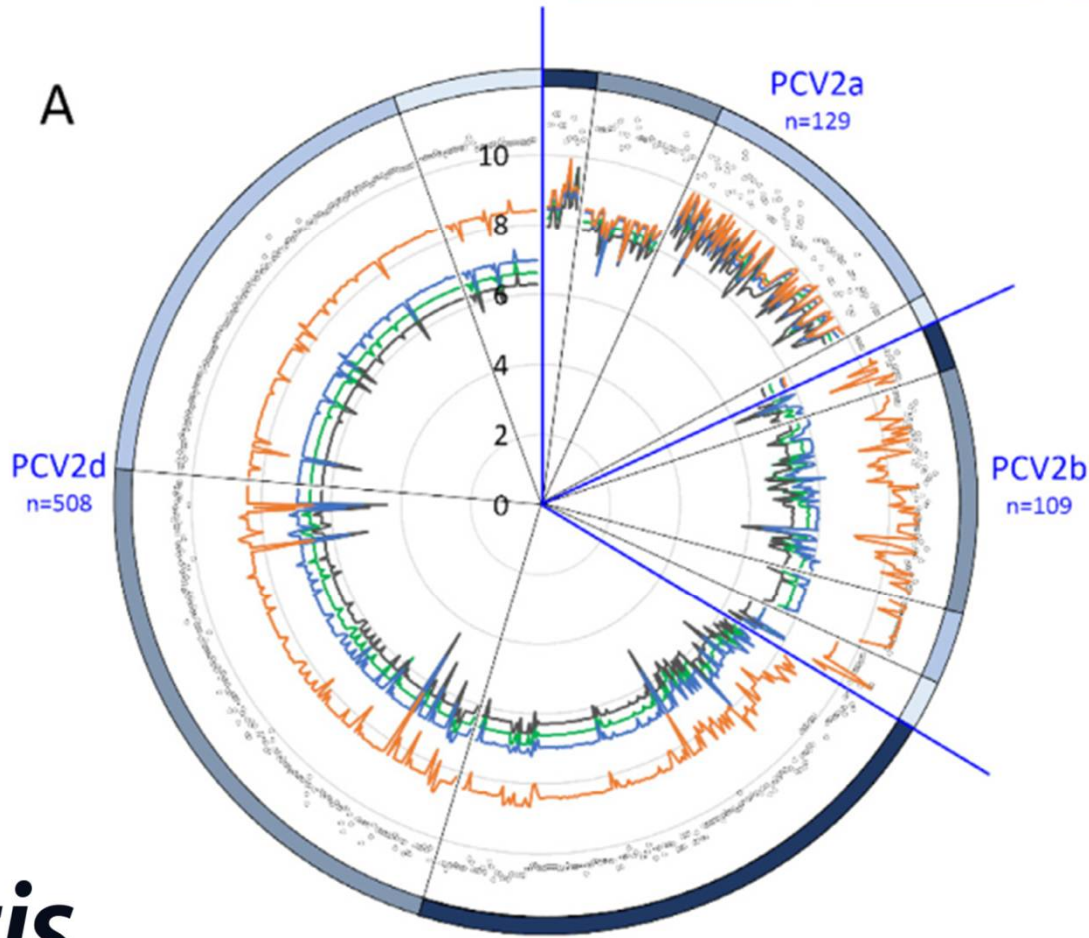
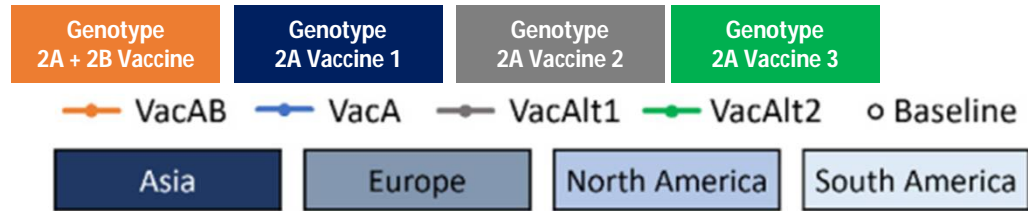


Distribution of tested PCV2 samples (N=746)



