







#### Sawang Kesdangsakonwut

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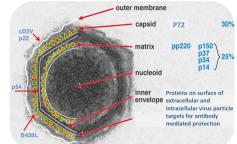


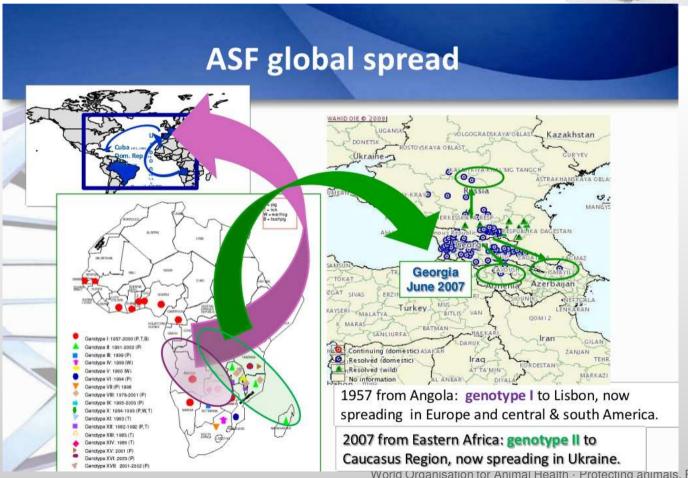
#### **Etiology**

: DNA virus, genus Asfivirus, Asfarviridae

: genome size between 170 - 190 kb

encodes between 160 - 175 genes.







#### **Chronology of ASF outbreak**

Year	ASF outbreak country	Transmission route
1921	Kenya*	Unknown
1957	Portugal	Pork or pig product from Africa
1960	Spain	Pork or pig product
1971	Cuba	Raw pork waste or pork product via an airplane from Portugal or Spain
1985	Belgium	Pork or pig product
2007	Georgia (Caucasus region)	Raw pork waste at an airport
2007	Russia	Wild boar
2015	Poland, Estonia	Wild boar
2018	China	Pork or pig product
2019	Mongolia	Pork or pig product†
2019	Vietnam	Pork or pig product
2019	North Korea	Illegal importation of Pork or pig product ‡
2019	Laos, Cambodia, Myanmar	Pork or pig product

