Update: 
Porcine epidemic diarrhoea and swine influenza

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Approach

• Review of the pathogen
• Review of the outbreak
• Research outcomes in last 2-3 years
• Key messages and lessons learned
PED virology (1)

Coronaviridae is a family of enveloped, positive-sense, single-stranded RNA viruses

- Family Coronaviridae, order Nidovirales, sub-family Coronavirinae (4 genera)
  - Alphacoronavirus: Transmissible gastroenteritis (TGE), PEDV, and porcine respiratory coronavirus (PRCV).
  - Betacoronavirus: Porcine haemagglutinating encephalomyelitis virus (HEV), SARS, and Middle eastern respiratory coronavirus (MERS-CoV)
  - Gammacoronavirus: Infectious bronchitis virus (IBV)
  - Deltacoronavirus: Poorly described, includes porcine Deltacoronavirus (PD-CoV) in China, the US, and Canada.
PED virology (2)

All coronaviruses cause localized infections of the respiratory or intestinal tracts

- Coronaviridae exhibit a relatively high degree of genetic heterology, even within a species
- Mutation, homologous and non-homologous recombination, and genome segment reassortment
- Replication of viral RNA as compared to cellular DNA
  - High rate of mutation that occurs (routinely) during RNA replication in the range of 0.1 to 0.001% per round
  - Main factor is the low efficiency of proof-reading and repair activities associated with RNA replicases and transcriptases
Clinical signs (1)

Transmissible gastroenteritis

- Transmissible gastroenteritis first described in the U.S. nearly 70 years ago.
- In pigs less than three weeks of age, characterised by profuse diarrhoea and vomiting, with high morbidity (approaching 100%).

Porcine epidemic diarrhoea

- Early 1970’s, ‘epidemic diarrhoea’ resembling TGE but less severe in Europe. Rotavirus?
- Prototype strain eventually identified and referred to as CV777; did not cross-react with TGE.

Photo courtesy Matt Ackerman (http://www.porkvet.com/)
Clinical signs (2)

Porcine respiratory coronavirus
- In Europe during the mid-1980s, decline in the occurrence of TGE.
- Eventually, a respiratory non-enteric coronavirus was identified; cross-reacted with TGE, but not PED.
- Late 1980s, US recognized a similar phenomenon.
- Believed to be a TGE virus mutant; PRCV has a large deletion in the S gene believed to play a role in the change in tropism.
- Assumed to be present in Australia.

Porcine Deltacoronavirus
- New genus, novel avian coronaviruses found in China in 2009. Further surveillance in both wild and farmed animals identified seven additional members in 2012.
- The reference Deltacoronavirus of pigs was identified as ‘PorCoV HKU15’ (was in 10% of pigs sampled in Hong Kong, no clinical disease reported).
- In early 2014 in the US, PED investigation revealed Deltacoronavirus infection in Ohio, then other locations.
- Clinical signs on this farm were similar to what have been described for virulent TGE and PED.
- The US virus was found to be nearly identical to Hong Kong strain.
US outbreak of PED (1)

April / May 2013

- Diagnosis by Iowa State University
- Index case unknown but likely in Midwest
- Diagnostic labs upskilled rapidly, ‘lack of a diagnostic test’ did not contribute to speed, geographic scope, or scale of outbreak

Discussions between ‘industry and government’ to determine a RESPONSE

- Not an FAD, instead classified as a TAD, therefore…
- Gov’t not obliged to respond, provide resources, initiate surveillance/reporting
- State veterinarians were the ‘meat in the sandwich’

Rapid, unexplained? spread

- In the space of a few months, all States with significant pig populations had epidemic disease
Looking forward (1)

Research outcomes

- Feed, feed ingredients, and feed hauling; aerosol are risk factors
- ‘My CT value is higher than your CT value’: Some investment in developing a molecular tool to indicate ‘live’ versus inactivated virus
- No shortage of diagnostic tests (primarily PCR): Utility of antibody tests not clear, but not a problem unique to PED
- Duration of immunity, persistence of virus in the environment, efficacy of vaccines: All somewhat different than what was known (suspected?) for TGE but fundamentally, outbreak management based on biofeedback. When does one stop feeding back?
- Likely, more than one strain was introduced and / or emerged

