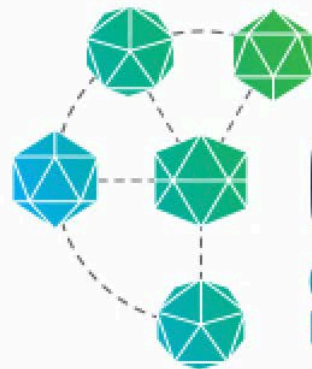


# SURVEILLANCE IN ANIMALS/AT THE HUMAN-ANIMAL INTERFACE

**Prof. Soren Alexandersen, DVM, PhD, DVSC, FRCPath, MRCVS**  
Director of Geelong Centre for Emerging Infectious Diseases

**Dr. James Fielding, MAppEpid, PhD**  
Epidemiologist and Honorary Senior Fellow  
Victorian Infectious Diseases Reference Laboratory  
The Peter Doherty Institute for Infection and Immunity



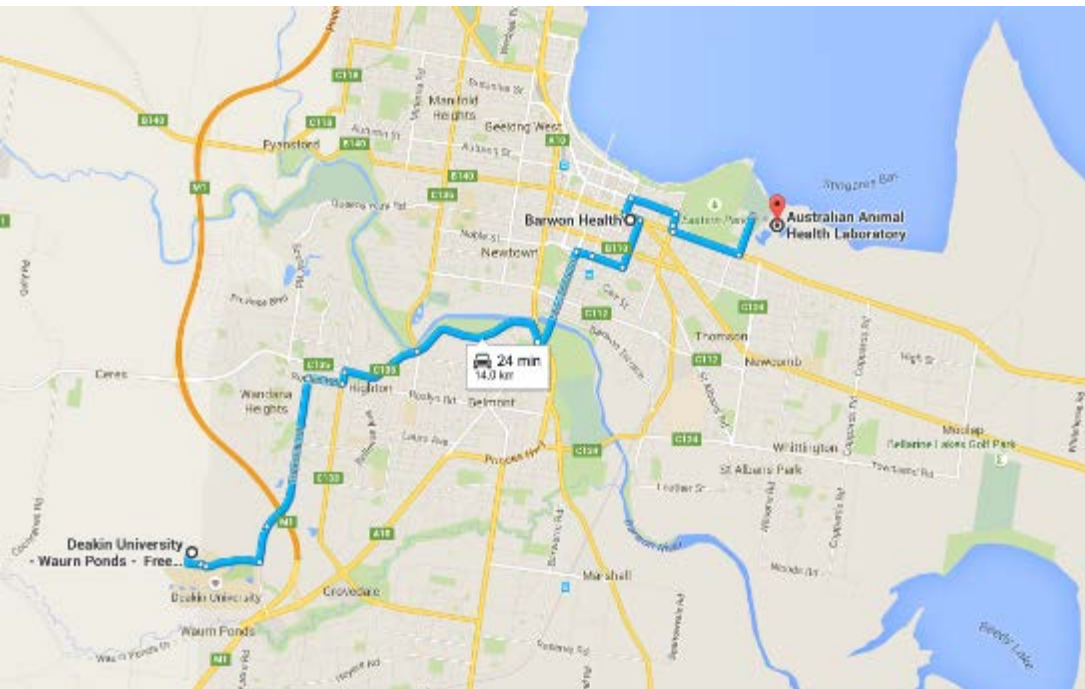
# GCEID

GEELONG CENTRE FOR  
EMERGING INFECTIOUS DISEASES



**APPRISE Annual Meeting**  
**15 August 2017**

## Geelong Centre for Emerging Infectious Diseases



## **Zoonotic diseases surveillance at the animal-human interface**

Scoping assessment to describe status of surveillance for established and emerging zoonotic diseases at the human animal interface in Australia:

- Compiling a list of zoonotic diseases regarded as important in the Australian context
- Defining the important animal-human interfaces in Australia
- Documenting the extent and nature of zoonotic disease surveillance at these interfaces in terms of humans, animals and e.g. arthropods
- Identifying gaps and opportunities for the establishment or improvement of zoonotic disease surveillance at the animal-human interface
- **TO FACILITATE OPTIMISATION AND USE OF ANIMAL SURVEILLANCE DATA???**

Zoonoses are estimated to comprise around 60% of both human diseases and of emerging diseases

### **Summary of key findings**

- Many important animal-human interfaces were identified in the assessment - most important including: veterinarians; farmers; abattoir/knackery workers; shearers; people assisting with animal births; pet owners; hunters (particularly pig hunters); wildlife management; and zoo and sanctuary staff
  - With several exceptions, zoonotic disease surveillance in Australia is largely passive, with responses mostly arising from notified cases of zoonotic infections in humans. Objectives of notifiable infectious diseases surveillance in animals and humans are different, with 22 diseases common to the respective lists of notifiable infectious diseases. Many zoonotic diseases are of little clinical importance in animal populations
- changes require funds, will and pressure!**