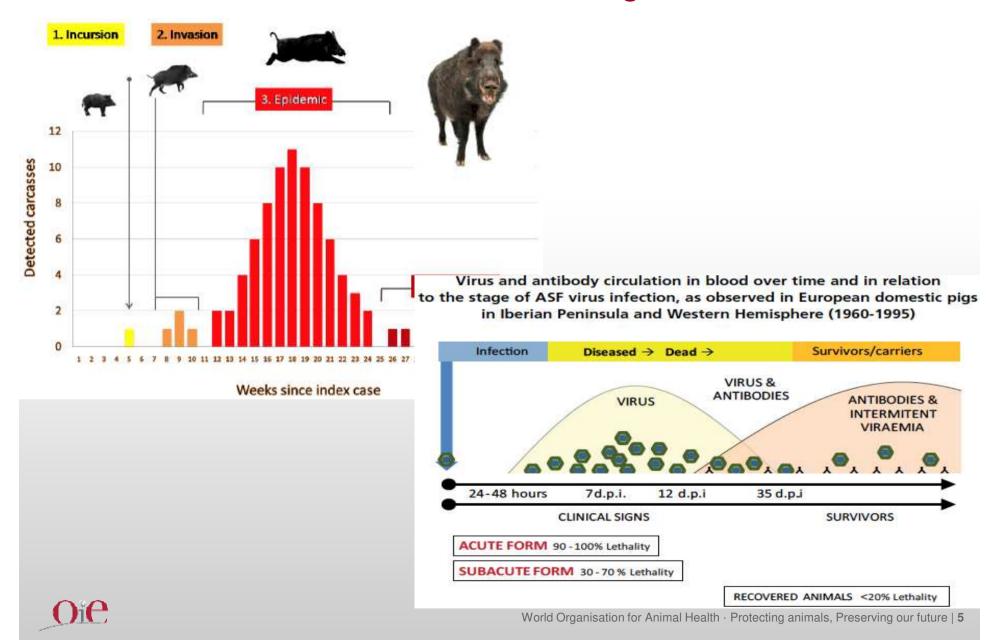




- A. Domestic pig/Sus scrofa domesticus (@FAO/Daniel Beltrán-Alcrudo).
- B. European wild boar/Sus scrofa ferus (@Swedish University of Agricultural Science (SVA)/Torsten Mörner).
- C. Bushpig/Potamochoerus porcus (©Swedish University of Agricultural Sciences (SLU) and Swedish Veterinary Institute (SVA)/Karl Stahl).
- D. Warthog/Phacochoerus africanus (@University of Pretoria/Mary-Louise Penrith).
- E. Giant forest hog/Hylochoerus meinertzhageni (©John Carthy).
- F. Ornithodoros erraticus (male & female) (©Institute of Natural Resources and Agrobiology of Salamanca (IRNASA), of the Higher Council of Scientific Investigations (CSIC)/Ricardo Pérez-Sánchez).



Source: FAO



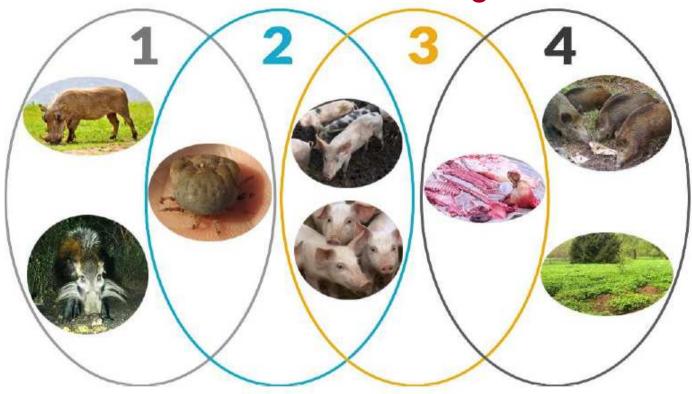


Figure 1.1. From Warthogs to Wild Boar: adaptive modification of ASFV transmission cycles on the way from Africa to Europe. 1) the natural African sylvatic cycle; 2) the anthropogenic cycle involving ticks (Africa and Iberian Peninsula); 3) the pure anthropogenic cycle (W Africa, Eastern Europe and Sardinia); 4) wild boar - habitat cycle (NE Europe, 2014-now) (Source: Chenais et al., 2018)



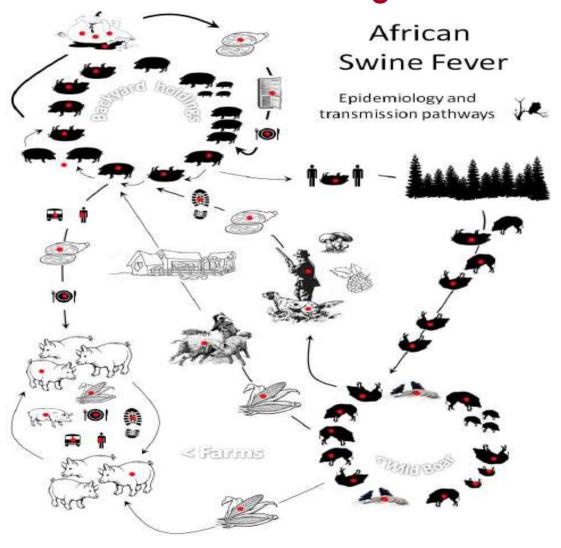
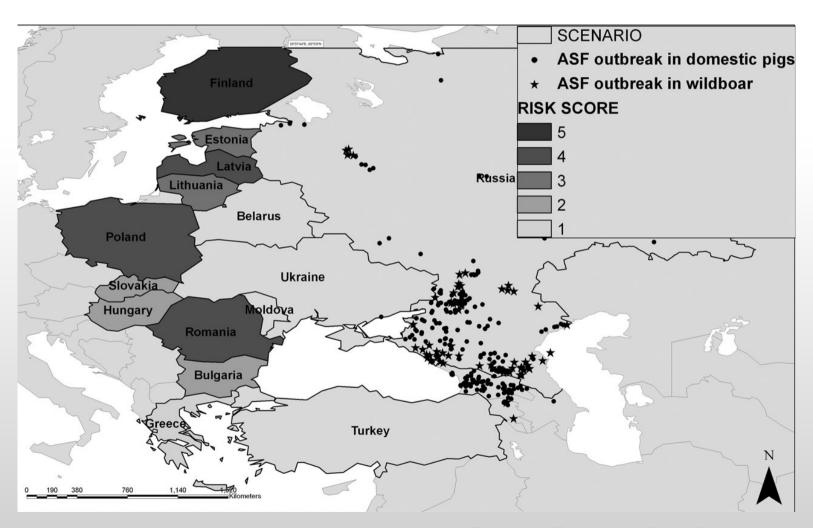