Lessons learned

- Transportation biosecurity was not as good as believed (or espoused).
- Robust, capable diagnostic system was critical: US model bases D-labs in Universities.
- ‘Emerging’ agent created a number of administrative hurdles that compromised reporting, surveillance, and lack of organised effort to contain the outbreak.
- Probably some lessons to be learned from how the Canadians managed their outbreak; they had a number of advantages over the US but the combination of factors limited spread and will likely allow eradication.
Cost of PED outbreak in the US

Assessment of the economic impacts of porcine epidemic diarrhea virus in the United States

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ABSTRACT: Porcine epidemic diarrhea virus (PEDV), which first emerged in the United States in 2013, spread throughout the U.S. hog population. Limited preemptive knowledge impeded the understanding of PEDV introduction, spread, and prospective economic impacts in the United States. To assess these impacts, this article reviews the timeline of PEDV in the United States and the corresponding impacts. PEDV is a supply-impacting disease and is not demand inhibiting, as pork demand remained strong since PEDV first appeared. Pig losses reached significant levels during September 2013 through August 2014, with the majority of pork production impacts occurring in 2014. PEDV had differing impacts for subsectors of the pork industry. A budget model demonstrates that producers could have had higher pig losses and decreases in productivity proportionally smaller than price increases, resulting in net returns above what was expected before the major outbreak of PEDV. Previous literature is reviewed to identify the potential main industry beneficiaries of the PEDV outbreaks in the United States. As a result of reduced volumes of available pig and hog supplies, reductions in annual returns likely occurred for packers, processors, distributors, and retailers. In addition, pork consumers who experienced reduced-supply-induced pork-price increases were likely harmed directly by higher prices paid for pork and indirectly as prices of competing meats were also likely strengthened by PEDV. This article also identifies future considerations motivated by the appearance of PEDV in the United States, such as discussions of industry-wide efficiency and competitive advantage, the future role of PEDV vaccines, enhancement in biosecurity measures, and consumer perceptions of food safety and insecurity.

Key words: animal health, economic impacts, PEDV, porcine epidemic diarrhea virus, pork, swine


UPDATED ESTIMATED ECONOMIC WELFARE IMPACTS OF PORCINE EPIDEMIC DIARRHEA VIRUS (PEDV)

by
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Working Paper #14-4

April 7, 2014

Dept. of Agricultural Economics
Purdue University

SIV short version

1) Viral disease of mammals
2) Has and will continue to co-evolve in avian and mammals
3) Vaccines unequivocally work, both commercial and autogenous. However…
4) Current thinking is that pigs are just part of the problem, and don’t really bear any more responsibility for the emergence of human pandemic strains than another species. However…
5) Vaccinate farm staff
6) Research
   ◦ ‘Carrier’ status in pigs
   ◦ ‘Viremic’ state in pigs
   ◦ Molecular evolution and epidemiology study
Influenza A virus (IAV) is a family of enveloped, negative-sense, single-stranded RNA viruses with a segmented genome

- **Family Orthomyxoviridae**
- Two surface glycoproteins most often used to describe the diversity of sub-types.
  - NA: Neuraminidasae (16)
  - HA: Hemagglutinin (9) – Most important determinant of virulence and host specificity
- Abundant permanent animal and avian reservoirs for IAV, some of which occasionally spill-over to people
- Waterfowl generally considered to be the most significant wild reservoir and harbour all sub-types
- Pigs (swIAV) have an import role in virus evolution because of their capacity to be infected with both avian and human viruses
SIV virology (2)

Avian influenza viruses occasionally spill-over into humans (e.g. H5N1, H7N9), usually with little onward transmission.