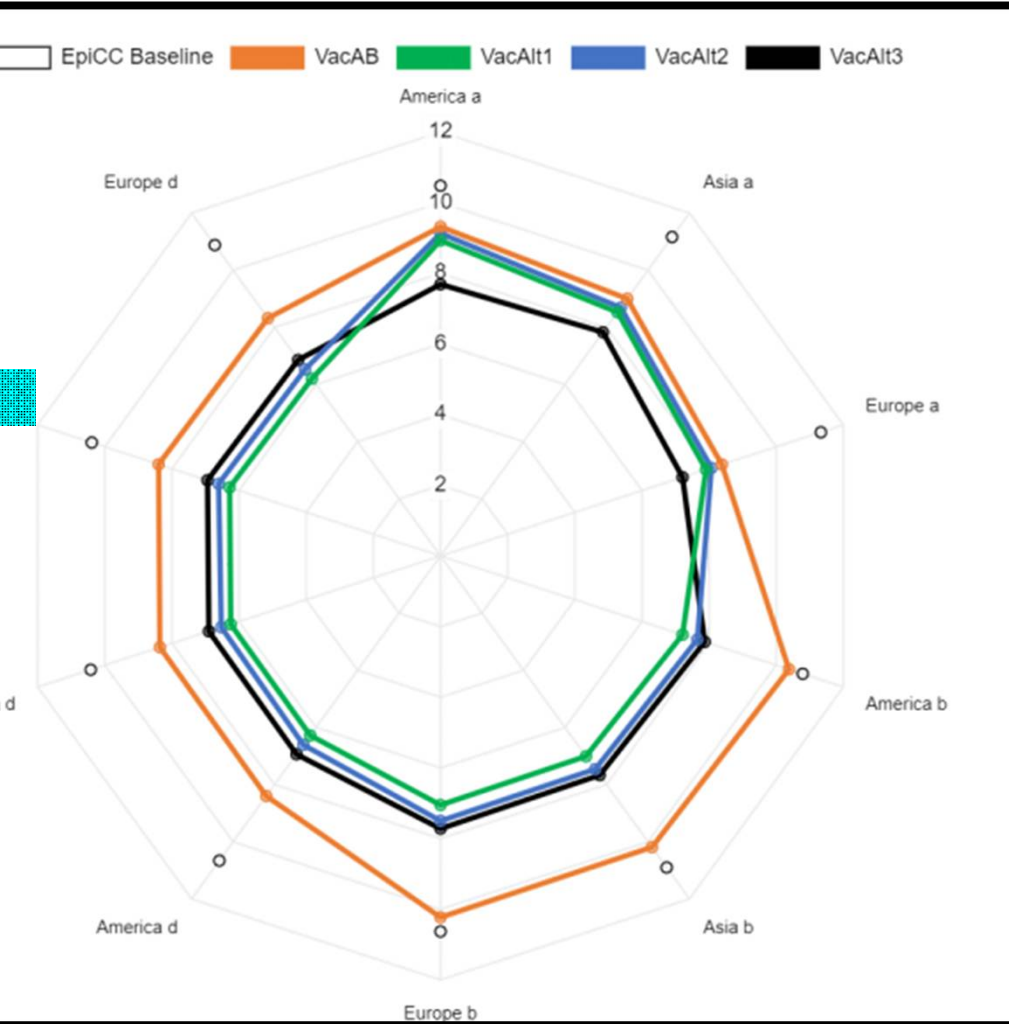
Capsid EpiCC scores of global PCV isolates and vaccines

# ANALYSIS 2. EpiCC BASELINE SCORES AND RADAR PLOT FOR PCV2 (GLOBAL STANDARDS)

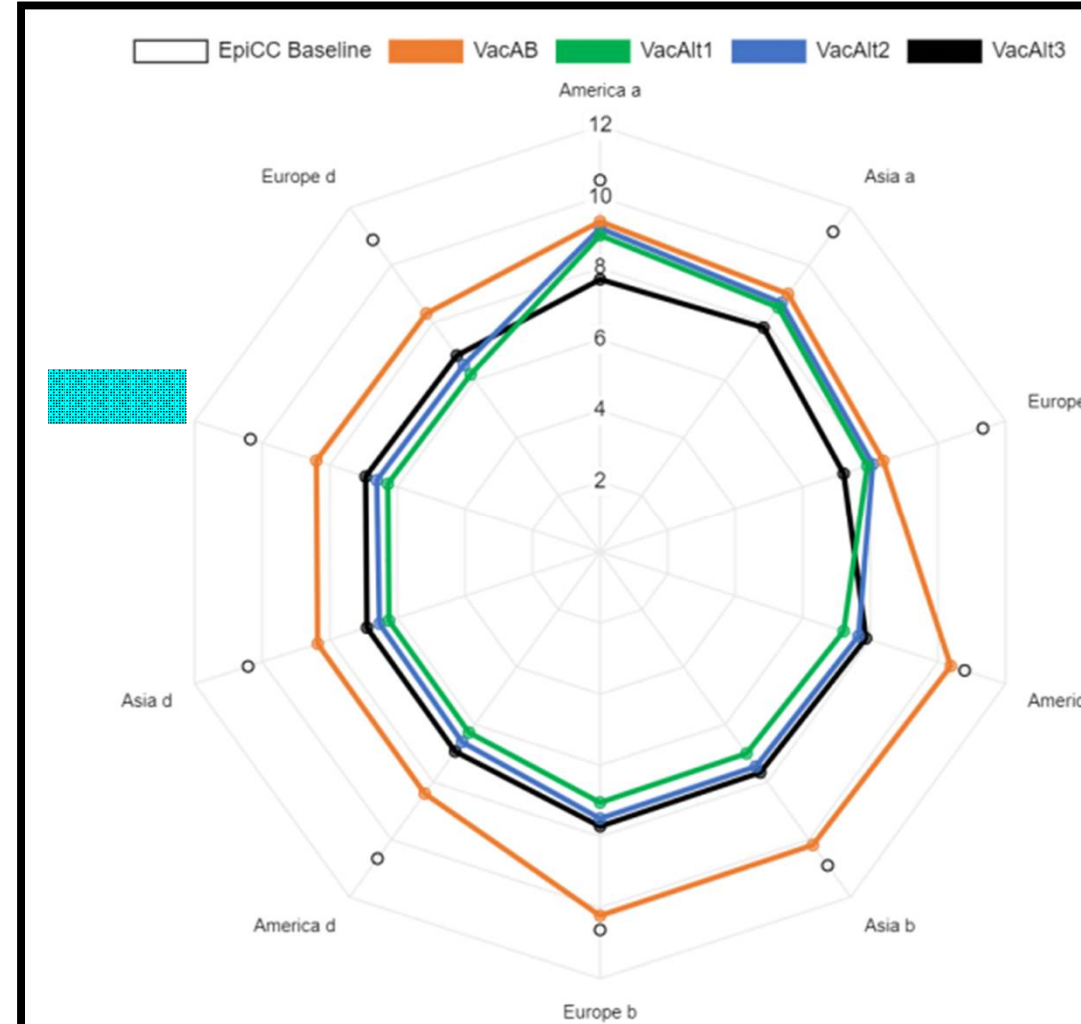




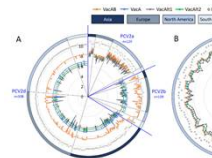
# ANALYSIS 2. EpiCC SCORES AND RADAR PLOT OF FIELD PCV2 SAMPLES



