

# African Swine Fever laboratory diagnosis in Spain



<https://www.mapa.gob.es/es/ganaderia/temas/laboratorios-sanidad-genetica/>

**Dr Manuel Durán-Ferrer**

Deputy Director General Animal and Plant Health Laboratories (MoA)

Laboratorio Central de  
Veterinaria

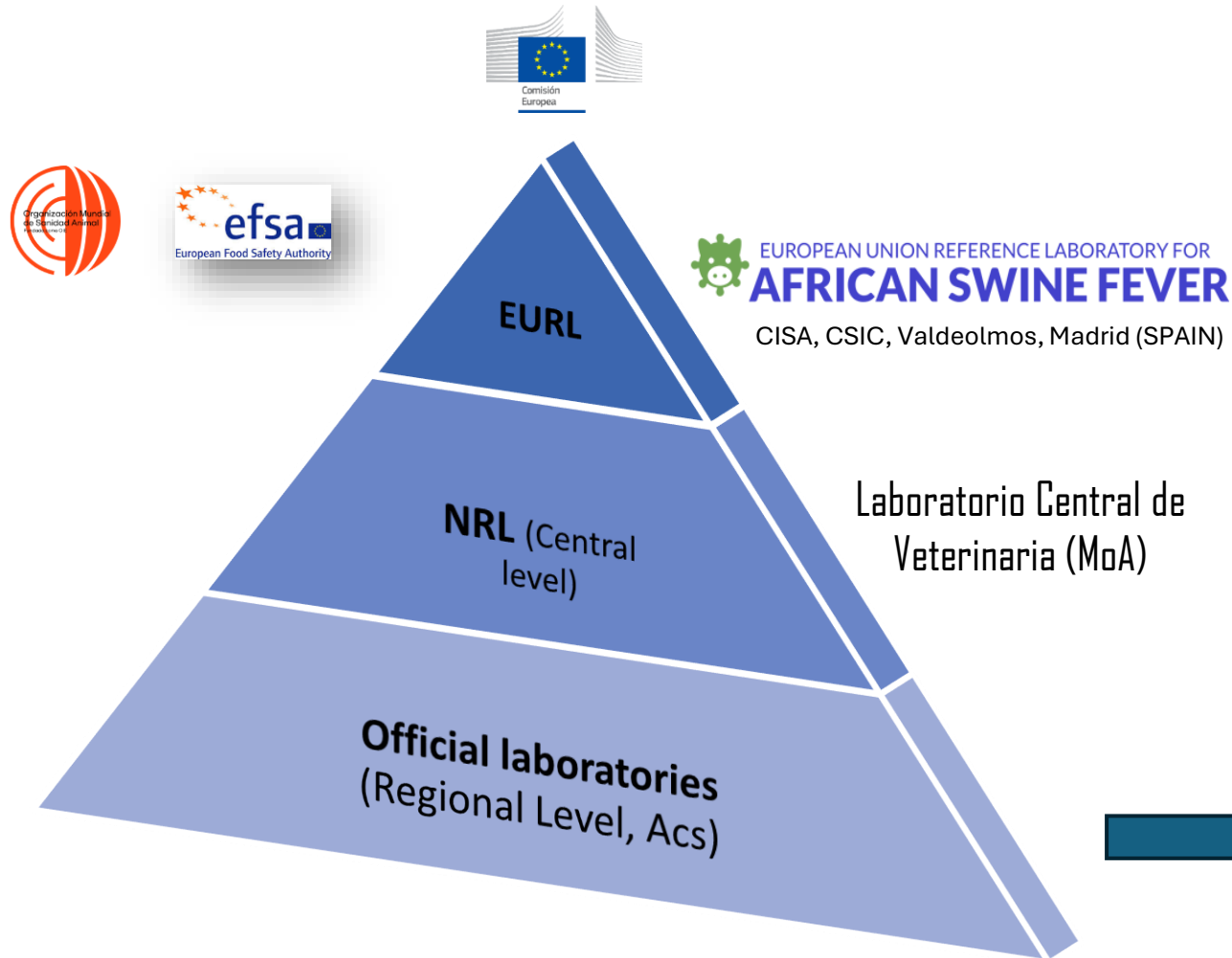


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# 1. African Swine Fever laboratory network (I)



