

INITIAL INVESTIGATION OF A SUSPICIOUS BIOLOGICAL EVENT-CASE STUDY OF ASF IN SPAIN



Strengthening Preparedness and Response to Biological Threats in Europe

23–25 March 2026

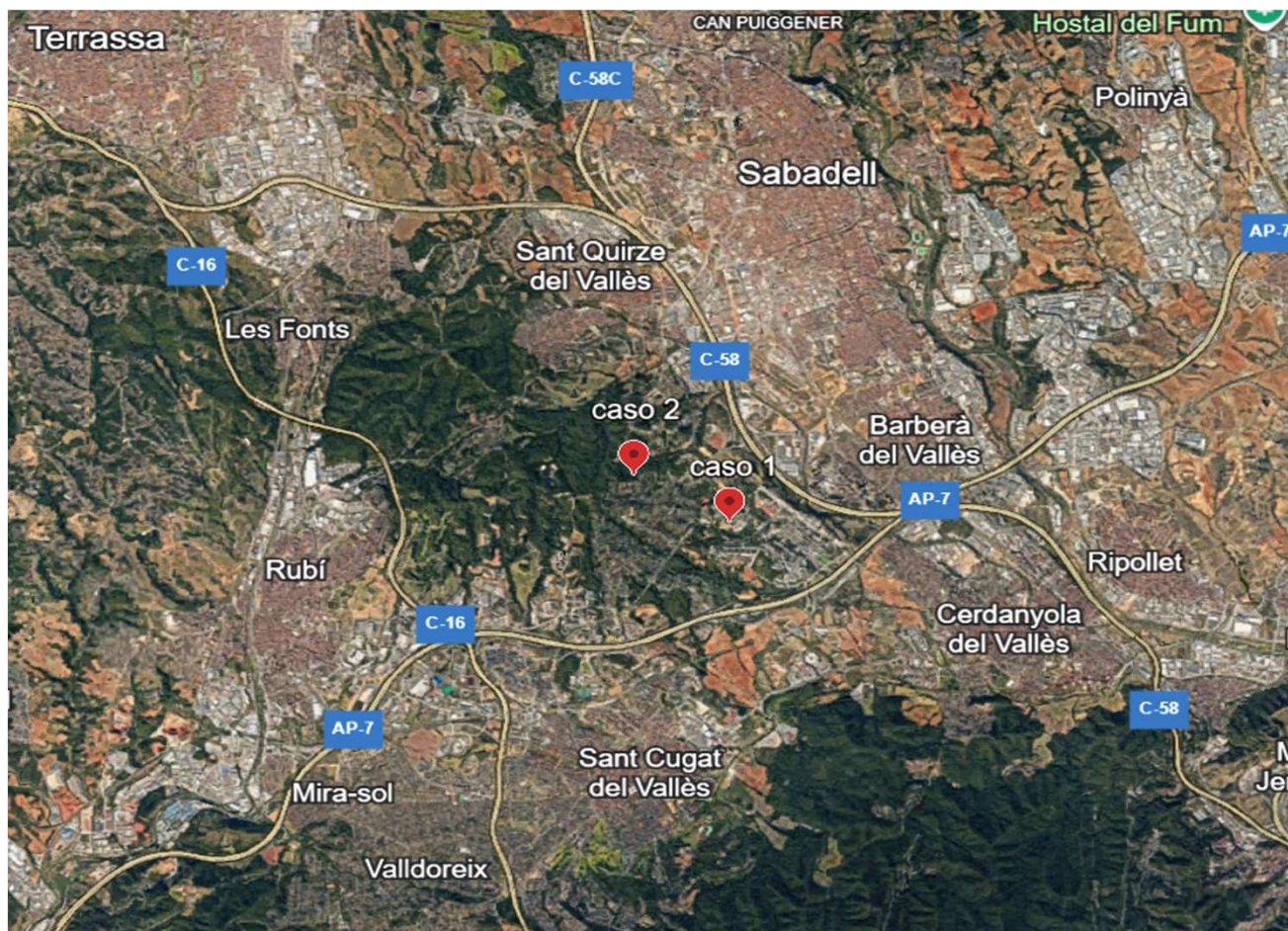
WOAH Headquarters, Paris, France

First cases detected in Cataluña

- 25 & 26/11/2025 – Detection of **two wild boar carcasses**, 1 km apart, near the campus of the Autonomous University of Barcelona, in Cerdanyola del Vallès municipality (Barcelona province).
- Carcasses in fresh conditions. Finding later of carcasses in older conditions → **Estimated entrance of the virus in late October in Spain.**
- Samples taken for analysis at the IRTA-CReSA laboratory → **Positive result in PCR** (26/11/2025) → Samples sent for confirmation in NRL.
- 27/11/25 – Sample reception and analysis at the LCV of Algete (NRL) → Positive PCR → **Confirmation of the presence of the African swine fever virus in Spain since its eradication in 1994.**
- Necropsy of the wild boars at the IRTA-CReSA laboratory → **Clear lesions consistent with African swine fever (ASF).**
- 28/11/2025 – Sequencing at the Algete National Laboratory → **Genotype II confirmed.**