**FARM 1A**

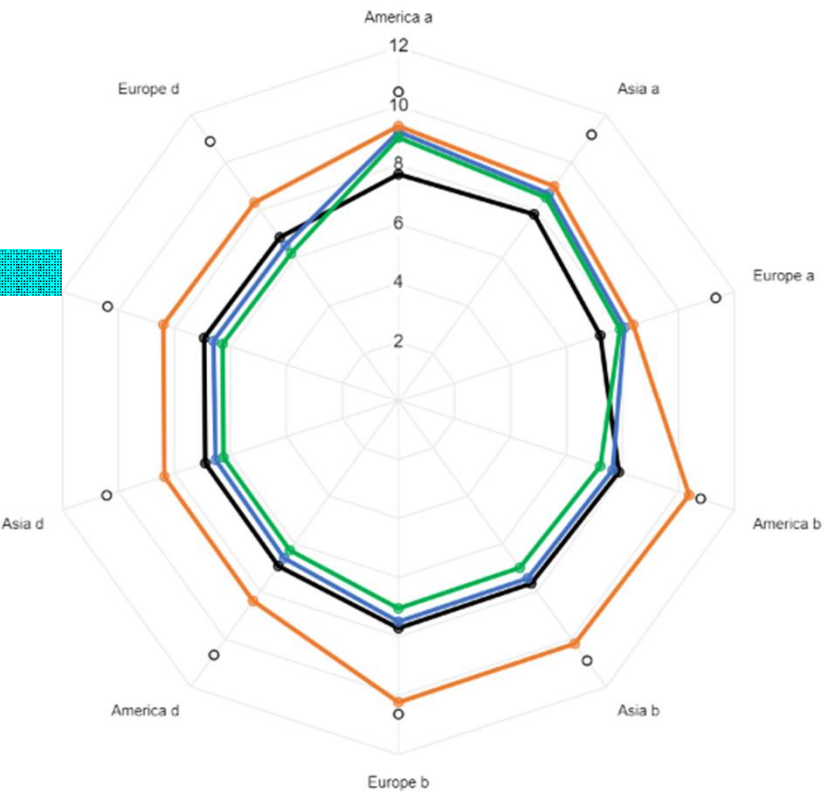


**FARM 1B**

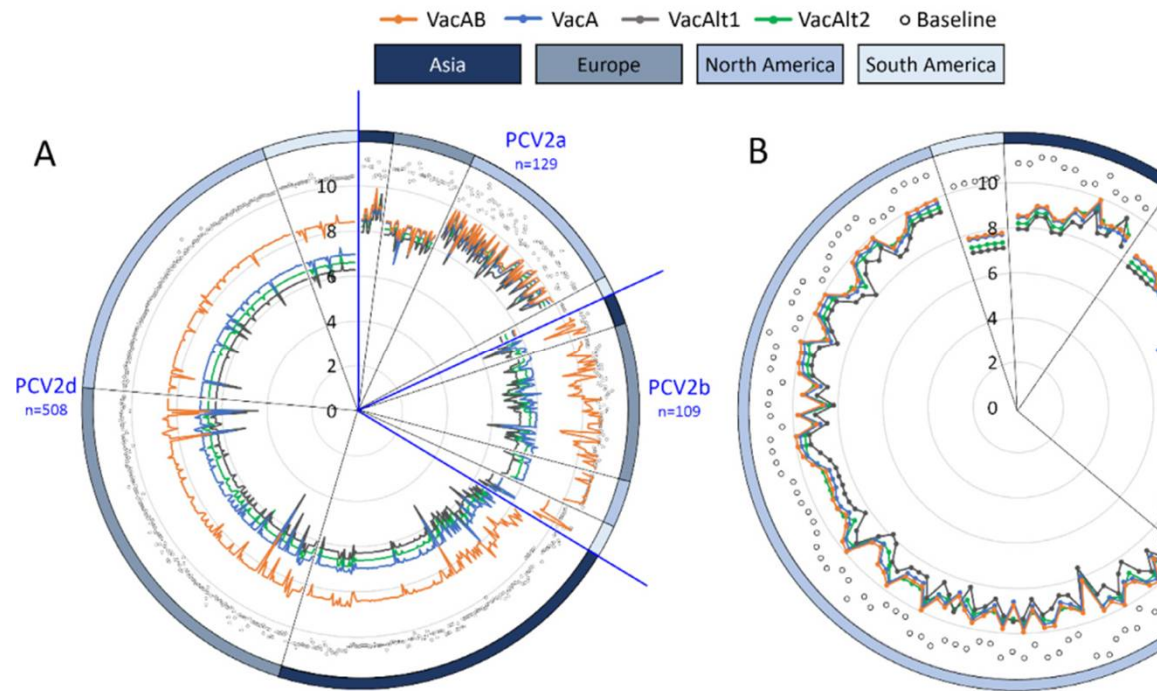


# ANALYSIS 2. EpiCC SCORES AND RADAR PLOT OF FIELD PCV2 SAMPLES

EpiCC Baseline VacAB VacAlt1 VacAlt2 VacAlt3



