PRRSV sequencing as epidemiological tool in outbreak management

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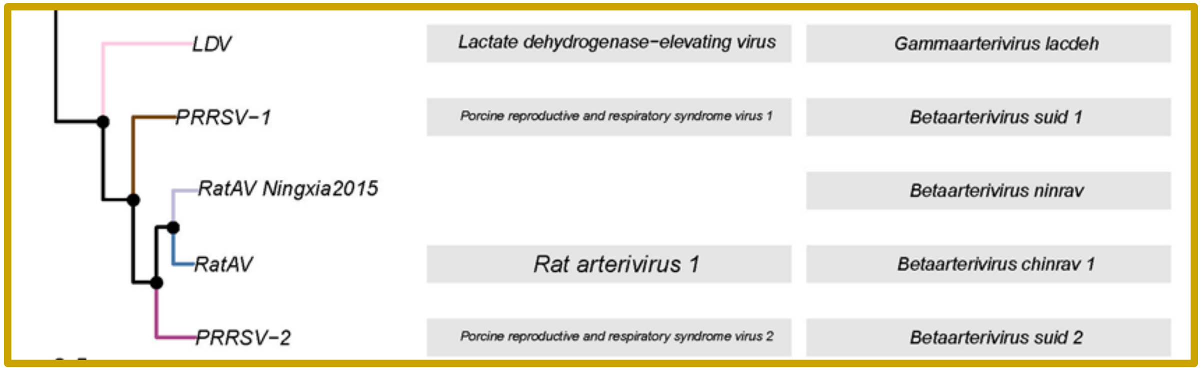
What's new about PRRSV

Porcine reproductive and respiratory syndrome virus

- PRRSV-1 (prior EU-genotype)
  - PRRSV-1.1 (Western and Central Europe), PRRSV 1.2-1.4 (Eastern Europe)
- PRRSV-2 (prior NA-genotype)
- New nomenclature: *Betaarterivirus suid 1* und *2*



LDV	Lactate dehydrogenase-elevating virus	Gammaarterivirus lacdeh
PRRSV-1	Porcine reproductive and respiratory syndrome virus 1	Betaarterivirus suid 1
RatAV Ningxia2015		Betaarterivirus ninrav
RatAV	Rat arterivirus 1	Betaarterivirus chinrav 1
PRRSV-2	Porcine reproductive and respiratory syndrome virus 2	Betaarterivirus suid 2

Quelle: ICTV 2018

- High genetic variability

PRRSV genetic variability

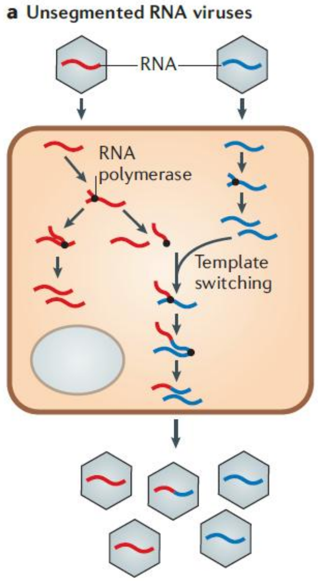
2 basic mechanisms

Point mutations (Drift)

- Errors during RNA replication
- High phylogenetic resolution
- Problems due to primer/probe mismatches with variant strains

Recombination (Shift)

- Template switching

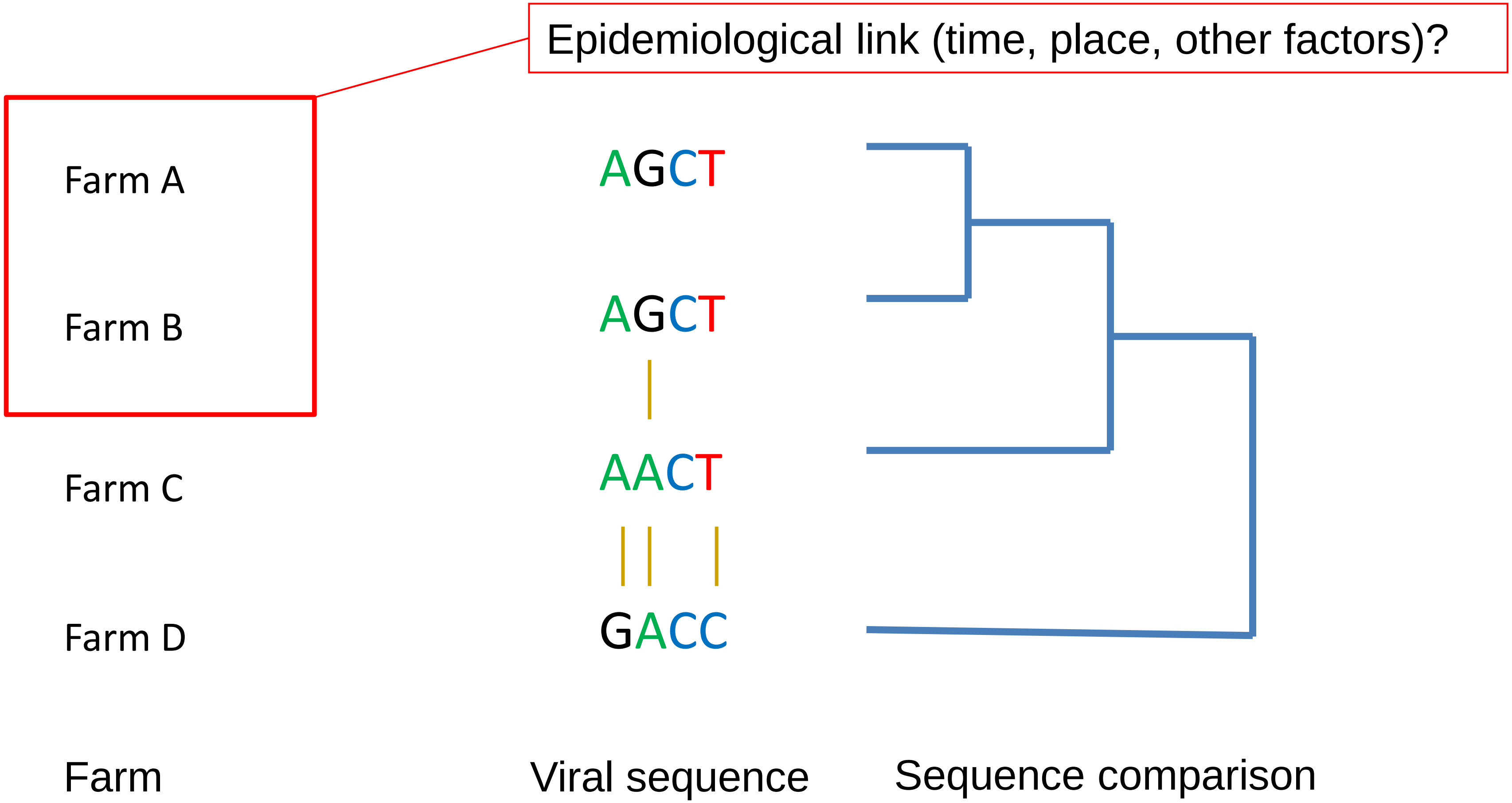


Simon-Loriere & Holmes, Nat Rev Microbiol 2011

- PRRSV-1 and -2
- Between field- and vaccine virus (Steinrigl et al., ESPHM 2017)

PRRSV sequencing

as epidemiological tool



Epidemiological link (time, place, other factors)?