First cases detected in Cataluña



- **Moderately dense forest area**
- **Moderate density of wild boar** in the area (about 4-5 WB/Km²)
- **Urban and residential neighborhoods** surrounding forest areas → Challenge in implementing many control measures.
- Presence of **fenced-highways and major roads** that delimit the area
- **Low density of pig farms** → total number of 57 pig holdings (of them, 41 were commercial) → Visit by OVS and enhancement of passive surveillance → **Pig sector remains unaffected so far.**

First cases detected in Cataluña

- Detection of a wild boar carcass on a **private garden with dense vegetation in a residential neighborhood** in the municipality of Cerdanyola del Vallès.
- The garden is **partially fenced** and has a known **permanent wild boar population**.
- **Daily garbage** is deposited in loose bins, which WB access to.
- It was adopted **partial restricted access to the area, which was cordoned off** by authorities.
- The following day, a second wild boar carcass was discovered **near the UAB campus**, approximately 1 km from the first.



Implemented control measures

- **Isolation of affected or potentially affected wild boar populations:** fences and enclosures anchored to the ground in critical passage areas, cattle grids, etc.
- **Active search for carcasses in the Infected Zone (IZ).** Large deployment of **trained search dogs** from various units and agencies.
- **Limited and restricted access** of non-authorized personnel to the area.
- Coordination between authorities & personnel: **UME (Militar Emergency Unit)**, **Civil Guard** (National Police), **Mossos d'Esquadra** (regional police), **local police**, **trained hunters**...
- **Hunting and other activities are prohibited in the high-risk zone (0-6 km) to prevent the dispersal of wild boar outside the IZ.**
- **Population control measures in the high-risk zone (0-6km) using silencers and thermal cameras**, carried out by members of the rural agents, SEPRONA (Nature Protection Service of the Civil Guard) and/or UME.
- **Reinforcement of hunting activities with trained and authorized hunters** by the Official Services (Wildlife Control Service), from February 7th, in some areas of the low-risk zone (12-20 km) to create a "white zone," without wild boar or with the lowest possible density, to reduce the risk of virus transmission to this area should any infected wild boar escape from the high-risk zone.
- Installation of **pig-brig traps** to increase the capture of wild boars in different areas depending on the success of the captures, in the quietest way possible.

Implemented control measures: Enhancement of carcass searches with trained dogs



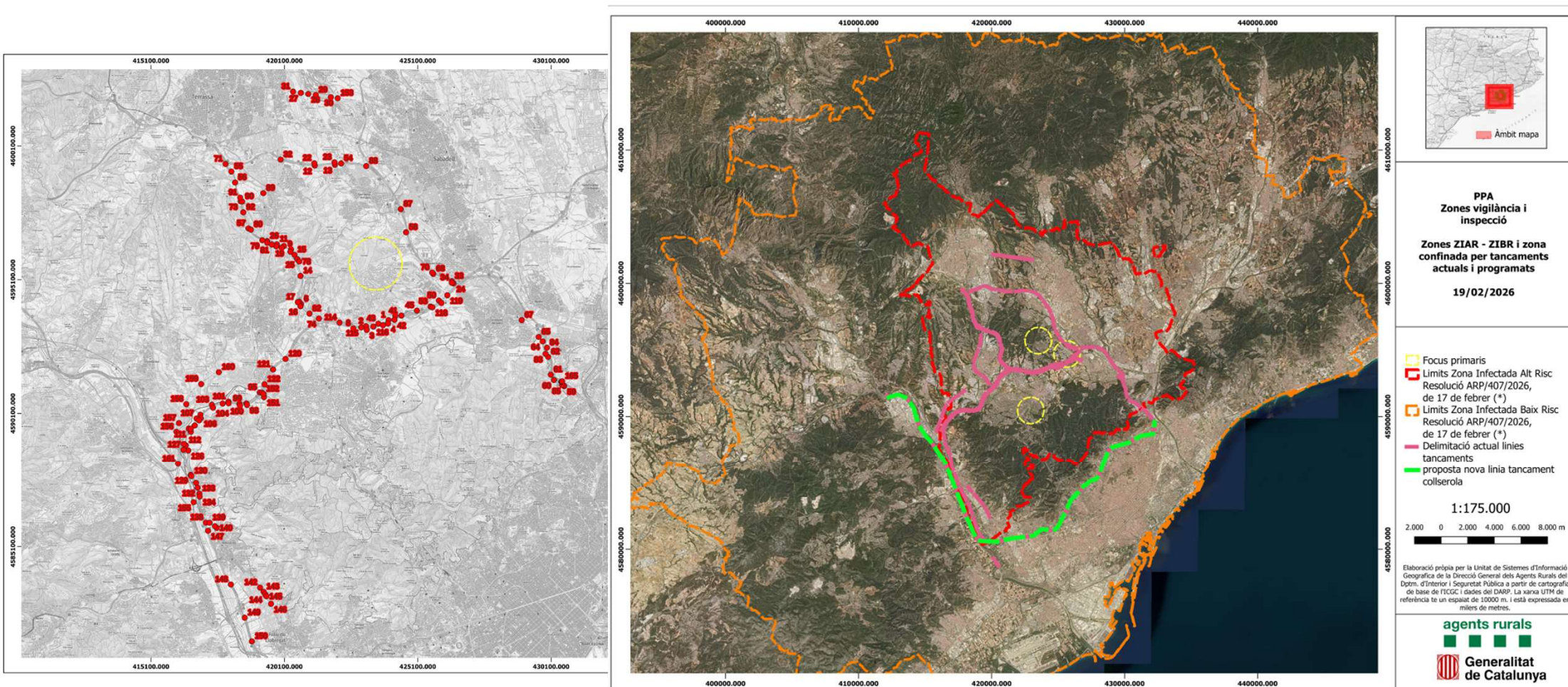
Teams using trained-search dogs (Agents Rurals, Guardia Civil, C. Madrid, Andorra, etc)