**FARM 2**



**GLOBAL STANDARD**

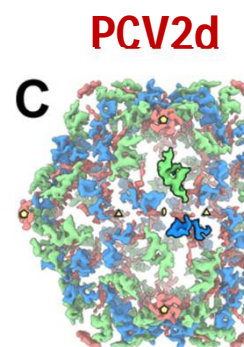
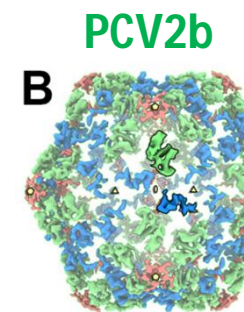
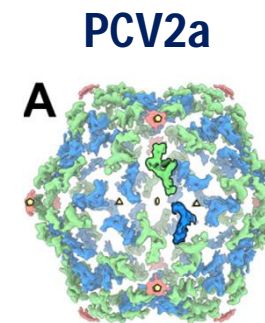
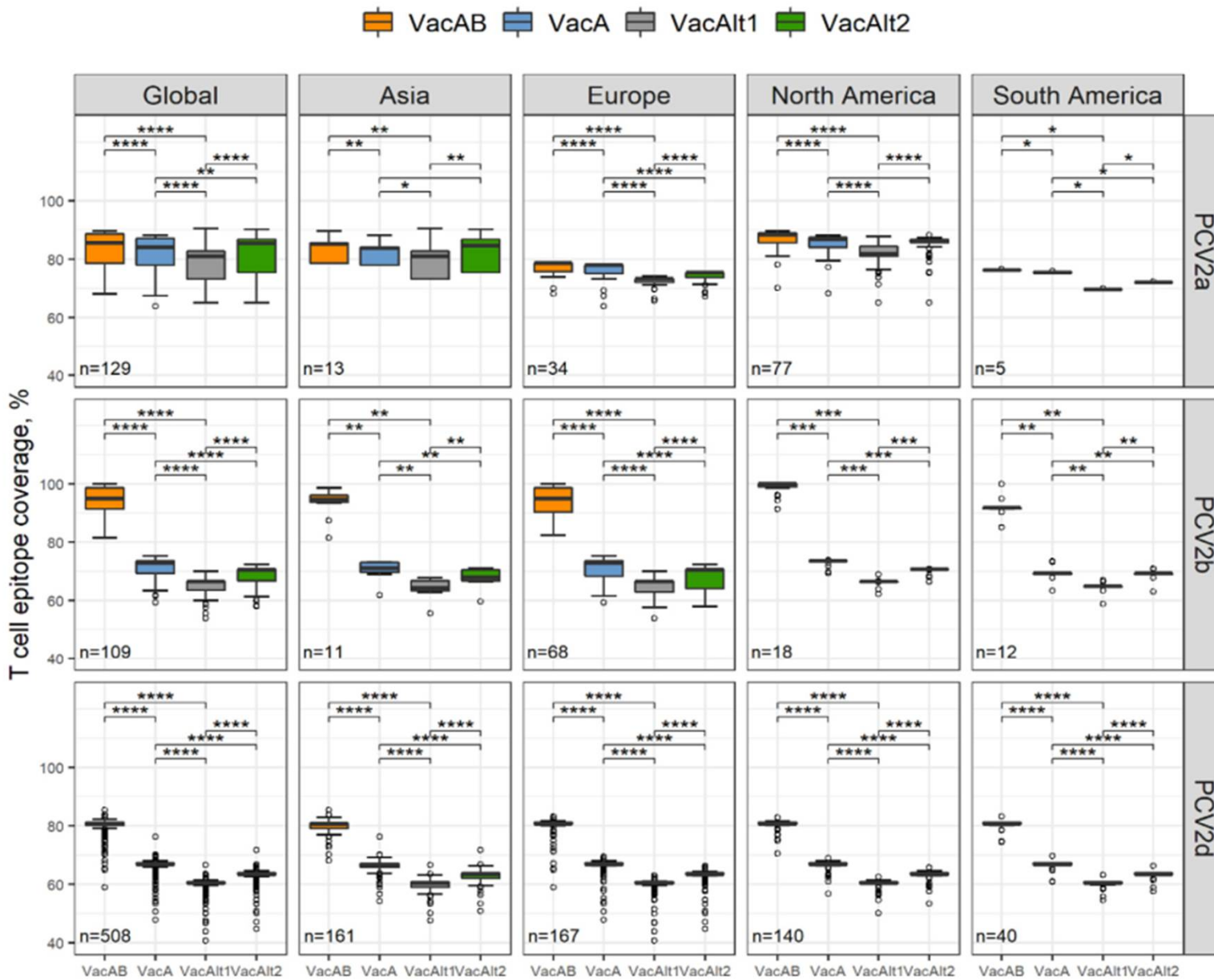
# ANALYSIS 3. PERCENT T-CELL EPITOPE COVERAGE (GLOBAL STANDARDS)