Farm A

Farm B

Farm C

Farm D

AGCT

AGCT

AACT

GACC

Farm

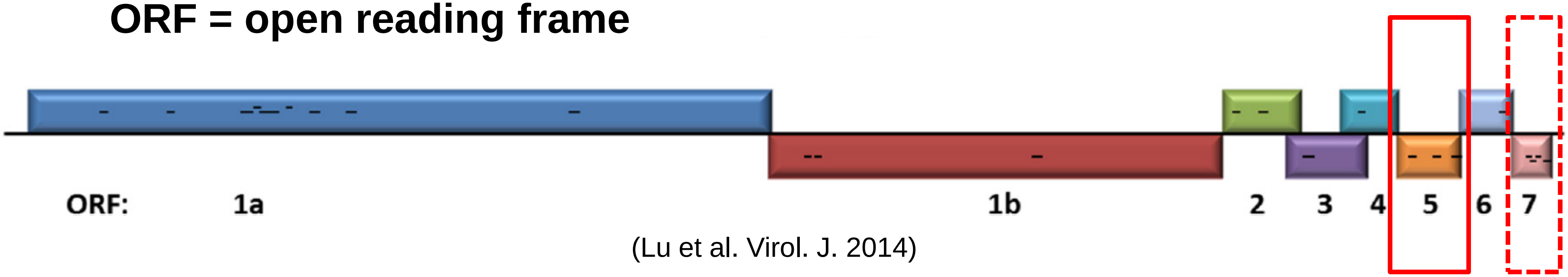
Viral sequence

Sequence comparison

PRRSV sequencing

Sequencing of subgenomic RT-PCR products

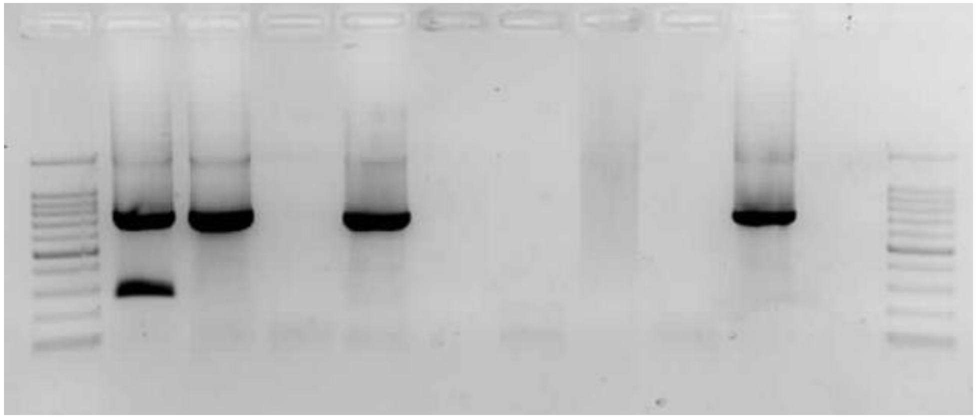
ORF = open reading frame

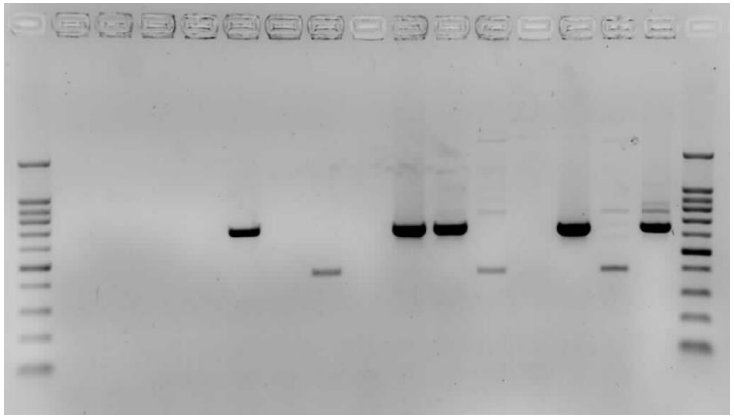


(Lu et al. Virol. J. 2014)