Implementation of a White Zone

Adoption of a wide and continuous **White Zone** (a strip clear of wild boar within the High-Risk Zone), meeting the characteristics proposed by the models (Lange et al. 2021) and by the analyses of European wild boar movement (Wielgus et al. 2025) **towards both north and south areas around the high-risk zone:**

- **At a safe distance from the high-risk zone.** Taking into account the rate of spread, the local density of wild boar, and the time horizon (capacity) of the planned depopulation measures.
- **Width of the White Zone** that prevents infected wild boar that may leave the high-risk zone from coming into contact with susceptible wild boar.
- **Remove the maximum amount of the population in the shortest possible time.** Furthermore, the wild boar in the area entered their rutting season in November and the birth of the young is expected in March (population resurgence must be avoided with reinforcement of population control activities).

Implemented control measures: fences



Implemented control measures: challenges with fences



Sabotage of fences, and substitution for tramex points

Implemented control measures: fences



Implemented control measures: UME Control Center and C&D installations



Vehicle C&D unit from IZ at the UME control center in Torreferrusa



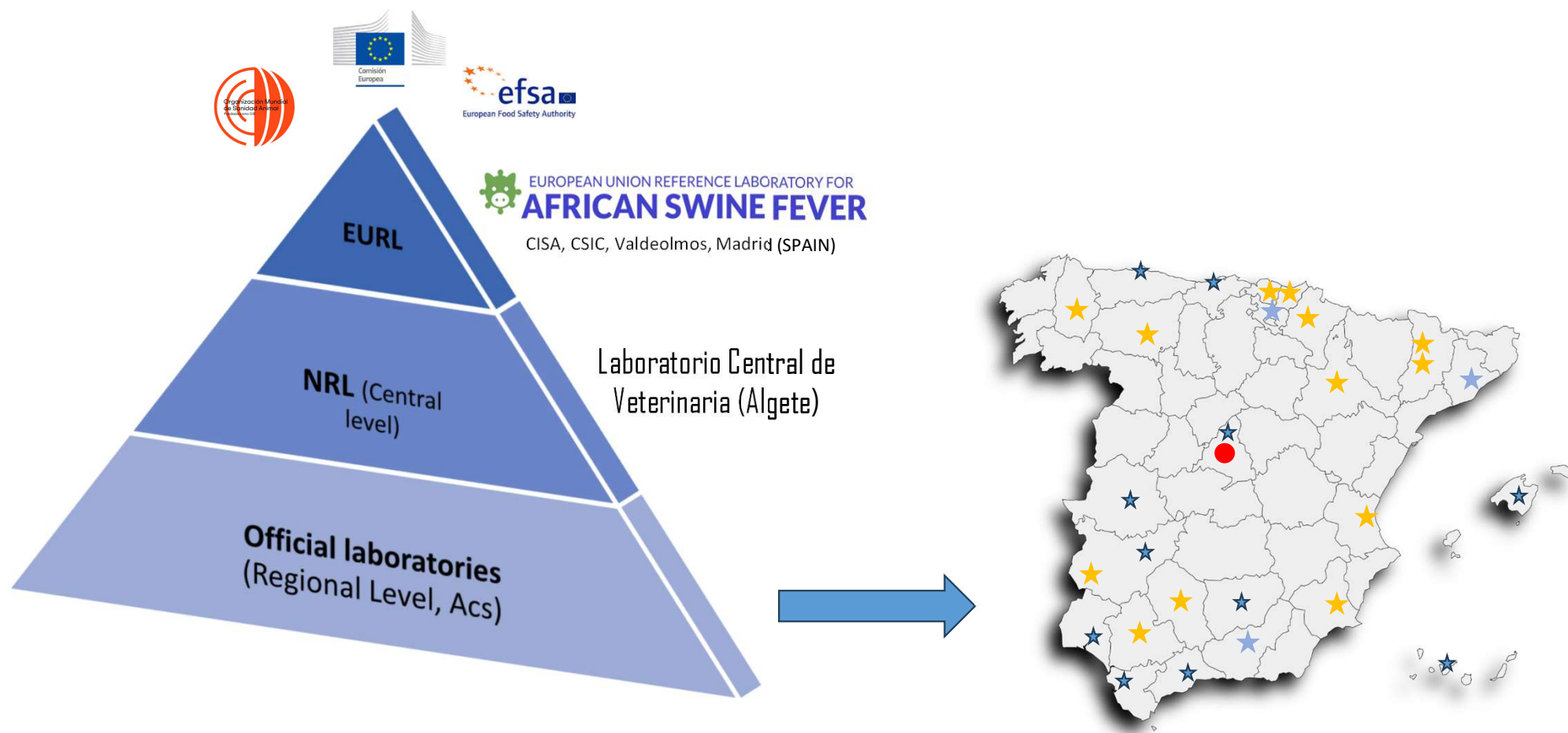
*Installation for the C&D of
trained dogs after searches*