Framework: **Regulation (EU) 2017/625**

# 1. African Swine Fever laboratory network (II)

The entire network of laboratories accredited in accordance to ISO 17025

**ASF laboratory network: 29 official labs + 1 NRL**

Labs carrying out only ELISA	12	★
Labs carrying out only PCR	3	★
Labs carrying out ELISA + PCR	14	★

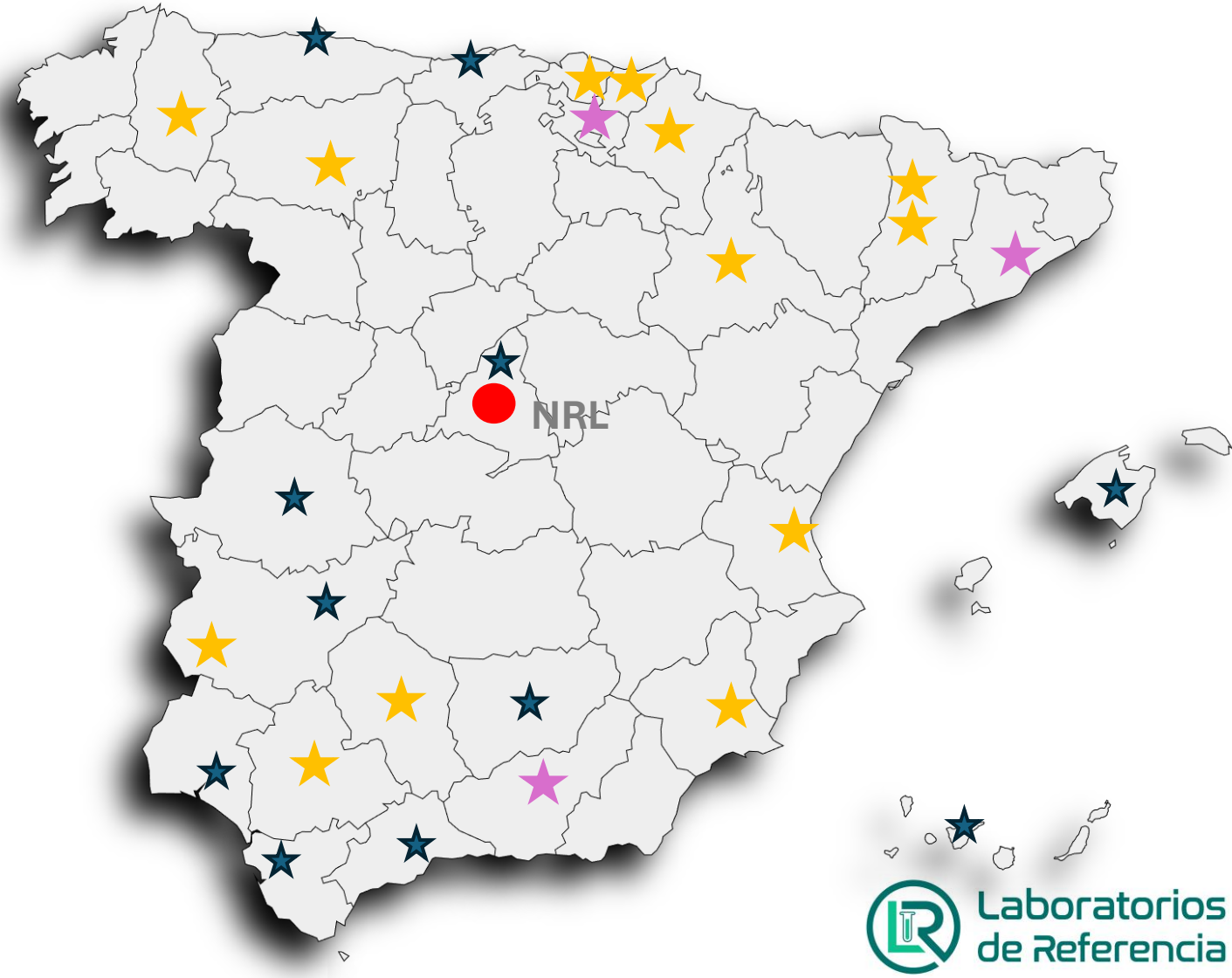
NRL ●

Laboratorio Central de Veterinaria

**Laboratory diagnosis at the NRL:**

- Screening tests (ELISAs, IPT)
- Confirmatory methods (PCR, virus isolation, Sanger sequencing)

