Coordinated surveillance of influenza viruses in European pigs: Enhanced Virological and Epidemiological analysis from the European Surveillance Network for Influenza in Pigs (ESNIP3)

I. H. Brown*, S. M. Reid, G. Simon, W. Loeffen,

L. E. Larsen, P. Kellam, S.Watson, N. Lewis, S. M. Brookes, O.Pybus & ESNIP3 Consortium

OFFLU SIV group meeting, Univ Minnesota, Minneapolis 19-20 March 2014 *Coordinator AHVLA-Weybridge, UK OIE reference laboratory for swine influenza EURL for Avian Influenza



http://www.esnip3.eu/index.html





ESNIP1 1999-2003 Coordinator Guus Koch, CVI Lelystad, NL



ESNIP2 2005-2008 Coordinator Kristien Van Reeth, Ugent, BE



ESNIP3 Coordinator Ian Brown, AHVLA, UK 2010-2013





ESNIP3 objectives

- Expand knowledge of epidemiology and evolution of SIVs in Europe
 - Surveillance for influenza in pigs; harmonised
 - Contemporary data available at EU level
 - Service to pig industry
- Rapid virus characterisation
 - Harmonised diagnostics; new tools
- Use of new technologies/improvements linking datasets
 - Antigenic characterisation/mapping
 - Genetic characterisation
 - Phylogeography
 - Genotypic data
- Provide timely insights to veterinary public health risk
 EFSA, ECDC
- EU SI Virus database and repository
 - Global dissemination of information/exchange
 - Network interaction





European enzootic Swine Influenza Viruses (SIVs)



Pandemic virus A/H1N1 2009





Brookes et al., 2009, 2010; Lange et al., 2009; Simon, Virologie, 2010

Project consortia

- 25 partners:
 - Veterinary institutes
 - Belgium, UK, The Netherlands, Italy, France, Germany, Denmark, Poland, Spain, Israel, Hungary, Finland, Greece, USA, China
 - Vaccine manufacturers
 - Merial (France), IDT (Germany) & Hipra (Spain)





Density of pig production in Europe



AHVLA Animal Health and Veterinary Laboratories Agency



	Country	Partner	Number of herds investigated	Number of positive cases	Frequency of positive cases (%)	Number of subtyped viruses
l	Jnited-Kingdom	P1-AHVLA	476	98	20,59	58
	Belgium	P2-UGent	96	29	30,21	29
	Netherlands	P2-UGent	46	25	54,35	25
		P12-CVI	28	14	50	11
		P8-IDT	8	1	12,5	1
	France	P3-Anses	1338	703	53,44	350
	Italy 📐	P4-IZSLER	2098	360	17,16	179
	Denmark	P5-DTU	1171	488	41,67	254
	Poland	P6-NVRI	153	55	35,95	29
		P8-IDT	31	1	3,23	1
	Slovak ia	P6-NVRI	3	1	33,33	1
5	Belarus	P6-NVRI	20	2	10,00	
	Russia	P6-NVRI	3	2	66,67	
	Lithuania	P6-NVRI	1	0	0,00	0
	Spain	P7-LCV	10	1	10	0
-		P22-HIPRA	355	79	22,25	29
	Germany	P8-IDT	2374	702	29,57	540
		P17-FLI	366	154	42,08	119
		P2-UGent	1	1	100	1
	Finland	P9-EVIRA	65	3	4,62	3
	Israel	P10-KVI	7	?	?	0
2	Hungary	P11-CAO	102	35	34,31	38
	Greece	P13-UTH	52	9	17,31	3
	Total Nov1	0-Oct13	8810	2763	31,36	1671
					(A	HVLA

Animal Health and Veterinary Laboratories Agency

Regional variation in the epidemiology of SI in Europe (ESNIP3)



Agency

New diagnostics PCR harmonisation

- Validated tools for detection of all SIVs
- Specific detection of North American swine H3N2v confirmed
- New methods under evaluation for rapid serotyping





Mapping changes in the virus

- Why do we need to do?
 - Changes in virus spread, infectivity, & pathogenesis
 - Changes in virus host range
 - Veterinary Public Health Implications
 - Diagnostics
 - Intervention through vaccination
- Two approaches
 - Mapping antigenic changes
 - Identifying genetic mutations
 - Linking two datasets



Antigenic mapping

- Understand how the pigs immune response to infection with influenza will reduce infection and spread with other strains
- Probe combinations of virus and different flu antibodies to reveal relationships
- Cartography visual tool for presenting datasets
- Applied in ESNIP3 for first time to European SIV's



A/swine/H1/





Genetic mapping/monitoring

- How are viruses mutating
- Determine the genetic code of SIV's and compare between strains
- Identify trends/patterns
- Identify new virus genotypes from genetic reassortment
- ESNIP3 has contributed c400 new SIV genomes
- Inform veterinary public health risk



17 unique genotypes observed

Blue = Eurasian avian-like Red = pandemic Purple = Human H1/H3 N1/N2 Blue/Greene = Classical swine Grey = Eurasian avian

PB2	PB1	ΡΑ	НА	NP	NA	MP	NS
pdm							
pdm	pdm	pdm	H1	pdm	N2	pdm	pdm
pdm	pdm	pdm	Н3	pdm	N2	pdm	pdm
pdm	pdm	pdm	pdm	pdm	N2	pdm	pdm
pdm	pdm	pdm	EA	pdm	N2	pdm	pdm
pdm	pdm	pdm	EA	pdm	EA	pdm	pdm
EA	EA	EA	Н3	EA	pdm	EA	EA
EA	EA	EA	Н3	EA	N2	pdm	EA
EA	EA	EA	Н3	EA	N2	EA	EA
EA	EA	EA	H1	EA	N2	EA	EA
EA	EA	EA	H1	EA	EA	EA	EA
EA	EA	EA	EA	EA	N2	EA	EA
EA	EA	EA	EA av	EA	N2	EA	EA
EA							
hu	hu	hu	Н3	hu	N2	hu	hu
CS							
EA av							



Genotype frequency throughout Europe





Pandemic genotype observed in 5 European countries





Pandemic segments observed throughout European swine







Implications of genotypic variation

- Continual virus mixing in the pig
- New introductions primarily from humans
- Viruses that are best fitted to replicating and spreading pigs will be 'selected'
- Contribute to virus change over time
- Importance of ongoing surveillance
- Implications for
 - control
 - economics
 - public health



Conclusions

- Surveillance approaches harmonised
- Four viruses cocirculating
- Significant regional variation
- Diagnostics fit for purpose
- Preliminary antigenic maps for H1 & H3
- Genomic data generated- genotypic evolution including with pdm09
- Data/knowledge exchanged with other networks, official bodies





The future?

- Project completion 31.10.13!
- Publication of work
- Continued engagement with stakeholders
- Future utility
- ESNIP4???
 - Lobbying & consultation
- Interest from commercial companies to sponsor an annual meeting

SNIPS No immediate prospect for continue

Acknowledgements

- EU commission
- Competent authorities supporting surveillance programmes
- Industry: producers, PVS's stakeholder groups etc
- Collaborating partners: WHO, OIE institutes





Thank you for your attention

Questions Your views & comments welcome



ian.brown@ahvla.gsi.gov.uk

Veterinary Laboratories