Implemented control measures: pig-brig traps



African Swine Fever laboratory network



Laboratory diagnosis and characterisation and monitoring of ASF outbreak 2025-2026



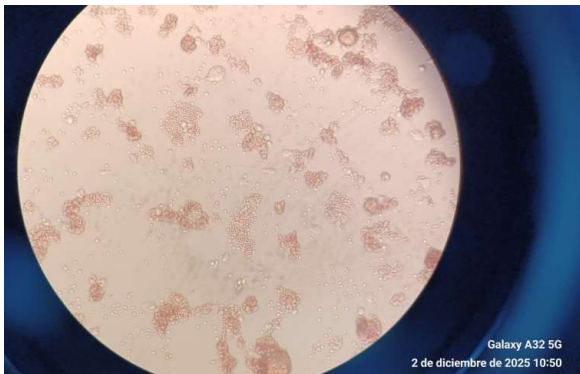
Laboratory diagnosis of index case at the NRL (LCV- Algete): outbreaks 1 and 2.

November 26th (evening): Notice that we will be receiving samples that have tested PCR positive in the official laboratory (IRTA-CreSa, Catalonia)

November 27th (18:30): two EDTA blood samples received at the NRL
(21:30): PCR results on EDTA blood samples (confirmed as **POSITIVE**)

November 28th (09:00): PCR results report is issued
(15:00): Partial sequencing Gen B646L (p72), Gen E183L (p54) and Gen B602L (CVR). Characterized as **GENOTYPE II**
(morning): primary monocyte culture preparation

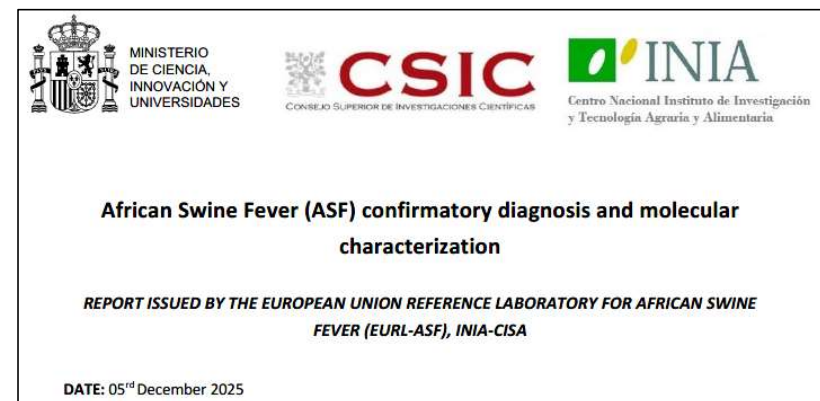
December 01st (morning): inoculation on primary monocyte culture
(confirmed as POS next day; presence of **Haemadsorbant Virus**)



Molecular characterization of ASFv Spain 2025

ASFv SPAIN 2025:

- **Genotype II** (as all virus currently circulating in EU)
- **Novel genetic group 29** (novel group close to genetic group Georgia 2007)
- **Differences between ASFv Spain 2025 and Georgia 2007:**
 - **30 changes** (single nucleotide polymorphism mutations and short insertions and deletions)
 - **1 large deletion** (around 10,000 pb) in the terminal left variable region)