type  
Vaccine

type  
Vaccine 1

type  
Vaccine 2

type  
Vaccine 3



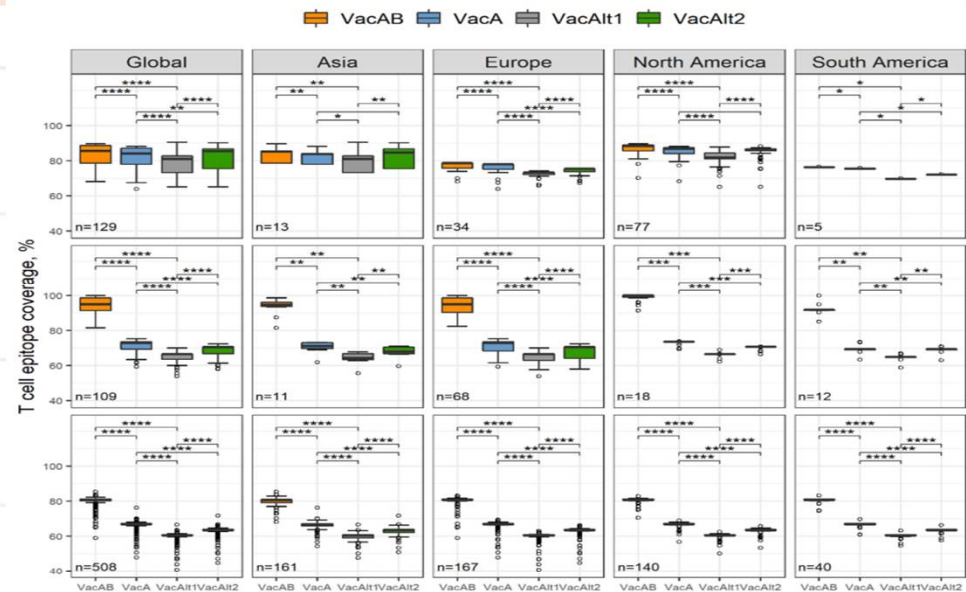
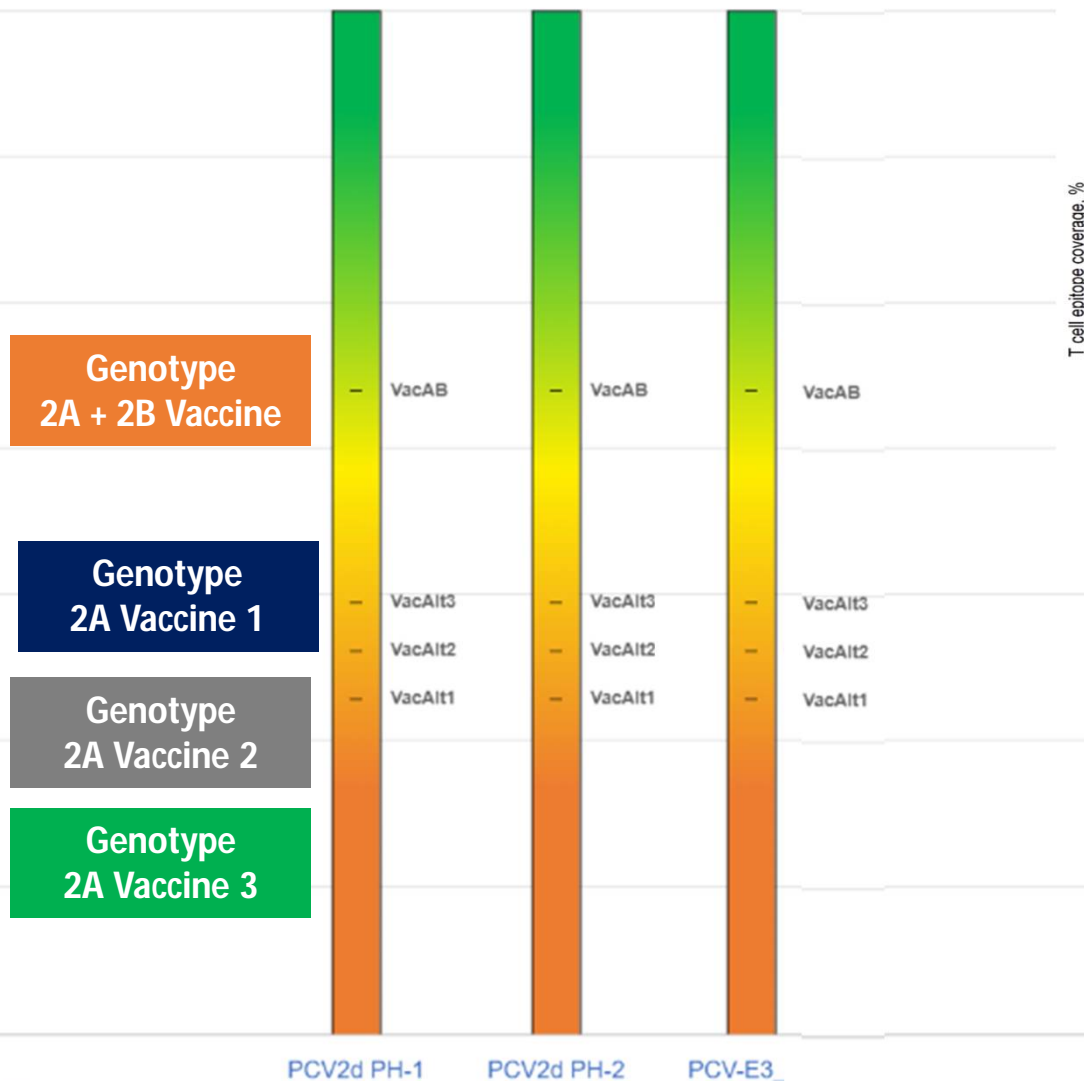
ptis