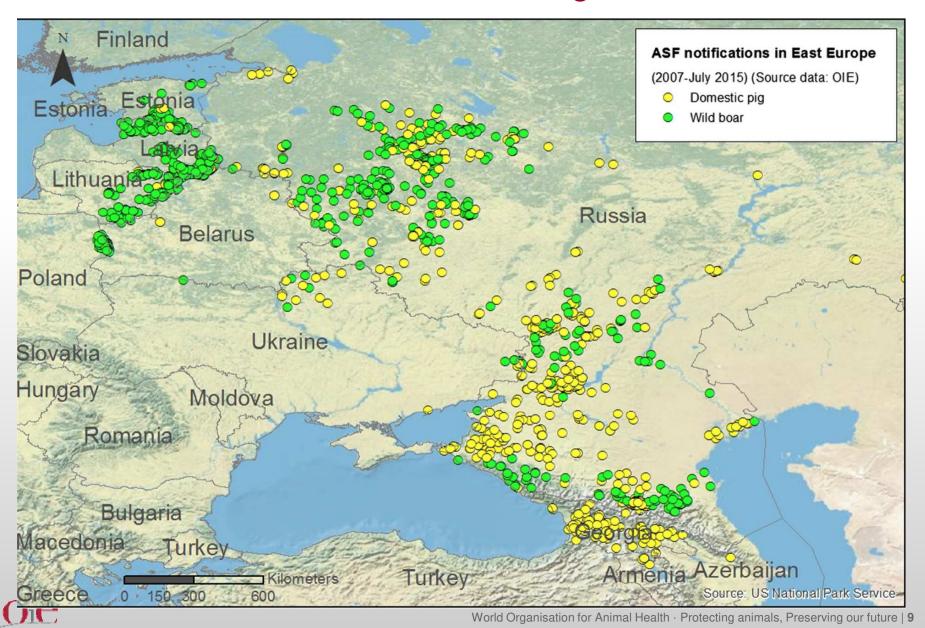


Figure 1.3. Complex of epidemiological factors and transmission pathways involved in sustaining endemicity and geographical expansion of ASFV in Eastern Europe (cycles 3 and 4, Fig. 1.1)

