European Food Safety Authority

EU Reference Laboratory for ASF
Animal Health Research Centre
(CISA), INIA
Ctra Algete-El Casar s/n
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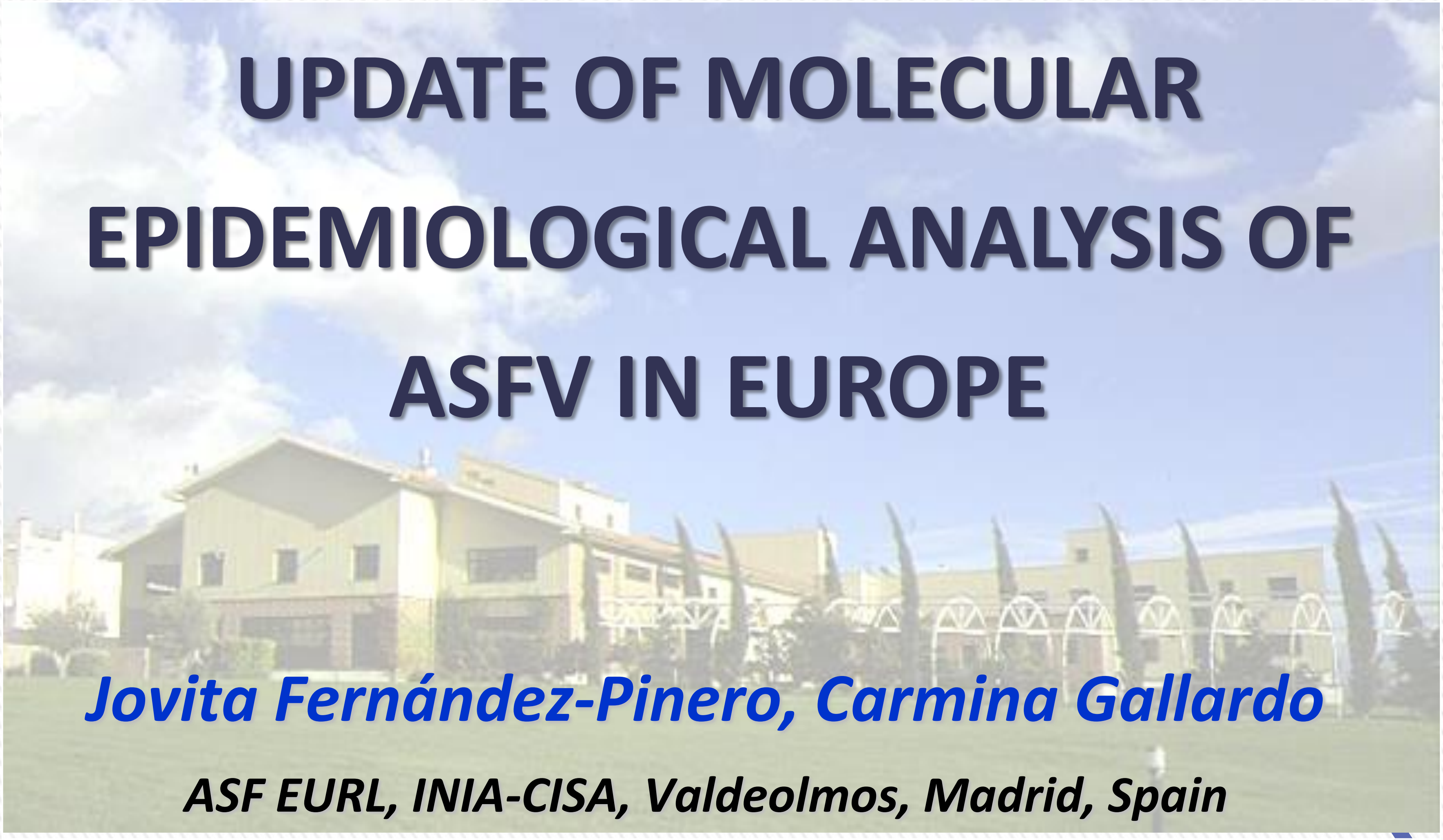
MINISTERIO DE ECONOMÍA Y COMPETITIVIDAD

INIA
Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria



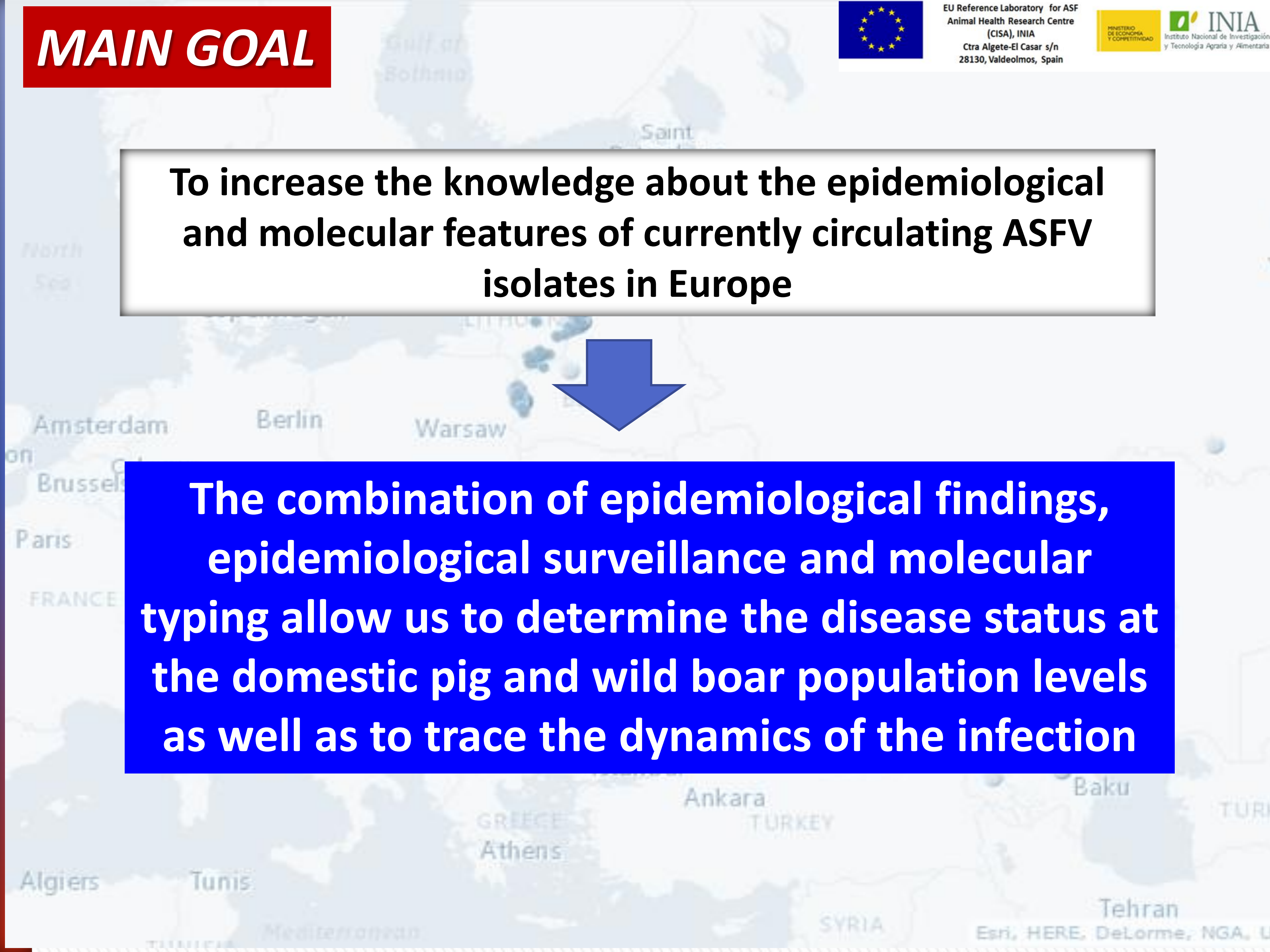
UPDATE OF MOLECULAR EPIDEMIOLOGICAL ANALYSIS OF ASFV IN EUROPE

Jovita Fernández-Pinero, Carmina Gallardo

ASF EURL, INIA-CISA, Valdeolmos, Madrid, Spain

WORKSHOP on Harmonisation of data collection on African Swine Fever (ASF) virus
November 23th – 25th, 2015
EFSA, Parma, Italy

MAIN GOAL

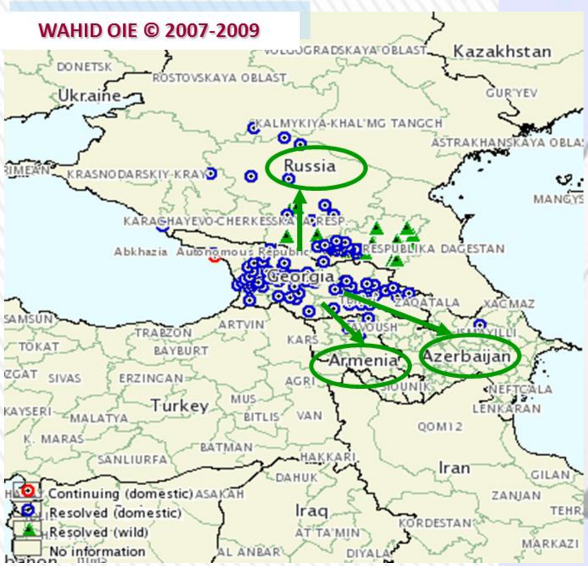


To increase the knowledge about the epidemiological and molecular features of currently circulating ASFV isolates in Europe

The combination of epidemiological findings, epidemiological surveillance and molecular typing allow us to determine the disease status at the domestic pig and wild boar population levels as well as to trace the dynamics of the infection