Host jumps of IAV that result in stable transmission in the new host are rare events:

Avian to human (3)
- 1918: H1N1 ‘Spanish flu’ epidemic
- 1957, 1968: H2N2/H3N2

Avian to swine (2)
- 1970s: Eurasian H1N1 viruses
- 1998: TRIG H3N2

Avian to equine (2)
- 1960s: H7N7
- 1990s: two H3N8

Avian to canine (1)
- 2000s: H3N2

Equine to canine (1)
- 2000s: H3N8

Swine to human (1)
- 2009: pH1N1
Influenza: a story of molecular evolution

1918 outbreak in people

- There is evidence of only one possible influenza virus outbreak in swine in England prior to the 1918 outbreak in people.
- During early stages of 1918 epidemic, there were multiple outbreaks of the disease in pigs and people.
- Impossible to determine which direction the virus travelled.
- ‘Classic H1N1’ in pigs isolated in 1930.
- Until the late 1990s, the classical swine lineage H1N1 (cH1N1) was relatively stable at the genetic and antigenic levels in the United States.

Beginning in the 1970s

- Global evolution of swIAV’s in European herds complicated by introduction of an avian H1N1 and a human seasonal H3N2 ‘Port Chalmers’.
Evolution (cont’d)

In 1998, a severe influenza-like disease was observed in pigs in the US (identified as H3N2 subtype). Two H3N2 viruses were identified:

- NC isolate was a double reassortant and contained gene segments from cH1N1 and from a human 1995 seasonal H3N2 (HA and NA).
- Midwest isolates were triple reassortants were similar to NC but also included a segment from an avian virus. Within 2 years, the triple reassortant was widespread while the double reassortant virus did not become established.

TRIG: triple reassortant internal gene constellation

- The vast majority of the resulting reassortant and drift variant viruses since 1998 contain the TRIG
2009 pandemic (1)

April 2009, the United States, Canada and Mexico reported community outbreaks of pneumonia in humans caused by a novel H1N1 influenza A virus.

- Spread globally at a high rate, prompting the WHO to declare a pandemic in June 2009.
- Retrospectively, the earliest known case was identified February 24, 2009, in a baby from San Luis Potosi, Mexico.
- This novel pH1N1 possessed a unique genome
  - Most closely related to the triple reassortant influenza viruses of the North American swine lineage…but with M and NA genes derived from a Eurasian lineage of swine influenza viruses.
  - Despite named ‘swine flu’, infection in humans was not connected to pig exposure.
  - The 2009 pandemic H1N1 was promptly shown to replicate efficiently in pigs and to cause a clinical disease comparable to that typically observed during common, enzootic influenza virus infection in swine.
  - The first case was in swine was detected on April 28, 2009 in Canada in a farm with pigs that were not previously vaccinated against swine influenza: the source of the outbreak was linked to a worker who showed symptoms of influenza-like disease.
The first identified case of pandemic H1N1 influenza in pigs in Australia

PK Holyoake, a,PD Kirkland, b RJ Davis, b KE Arzey, b J Watson, c RA Lunt, c J Wang, c F Wong, c BJ Moloney d and SE Dunn d
2009 pandemic (2)

True origin of the pH1N1 virus is unknown.

- Suggestions that it circulated in swine (undetected) for perhaps as long as a decade before 1st human case.
- Where did the Eurasian swine segments come from?
  - Was not known to be circulating in North or South American pigs.
  - Virus became more fit for people while circulating in Mexican pigs?
  - Arose in a combined human-pig-avian strain that had been circulating (undetected) in Asia?
  - Perhaps humans had a more primary role?
- Since 2009, there have been at least 49 introductions of pH1N1 from people to swine.
  - Still little evidence that the human-adapted pH1N1 readily transmits back to humans (at least as a ‘stable’ introduction with onward human-to-human transmission)
Two papers to recommend


SIV short version (cont’d)

Why is SIV not a particular problem in AU/NZ?
- Terminal end of the major migratory waterfowl flyways – less virus source
- Relatively small pig populations (country, farm)
- Relatively low numbers of pig movements and co-mingling events

Research and lessons learned
- Practically, we’re managing SIV the same as we always have
- Need to begin/encourage/maintain dialogue with regulatory organisations
- Need to be doing surveillance in pigs – you’re not just vets, you’re people too!
- Pessimist in me says the research on SIV per se is becoming more academic
  - ‘Predicting the great unknown’
  - No therapeutics or novel vaccine constructs that are imminent
Questions and contact me

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