EURL
December 5th 2025

Virus sequence is published in **GenBank** database and in a peer-reviewed **scientific journal**

COMMUNICATION: A NEW CHALLENGE



MINISTERIO
DE AGRICULTURA, PESCA
Y ALIMENTACIÓN



En el marco del cumplimiento de la norma de la Unión Europea (UE)

El Ministerio de Agricultura, Pesca y Alimentación abre una investigación complementaria sobre el origen del virus de la peste porcina africana en España

05 de diciembre de 2025. El Ministerio de Agricultura, Pesca y Alimentación abre una nueva investigación sobre el origen de la peste porcina africana (PPA) en España, tras haber recibido hoy el informe del laboratorio de referencia de la UE en el que se comunican los resultados de secuenciación del genoma del virus de la PPA.

Se trata de una investigación complementaria a la iniciada el pasado 28 de noviembre, fecha en la que se detectó el brote de peste porcina africana en Cerdanyola del Vallés (Barcelona).

El informe del Centro de Investigación en Sanidad Animal (CISA-INIA), de Valdeolmos (Madrid), laboratorio de referencia de la UE, recoge la caracterización molecular por secuenciación del genoma del virus de la PPA y los compara con los distintos virus de peste porcina africana detectados en toda la Unión Europea.

Todos los virus circulantes en la actualidad en los Estados miembros pertenecen a los grupos genéticos 2-28 y no al nuevo grupo genético 29 al que pertenece el virus causante del foco en la provincia de Barcelona -muy similar al grupo genético 1 que circuló en Georgia en 2007-.

Los virus, en condiciones naturales, cuando se propagan mediante ciclos de infección en animales sufren en mayor o menor medida cambios en su genoma. El hallazgo de un virus similar al que circuló en Georgia no excluye, por tanto, que su origen pueda estar en una instalación de confinamiento biológico.

La cepa del virus "Georgia 2007" es un virus de "referencia" que se utiliza con frecuencia en infecciones experimentales en instalaciones de confinamiento para realizar estudios del virus o para evaluar la eficacia de las vacunas, que actualmente están en fase de desarrollo.

Del informe se deduce que cabe la posibilidad de que el origen del virus no esté en animales o productos de origen animal provenientes de alguno de los países en los que actualmente está presente la infección.

Por ello, la Dirección General de Sanidad de la Producción Agroalimentaria y Bienestar Animal del Ministerio de Agricultura, Pesca y Alimentación ha iniciado las siguientes actuaciones:

- 1) Comunicar al Servicio de Protección de la Naturaleza (SEPRONA) de la Guardia Civil la necesidad de investigar estos hechos, como autoridad competente para la investigación de posibles infracciones o delitos medioambientales.
- 2) Iniciar un procedimiento de investigación del origen del virus en el marco del artículo 57.2 del Reglamento (UE) 2016/429, del Parlamento Europeo y del Consejo, de 9 de marzo de 2016.

PRESS RELEASE

The Ministry of Agriculture, Fisheries and Food opens a complementary investigation on the origin of the ASF virus in Spain

All viruses currently circulating in the Member States do not belong to the new **genetic group 29** to which the virus causing the outbreak in the province of Barcelona belongs - very similar to genetic group 1 that circulated in Georgia in 2007.

Viruses, under natural conditions, when spread through cycles of infection in animals undergo changes in their genome to a greater or lesser extent. The finding of a virus similar to the one that circulated in Georgia **does not, therefore, exclude that its origin may be in a biological confinement facility.**

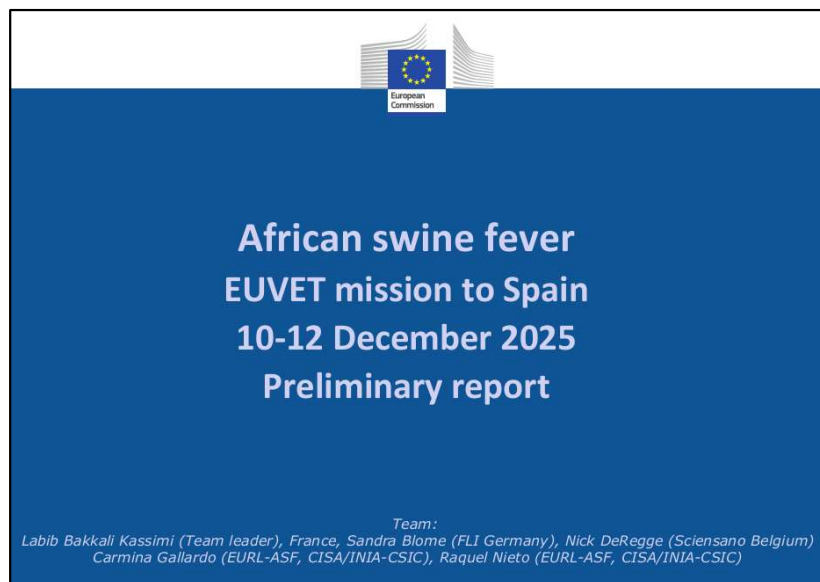
The “Georgia 2007” virus strain is a “reference” virus that is frequently used in experimental infections in confinement facilities to conduct virus studies or to evaluate the efficacy of vaccines, which are currently under development.