# Assessing the Risk of African Swine Fever Introduction into the European Union by Wild Boar







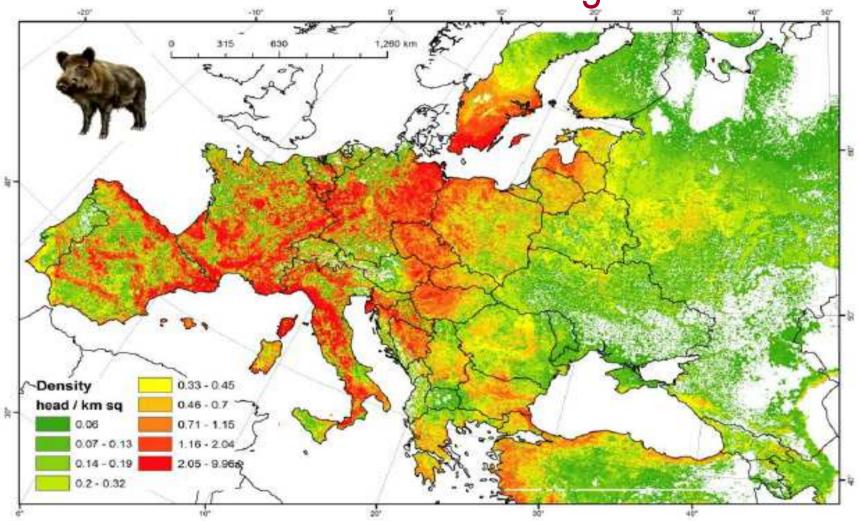
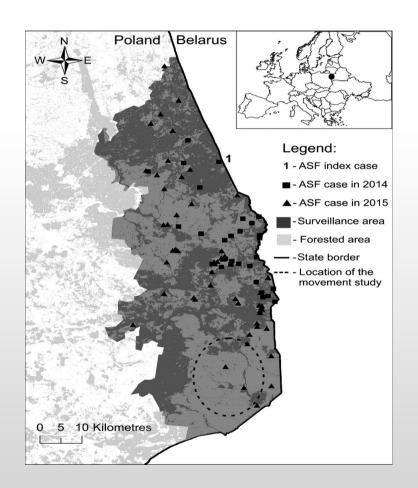
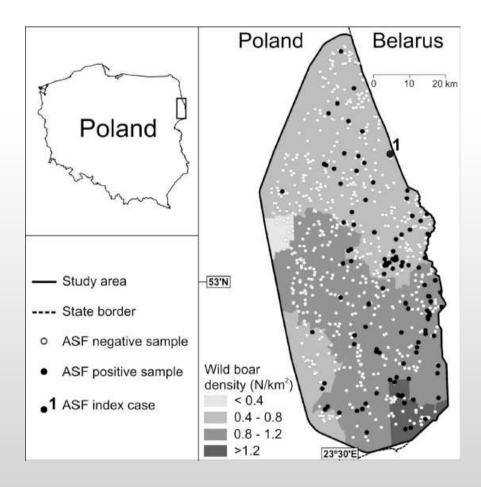


Figure 2.2. Modelled wild boar population density map based on official hunting statistic and population estimates for the period 2000-2010 (Source: FAO/ASFORCE, 2015; Pittiglio, Khomenko, Alcrudo, 2018)

Do wild boar movements drive the spread of African Swine Fever?

Spatial epidemiology of African swine fever: Host, landscape and anthropogenic drivers of disease occurrence in wild boar





Podgorski & Smietanka Transbound Emerg Dis 65(2018):1588-96. Podgórski et al. Prev Vet Med, doi: 10.1016/j.prevetmed.2019.104691