ASF: BACKGROUND

2007-2013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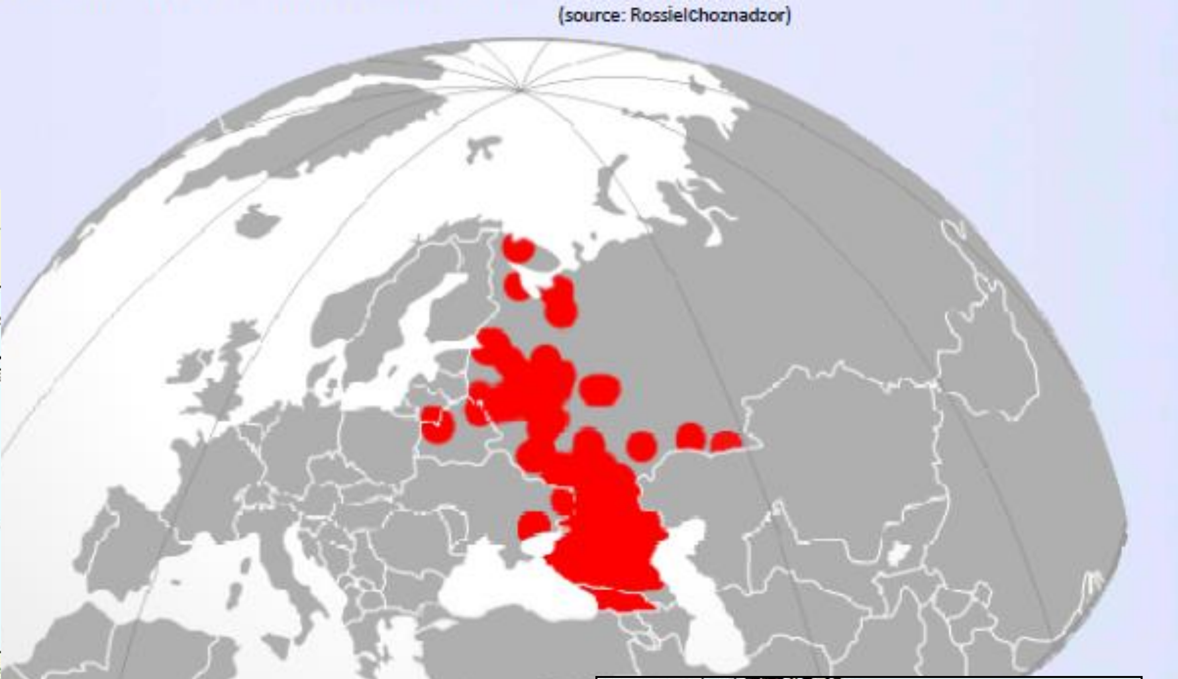
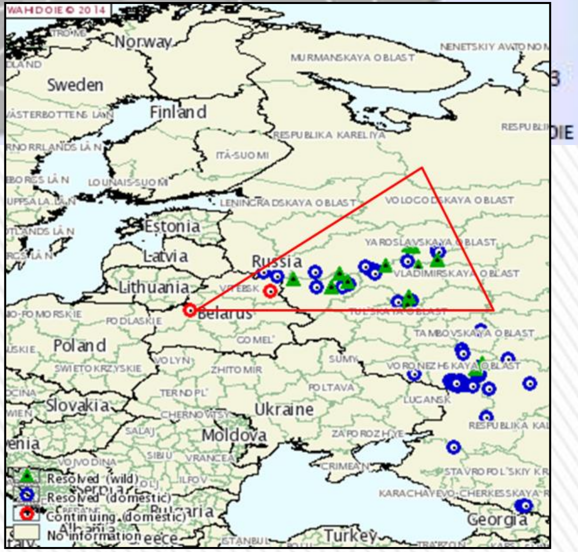

(source: RossielChoznadzor)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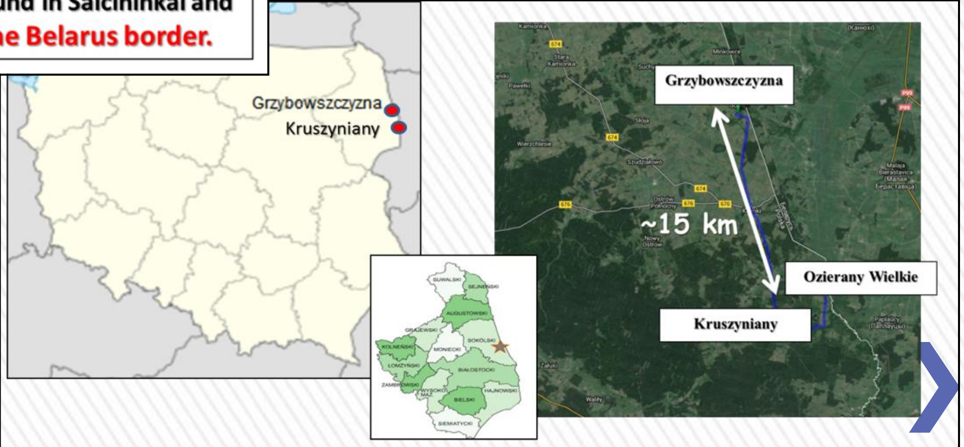
- **6 affected countries in Eastern Europe** (Georgia, Azerbaijan, Armenia, Russian Federation, Ukraine, Belarus)
- **Ongoing spread of ASFV towards west affecting eastern European countries**, such as Ukraine (2012) and Belarus (2013)

ASF: BACKGROUND

2014 → ASF spreads to the East EU countries.

2 cases of ASF in wild boars. One of the infected animals was found in Salcininkai and the other in Varena, 5 km and 40 km, respectively, from the Belarus border.

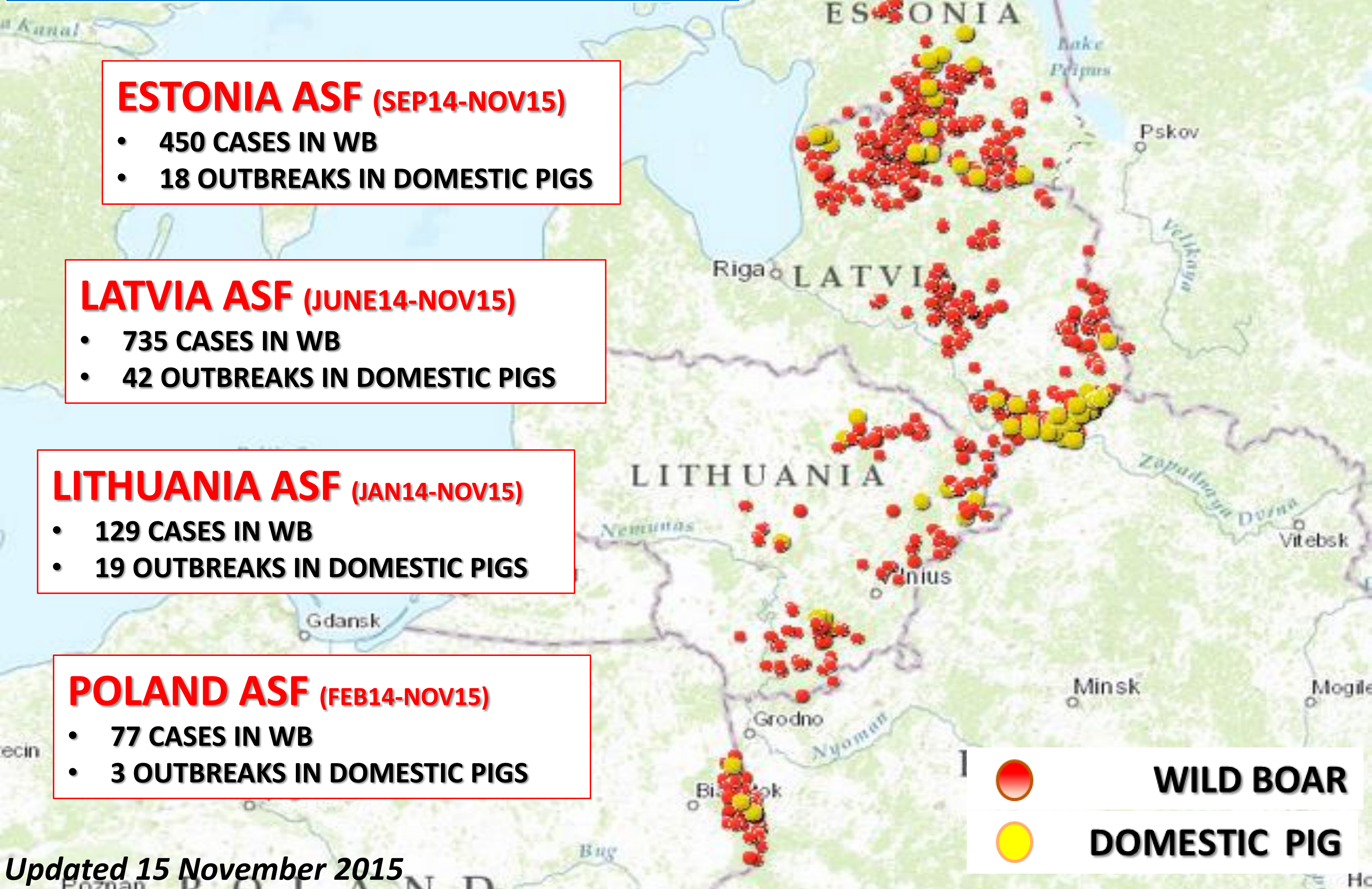
In January and February 2014, cases of African swine fever in wild boar, occurred in **Lithuania and Poland** due to the introduction of the ASF virus from neighboring non EU where the disease is present (epidemiological and molecular findings).



On February 14 and 17, 2014, reports of 2 cases of ASF in wild boars in Poland which were found dead ≈900 m and ≈200 m, respectively, from Poland's border with Belarus.

2 CASES IN WILD BOAR LITHUANIA (JANUARY 2014)
2 CASES IN WILD BOAR POLAND (FEBRUARY 2014)

1390 CASES IN WILD BOAR AND 82 DOMESTIC PIGS OUTBREAKS



ESTONIA ASF (SEP14-NOV15)

- 450 CASES IN WB
- 18 OUTBREAKS IN DOMESTIC PIGS

LATVIA ASF (JUNE14-NOV15)

- 735 CASES IN WB
- 42 OUTBREAKS IN DOMESTIC PIGS

LITHUANIA ASF (JAN14-NOV15)

- 129 CASES IN WB
- 19 OUTBREAKS IN DOMESTIC PIGS

POLAND ASF (FEB14-NOV15)

- 77 CASES IN WB
- 3 OUTBREAKS IN DOMESTIC PIGS

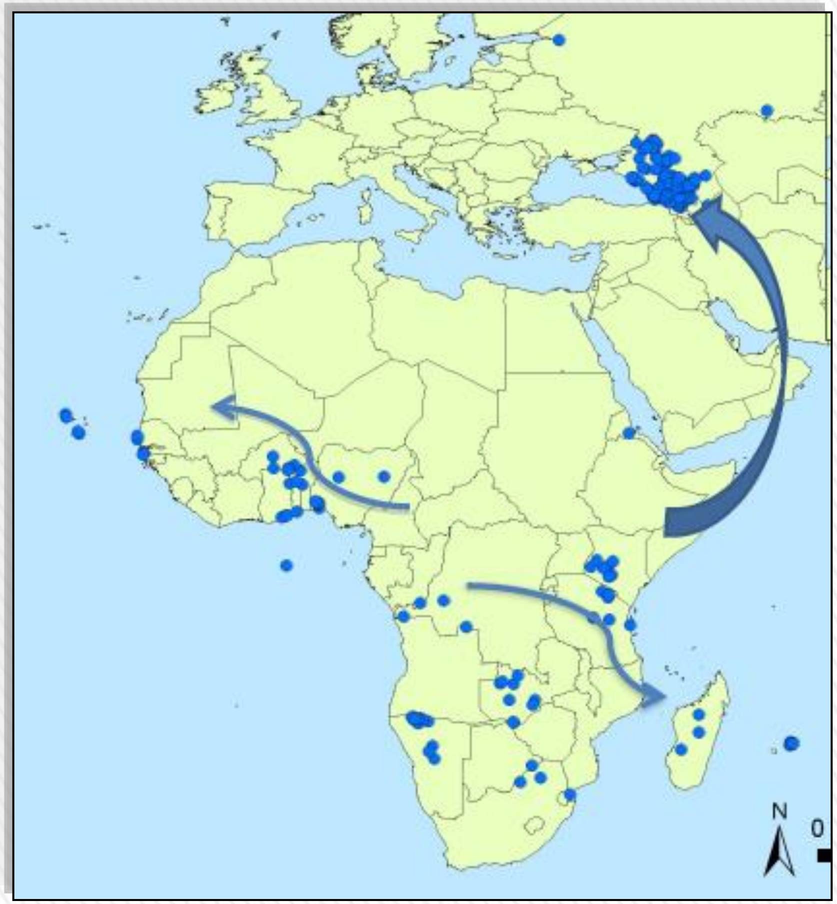
🔴 **WILD BOAR**

🟡 **DOMESTIC PIG**

Updated 15 November 2015

ASFV: MOLECULAR CHARACTERIZATION

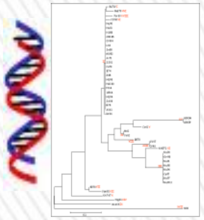
- Which is the origin of the virus?
- How is moving the virus?
- Is the virus changing over the time?