ORF5 RT-PCR

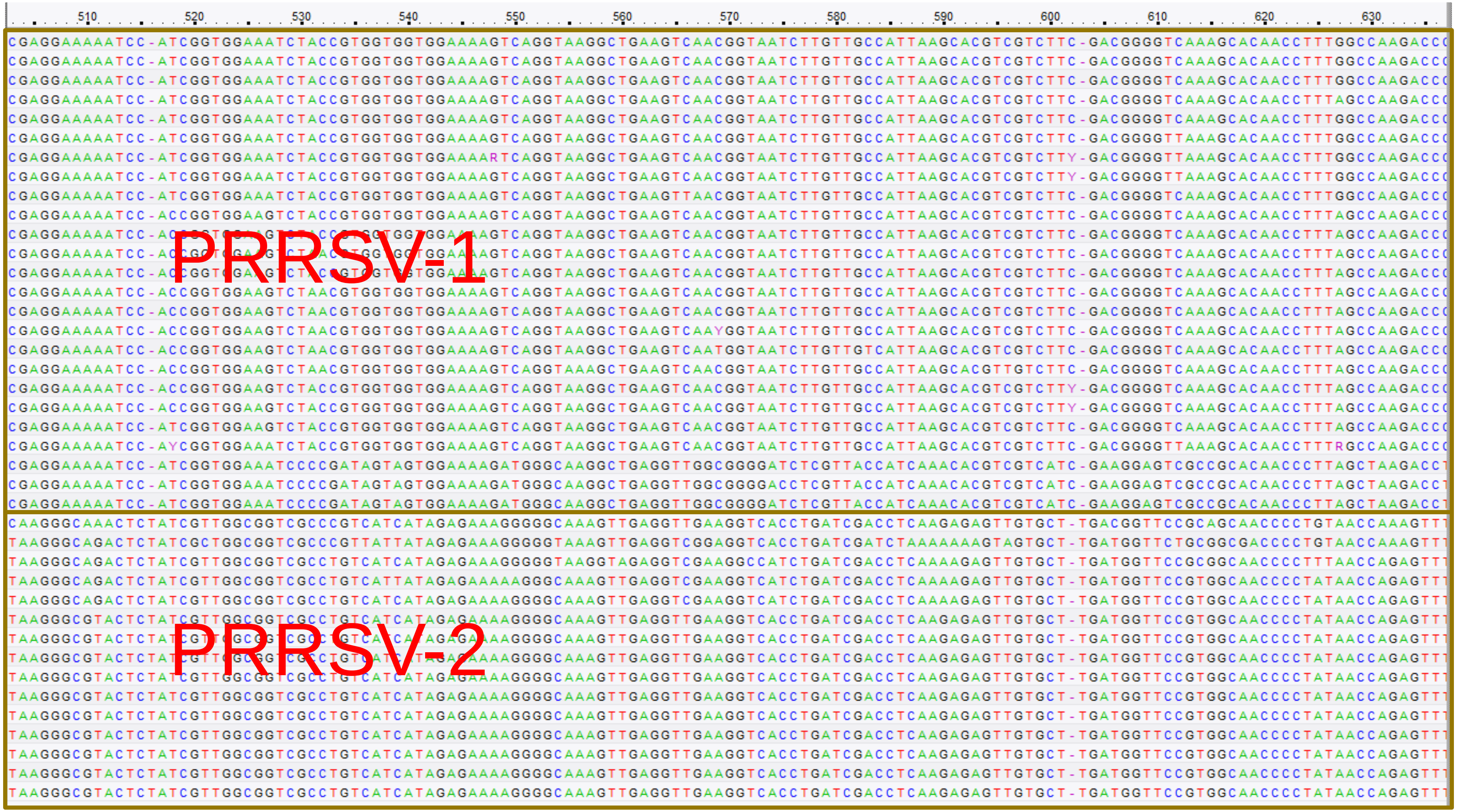
ORF7 RT-PCR





ORF5 sequence database – since 2012

>760 PRRSV ORF5 sequences from Austria



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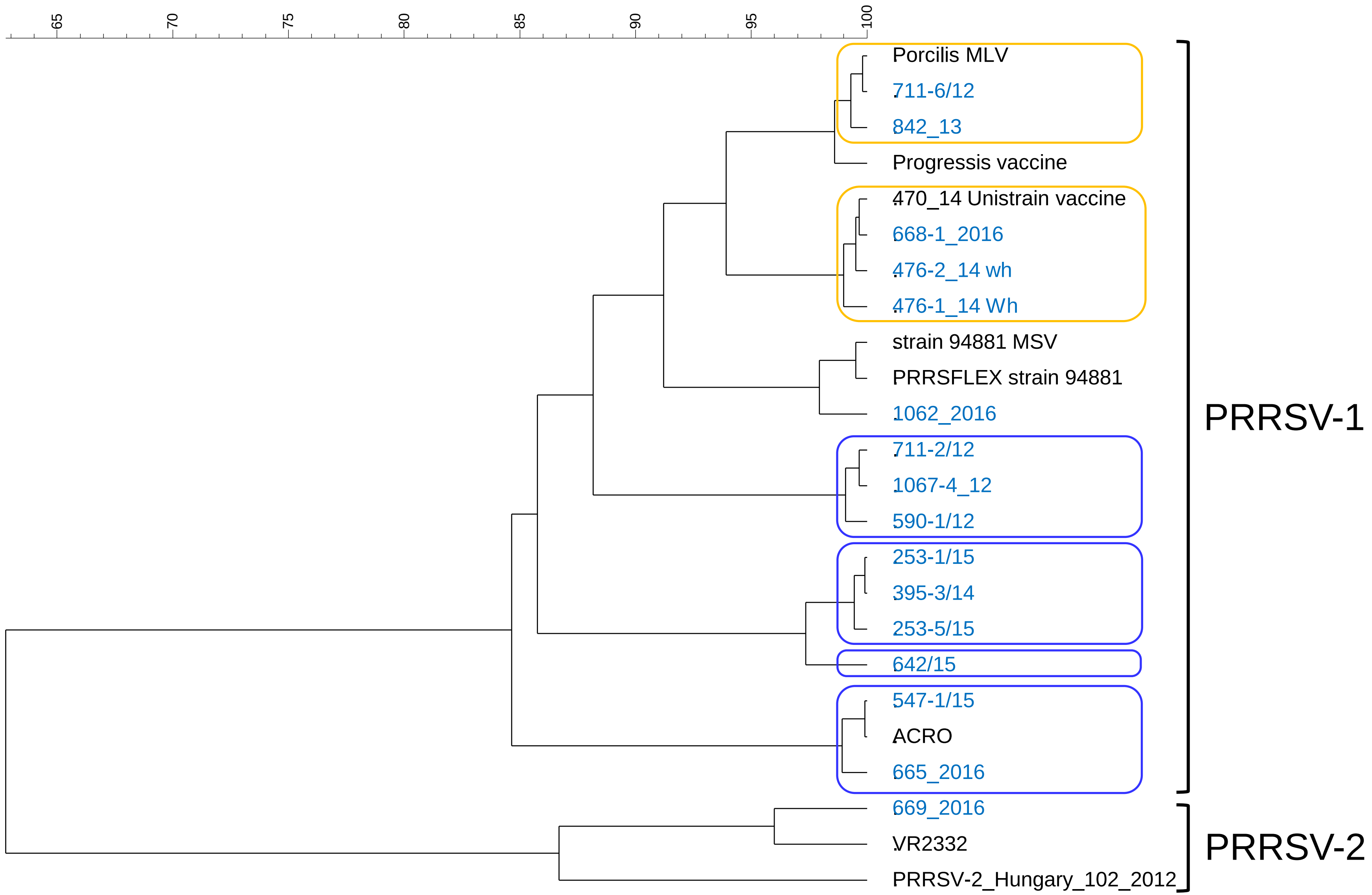
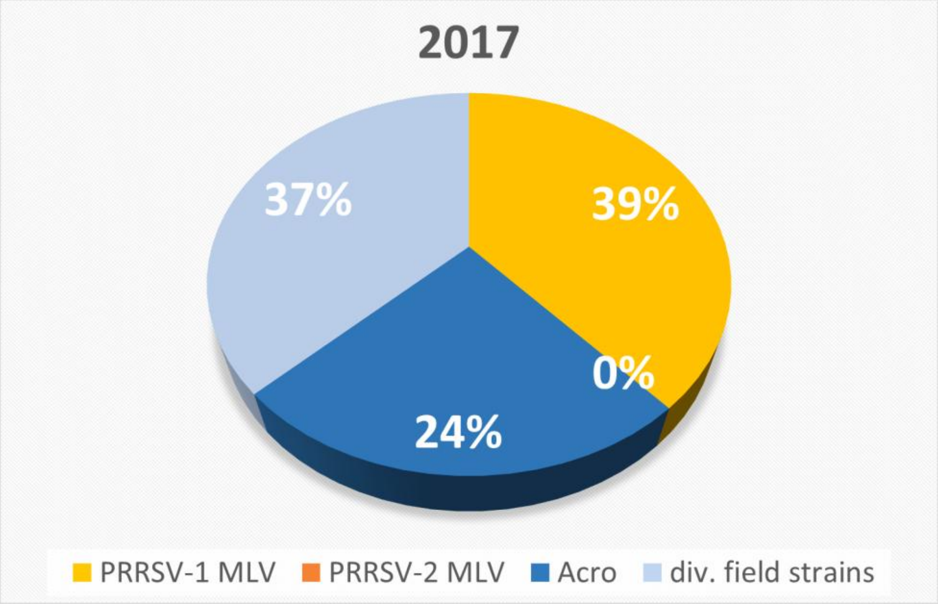
Sequence comparison