Foss et al., 2022

Khayat, et al., 2022



# ANALYSIS 3. PERCENT T-CELL EPITOPE COVERAGE OF FIELD PCV2 SAMPLE



Foss et al., 2022

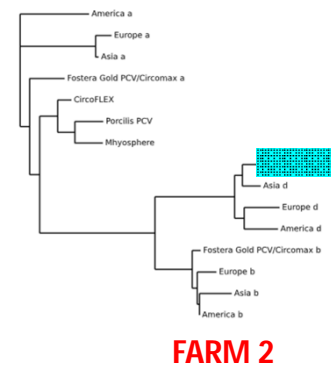
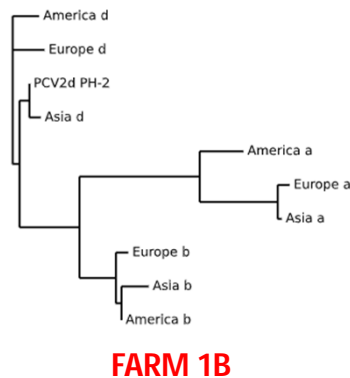
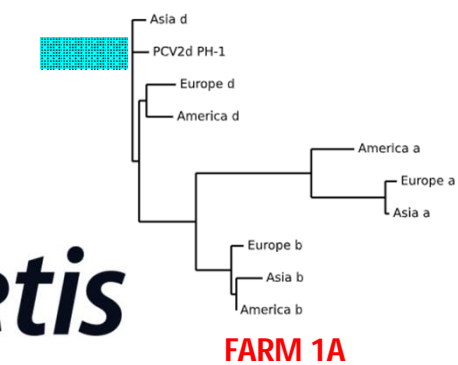
TABLE 1. Epitopes of PCV1 and PCV2

Epitope	Residues <sup>a</sup>	Aligned sequence <sup>b</sup>	MAb binding residue(s)
A	69–83	NV <b>N</b> ELRFNIG <b>Q</b> FLPP VDMMRFN <b>I</b> DFLPPG	Asp70, Met71, Asn77, Asn78
B <sup>d</sup>	113–127	TS <b>N</b> Q <b>R</b> GVG <b>S</b> TV <b>I</b> L <b>D</b> Q <b>G</b> DRGVG <b>S</b> SA <b>V</b> IL <b>D</b> D	Gln113, Asp115
C <sup>d</sup>	117–131	RGV <b>G</b> ST <b>V</b> IL <b>D</b> AN <b>F</b> V GV <b>G</b> SS <b>A</b> VIL <b>D</b> DN <b>F</b> VT	Asp127
D	169–183	D <b>Q</b> T <b>I</b> D <b>F</b> Q <b>P</b> NN <b>K</b> R <b>N</b> Q F <b>T</b> I <b>D</b> Y <b>F</b> Q <b>P</b> NN <b>K</b> R <b>N</b> Q <b>L</b>	Thr170
E	193–207	N <b>V</b> E <b>H</b> T <b>L</b> G <b>L</b> G <b>Y</b> A <b>L</b> Q <b>N</b> A <b>T</b> T V <b>D</b> H <b>V</b> G <b>L</b> G <b>T</b> A <b>F</b> E <b>N</b> S <b>I</b> Y	Glu203, Ile206, Tyr207
F	25–39	R <b>R</b> P <b>L</b> V <b>H</b> P <b>A</b> F <b>R</b> N <b>R</b> Y <b>R</b> W <b>R</b> R <b>R</b> P <b>L</b> V <b>H</b> P <b>--</b> R <b>H</b> Y <b>R</b> W <b>R</b>	

Khayat, et al., 2019

# SUMMARY OF EpiCC RESULTS

ID	Country	Genotype	EpiCC Baseline	Vaccines	Vaccine Genotypes	EpiCC Score <sup>1</sup>	T cell epitope Coverage %	Deficit relative to VacAB	VacAB coverage i ove each mon vacci
A	Philippines	PCV2d	10.388	VacAB	PCV2a, PCV2b	8.397	80.83%	-	-
				VacAlt1	PCV2a	6.282	60.47%	20.36%	33.67
				VacAlt2	PCV2a	6.61	63.63%	17.21%	27.05
				VacAlt3	PCV2a	6.941	66.81%	14.02%	20.99
B	Philippines	PCV2d	10.349	VacAB	PCV2a, PCV2b	8.397	81.14%	-	-
				VacAlt1	PCV2a	6.282	60.7%	20.44%	33.67
				VacAlt2	PCV2a	6.61	63.87%	17.27%	27.05
				VacAlt3	PCV2a	6.941	67.07%	14.07%	20.99
C	Philippines	PCV2d	10.388	VacAB	PCV2a, PCV2b	8.397	80.83%	-	-
				VacAlt1	PCV2a	6.282	60.47%	20.36%	33.67
				VacAlt2	PCV2a	6.61	63.63%	17.21%	27.05
				VacAlt3	PCV2a	6.941	66.81%	14.02%	20.99



# KEY TAKE AWAYS

PCV2 is an economically important pathogen that can lead to several **porcine coronavirus-associated diseases (PCVAD)**.

PCV2's evolutionary rate is unusually high for DNA virus resulting to the **emergence of at least 8 genotypes**.