## **James Fielding – DRAFT APPRISE Discussion Paper**

- **Some jurisdictions have well established and coordinated One Health Networks with representatives from across the environmental, human and animal health sectors. Some ongoing, others fixed term in response to acute events, but all highly valued**
- **The scoping exercise did not identify any human population-targeted zoonotic disease surveillance at animal-human interfaces, but there are a number of opportunities that could be explored**
- **Further work in this area should be done in collaboration with the Office of Health Protection's evaluation of Australia's "behaviours, policies and practices to minimise the transmission of zoonotic diseases from animals into human populations"**

**IMPORTANT TO FACILITATE OPTIMISATION AND USE OF ANIMAL SURVEILLANCE DATA???**

Table 1: Zoonotic diseases listed on state/territory government department websites

Disease	New South Wales	Victoria	Queensland	Northern Territory
Animal influenza*	✓		✓	
Anthrax	✓	✓	✓	
Australian bat lyssavirus	✓	✓	✓	✓
Babesiosis	✓			
Bacterial infections from animal bites		✓	✓	
Beef measles	✓			
Brucellosis	✓	✓	✓	
Cat scratch fever		✓	✓	✓
Cryptosporidiosis	✓	✓	✓	✓
Giardiasis	✓	✓	✓	✓
Hantavirus			✓	
Hendra virus	✓	✓	✓	✓
Hydatid disease	✓	✓	✓	✓
Leishmaniasis	✓			
Leptospirosis	✓	✓	✓	✓
Listeriosis	✓	✓	✓	✓
Liver fluke	✓			
Lyme disease	✓			
Melioidosis			✓	✓
Menangle virus		✓		
Mycobacterium infections (non-tuberculosis)		✓		
Nipah virus		✓		
Orf		✓		
Plague	✓		✓	
Psittacosis	✓	✓	✓	✓
Q fever	✓	✓	✓	✓
Rabies	✓	✓	✓	
Rat lung worm	✓			
Ringworm		✓	✓	✓
Salmonellosis	✓	✓	✓	✓
Scrub typhus	✓			✓
Shiga toxin-producing <i>Escherichia coli</i>	✓	✓		
<i>Sparganosis</i>			✓	✓
<i>Streptococcus suis</i>		✓		
Tetanus	✓			
Toxocariasis		✓	✓	
Toxoplasmosis	✓	✓	✓	✓
Transmissible spongiform encephalopathies^	✓			
Tuberculosis (bovine)		✓		
Tularemia	✓		✓	
Yersiniosis		✓		

\* includes avian and swine influenza

^ includes bovine spongiform encephalopathy and variant Creutzfeldt Jakob disease



# **State, Territory and National Animal Surveillance**

Tasmanian Department of Primary Industries, Parks, Water and Environment

Queensland Department of Agriculture and Fisheries

Department of Agriculture and Food, Western Australia

Northern Territory Department of Primary Industry and Resources

Department of Primary Industries and Regions, South Australia

**New South Wales Department of Primary Industry (EMAI)**

**Victorian Dept. of Economic Development, Jobs, Transport and Resources (AGRIBIO)**

**CSIRO Australian Animal Health Laboratory (AAHL)**

**Wildlife Health Australia**

# Animal Health Surveillance QUARTERLY -October to December 2016

**Table 14 Disease testing and pest surveillance under the Northern Australia Quarantine Strategy (NAQS), 1 October 2015 to 31 December 2016**

Target disease	Oct–Dec 2015		Jan–Mar 2016		Apr–Jun 2016		Jul–Sep 2016		Oct–Dec 2016	
	Tested	Positive	Tested	Positive	Tested	Positive	Tested	Positive	Tested	Positive
Aujeszký's disease <sup>a</sup>	154	0	45	0	146	0	196	0	189	0
Avian influenza <sup>a</sup>	0	0	0	0	103	0	0	0	0	0
Classical swine fever	154	0	58	0	206	0	196	0	189	0
Japanese encephalitis	0	0	36	0	59	1 <sup>b</sup>	0	0	45	0
Surra ( <i>Trypanosoma evansi</i> )	183	0	16	0	199	0	244	0	207	0

a Excludes testing in wild birds.

b A single pig from Moa Island, Torres Strait, tested positive to Japanese encephalitis (JE) on ELISA test for antibodies. Results from follow-up testing with Flavivirus group plaque reduction neutralisation test were consistent with an antibody response following exposure to JE virus (i.e. antibody titres for JE virus were four-fold higher than titres for Murray Valley encephalitis and Kunjin viruses). No clinical signs consistent with JE were observed in this pig (or other animals) sampled during this survey. JE virus is endemic in Papua New Guinea and is known to circulate in Torres Strait on a seasonal basis. Surveillance for JE conducted by both NAQS and Queensland Health has found no evidence of circulation of JE on the mainland this year. Queensland Health was notified of this finding and they have since conducted follow-up investigations and awareness campaigns in Torres Strait as a public health measure.