PRRSV typing results

Recent results: 2017, 2018



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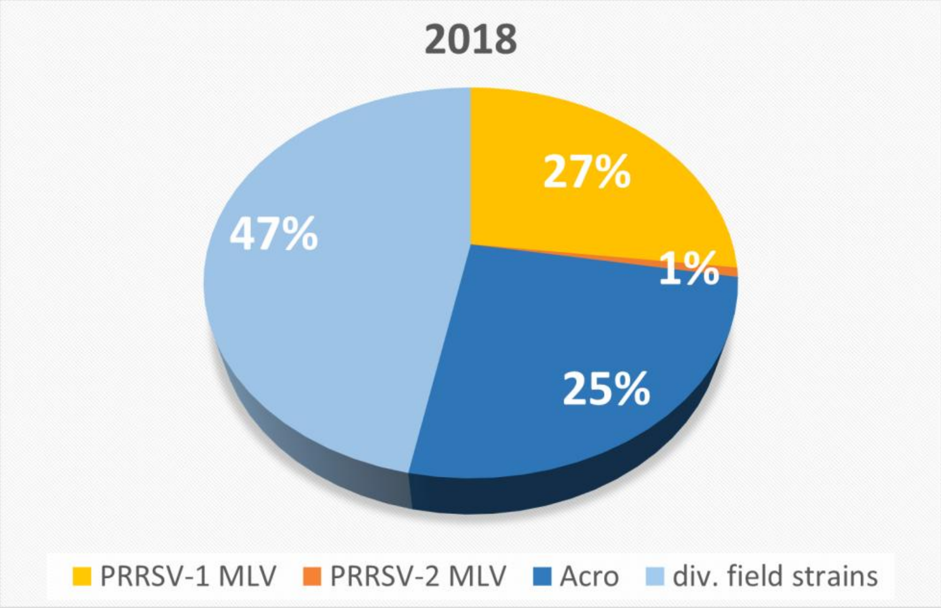
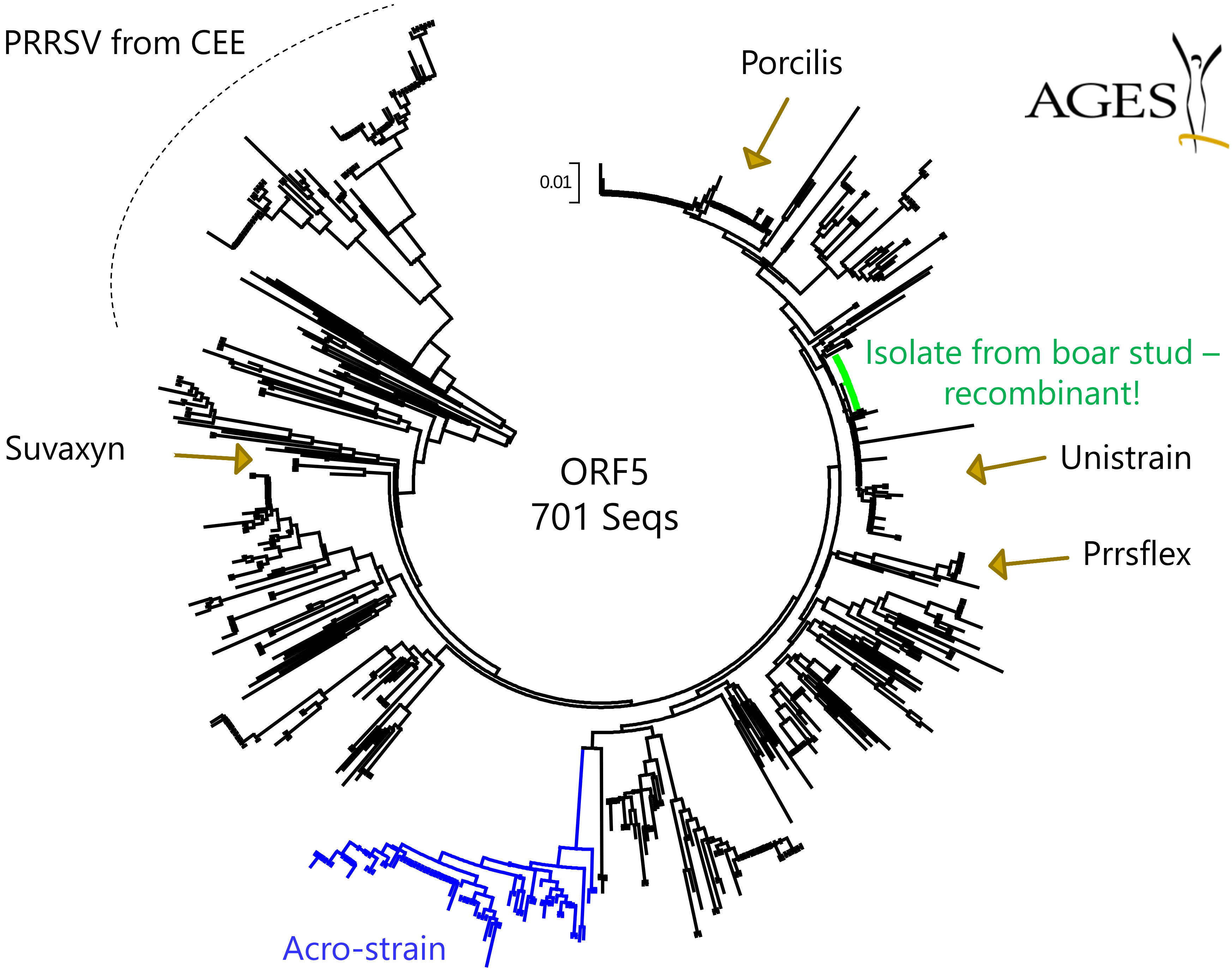
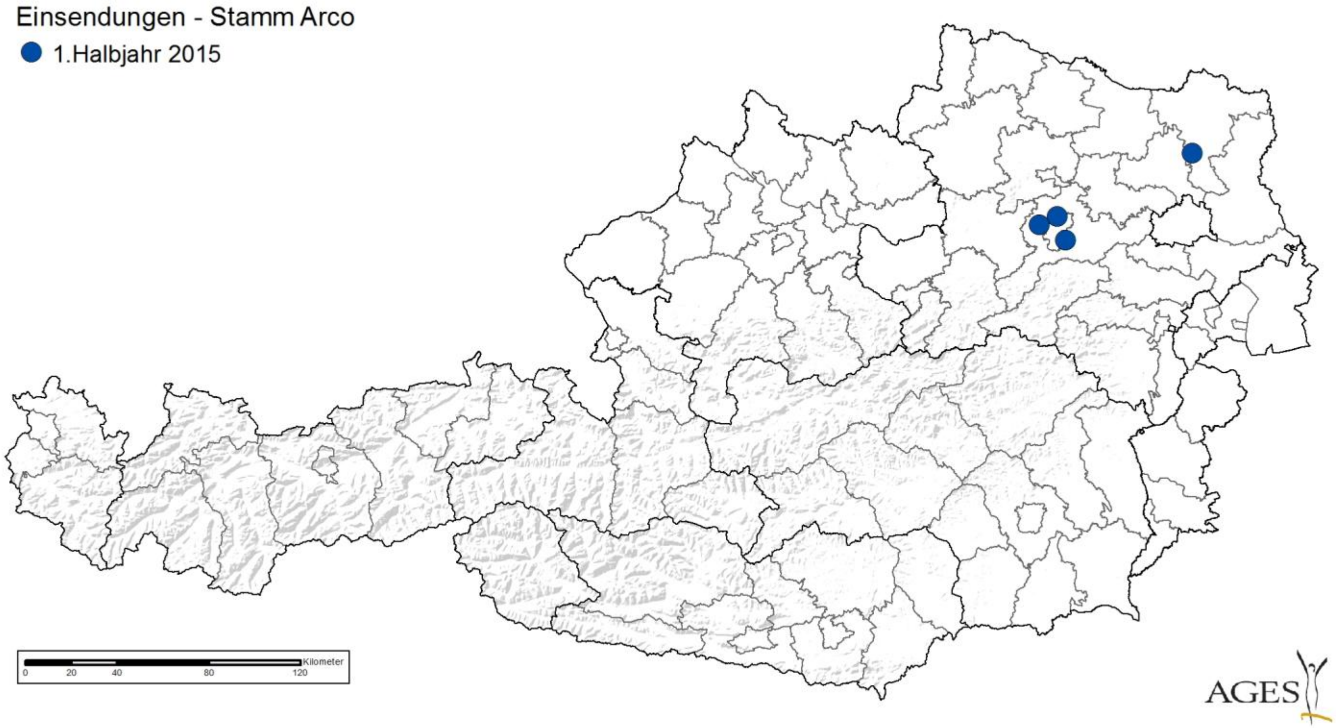