All methods accredited (ISO 17025)



# 1. African Swine Fever laboratory network (III)

## National Reference Laboratory: tasks and responsibilities (Regulation (EU) 2017/625, Law 8/2003)



Harmonization of diagnostic methods



Technical advice to OVS



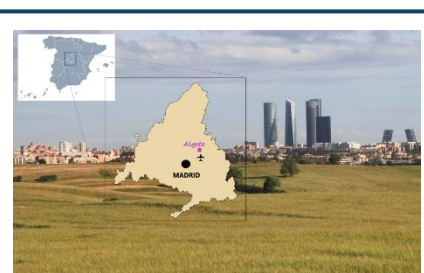
Control of diagnostic reagents



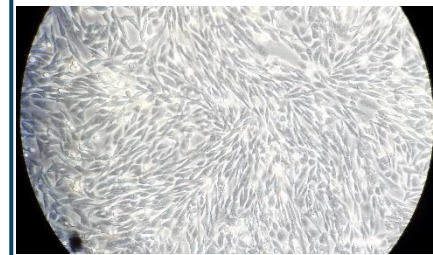
Confirmation of the diagnosis



Coordination with EURL (WS, participation in PTs, etc.)



Organization of Proficiency tests



Dissemination of information from EURL to OC labs.



Training courses, if necessary

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## 2. Laboratory diagnostic workflow

### FLOW DIAGNOSTIC CHART

### AR of CATALONIA

Muestras de elección para el diagnóstico



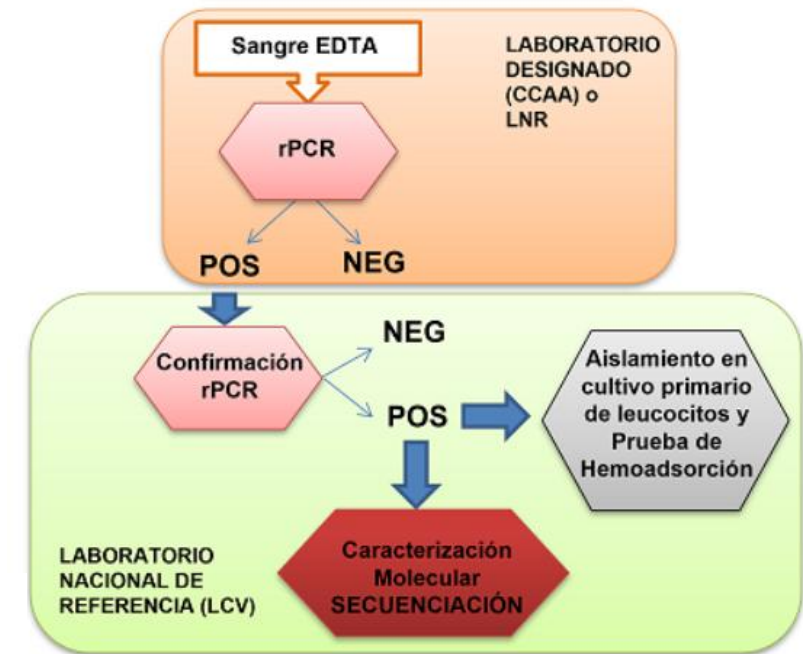
**Regional official lab (IRTA CReSA):**  
 Necropsies and sampling  
**Screening by qPCR**

If POS/Non conclusive

Samples sent to **NRL** for  
**Confirmation by qPCR & Characterization (Sanger sequencing)**

**Ongoing collaborative serological study**

### DIAGNÓSTICO VIROLÓGICO



rPCR: reacción en cadena de la polimerasa en tiempo real

**Active and pasive surveillance in other Autonomous Regions**

**Serology and/or PCR by official labs, and confirmation at the NRL**

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### 3. Laboratory diagnosis and characterisation and monitoring of ASF outbreak 2025-2026 (I)