**Table 17 Investigations for national notifiable animal diseases, October to December 2016**

Disease	Species	State	Month	Response code <sup>a</sup>	Finding
Infection with influenza A viruses in swine <sup>d</sup>	Pig	SA	Oct	3	Positive
	Pig	WA	Dec	2	Negative (2 unrelated investigations)
	Pig	WA	Nov	2	Negative
	Piq	WA	Nov	3	Positive

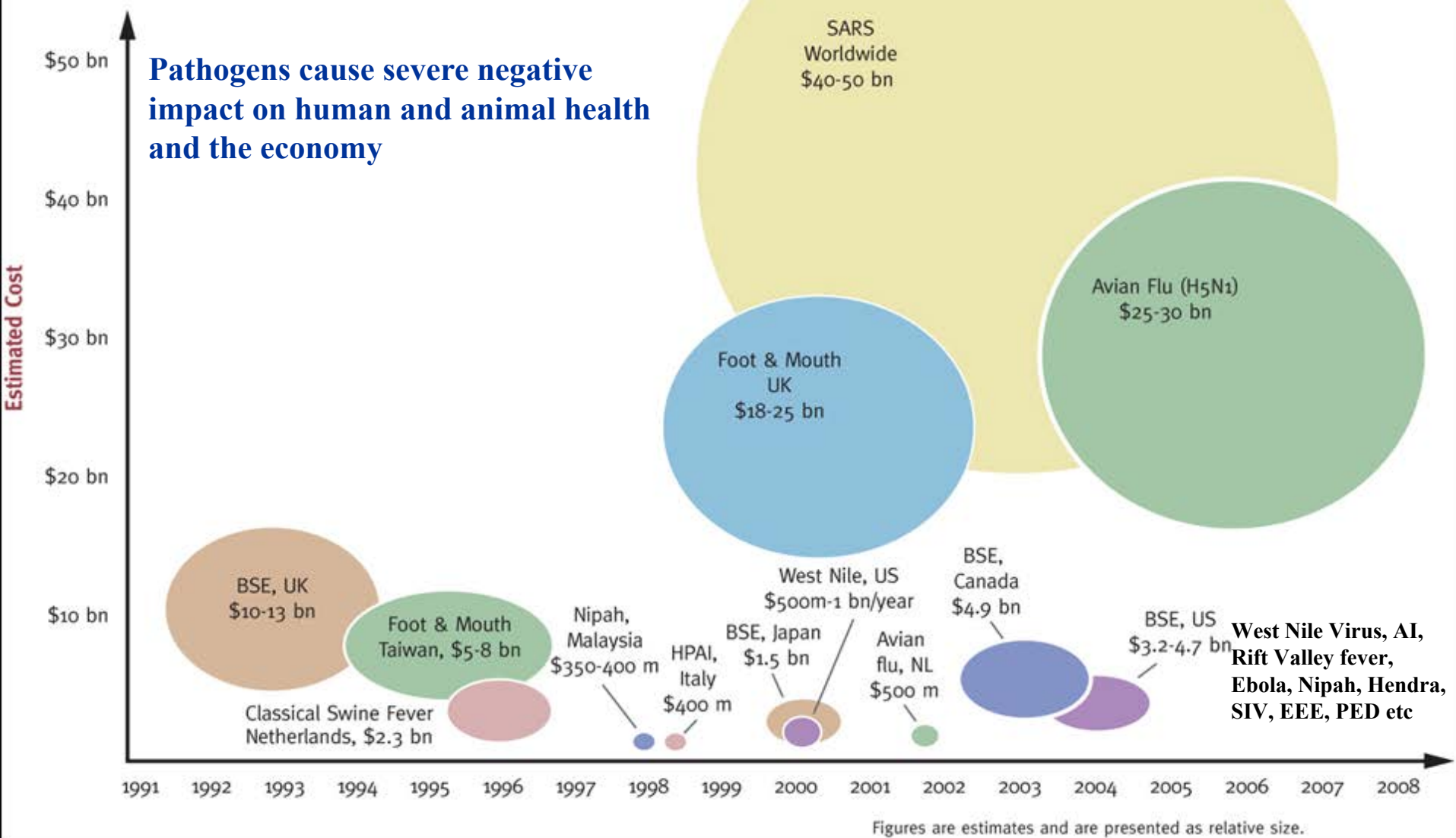
d Laboratory detection was determined to be an incidental finding. Sequencing of the influenza virus most closely correlated with older human-origin ‘seasonal’ influenza A viruses for the HA and NA genes, and to pandemic H1N1 2009 viruses for the internal genes.