PCV2 continues to evolve and EpiCC analysis provides a new tool to assess the possible impact of virus genetic divergence on T cell epitope coverage of vaccine strains.

Circulating field PCV strains that share more T cell epitope content with vaccine strains will have higher EpiCC scores and higher vaccine coverage.

**etis**



**PROJECT TITLE**

**DEVELOPMENT OF SURVEILLANCE SYSTEM FOR ASFV IN RURAL ENVIRONMENT AND FOMITES OF ASF-AFFECTED SWINE FARM AS AN ADDED TOOL FOR ASF SENTINEL, REPOPULATION AND RECOVERY PROGRAMS**

**General Objective**

The general objective of the study is to develop a surveillance system for ASFV that utilizes the rural environment and fomites as an added tool for ASF sentinel, repopulation and recovery programs in the Philippines.



Dennis V. Umali, DVM, PhD  
Veterinary Molecular Epidemiology/ Veterinary Diagnostics and Disease Control



Jorge Gil C. Angeles, MS, PhD  
Molecular Biology and Biotechnology/ Epigenetics and Bioinformatics



Jomar F. Rabajante, MS, PhD  
Mathematical and Systems Engineering/ Biomathematics



Fletcher P. Del Valle, DVM, PhD  
Veterinary Virology/ Food Animal Medicine



Sherwin L. ...  
Veterinary ...  
Food A...



Mark Lawrence G. Alienz  
Veterinary Medicine



Leni Anjela DC. Leynes, Rmircr  
Microbiology



Gianne May R. Gagan, DVM  
Veterinary Medicine/ Tropical Animal Health



Erika Joyce Arellano, RMT  
Medical Technology



Ang ...  
Admini...



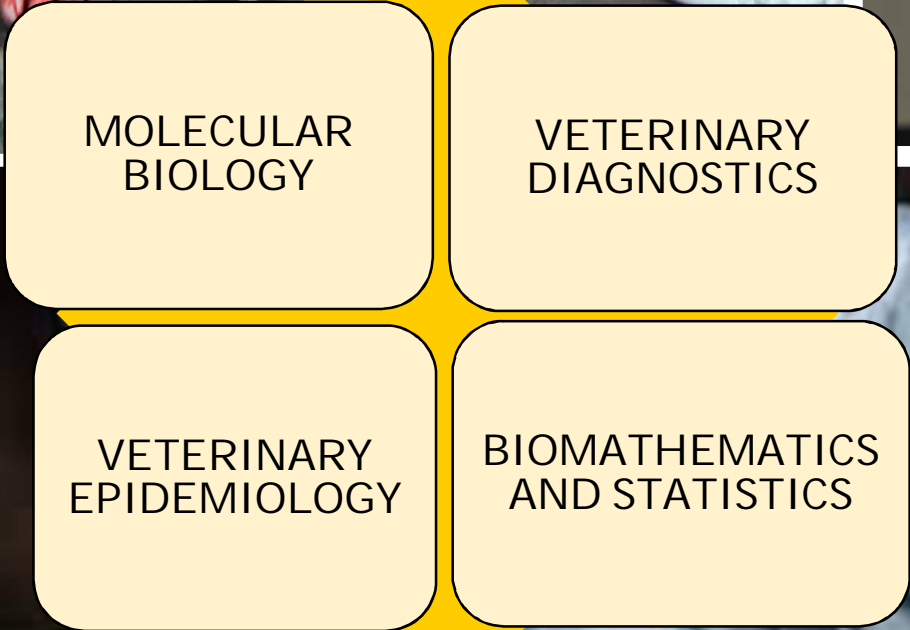
# MOLECULAR EPIDEMIOLOGICAL-BASED REPOPULATION SYSTEM

## RESEARCH TEAM

- MOLECULAR EPIDEMIOLOGIST
- VIROLOGIST
- MOLECULAR BIOLOGIST
- MICROBIOLOGIST
- ANIMAL SCIENTIST
- BIOMATHEMATICIAN
- VETERINARIANS