n=130

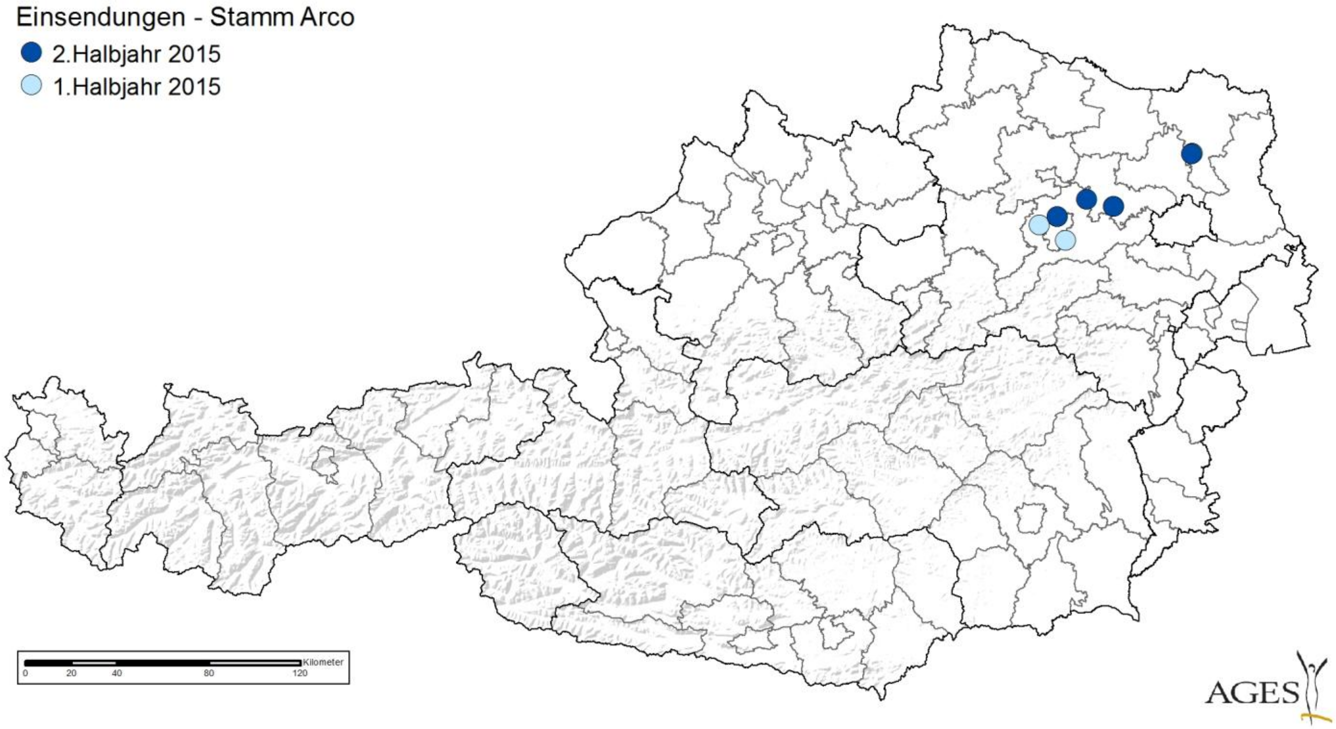
MLV = vaccine sequences (4 MLVs), or vaccine-like seqs


PRRSV from CEE
Porcilis
0.01
Isolate from boar stud – recombinant!
Unistrain
Prrsflex
Suvaxyn
ORF5
701 Seqs
Acro-strain