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

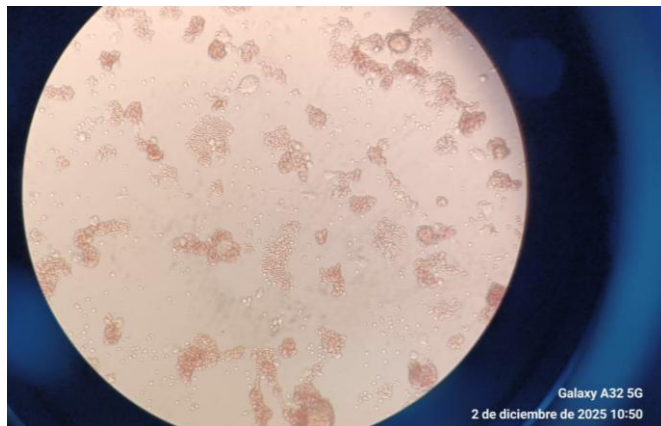
**November 26th (evening):** Notice that we will be receiving samples that have tested PCR positive in the official laboratory (**IRTA-CreSa**, AR of Catalonia)

**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**

**Rapid response:** confirmation in 3 hours, genotyping in around 20 hours, isolation in 2 working days.

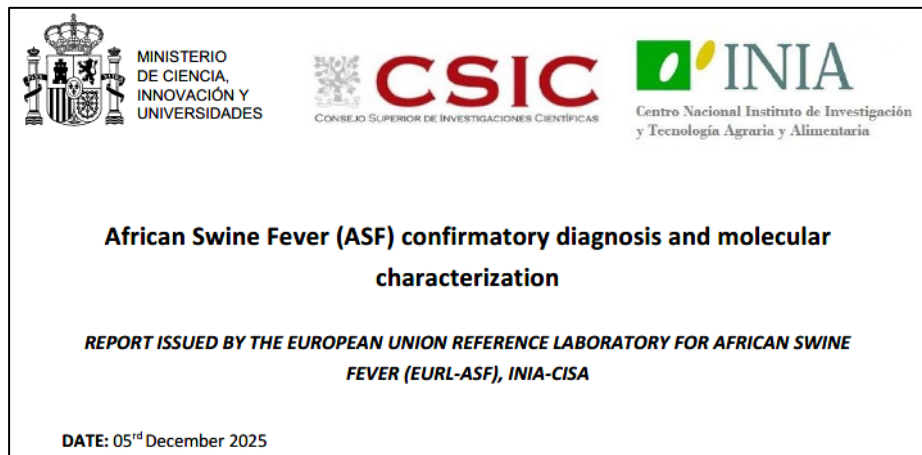


### 3. Laboratory diagnosis and characterisation and monitoring of ASF outbreak 2025-2026 (II)

#### Collaborative studies between NRL and EURL

- **Molecular characterisation** for the follow up of outbreaks (Sanger, WGS)
- **Serological** studies

#### EURL: full molecular characterization of ASF virus SPAIN 2025:



Virus sequence is already published at **GenBank** (<https://www.ncbi.nlm.nih.gov/>).  
Accession number: **PZ023911**.  
(<https://www.ncbi.nlm.nih.gov/nuccore/PZ023911.1>)

EURL  
December, 5. 2025

## 4. Monitoring of disease outbreaks: molecular markers

### First detection:

- **qPCR** for the detection of ASFv (Fernández-Pinero *et al.*, 2013; WOAHA, 2025)
- **partial sequencing** (Sanger) for genotype determination: gen B646L (p72), gen E183L (p54) and gen B602L (CVR) (Genotype II)