# African Swine Fever Virus, Siberia, Russia, 2017

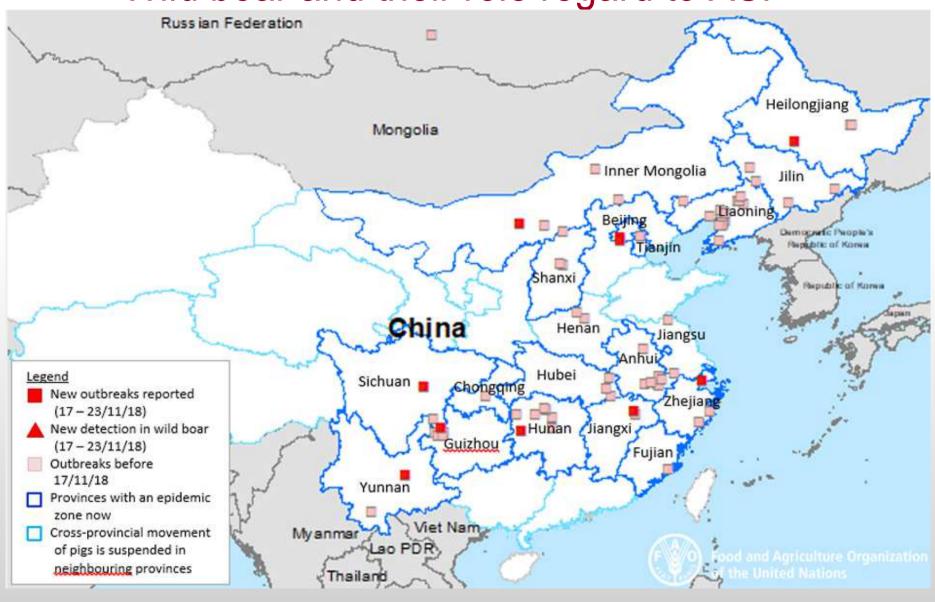
Denis Kolbasov, Ilya Titov, Sodnom Tsybanov, Andrey Gogin, Alexander Malogolovkin



Since the outbreak in Irkutsk, subsequent ASF outbreaks have occurred in Siberia (Mar–Oct 2017) and near the border with China.

Kolbasov et al., 2018. Emerg infect Dis, 24: 796-7.







# Molecular Characterization of African Swine Fever Virus, China, 2018

Shengqiang Ge,¹ Jinming Li,¹ Xiaoxu Fan,¹ Fuxiao Liu,¹ Lin Li,¹ Qinghua Wang, Weijie Ren, Jingyue Bao, Chunju Liu, Hua Wang, Yutian Liu, Yongqiang Zhang, Tiangang Xu, Xiaodong Wu, Zhiliang Wang

During July 1–August 1, 2018, a total of 47 of 383 pigs died on a farm in the Shenbei District of Shenyang, Liaoning Province, China. Postmortem analysis performed by local veterinarians showed an ASF-typical lesion in pig spleens that were extremely swollen and severely necrotic. Other pathologic changes included hemorrhages in tonsils and lungs, marbled lesions in mandibular and mesenteric lymph nodes, and diffuse hemorrhages in a large part of gastric serosa.

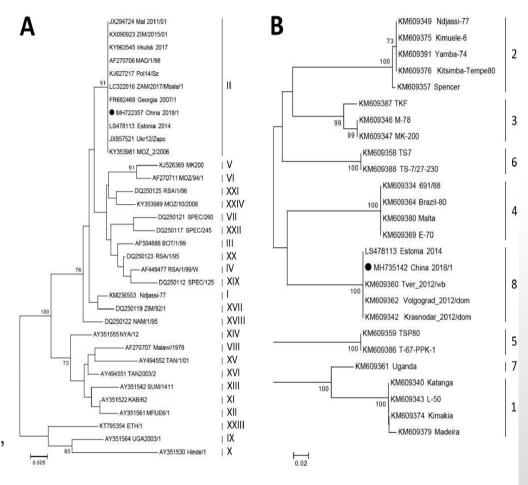
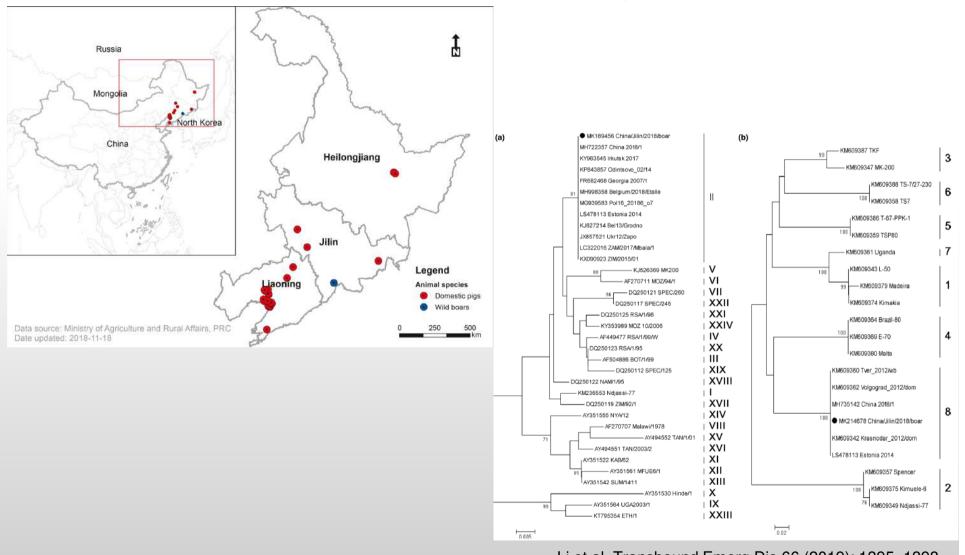