# James Fielding – **DRAFT** APPRISE Discussion Paper

## **Key decisions to be made:**

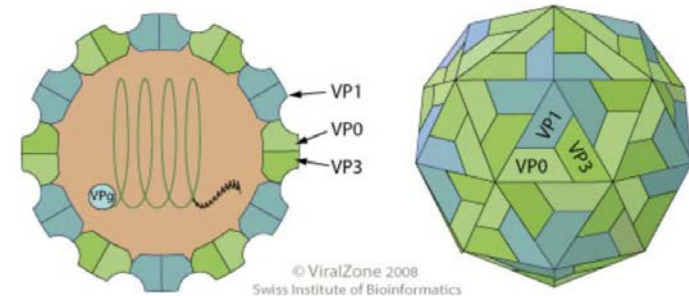
- 1. Determine the means by which APPRISE could collaborate with the Zoonoses, Foodborne and Emerging Infectious Diseases Section in the next phases of the Joint External Evaluation for behaviours, policies and practices to minimise the transmission of zoonotic diseases from animals into humans**
- 2. What animal-human interfaces (and animal, human, arthropod populations) should be prioritised for surveillance? Are there risk assessments to support decisions? How to engage these groups?**
- 3. Assess the feasibility of an exercise to map all systems, survey and projects involving zoonotic diseases in Australia**
- 4. What is the willingness, capacity and extent to which zoonotic disease surveillance could be incorporated into existing animal surveillance programs?**
- 5. Networks made up of people from the different disciplines of One Health – environment, human health and animal health – have been identified as critical for the **sharing of information about zoonotic diseases**. What technological solutions for data sharing of surveillance data collection can augment these networks?**
- 6. Consider the priority and value of deep sequencing for pathogen discovery within the context of current zoonotic disease surveillance at the animal-human interface and in animals - relatively weak, and **not communicated and shared**.**



**What may be next:** Likely an RNA virus or a single stranded DNA virus originating in another species or another geography and perhaps being vector-borne (e.g. Zika virus). Important to do surveillance for potential new pathogens: One World – One Health. Not only preparing for the next outbreak, but doing surveillance and disease control world-wide.



2015 Geelong outbreak of human parechovirus type 3 identified by UHG paediatric team – 17 severely sick infants  
Recombinant (natural) virus with highly conserved virus capsid - may be helpful in directing energy towards the development of a preventive vaccine or antibody treatment of young infants



From:  
Nat Commun. 2016; 7: 11387.  
Published online 2016 July 20. doi: 10.1038/ncomms11387  
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Figure 4

Structure of Ljungan virus provides insight into genome packaging of this picornavirus

Ling Zhu, Wang Wang, Jinghan Ren, Claudine Forta, Hannah Wentham, Jens Ole Ekdorp, Anusha Paranjani, Nick J. Knowles, Ashay Kotecha, C. Alexander Seibert, A. Michael Lindberg, Elizabeth E. Fry, Zhen Rao, Tobias J. Tjeldt & David I. Stuart

Nature Communications 6, Article number: 6358 (2015)  
doi:10.1038/ncomms6358

Received: 28 May 2015  
Accepted: 07 August 2015  
Published online: 08 October 2015