For this reason, the Directorate-General for Health of Agri-Food Production and Animal Welfare of the Ministry of Agriculture, Fisheries and Food has initiated the following actions:

- **Communicate to the Nature Protection Service (SEPRONA) of the Guardia Civil (Civil Guard)** the need to investigate these facts, as the competent authority for the investigation of possible infringements or environmental crimes.
- Initiate **an investigation procedure** for the origin of the virus in the framework of Article 57(2) of Regulation (EU) 2016/429, of the European Parliament and of the Council of 9 March 2016.

Origin of virus strain: hypothesis and lab. investigation

EU Veterinary Emergency Team (EUvet) - laboratories.



PAFF Animal Health and Welfare committee
December 15-16, 2025

Main conclusion: “Based on the data presented, the **EUVET** team **could not identify any obvious route** by which the **virus** **could have been released from the IRTA-CReSA facilities**”.

Main recommendations:

- Perform **sequencing analysis** of samples collected from **outbreaks** to **follow up the virus variation** (ongoing by the NRL and EURL)
 - Analytical approach: Implementation of partial (Sanger) sequencing of virus to identified **relevant mutations (SNPs)** and a real time PCR for detection and screening for the **deletion** observed in the 5' end of the virus genome.
- Perform sequencing analysis (Sanger and or WGS) of **relevant viruses available in IRTA-CReSA** to exclude any possibility of laboratory scape based on a selection of viral isolates and samples from animals experimentally infected with ASF virus in the last year (ongoing by the NRL and EURL)
- Perform sequence comparison of **relevant viruses kept in other laboratories** in Spain to exclude any possibility of laboratory scape (two laboratories under investigation).
- Address the critical points pointed in the facility or protocols by performing an **audit of CReSA** (done with satisfactory results)

Origin of virus strain: hypothesis and lab. investigation

Hypothesis of virus origin and probability of occurrence

Hypothesis 1. Accidental release from a research laboratory

- Index case located in a geographical **area close to the CReSA-IRTA** facilities (Bellaterra, Catalonia)
- High homology with lineage **Georgia 2007**, not currently circulating in the EU according to available info.
- Georgia 2007 is a **reference strain** use in experimental infections

Unlikely (at the moment): no evidence of relationships after preliminary laboratory investigation by:

- **Partial (Sanger)** sequencing of **81 samples** from CReSA (12 virus isolates, 69 samples of pigs experimentally infected with Georgia 2007/Armenia 2007 in 2025)
- **Whole Genome Sequencing** of **17 virus isolates** from CReSA (Institut de Recerca Biomédica, IRB).

The samples analyzed **do not show the significant mutations (SNPs) or the large deletion** characteristic of the virus pf Spanish outbreak.

Origin of virus strain: hypothesis and lab. investigation

Hypothesis of virus origin and probability of occurrence

Hypothesis 2. Introduction from active European sources through natural or progressive transmission.

Unlikely, because:

- The geographically **closest active European outbreak** is in Northern Italy (Piedmont region), is located **500–600 km** far from Catalonia, and the virus is associated with genetic groups different from those identified in the Spanish virus.
- Countries located between the affected areas and Catalonia, particularly France, maintain **intensive wildlife surveillance systems**.
- The genetic profile of the **virus detected in Spain did not show a close relationship with the dominant lineages in the nearest European outbreaks**.

4. Origin of virus strain: hypothesis and lab. investigation

Hypothesis of virus origin and probability of occurrence

Hypothesis 3. Deliberate introduction.

Unlikely, because:

- The identified virus has a **large structural deletion in the left variable region of the genome**, along with a genetic profile not previously described in European outbreaks. From a virological point of view, it is therefore an isolate with uncertain biological behavior, which **reduces its predictability in terms of transmission and pathogenicity**.
- In this context, **the use of a virus with these characteristics in a hypothetical scenario of deliberate introduction is inconsistent**, given that this type of event is usually associated, based on the data known to date, with well-characterized strains with known epidemiological behavior.