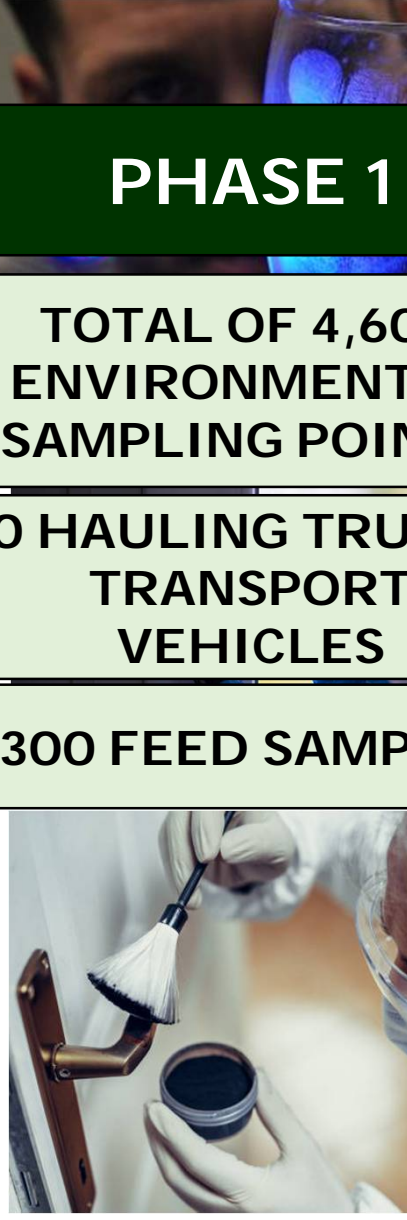
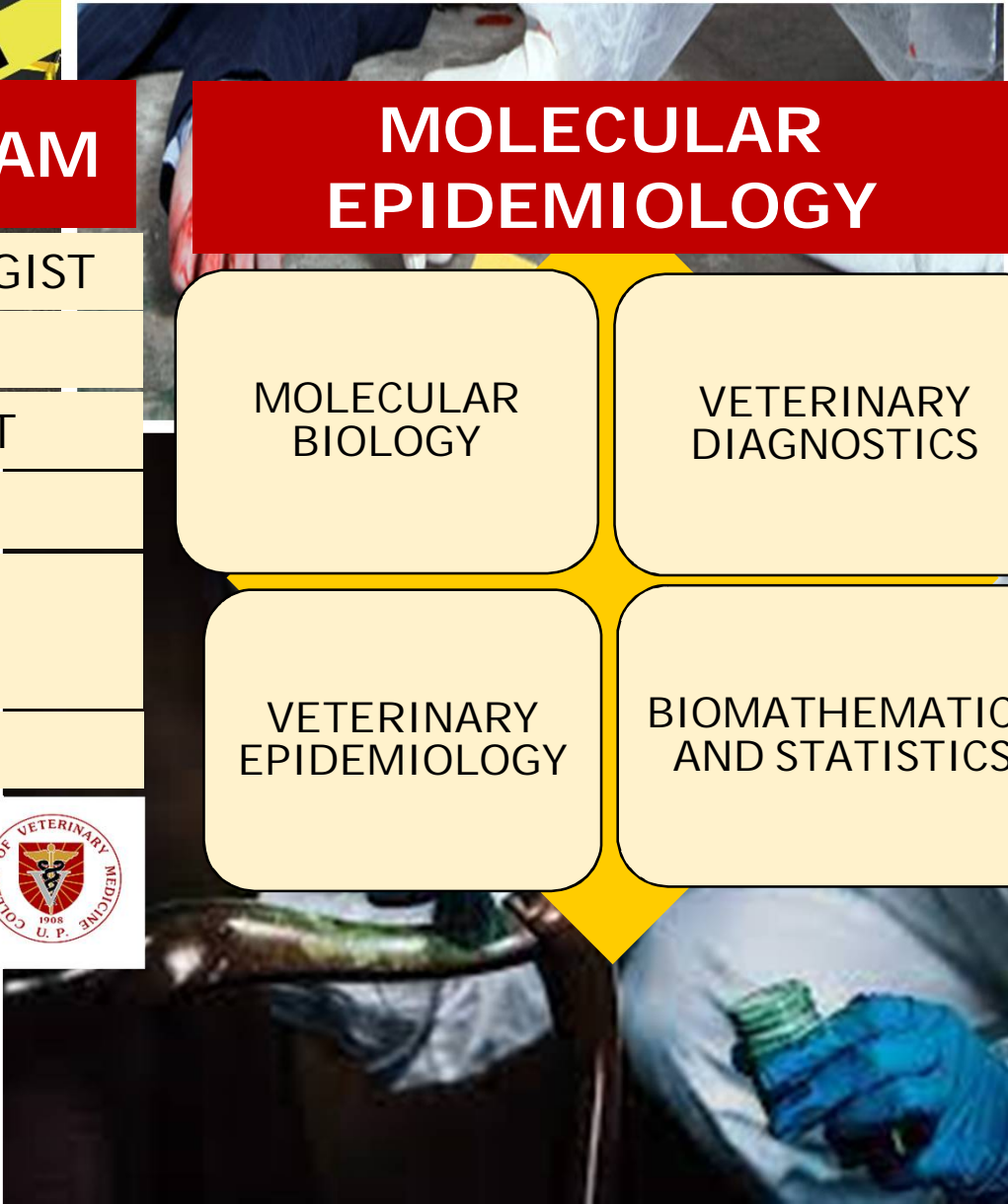


## MOLECULAR EPIDEMIOLOGY



## PHASE 1

- TOTAL OF 4,600 ENVIRONMENTAL SAMPLING POINTS
- 30 HAULING TRUCKS TRANSPORT VEHICLES
- 300 FEED SAMPLES



# AREAS OF POSSIBLE COLLABORATIONS

## POTENTIAL COLLABORATORS

SMALLHOLDER FARMS

SEMI-COMMERCIAL FARMS

COMMERCIAL FARMS

ASSOCIATION-GROUPS

LGUs

**PLANNING TO (2023-2024):**

**Perform Sentinelling**

**Partial/Full Repopulation**

**Build-up of In-House Farm**

**Laboratory Capabilities**

## PHASE 2 (FIELD VALIDATION)

**FREEDOM FROM PREVIOUS  
INFECTION OF THE FARM  
ENVIRONMENT**

**BIOSECURITY  
ENHANCEMENTS -  
qPCR-BASED MOLECULAR  
SURVEILLANCE SYSTEM**

**MOLECULAR  
EPIDEMIOLOGICAL-BASED  
REPOPULATION SYSTEM**

**RISK-BASED APPROACH TO  
SEGMENTAL  
DEPOPULATION**

**EARLY DETECTION OF  
REINFECTION THROUGH  
SYNDROMIC SURVEILLANCE  
SYSTEM**

**EMAIL ADDRESS: [dvumali@up.edu.ph](mailto:dvumali@up.edu.ph)**