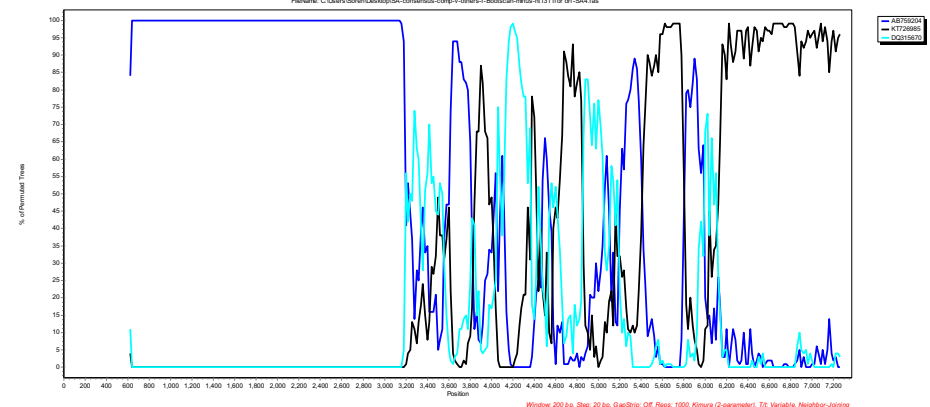
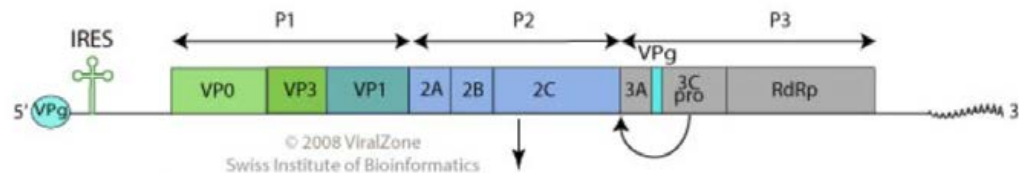
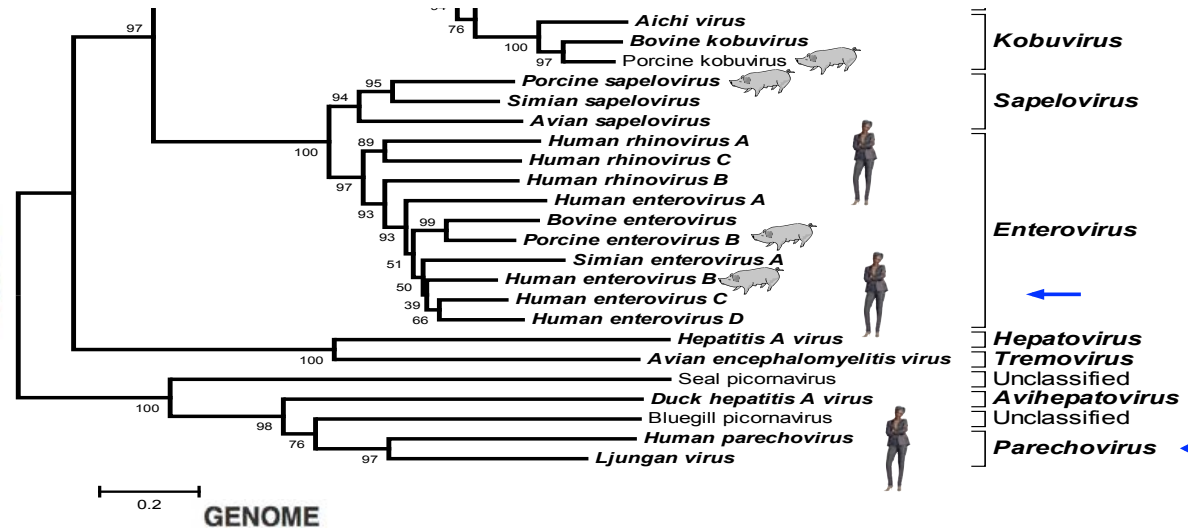
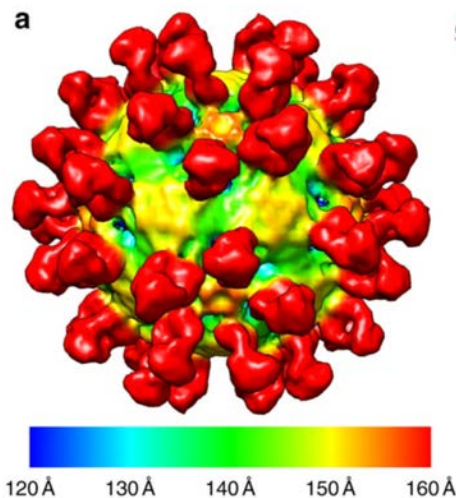
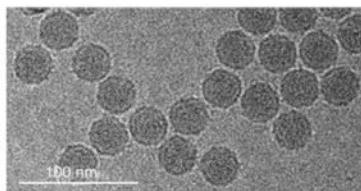
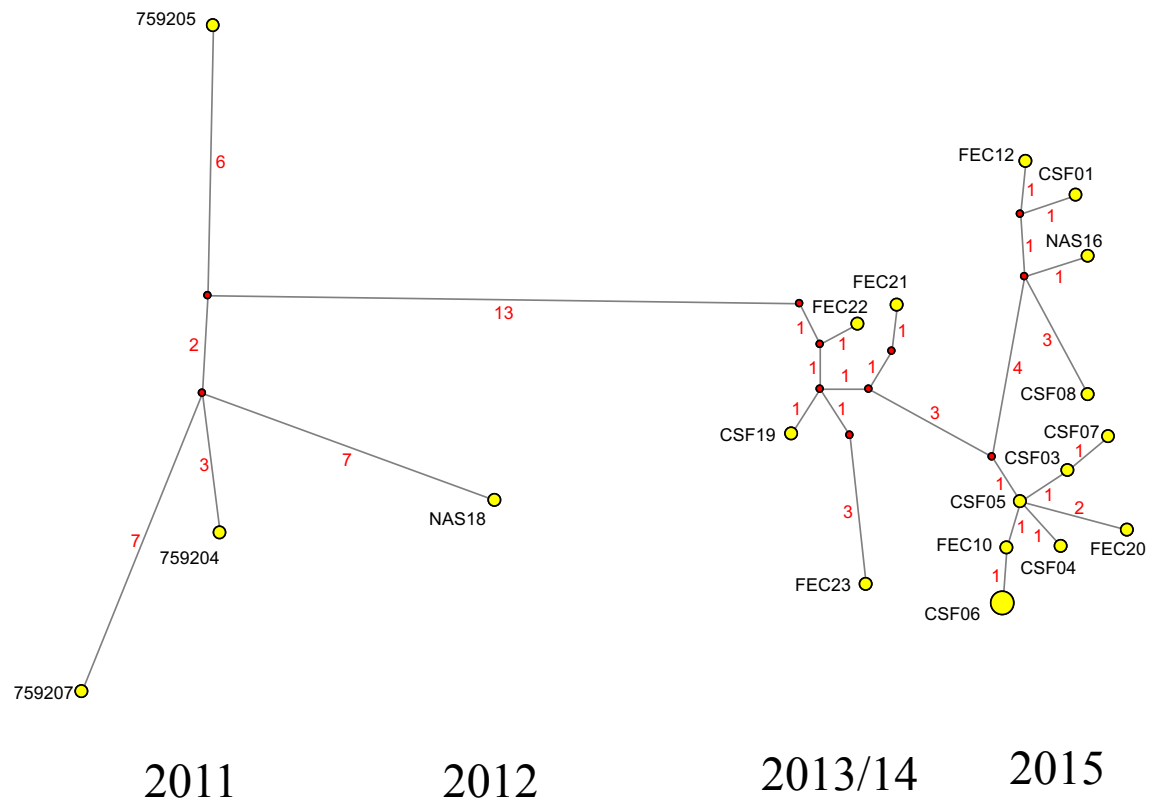