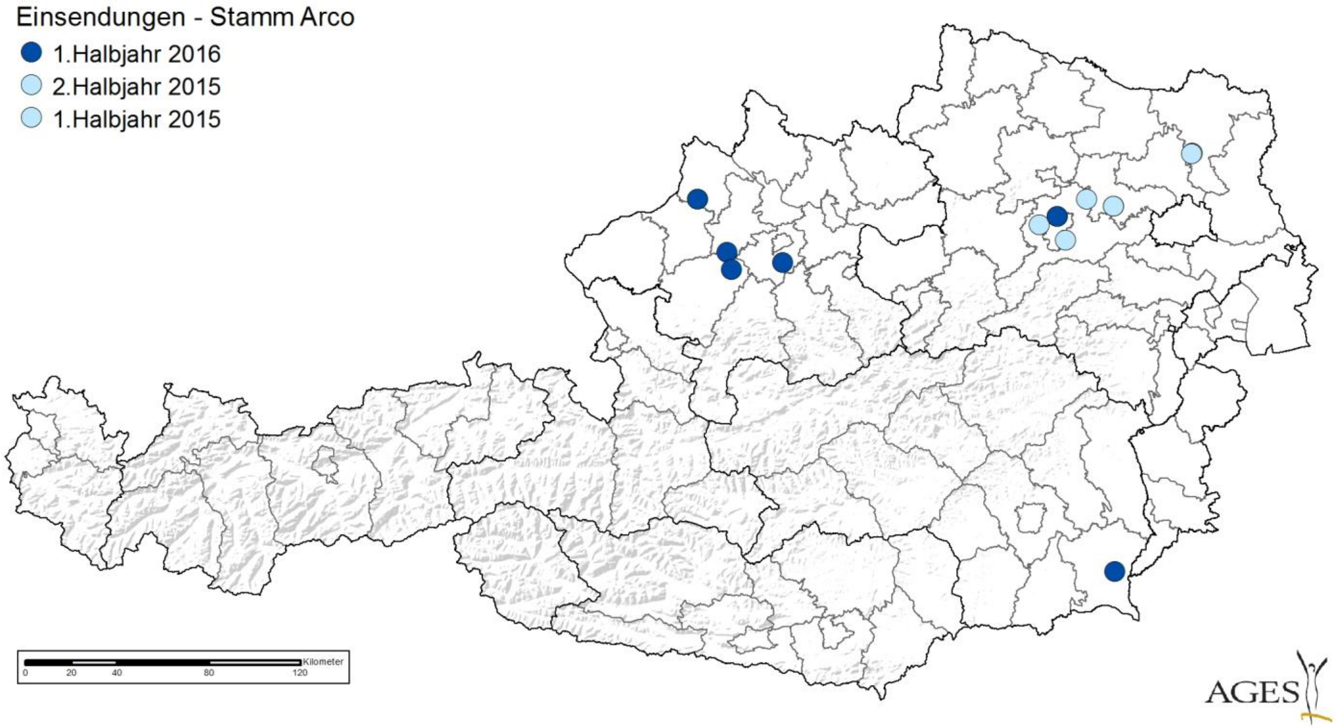
Spread of Acro-strain 2015-2019



Spread of Acro-strain 2015-2019

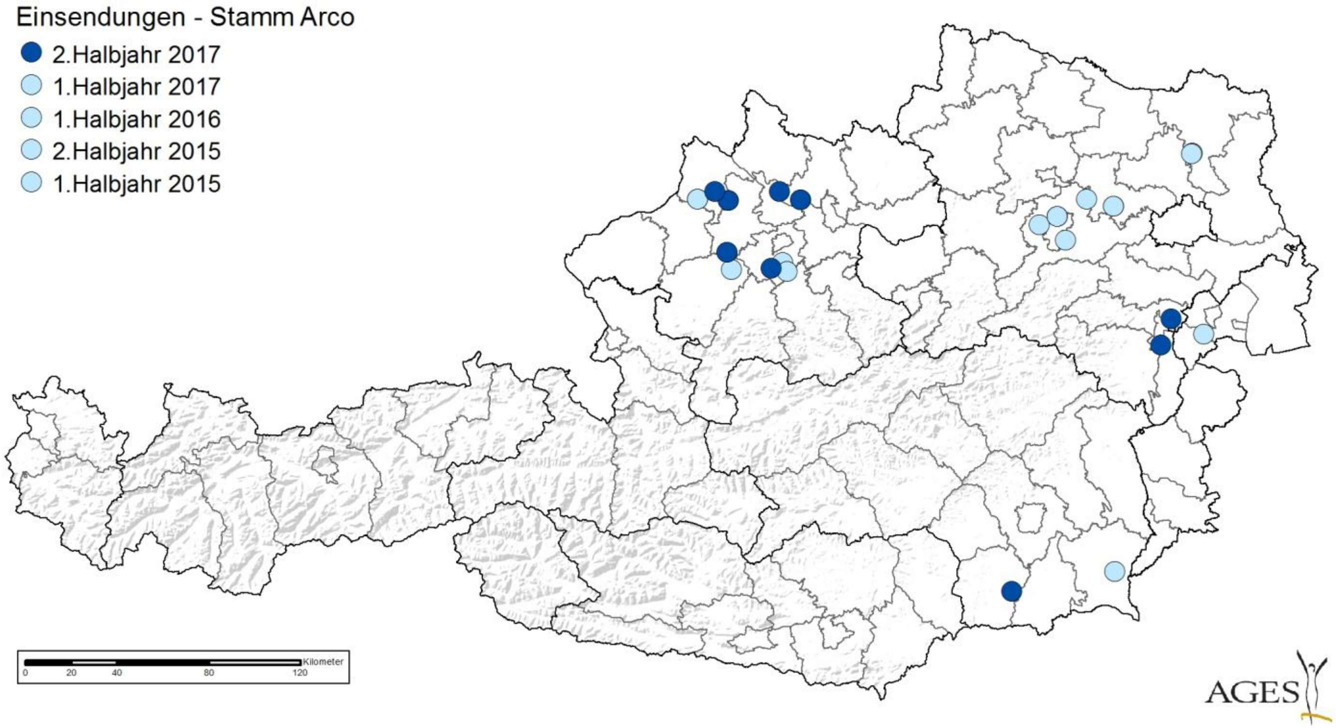


Spread of Acro-strain 2015-2019

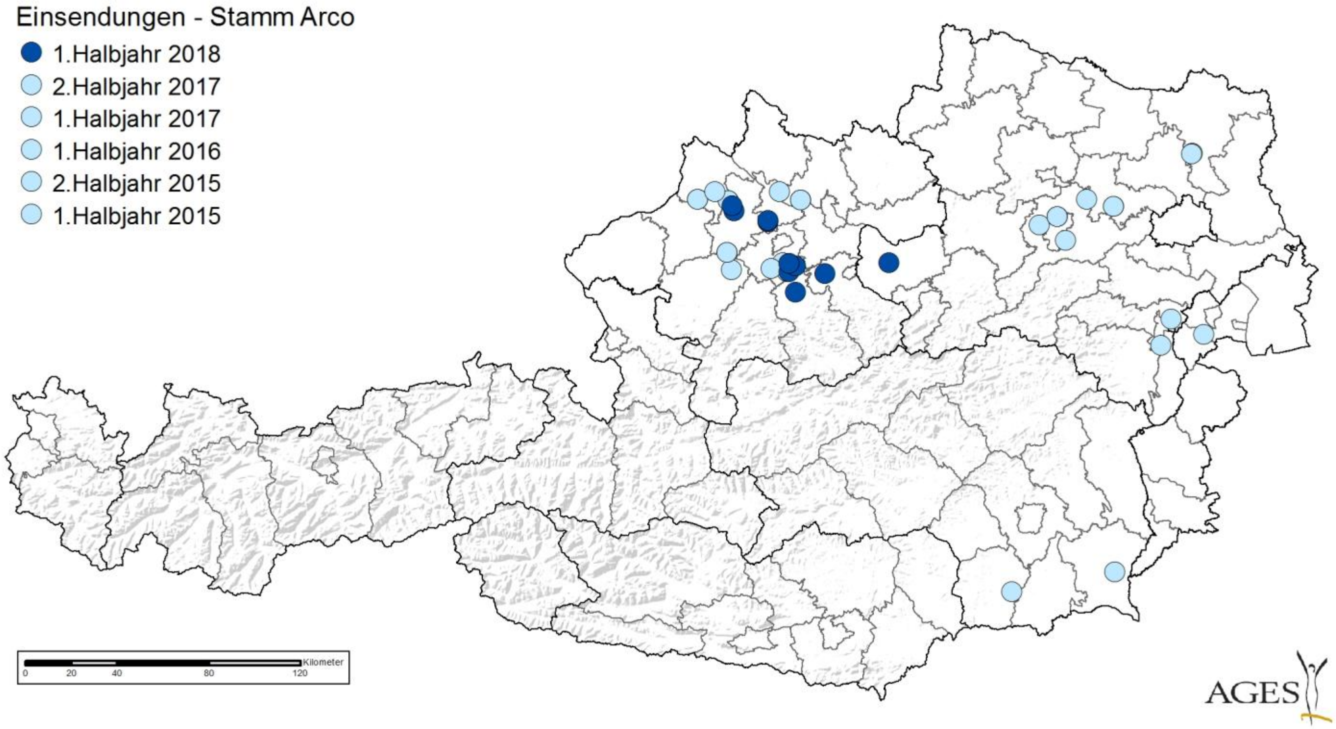


Spread of Acro-strain 2015-2019

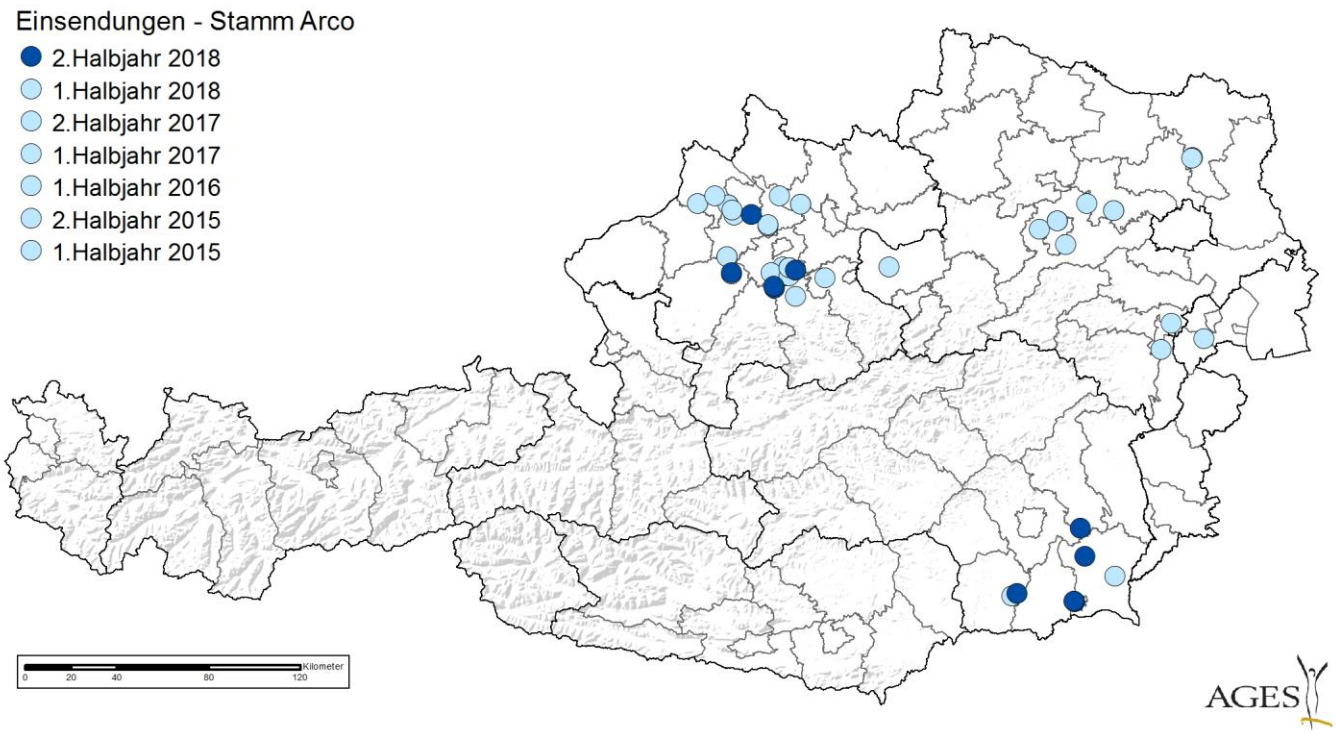
Spread of Acro-strain 2015-2019



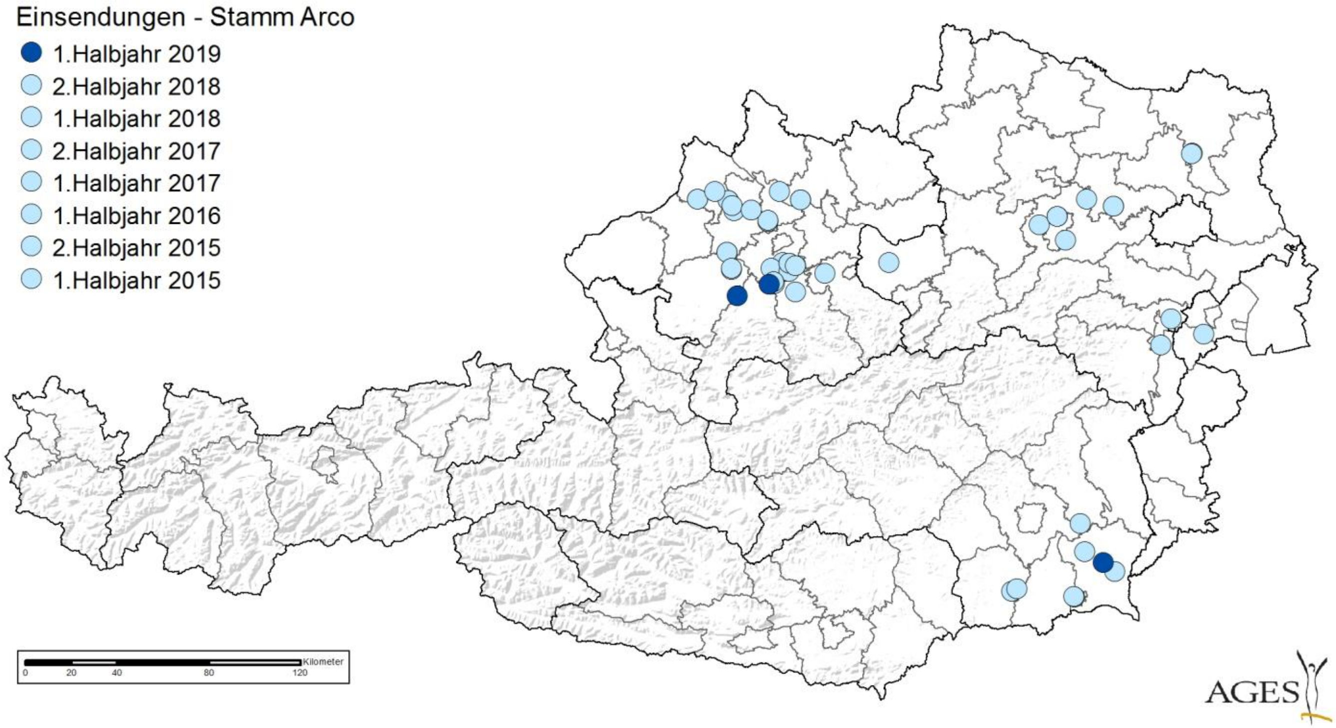