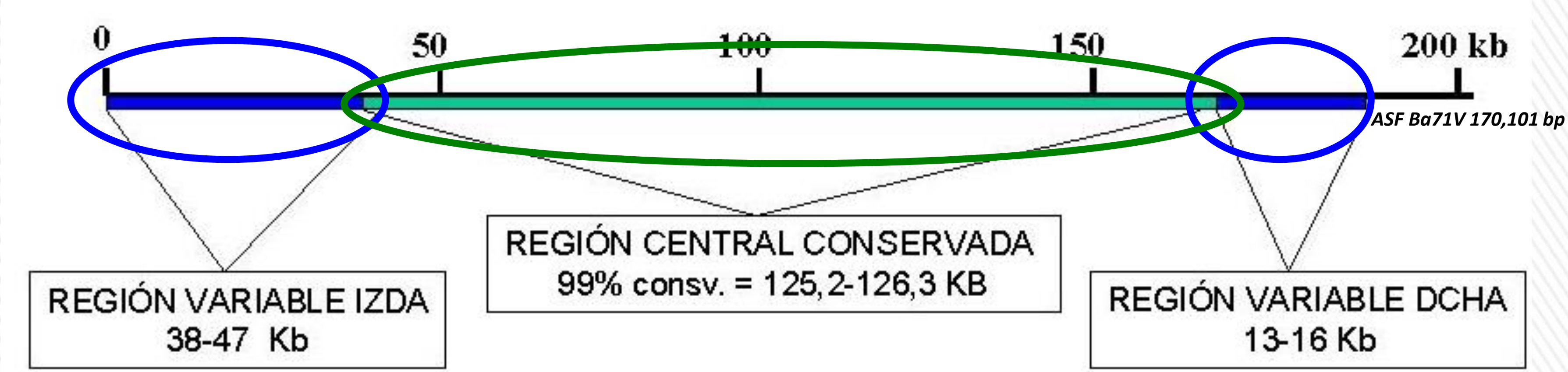
Molecular techniques are highly useful to **trace the source and dynamics** of ASF infections

Improvement of knowledge **on the epidemiological situation of ASF**

ASFV genome



Lineal dsDNA with a size between 170-193 kbp



REGIÓN VARIABLE IZDA
38-47 Kb

REGIÓN CENTRAL CONSERVADA
99% consv. = 125,2-126,3 KB

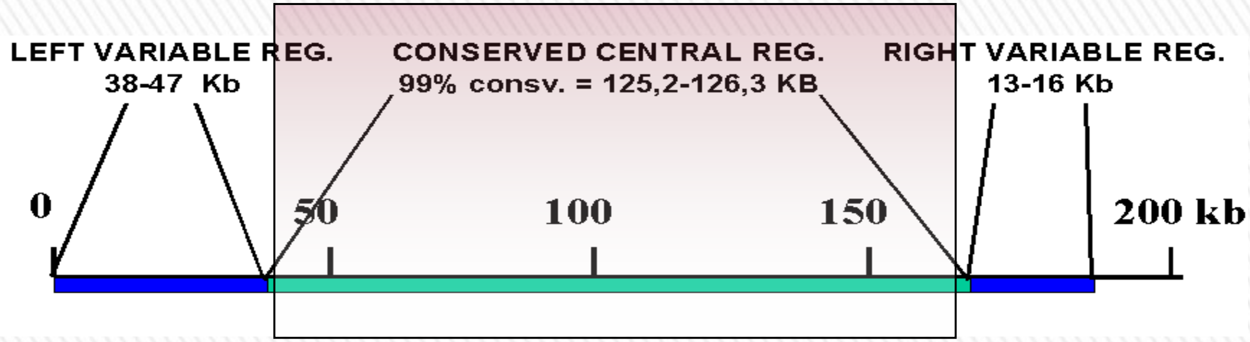
REGIÓN VARIABLE DCHA
13-16 Kb

Small variations due to the presence of tandem repeats sequences (TRS) located in the central part of the genome.

Loss or acquisition of DNA fragments causing length change between 3 and 20 kb. Variable ends of ASFV genome **MGFs: MGF 100, 110, 300, 360 and 505/530**

ASFV: MOLECULAR CHARACTERIZATION

Traditional standardized procedures



FIRST GENOTYPING ON ASFV ISOLATES

- C-terminal end gene *B646L*→ **protein p72** → **22 genotypes**
- Complete gene *E183L*→ **protein p54**

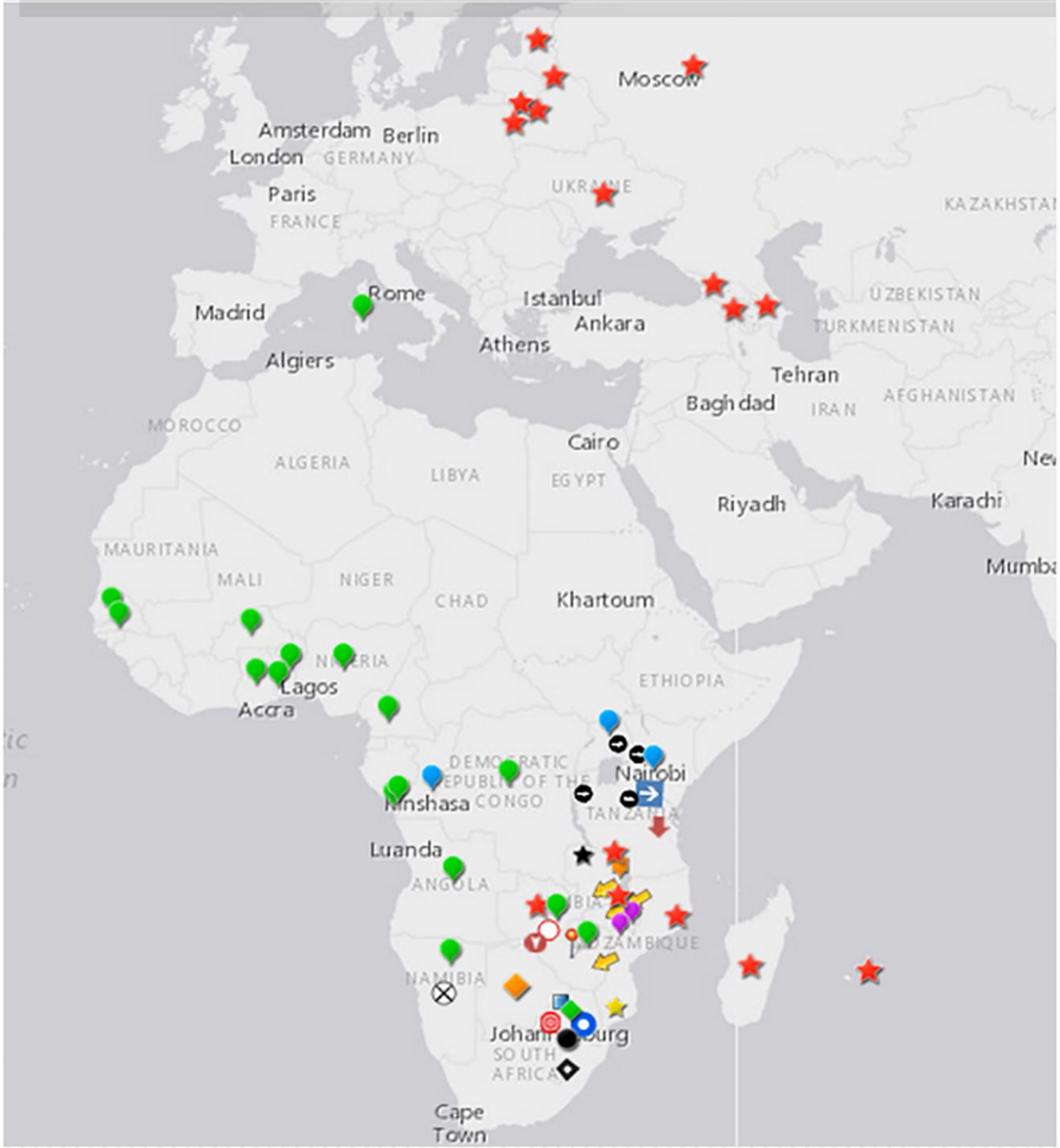
INTRAGENOTYPIC VARIABILITY

CVR: Analysis of the **central variable region** *of the B602L gene* characterized by the presence of tandem repeat sequences (TRS)

ASFV: MOLECULAR CHARACTERIZATION

ASFV P72-GENOTYPING → 22 GENOTYPES

- GENOTYPE I 🟢
- GENOTYPE II ★
- GENOTYPE III ◆
- GENOTYPE IV ●
- GENOTYPE V 🟣
- GENOTYPE VI ★
- GENOTYPE VII ◆
- GENOTYPE VIII ➘
- GENOTYPE IX 🔵
- GENOTYPE X ●
- GENOTYPE XI ●
- GENOTYPE XII ▼
- GENOTYPE XIII ★
- GENOTYPE XIV ○
- GENOTYPE XV ⬇
- GENOTYPE XVI ⬆
- GENOTYPE XVII 📍
- GENOTYPE XVIII ⊗
- GENOTYPE XIX ■
- GENOTYPE XX ◎
- GENOTYPE XXI ○
- GENOTYPE XXII ◇



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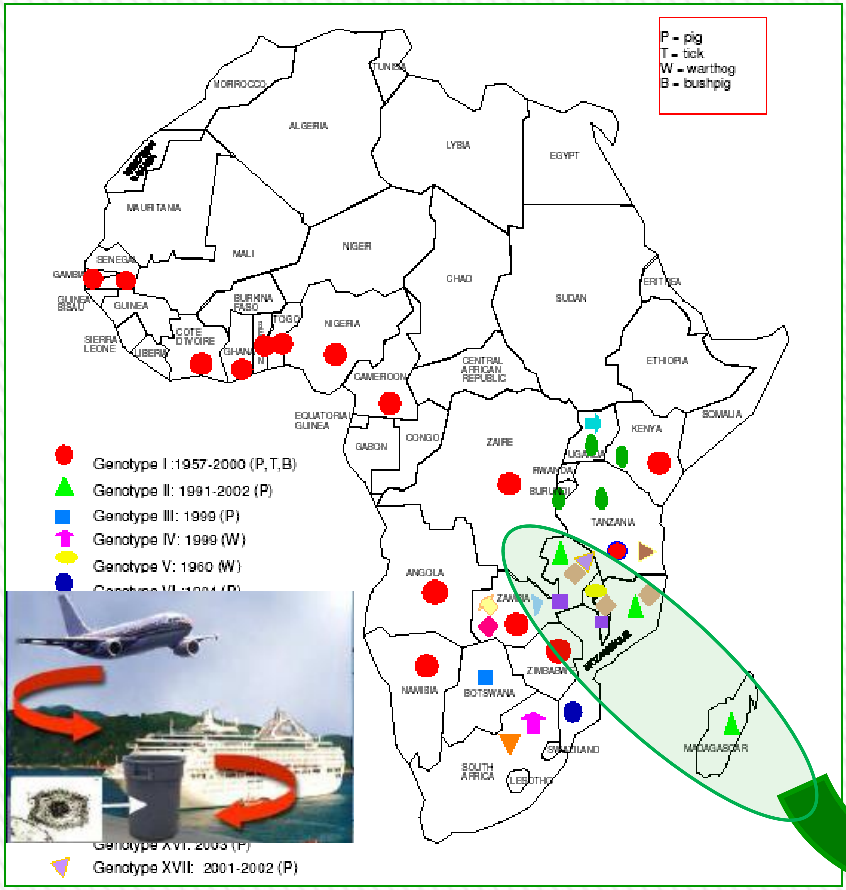
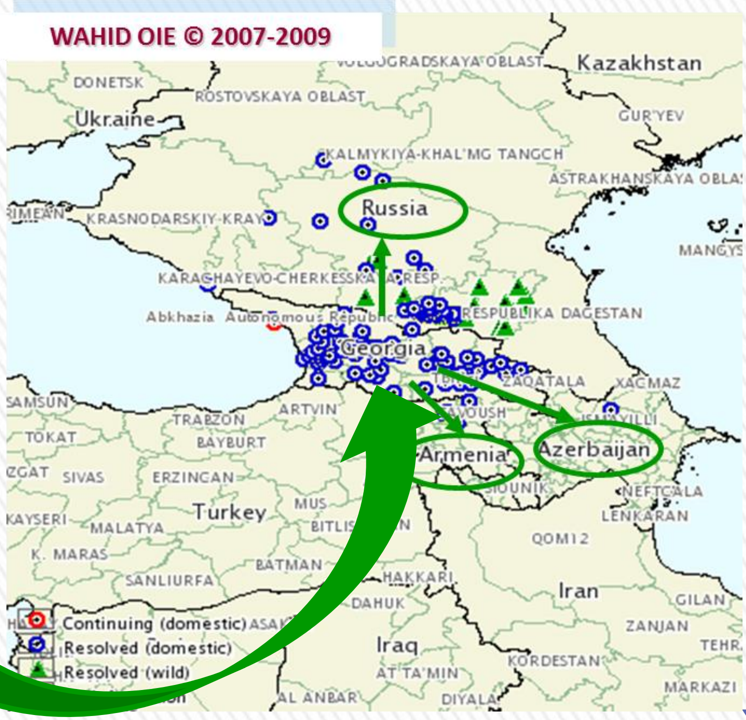
Tracing the origin