FIG. 4A



# Picornaviruses

## Small ssRNA

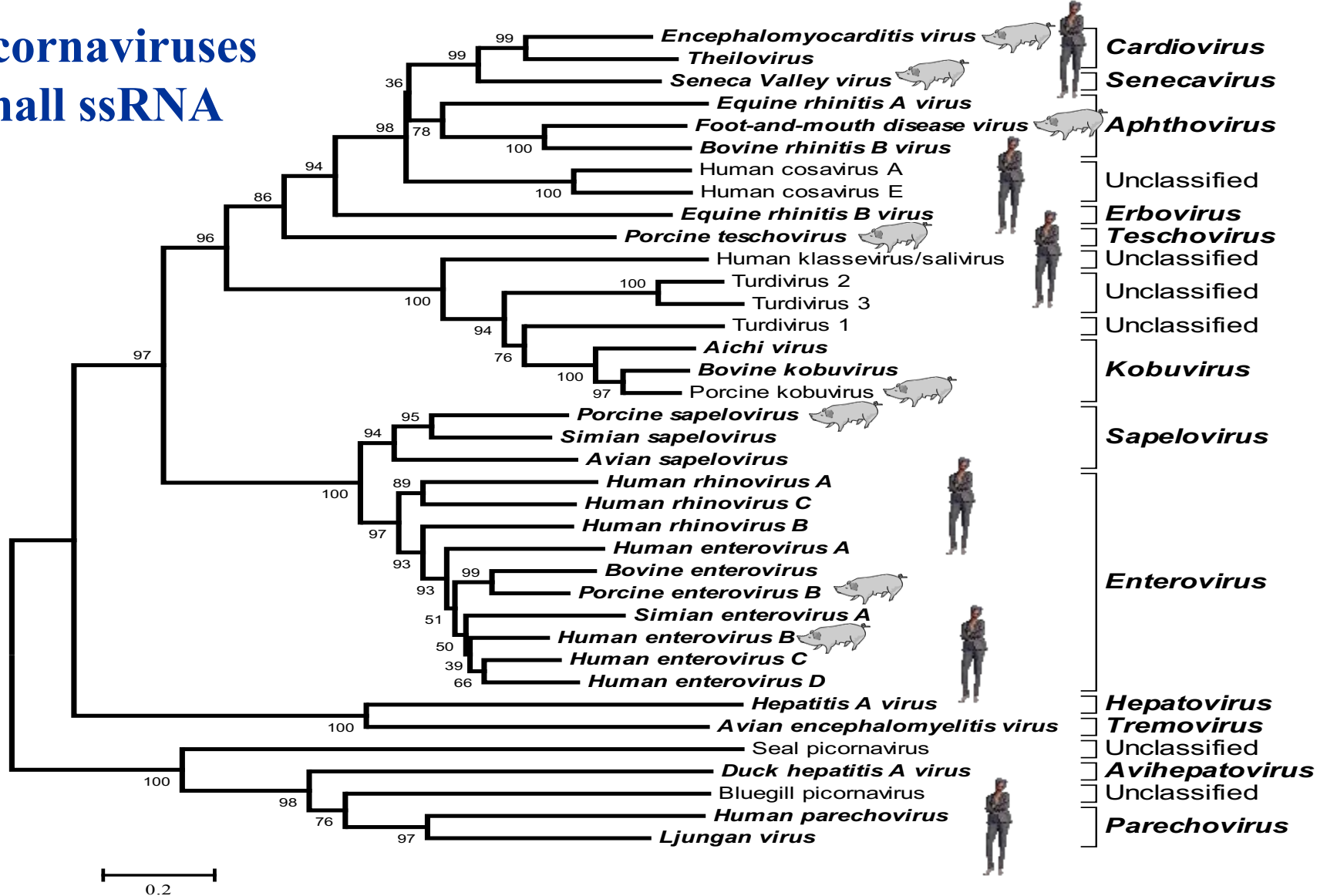


Figure 1. Midpoint-rooted Neighbor-joining tree showing the relationships between the polymerase sequences of 37 picornaviruses. The tree was constructed using MEGA 4.0. The evolutionary distances were computed using the JTT matrix-based method. Formally recognised taxa are indicated in bold-italics. Picornaviruses which infect pigs are indicated by the cartoon pig.