Spread of Acro-strain 2015-2019



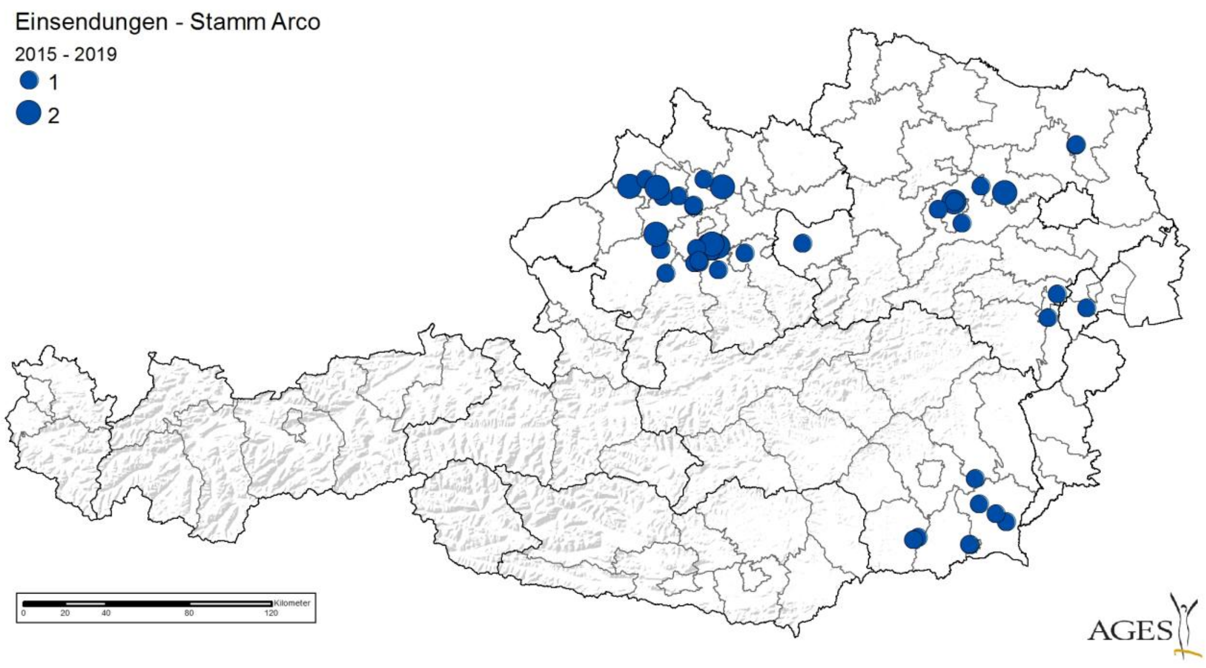
Spread of Acro-strain 2015-2019

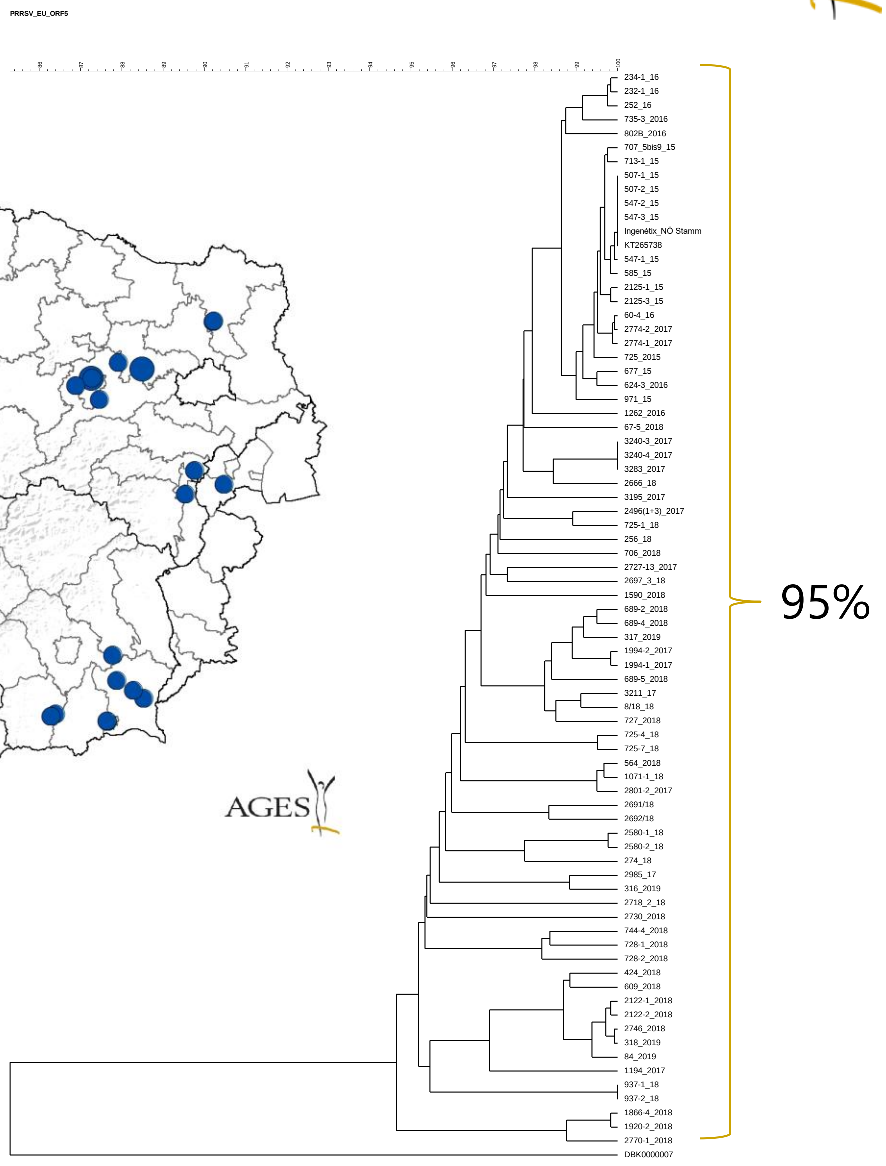


Spread of Acro-strain 2015-2019



Spread of Acro-strain 2015-2019





Summary & outlook

- PRRSV sequencing is a valuable epidemiological tool in outbreak management
  - Not for prognosis of strain virulence or vaccine matching
- High sequence variability in AT, only PRRSV-1.1, MLV-(like) sequences frequently seen (all four AT-registered MLV)
- Two complete genomes sequenced – boar stud (recombinant between field-virus/MLV(-like)) and Acro-strain
- WGS still difficult as standard sequencing method, but highly interesting for research! Will definitely come for routine use!

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