Georgia
June 2007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New ASFV belonging to genotype II associated to those circulating in East African countries

ASF IN EASTERN EUROPE

MOLECULAR CHARACTERIZATION OF EASTERN EUROPEAN ASFV ISOLATES (2007-2015)

346 ASFV sequenced by standardized procedures (EURL):

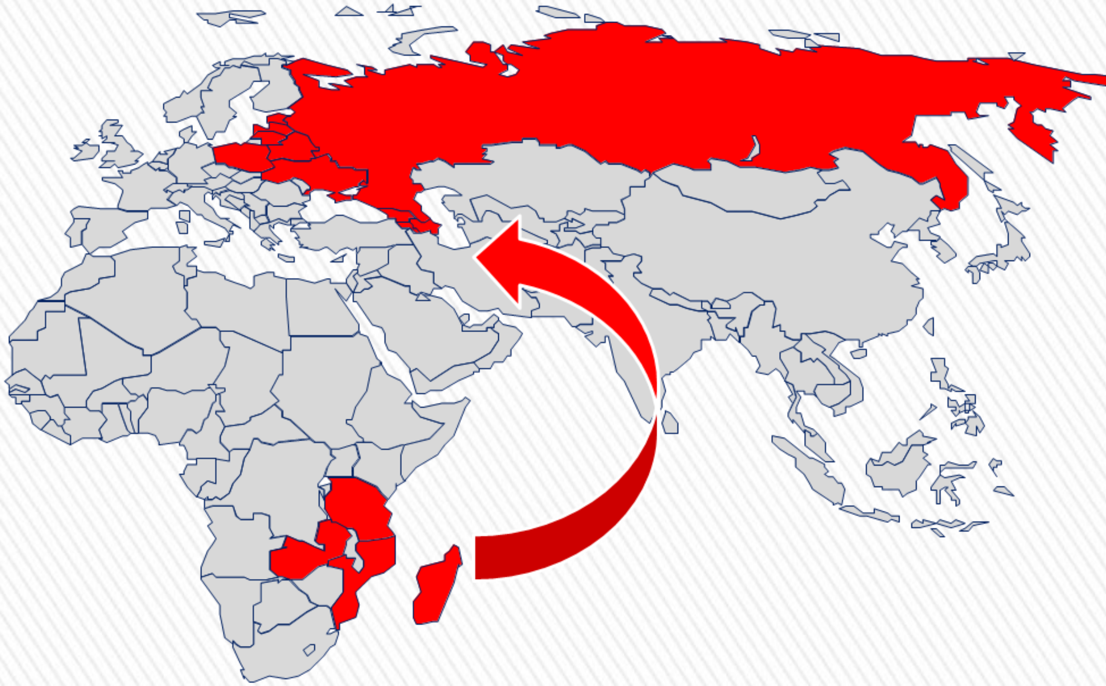
- 1 ASFV Georgia 2007
- 1 Armenia 2007
- 2 ASFV Azerbaijan 2008
- 15 Russia Federation 2007-2012
- 1 Belarus 2013
- 2 Ukraine 2012-2015
- **84 Estonia 2014-2015**
- **29 Latvia 2014-2015**
- **107 Lithuania 2014-2015**
- **104 Poland 2014-2015**

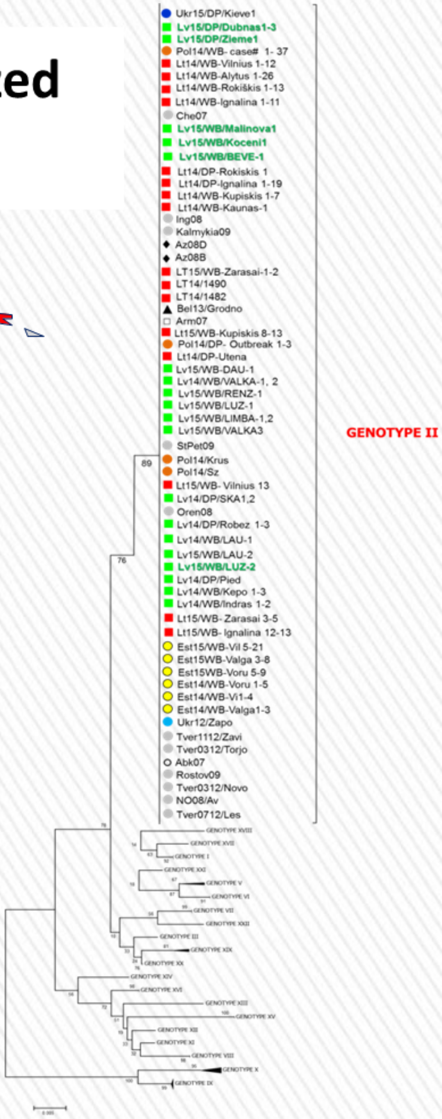
Updated 15 November 2015

ASF IN EASTERN EUROPE

From the GENETIC DATA

All Eastern European ASFV isolates characterized clustered within p72 genotype II





Single introduction → Since its introduction in 2007 in Georgia all ASFV isolates circulating in Eastern and Central Europe are classified within p72 genotype II.

ASF IN EASTERN EUROPE

From the GENETIC DATA

2014

• 100% nt/aa homology in C-term p72 and full p54 gene sequences and

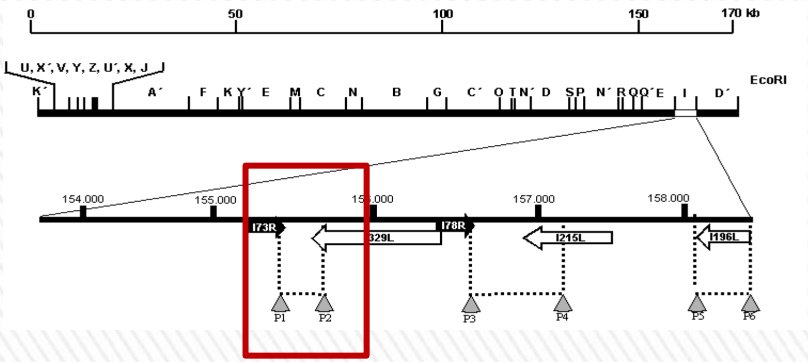
• unique and identical pattern of TRS within CVR

between all analysed ASFV genotype II isolates coming from Central and Eastern Europe since 2007

Need to define new genetic markers to determine with higher resolution the origin of a new ASF incursion and to trace the evolution of closely related ASFV isolates.

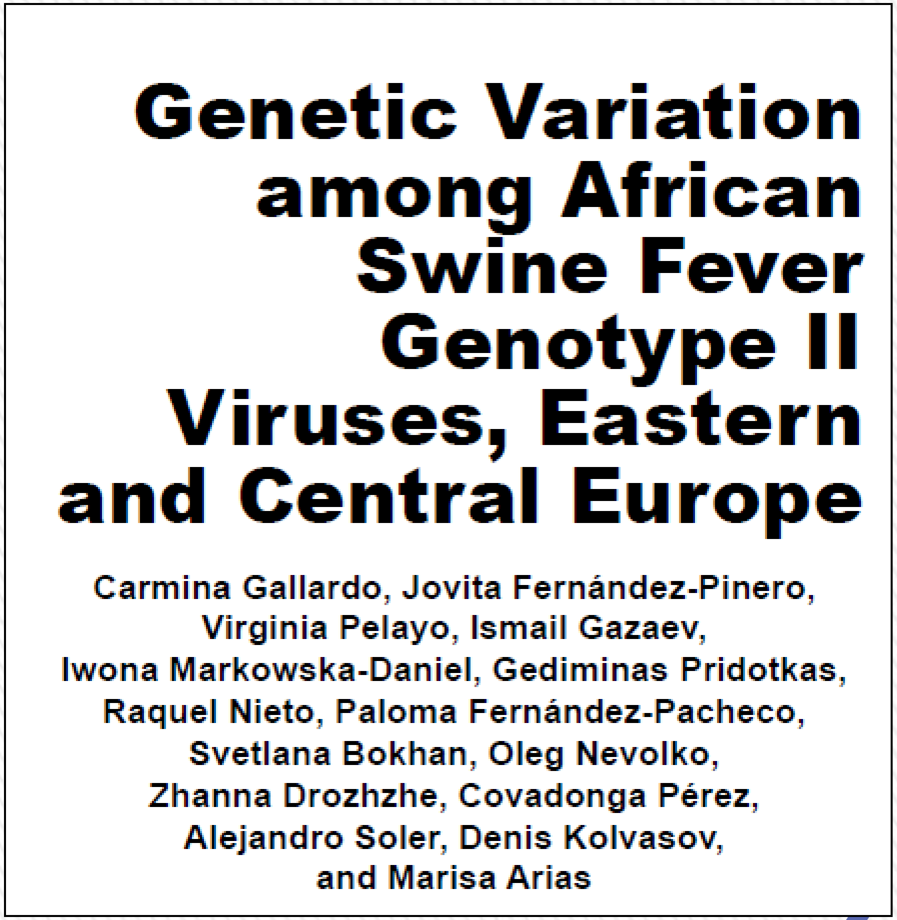
ASF IN EASTERN EUROPE

SUBTYPING BY THE ANALYSIS OF TRS



Analysis of the I73R/I329L intergenic region

NEW GENETIC MARKER IDENTIFIED TO TRACE THE OUTBREAKS



Genetic Variation among African Swine Fever Genotype II Viruses, Eastern and Central Europe