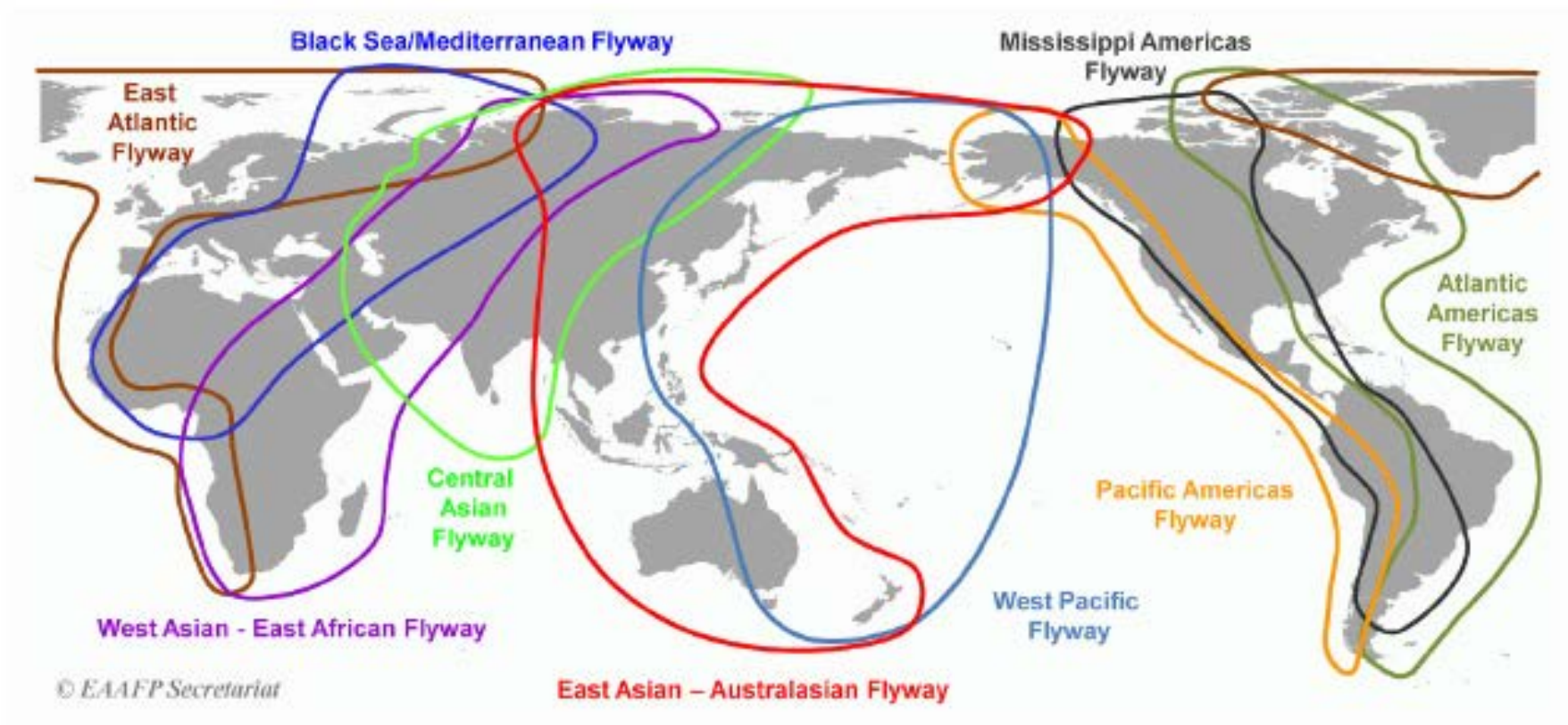
Coronaviruses in wild birds – very promising

The virome (virus community) of Australian wild birds –  
Very interesting preliminary results using novel  
methods together with Next Generation Sequencing

Animal influenza viruses – PhD project to be done in  
collaboration with University of Copenhagen