### Disease outbreaks monitoring:

- **qPCR** for the **detection** of ASFv (Fernández-Pinero *et al.*, 2013; WOAHA, 2025)
- **Unique molecular markers** of ASFv SPAIN 2025 used **to track** disease outbreaks at the **NRL**:
  - SNP in gen E183L (**p54**): Partial sequencing by Sanger (Gallardo *et al.*, 2009) (635 pb)
  - SNP in **MGF505 9R/10R** intergenic region: Partial sequencing by Sanger (Giammaroli *et al.*, 2014) (551 pb)
  - **Large deletion** in the terminal left end of the viral genome: qPCR (EURL 2026, unpublished)

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## 5. Origin of virus strain: hypothesis and lab. investigation

### Hypothesis of virus origin and probability of occurrence

#### Facts:

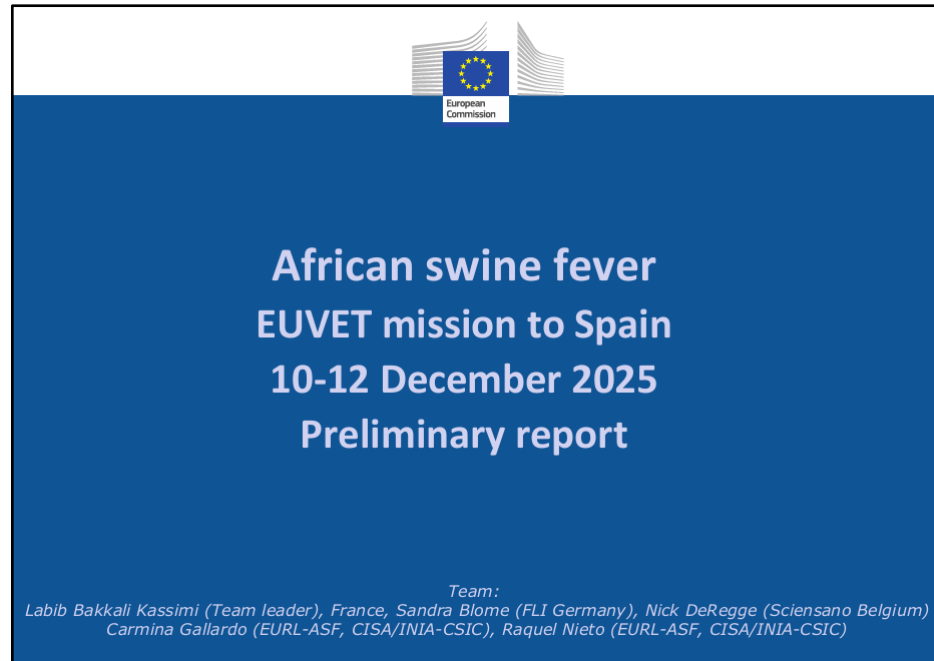
- The **geographically closest active European outbreak is located 500–600 km far** from Catalonia (Piedmont region, Italy)
- **Countries** located between the affected areas and Catalonia maintain **intensive wildlife surveillance** systems.
- The **genetic profile** of the virus detected in Spain did not show a close relationship with the dominant lineages in the European Union outbreaks. The 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.
- Although **the 2 first outbreaks** detected were **closed to a ASF research laboratory**, **laboratory tests** results have **not found relationship** between the samples (**81** samples investigated for 3 specific markers, **17** virus strains studied by WGS) held at this facility and the virus responsible for the outbreak in Spain
- Location of the outbreak in a highly connected environment, with **high human mobility** and a dense **road and rail infrastructure network**.

- Hypothesis 1. **Accidental release** from a research laboratory. **Unlikely**
- Hypothesis 2. Introduction from active European sources through **natural or progressive transmission**. **Unlikely**
- Hypothesis 3. **Deliberate introduction**. **Unlikely**

- Hypothesis 4. **Introduction over long distances mediated by human activities** (contaminated meat products or food waste). **Most likely hypothesis:** 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.

## 5. 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)

## 5. Take-home messages

1. The **network of laboratories** is appropriately sized and **operates** in a coordinated manner in accordance with **EU (and WOAH) standards**.
2. This network is led by the **national reference laboratory**, which carries out **intensive work in confirming and characterizing outbreaks**.
3. **Coordination** between the NRL and the EU reference laboratory (EURL) has been **key** for tackling disease outbreaks.
4. **Extensive laboratory work** is being conducted to determine the **origin of the virus**.