Carmina Gallardo, Jovita Fernández-Pinero,
Virginia Pelayo, Ismail Gazaev,
Iwona Markowska-Daniel, Gediminas Pridotkas,
Raquel Nieto, Paloma Fernández-Pacheco,
Svetlana Bokhan, Oleg Nevolko,
Zhanna Drozhzhe, Covadonga Pérez,
Alejandro Soler, Denis Kolvasov,
and Marisa Arias

ASF IN EASTERN EUROPE

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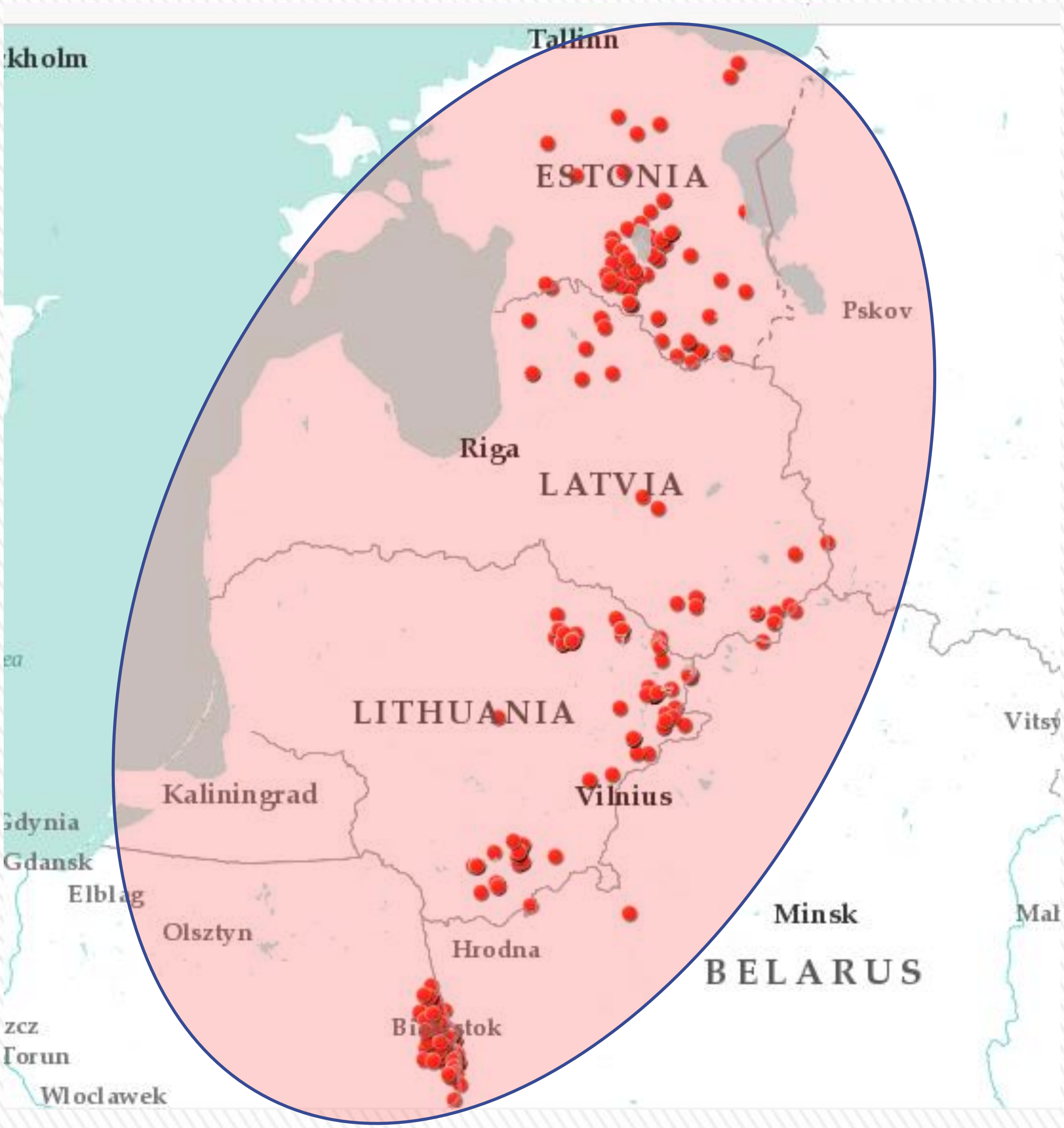
I73R/I329L intergenic region of Lithuanian and Polish ASFV isolates

```
                61                                                                         136
Georgia2007     TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Abk07           TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Arm07           TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Che07           TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Az08D           TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Az08B           TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Ing08           TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Oren08          TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
NO08/Av         TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
NO08/Ap         TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Dagestan09      TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
StPet09         TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Kalmykia09      TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Rostov09        TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Tver0511/Torjo  TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Tver0312/Torjo  TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Tver0313/Novo   TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Ukr12/Zapo      TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATAGGAATATATAGAAATATATAGAAATAGCTAAGCTTAATACTAAT
Tver0712/Les    TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Tver0812/Bolo   TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATA----------GAAATATATAGAAATAGCTAAGCTTAATACTAAT
Bel13/Grodno    TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATAGGAATATATAGAAATATATAGAAATAGCTAAGCTTAATACTAAT
Lt14/1490       TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATAGGAATATATAGAAATATATAGAAATAGCTAAGCTTAATACTAAT
Lt14/1482       TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATAGGAATATATAGAAATATATAGAAATAGCTAAGCTTAATACTAAT
Pol14/Sz        TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATAGGAATATATAGAAATATATAGAAATAGCTAAGCTTAATACTAAT
Pol14/Krus      TAGTTTAAGCAGTAAATGTAGAATAACACAGTTAAGCAATAAATAACAAGTATATAGGAATATATAGGAATATATAGGAATATATAGAAATATATAGAAATAGCTAAGCTTAATACTAAT
```

The viruses obtained from the first cases occurred in Poland and Lithuania at the beginning of 2014 **had a TRS insertion identical to that present in ASFV isolates from Belarus 2013 and Ukraine 2012**.

ASF IN EASTERN EUROPE



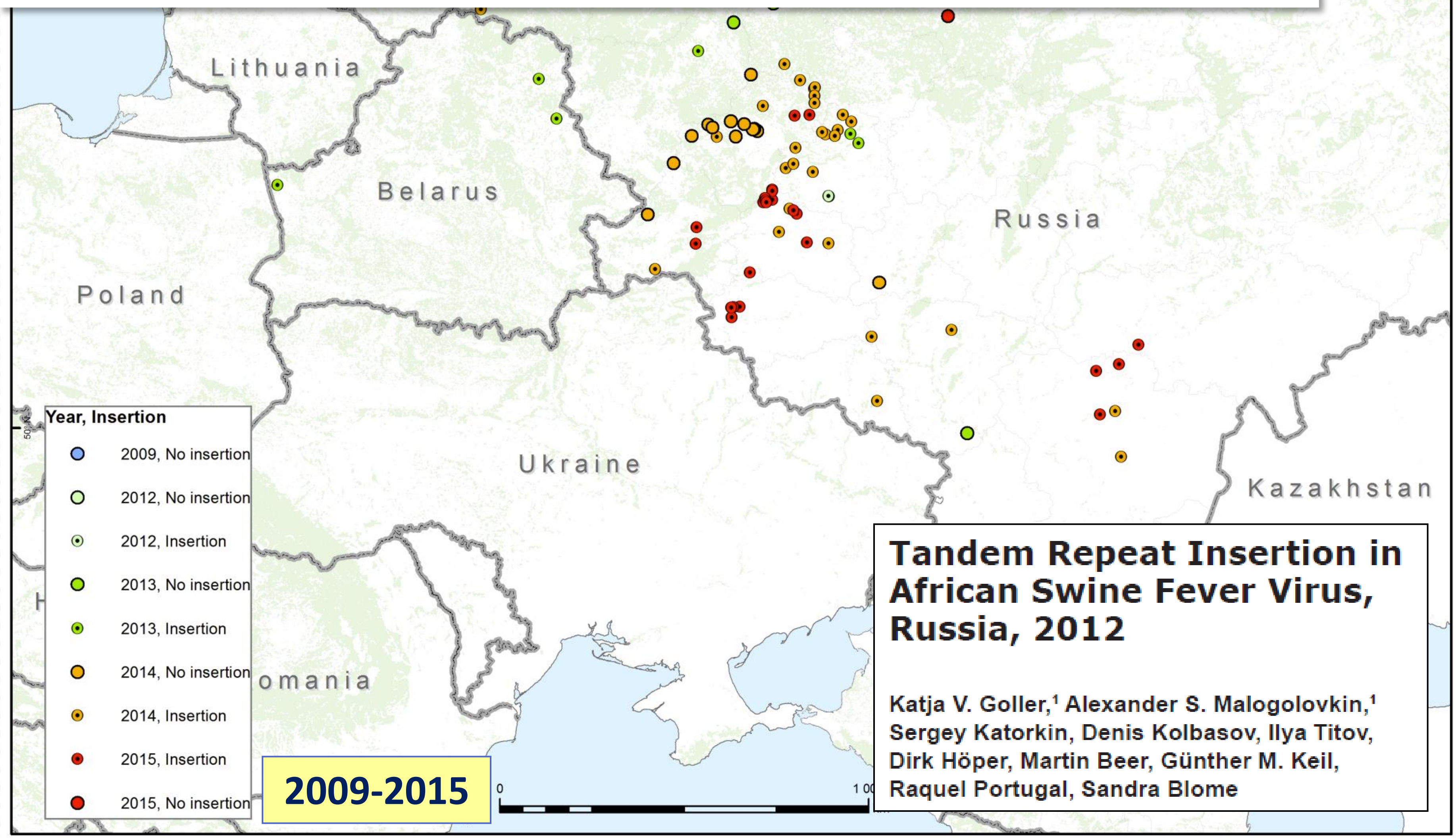
ASFV isolates with TRS insertion (TRS+) circulating in the EU countries

↓

The analysis of the **I73R/I329L intergenic region** showed a **100% sequence homology between all EU ASFV isolates** (Lithuania, Poland, Estonia and Latvia).