4. Origin of virus strain: hypothesis and lab. investigation

Hypothesis of virus origin and probability of occurrence

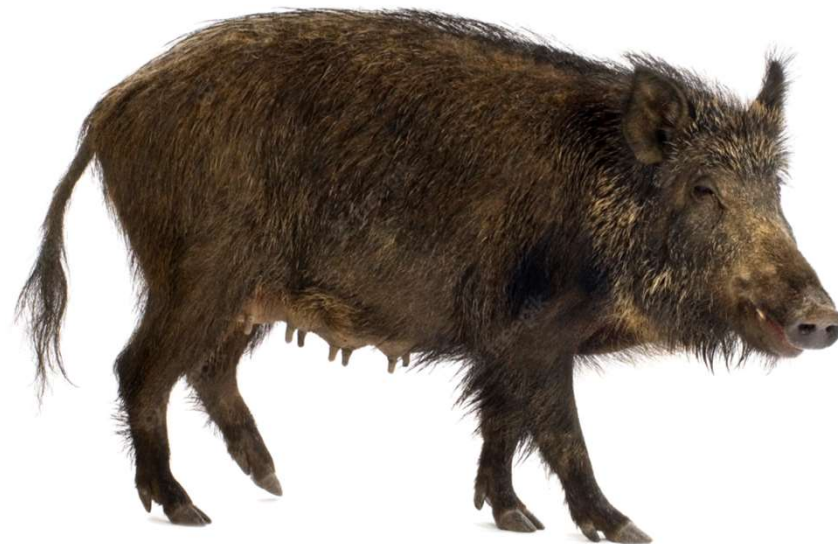
Hypothesis 4. Introduction over long distances mediated by human activities (contaminated meat products or food waste)

This scenario is **consistent** with historical patterns of ASFv spread and compatible with various epidemiological elements observed in the outbreak detected in Catalonia, including:

- **Outbreak in Catalonia with no epidemiological link** with previously affected areas.
- **Absence of intermediate outbreaks** in neighboring countries, including territories with high detection and surveillance capacity.
- **Location of the outbreak in a highly connected** environment, with high human mobility and a dense **road and rail infrastructure network**.
- **Genetic divergence from the dominant lineages in Europe**, including those closest to northern Italy, suggesting an introduction unrelated to known geographical expansion.

This route of introduction is the **most common mechanism** for the long-distance spread of ASFv and is widely **documented in the epidemiology of the disease**, having been responsible for numerous episodes of transcontinental and long-distance introduction both in Europe and on other continents.

Thank you for your attention!