Figure. Phylogenetic analysis of a causative virus strain (China 2018/1) of an African swine fever outbreak, China, 2018. A) p72 genotype; B) CD2v serogroup. The neighbor-joining method and Kimura 2-parameter model were used for construction of phylogenetic trees in MEGA 5.0 software (https://www.megasoftware.net/). Numbers along branches indicate bootstrap values >70% (1,000 replicates). Black circles indicate causative virus from this study. Roman numerals to the right in panel A indicate p72 genotypes. Numbers to the right in panel B indicate CD2v serogroups. GenBank accession numbers are provided for all sequences. Scale bars indicate nucleotide substitutions per site.

Ge et al., 2018. Emerg infect Dis, 24: 2131-33.



#### Infection of African swine fever in wild boar, China, 2018

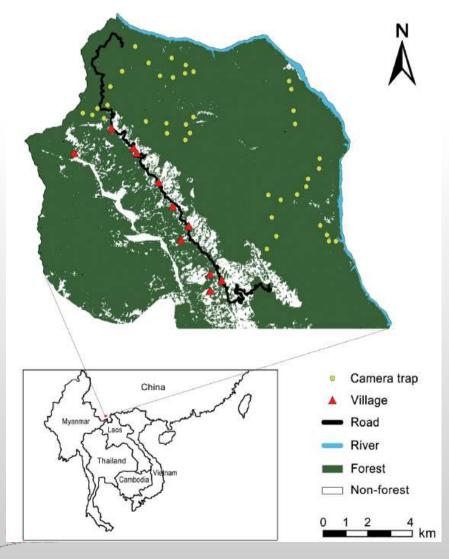


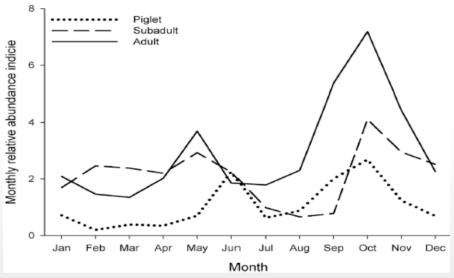


Li et al. Transbound Emerg Dis 66 (2019): 1395–1398.

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Population dynamics and space use of wild boar in a tropical forest, Southwest China





- The sex ratio was unchanged during the four years.
- Space use differed among ages and sexes:

; adult males were active near villages while piglets avoided forest edges

Guo et al. Glob Ecolo Conserv 11 (2017):115-124.

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สัตวแพทย์บริการวิชาการสุกร I SWINE VETERINARY SERVICE TEAM



#### **AFRICAN SWINE FEVER**

REPORT

WEEK 30<sup>th</sup> 21 - 31 JULY 2019

#### สถานการณ์การระบาดโรค ASF



Posted by Global New Light of Myanmar
Date: August 06, 2019 in: Local News



Number of dead pigs seen in Tachilek Township. Photo: Myint Mo (Tachilek)





Wild boar ( หมูป่า, Moopa) in Thailand

: conservation area

- national park

- wildlife sanctuary

: farm wild boar

- backyard
- small farm





The crucial roles for ASF prevention in THAILAND.

- > Strict biosecurity
- > Multisector coporations
  - farmer
  - government
  - academic





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