2014-2015

Two analogous genetic variants co-circulating in Russian Federation since 2012

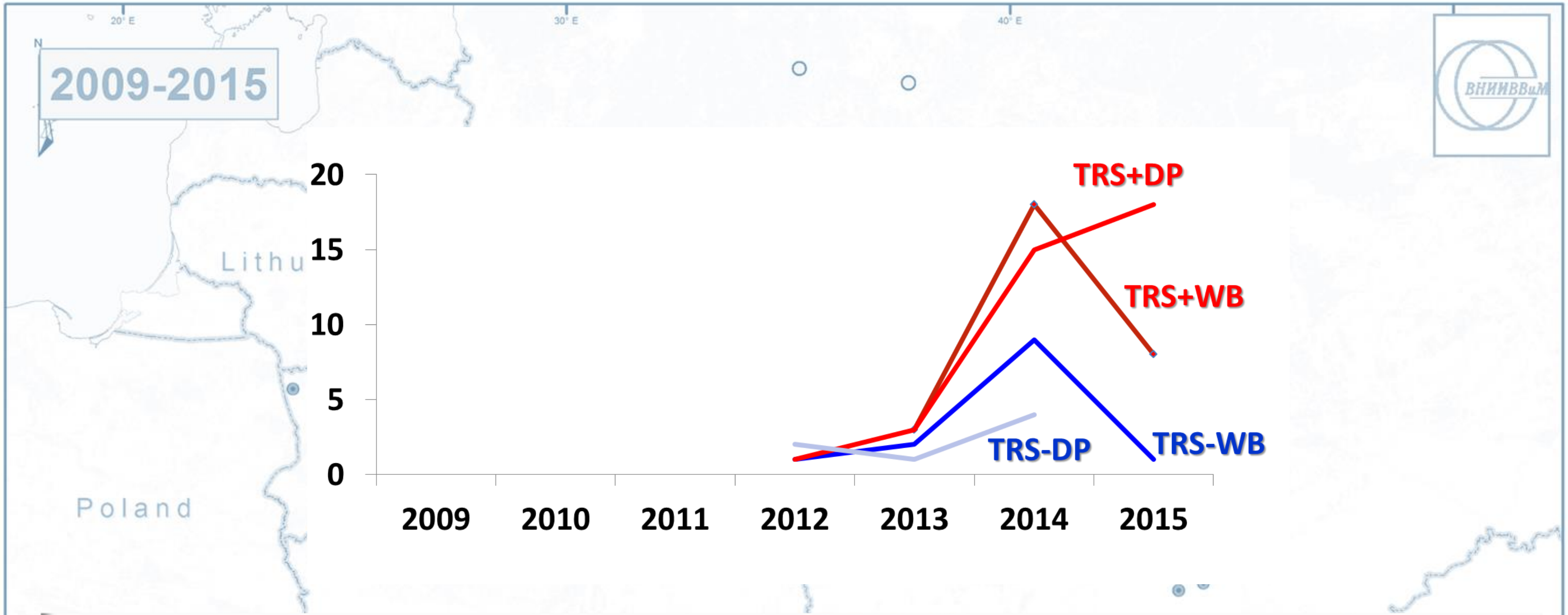


2009-2015

Tandem Repeat Insertion in African Swine Fever Virus, Russia, 2012

Katja V. Goller,[1] Alexander S. Malogolovkin,[1] Sergey Katorkin, Denis Kolbasov, Ilya Titov, Dirk Höper, Martin Beer, Günther M. Keil, Raquel Portugal, Sandra Blome

ASF IN EASTERN EUROPE



- ASFV isolates **with TRS insertion (TRS+) prevail among current disease outbreaks** (88 Russian ASFV isolates sequenced)
- ASFV with TRS insertion was found in domestic and wild boars population
- ASFV isolates with/without TRS insertion spread across Russia randomly

CVR subtyping of Eastern EU ASFV

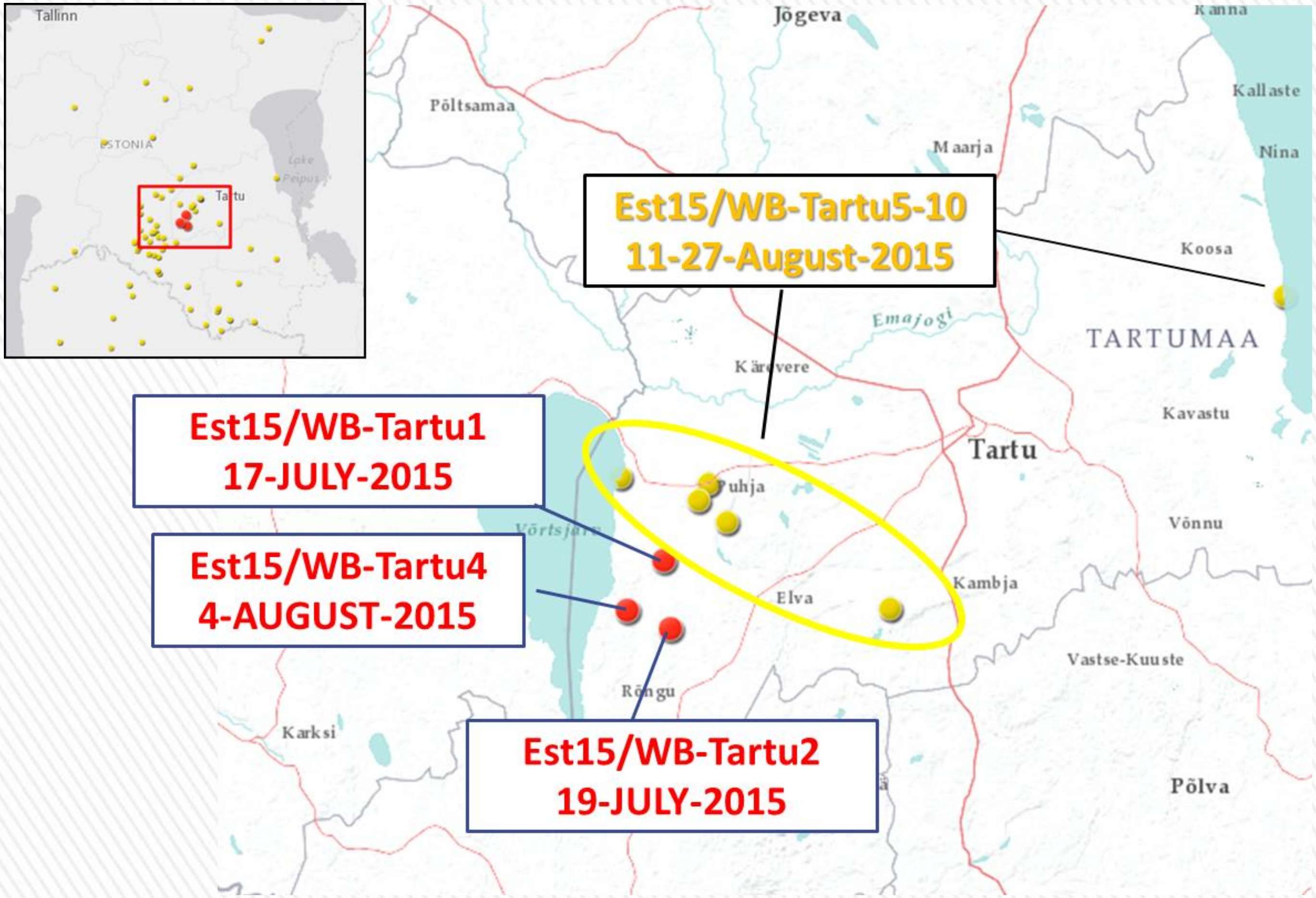
```
Est15/WB-Valga-9        SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-Valga-10       SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-Parnu1         SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-Vil22          SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-IDA2           SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-Tartu1         SAYTCADTNVDTCASMCADTNVDT------------CASTCTSTEY
Est15/WB-Tartu2         SAYTCADTNVDTCASMCADTNVDT------------CASTCTSTEY
Est15/WB-Tartu3         SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-Tartu4         SAYTCADTNVDTCASMCADTNVDT------------CASTCTSTEY
Est15/WB-Tartu5         SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-Tartu6         SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-VORU-10        SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-POLVA-1        SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-RAPLA-1        SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/WB-JARVA1         SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/DP-Tartu1         SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/DP-Vil1           SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/DP-Vil2           SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/DP-VALGA1         SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/DP-Vil3           SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
Est15/DP-VALGA2         SAYTCADTNVDTCASMCADTNVDTCASMCADTNVDTCASTCTSTEY
```

New CVR genetic variant found in Estonia: This CVR variant is characterized by the deletion of three aminoacid tetramer repeats (CASMCADTNVDT)

July 2015

ASF IN EASTERN EUROPE

Using standardized subtyping procedures: Co-circulation of two different CVR variants in the same region in Estonia within the wild boar population.



Est15/WB-Tartu5-10
11-27-August-2015

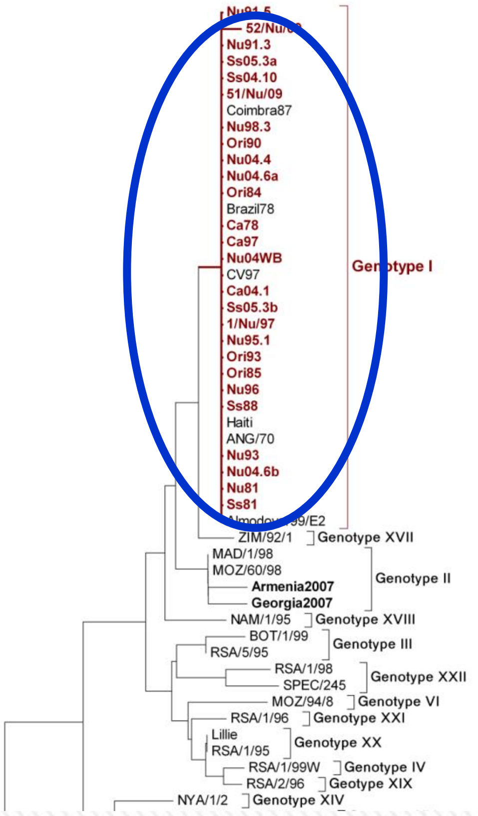
Est15/WB-Tartu1
17-JULY-2015

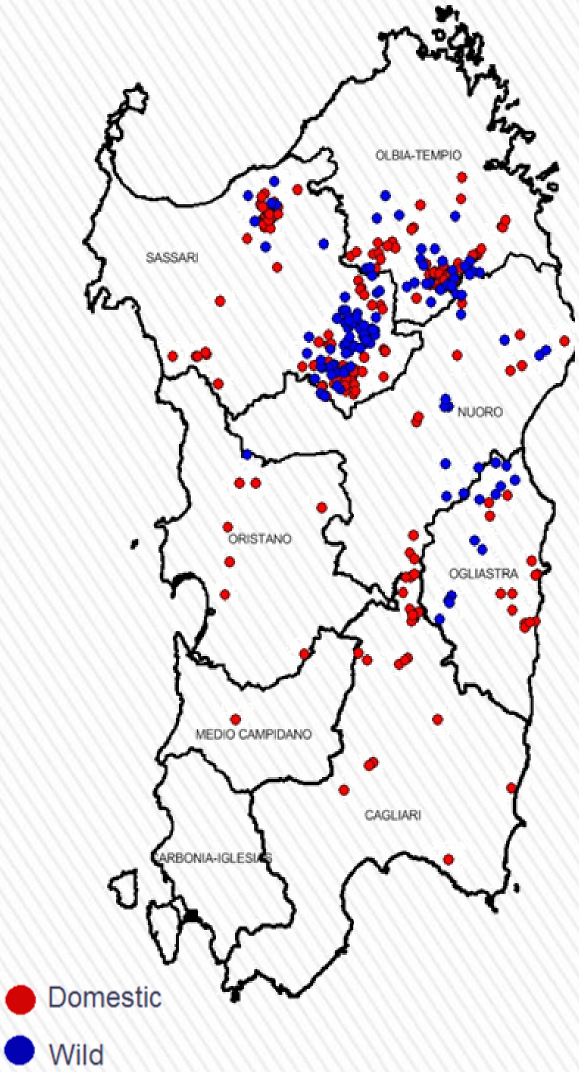
Est15/WB-Tartu4
4-AUGUST-2015

Est15/WB-Tartu2
19-JULY-2015

ASF IN SARDINIA

What´s about Sardinia?