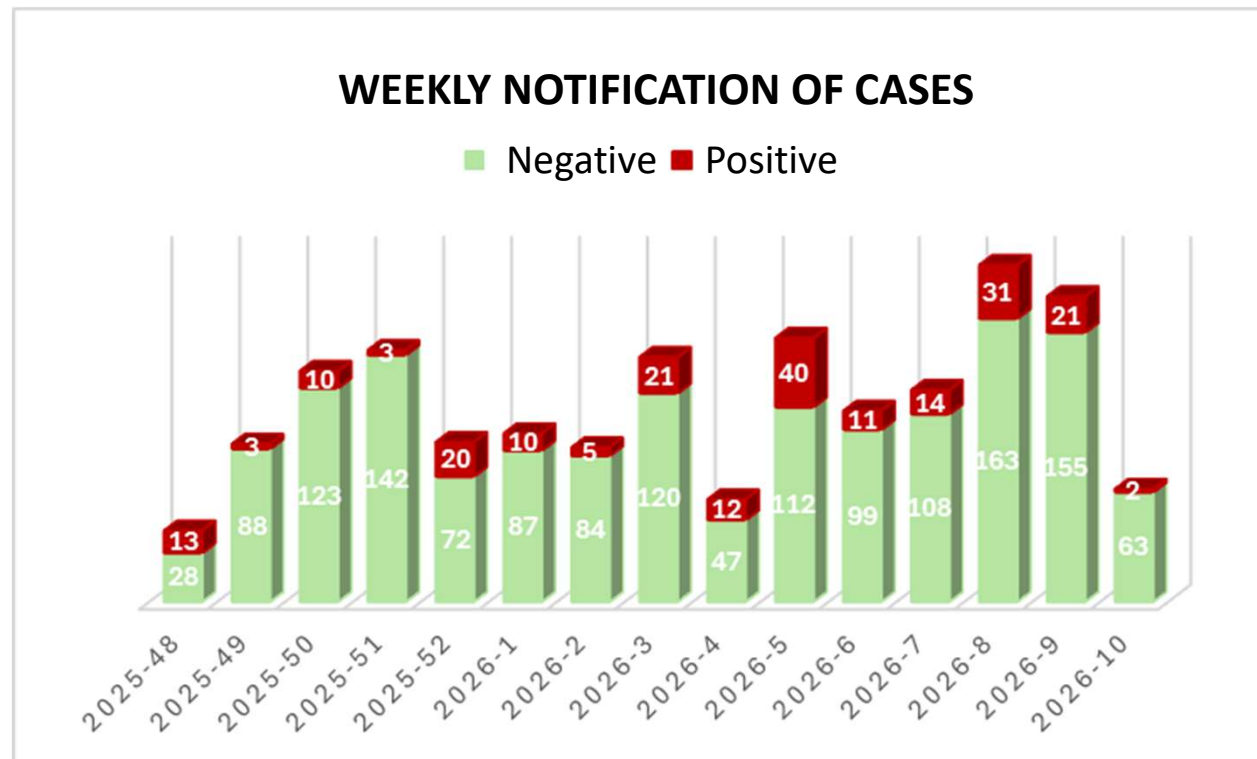


ASF website MAPA

https://www.mapa.gob.es/es/ganaderia/temas/sanidad-animal-higiene-ganadera/sanidad-animal/enfermedades/peste-porcina-africana/peste_porcina_africana.aspx

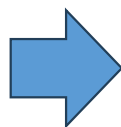
Positive and negative wild boars/week and zone

	TOTAL ANALIZADOS ZONA		
	POSITIVOS	NEGATIVOS	TOTAL
2025-48	13	28	41
2025-49	3	88	91
2025-50	10	123	133
2025-51	3	142	145
2025-52	20	72	92
2026-1	10	87	97
2026-2	5	84	89
2026-3	21	120	141
2026-4	12	47	59
2026-5	40	112	152
2026-6	11	99	110
2026-7	14	108	122
2026-8	31	163	194
2026-9	21	155	176
2026-10	2	63	65
TOTAL	216	1491	1707



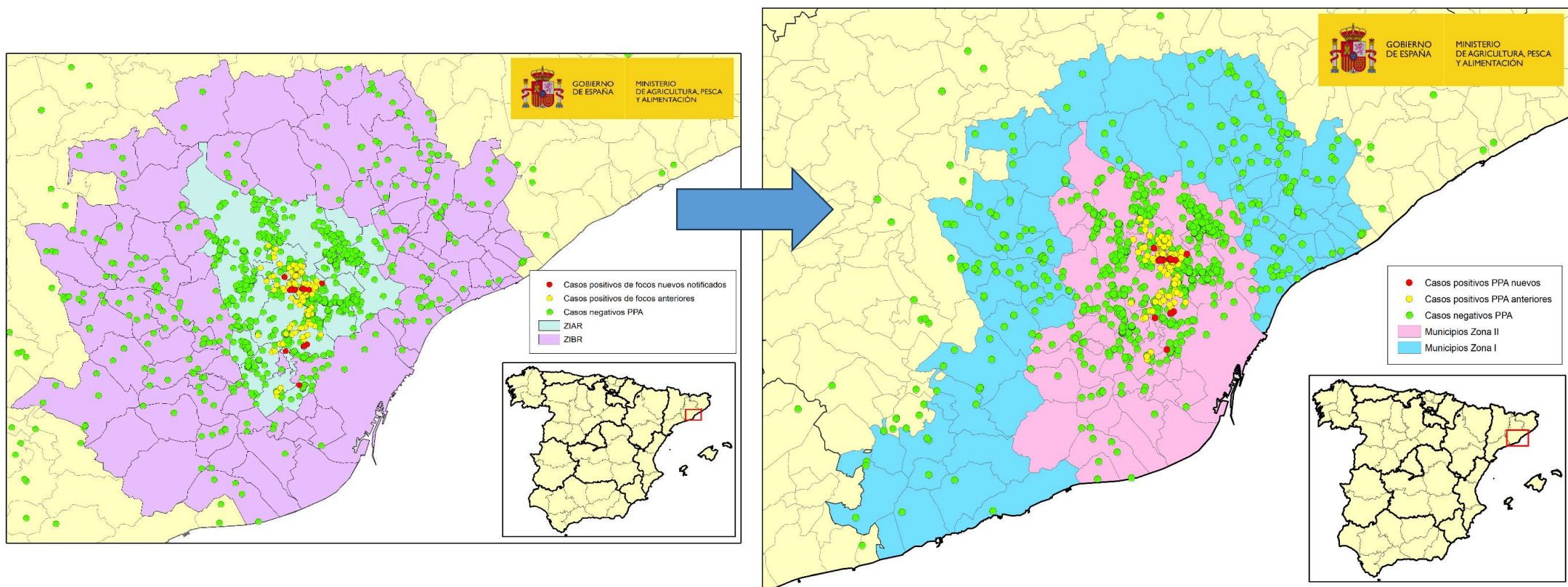
1707 PCR

1215 ELISA → 6 ELISA
+; 24 IPT +
Todos también PCR +



Given the moderate mortality observed, there is a possibility of an acute/subacute strain (detection of a deletion affecting virulence genes). This could also be due to low transmissibility in the area.

Initial Infected Zone → EU Zoning



Short/medium-term challenges