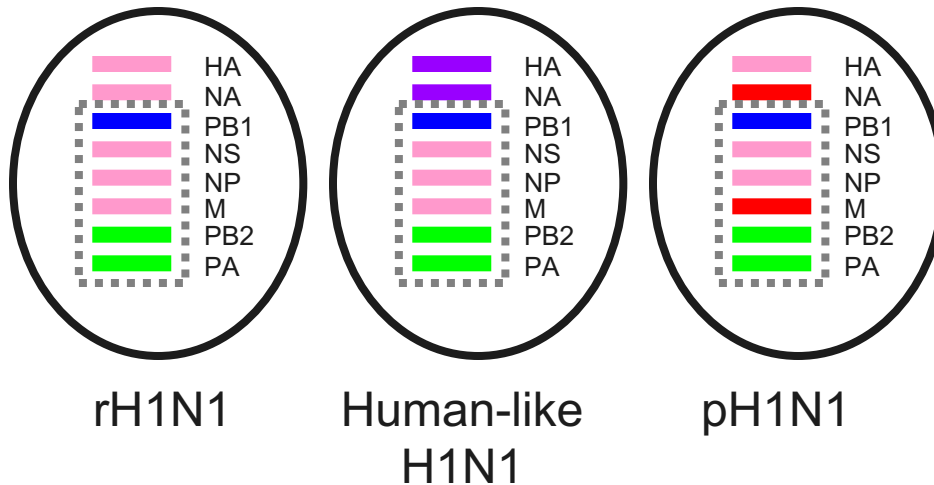
*Mycobacterium ulcerans* – Buruli or Bairnsdale ulcer, a  
disease of West Africa and our local region





Migration routes of migratory bird all around the world (Adopted from <http://www.waderquest.org/2014/05/>)

## Gene Constellations Detected in H1N1 Subtype Swine Influenza Viruses in Canada in 2009/2010



Weingartl et al., Genetic and Pathobiologic Characterization of Pandemic H1N1 2009 Influenza Viruses from a Naturally Infected Swine Herd. *JOURNAL OF VIROLOGY*, Mar. 2010, p. 2245–2256

Berhane, Pasick et al., Molecular characterization of pandemic H1N1 influenza viruses isolated from turkeys and pathogenicity of a human pH1N1 isolate in turkeys. *Avian Dis.* 2010 Dec;54(4):1275-85.

## Genetic Characterization of Turkey H3N2 Isolates Ontario 2011

### A/Tk/ON/FAV3/11

- All segments swine origin trH3N2

1<sup>st</sup> Outbreak  
- February

### A/Tk/ON/FAV9/11

- PB1, HA, NA and NS – trH3N2
- PB2, PA, NP and M – H1N1pm2009

### A/Tk/ON/FAV10/11

- PB1, HA, NA and NS – trH3N2
- PB2, PA, NP and M – H1N1pm2009

2<sup>nd</sup> & 3<sup>rd</sup>  
Outbreaks  
- June

Nfon, Berhane, Pasick et al., Molecular and antigenic characterization of reassortant H3N2 viruses from turkeys with a unique constellation of pandemic H1N1 internal genes. *PLoS One.* 2012;7(3):e32858. Epub 2012 Mar 21.

# Identification of novel influenza A viruses in Australian swine

OFFLU SIV Group Annual Meeting, Rome, 16-17 April 2013

Frank Wong<sup>1</sup>, Ian Barr<sup>2</sup>, David Smith<sup>3</sup>, David Williams<sup>1</sup>, Kelly Davies<sup>1</sup>, Vicky Stevens<sup>1</sup>,  
Songhua Shan<sup>1</sup>, Peter Mohr<sup>1</sup>, Kerri Bruce<sup>1</sup>, Naomi Komadina<sup>2</sup>, Yi-Mo Deng<sup>2</sup>, James Watson<sup>1</sup>,  
Sam McCullough<sup>1</sup>, Peter Daniels<sup>1</sup>

## Western Australia and Queensland (AAHL & WHO-CC)

SAN	Subtype	Origin	Date	Isolation*	
				Eggs	MDCK
12-02246	nH1N2	Gingin, WA	7/8/2012	Y	N
12-02281	nH1N2 nH3N2	Gingin, WA	10/8/2012	N	Y
12-02404	nH1N2	Kingaroy, Qld	23/8/2012	Y	N
12-02476	nH1N2	Kingaroy, Qld	31/8/2012	Y	Y
12-02693	pH1N1	Kingaroy, Qld	21/9/2012	Y	N

\*All isolates confirmed by FLU-A TQM PCR and WGS

# Synopsis

- Novel H1N2 viruses in WA and QLD pigs appear to be independent “triple reassortant” viruses with HA and NA genes from older human H1N1 and H3N2 strains respectively, on an pH1N1/2009 genomic backbone (all internal genes from pandemic H1N1 virus).
- The H1N2 reassortants likely occurred after 2009 when the pandemic H1N1 virus was introduced to Australian swine from the human population.
- An novel H3N2 reassortant was also present in WA pigs containing a huH1N1 PA gene on an huH3N2 genomic backbone [“strange virus”].
- The current H1N2 and H3N2 viruses in WA and QLD represent the first report of non-pandemic influenza A virus in Australian pigs.
- Molecular evidence supports the probable long-term circulation of human-derived H1 and H3 viruses in Australian swine, previously unsampled due to the absence of influenza A surveillance in pigs.
- The viruses in Australian pigs are not the H3N2v and H1N2v variant viruses currently circulating in North American domestic pigs and causing concern to public health due to incidences of pig-to-human transmissions.





**The (business) END** – realities for a laboratorian outside his/her lab