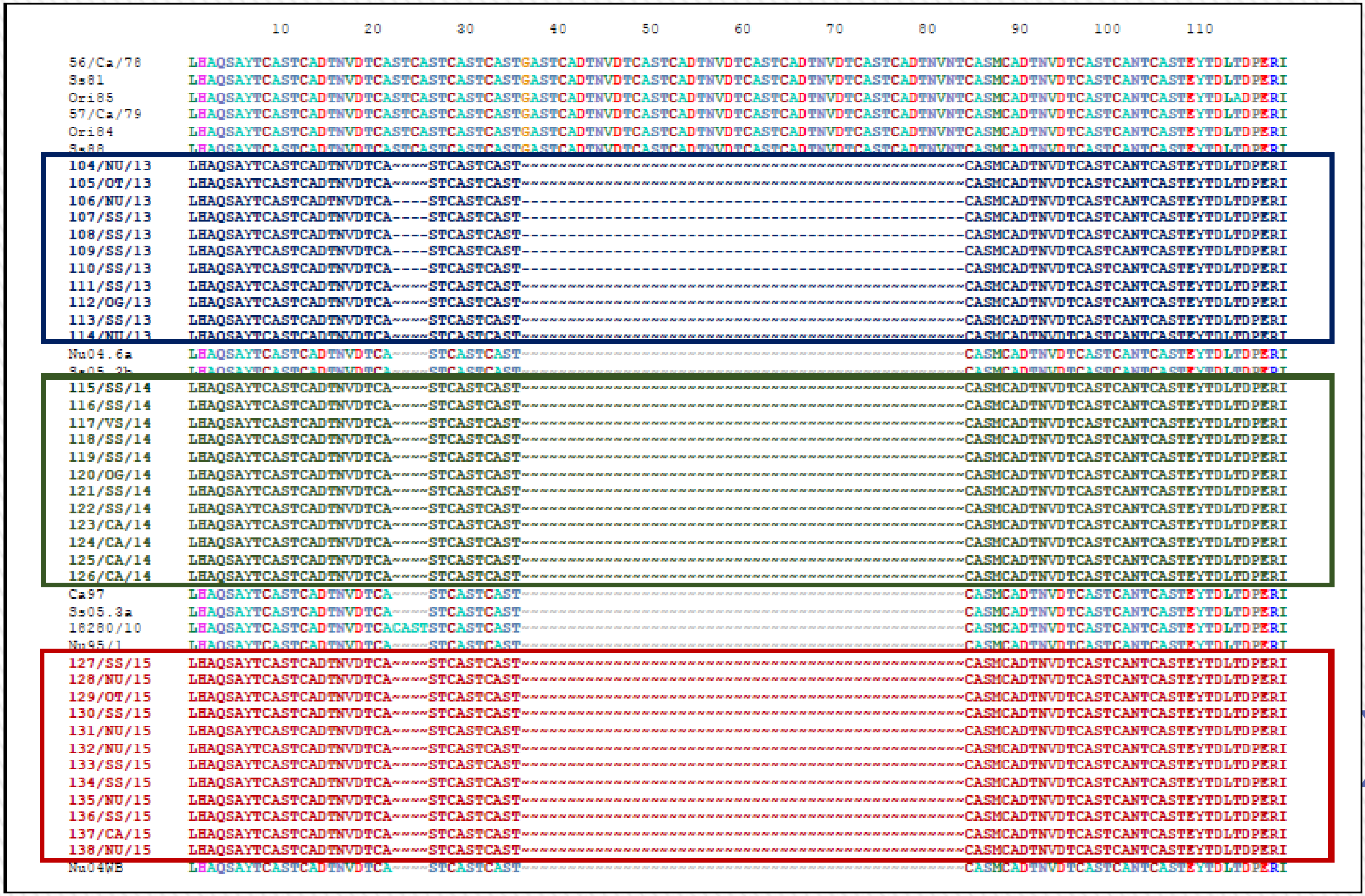
ASFV p72 genotype I

circulating in both wild and domestic pigs→

SINGLE INTRODUCTION 1978

P72 GENOTYPE	P54 GENOTYPE	CVR SUBTYPING	YEARS
I	I a	III	1978-1997
I	I a	X	1997-2014

No recent genetic changes, same CVR variant (gene *B602L*) present since 90´s



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                    10        20        30        40        50        60        70        80        90       100       110
56/Ca/78    LHAQSAYTCASTCADTNVDTCASTCASTCASTCASTGASTCADTNVDTCASTCADTNVDTCASTCADTNVDTCASTCADTNVNTCASMCADTNVDTCASTCANTCASTEYTDLTDPERI
Ss81        LHAQSAYTCASTCADTNVDTCASTCASTCASTCASTGASTCADTNVDTCASTCADTNVDTCASTCADTNVDTCASTCADTNVNTCASMCADTNVDTCASTCANTCASTEYTDLTDPERI
Ori85       LHAQSAYTCASTCADTNVDTCASTCASTCASTCASTGASTCADTNVDTCASTCADTNVDTCASTCADTNVDTCASTCADTNVNTCASMCADTNVDTCASTCANTCASTEYTDLADPERI
57/Ca/79    LHAQSAYTCASTCADTNVDTCASTCASTCASTCASTGASTCADTNVDTCASTCADTNVDTCASTCADTNVDTCASTCADTNVNTCASMCADTNVDTCASTCANTCASTEYTDLTDPERI
Ori84       LHAQSAYTCASTCADTNVDTCASTCASTCASTCASTGASTCADTNVDTCASTCADTNVDTCASTCADTNVDTCASTCADTNVNTCASMCADTNVDTCASTCANTCASTEYTDLTDPERI
Ss88        LHAQSAYTCASTCADTNVDTCASTCASTCASTCASTGASTCADTNVDTCASTCADTNVDTCASTCADTNVDTCASTCADTNVNTCASMCADTNVDTCASTCANTCASTEYTDLTDPERI
104/NU/13   LHAQSAYTCASTCADTNVDTCA~~~~STCASTCAST~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~CASMCADTNVDTCASTCANTCASTEYTDLTDPERI
105/OT/13   LHAQSAYTCASTCADTNVDTCA~~~~STCASTCAST~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~CASMCADTNVDTCASTCANTCASTEYTDLTDPERI
106/NU/13   LHAQSAYTCASTCADTNVDTCA----STCASTCAST------------------------------------------------CASMCADTNVDTCASTCANTCASTEYTDLTDPERI
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112/OG/13   LHAQSAYTCASTCADTNVDTCA~~~~STCASTCAST~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~CASMCADTNVDTCASTCANTCASTEYTDLTDPERI
113/SS/13   LHAQSAYTCASTCADTNVDTCA~~~~STCASTCAST~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~CASMCADTNVDTCASTCANTCASTEYTDLTDPERI
114/NU/13   LHAQSAYTCASTCADTNVDTCA~~~~STCASTCAST~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~CASMCADTNVDTCASTCANTCASTEYTDLTDPERI
Nu04.6a     LHAQSAYTCASTCADTNVDTCA~~~~STCASTCAST~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~CASMCADTNVDTCASTCANTCASTEYTDLTDPERI
Ss05.2b     LHAQSAYTCASTCADTNVDTCA~~~~STCASTCAST~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~CASMCADTNVDTCASTCANTCASTEYTDLTDPERI
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ASFV: MOLECULAR CHARACTERIZATION

Summary

COUNTRY	YEAR	P72 GENOTYPE	CVR SUBTYPING	INTERGENIC SUBTYPING
Georgia	2007	II	GII-CVR1	GII-IGR1
Armenia	2007	II	GII-CVR1	GII-IGR1
Azerbaijan	2008	II	GII-CVR1	GII-IGR1
Russia Federation	2007-2012 (EURL)	II	GII-CVR1	GII-IGR1
	2012-2015 (Pokrov)	II	GII-CVR1	GII-IGR1 + GII-IGR2
Ukraine	2012, 2015	II	GII-CVR1	GII-IGR2
Belarus	2013	II	GII-CVR1	GII-IGR2
Lithuania	2014-2015	II	GII-CVR1	GII-IGR2
Poland	2014-2015	II	GII-CVR1	GII-IGR2
Latvia	2014-2015	II	GII-CVR1	GII-IGR2
Estonia	2014	II	GII-CVR1	GII-IGR2
	2015	II	GII-CVR1 + GII-CVR2	GII-IGR2
Sardinia	1978-1997	I	GI-CVRIII	
	1997-2015	I	GI-CVRX	

EURL SEQUENCE DATABASE

Welcome to the African Swine Fever Virus Sequence Database

Genetic typing in combination with epidemiological findings is an essential method for tracing relations between outbreaks of ASF and to trace the dynamic of the disease. In this context, a computerized database containing all available information concerning the African swine fever (ASF) virus strains and isolates kept in the EU Reference Laboratory (EU-RL) has been established and is being continuously updated upon arrival of new isolates. **The purpose is to compile sequence information of the ASFV isolates from all epidemics in or near the European Union, as well as from all over the world and to make the data available to other laboratories for the rapid typing of isolates from new outbreaks.**

VIRUS DATABASE

SEARCH

Virus name:
Region: <Any>
Country of origin: <Any>
Date of outbreak:
Host Species: <Any>
Gene: <Select>
P72 genotype:

Checked Sequences: View in browser or Download in FASTA format

☐	Virus name	Host Species	Scientific Name	Date of outbreak	Region	Country of origin	Sampling Location		
							Locality	Department	Province
No results to show, please, select a Gene.									

Checked Sequences: View in browser or Download in FASTA format

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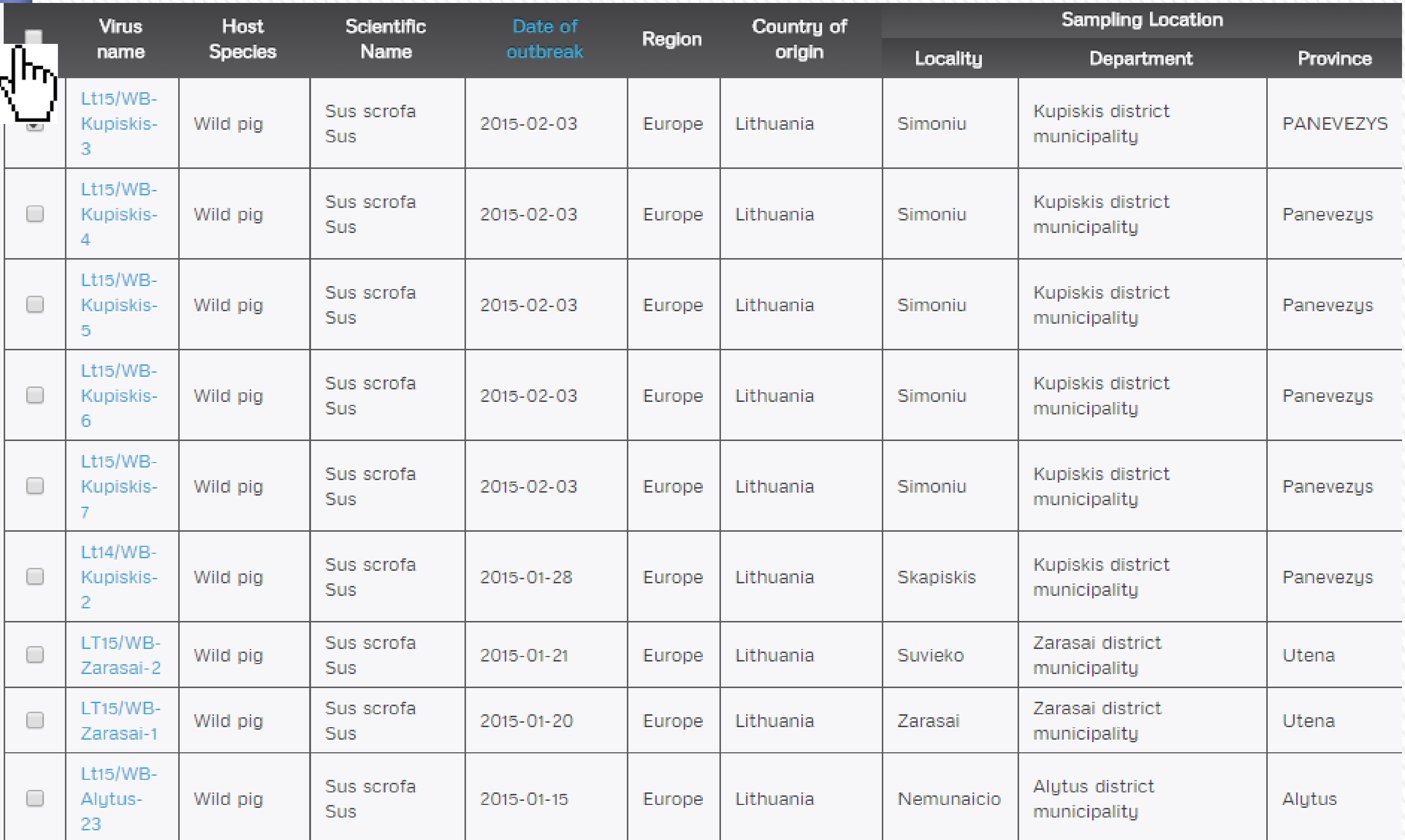
Web by interbionet.com

The data base includes sequence information of **three defined regions of ASFV genome** using for classical genotyping comprising: i) partial sequence of the C-terminal end of the gene *B646L* encoding the major protein p72 (Bastos et al., 2003) which allow us to classify the ASFV in 22 major genotypes (Boshoff et al., 2007), ii) to sequence the full E183L-gene encoding the p54 protein (Gallardo et al., 2009) as a valuable additional genotyping method for molecular epidemiological studies of each p72 genotype viruses, and iii) the sequencing of the central variable region within B602L-gene (CVR) characterized by the presence of amino acid tandem repeats (Nix et al., 2006; Gallardo et al., 2011). The CVR remains the genome target of choice when attempting to determine the origin and map the spread of closely related virus.

Apart from the sequences, it contains epidemiological data for more than 500 ASFV isolates such as the year of isolation, country, region, and host species, which are necessary for identifying new isolates. Individual p72, p54 and/or CVR sequences can be downloading and exported for further use, i.e. for performing the alignment and for calculating the phylogenetic tree.

To access to the sequence data base is required a user name and a password, which can be obtained by sending an EMAIL to the eurl.asf@inia.es

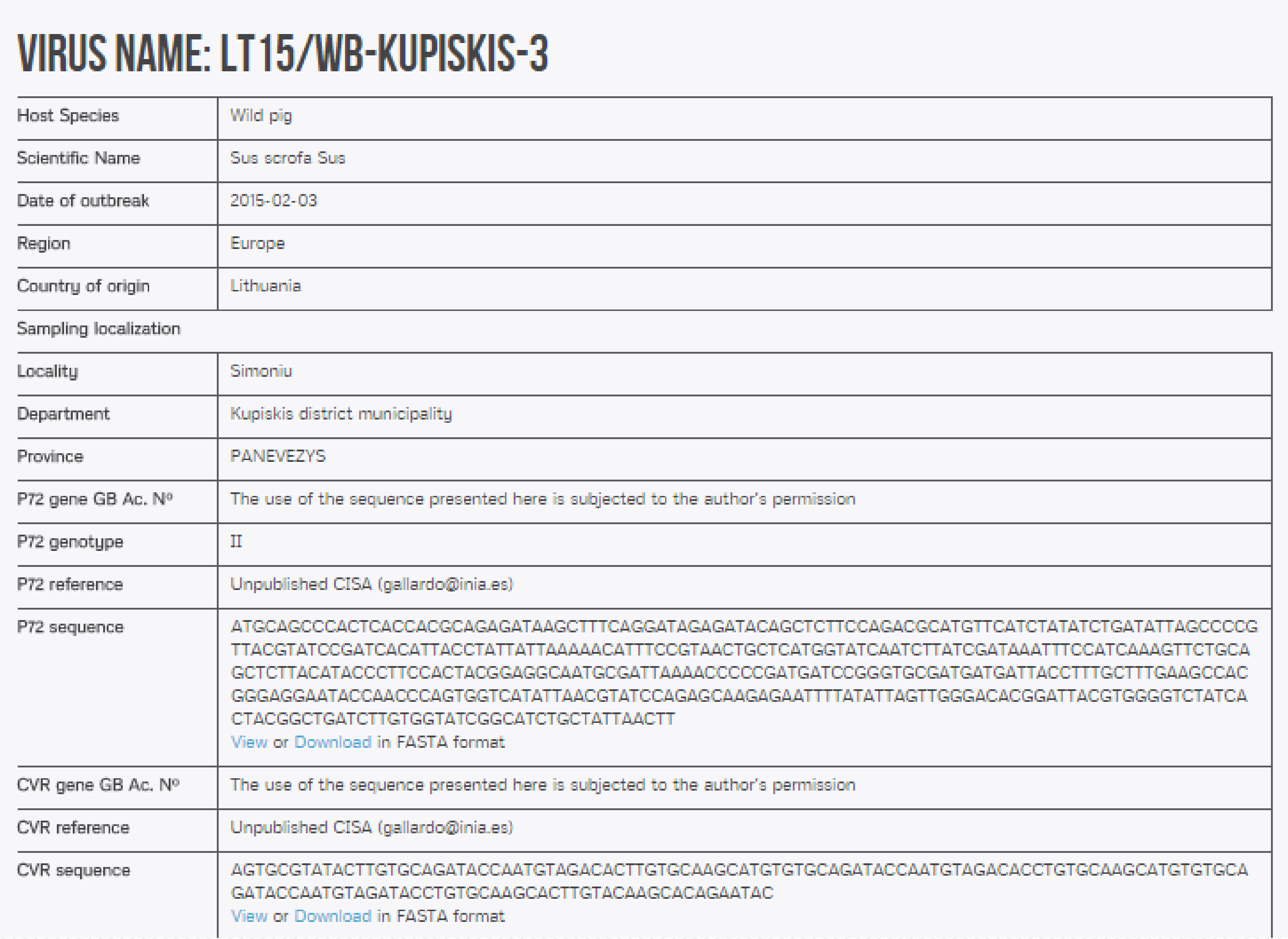
EURL SEQUENCE DATABASE



☐	Virus name	Host Species	Scientific Name	Date of outbreak	Region	Country of origin	Sampling Location		
							Locality	Department	Province
☐	Lt15/WB-Kupiskis-3	Wild pig	Sus scrofa Sus	2015-02-03	Europe	Lithuania	Simoniu	Kupiskis district municipality	PANEVEZYS
☐	Lt15/WB-Kupiskis-4	Wild pig	Sus scrofa Sus	2015-02-03	Europe	Lithuania	Simoniu	Kupiskis district municipality	Panevezys
☐	Lt15/WB-Kupiskis-5	Wild pig	Sus scrofa Sus	2015-02-03	Europe	Lithuania	Simoniu	Kupiskis district municipality	Panevezys
☐	Lt15/WB-Kupiskis-6	Wild pig	Sus scrofa Sus	2015-02-03	Europe	Lithuania	Simoniu	Kupiskis district municipality	Panevezys
☐	Lt15/WB-Kupiskis-7	Wild pig	Sus scrofa Sus	2015-02-03	Europe	Lithuania	Simoniu	Kupiskis district municipality	Panevezys
☐	Lt14/WB-Kupiskis-2	Wild pig	Sus scrofa Sus	2015-01-28	Europe	Lithuania	Skapiskis	Kupiskis district municipality	Panevezys
☐	LT15/WB-Zarasai-2	Wild pig	Sus scrofa Sus	2015-01-21	Europe	Lithuania	Suvieko	Zarasai district municipality	Utena
☐	LT15/WB-Zarasai-1	Wild pig	Sus scrofa Sus	2015-01-20	Europe	Lithuania	Zarasai	Zarasai district municipality	Utena
☐	Lt15/WB-Alytus-23	Wild pig	Sus scrofa Sus	2015-01-15	Europe	Lithuania	Nemunaicio	Alytus district municipality	Alytus

ASFV: MOLECULAR CHARACTERIZATION

EU Reference Laboratory for ASF
Animal Health Research Centre
(CISA), INIA
Ctra Algete-El Casar s/n
28130, Valdeolmos, Spain



VIRUS NAME: LT15/WB-KUPISKIS-3

Host Species	Wild pig
Scientific Name	Sus scrofa Sus
Date of outbreak	2015-02-03
Region	Europe
Country of origin	Lithuania
Sampling localization	
Locality	Simoniu
Department	Kupiskis district municipality
Province	PANEVEZYS
P72 gene GB Ac. Nº	The use of the sequence presented here is subjected to the author's permission
P72 genotype	II
P72 reference	Unpublished CISA (gallardo@inia.es)
P72 sequence	ATGCAGCCCACTCACCACGCAGAGATAAGCTTTCAGGATAGAGATACAGCTCTTCCAGACGCATGTTCATCTATATCTGATATTAGCCCCG TTACGTATCCGATCACATTACCTATTATTAAAAACATTTCCGTAACTGCTCATGGTATCAATCTTATCGATAAATTTCCATCAAAGTTCTGCA GCTCTTACATACCCTTCCACTACGGAGGCAATGCGATTAAAACCCCCGATGATCCGGGTGCGATGATGATTACCTTTGCTTTGAAGCCAC GGGAGGAATACCAACCCAGTGGTCATATTAACGTATCCAGAGCAAGAGAATTTTATATTAGTTGGGACACGGATTACGTGGGGTCTATCA CTACGGCTGATCTTGTGGTATCGGCATCTGCTATTAACTT View or Download in FASTA format
CVR gene GB Ac. Nº	The use of the sequence presented here is subjected to the author's permission
CVR reference	Unpublished CISA (gallardo@inia.es)
CVR sequence	AGTGCGTATACTTGTGCAGATACCAATGTAGACACTTGTGCAAGCATGTGTGCAGATACCAATGTAGACACCTGTGCAAGCATGTGTGCA GATACCAATGTAGATACCTGTGCAAGCACTTGTACAAGCACAGAATAC View or Download in FASTA format

CONCLUSIONS

EAST EUROPE

- **Single ASFV p72 genotype II** circulating since 2007 up to now in both wild and domestic pigs; **single introduction in East Europe in 2007.**

Identification of A NEW GENETIC MARKER TO TRACE THE DYNAMIC OF THE INFECTION (I73R/I329L intergenic region)

Presence of **two genetic variants co-circulating in Russian Federation** being the **variant emerged in 2012** the one circulating in the four affected **EU countries**.

CONCLUSIONS

EAST EUROPE

- By the use of standardized subtyping procedures **two genetic variants co-circulating in Estonia** has been recently identified **within the wild boar population**.

SARDINIA

- **Single ASFV p72 genotype I** circulating in both wild and domestic pigs; **single introduction in Sardinia in 1978.**
- **No genetic changes** has been identified in the last years by the use of standardized subtyping procedures with the **same variant present since 90´s**

It would be desired to identify further genetic markers for a more precise tracing of the ASFV spread and for a deeper understanding of the epidemiology of the disease.

efsa

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MINISTERIO DE ECONOMÍA Y COMPETITIVIDAD

INIA Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria

THANK YOU!

ASFORCE

TARGETED RESEARCH EFFORT ON AFRICAN SWINE FEVER

PIWet

BIOR

INSTITUTE OF FOOD SAFETY, ANIMAL HEALTH AND ENVIRONMENT

Istituto Zooprofilattico Sperimentale Umbria Marche

BELARUS

UKRAINE

ВНИИВВиМ