

# TEMPORAL EVOLUTION OF RABBIT HAEMORRHAGIC DISEASE VIRUS (RHDV) AND IMPACT OF VACCINATION DURING THE RHD EPIDEMIC IN SPAIN 2013-2015

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In response to RHDV-2 emergence in Spain, the evolution of the virus and the role of vaccination were evaluated. The results support a fast RHDV-2 spread and reveal the positive effect of vaccination on disease control.

## INTRODUCTION

A new RHD variant (RHDV-2) emerged in Spain in 2011, sparking an emergency response that included the provisional licencing of RHDV-2 vaccines. The aim of this study was to investigate the temporal evolution of RHDV (2013-2015), and the impact of vaccination as a control measure in Spain.

## METHODS

**Study period:** It was divided into two phases, namely pre-vaccine authorisation (10/2013-07/2014), and post-vaccine authorisation (07/2014-08/2015).  
**Samples:** Individual and pooled (homogenates) samples of liver, spleen, lung and kidney from animals suspected of being affected by RHDV by clinical evaluation. Samples came from all rabbit producing areas in Spain.  
**Laboratorial assays:** Haemagglutination (liver); end-point RT-PCR, partial sequencing (VP60 gene) and phylogenetic analysis (pooled samples).

## RESULTS

A total of 134 samples from suspected RHD outbreaks occurring in 104 rabbitries all over Spain were analysed. All RHDV-positive specimens (48.5%) contained RHDV-2 alone, indicating that it was the most likely cause of all RHD outbreaks recorded in the time period studied (Figures 1 and 2). The phylogenetic analysis confirmed a geographic association among outbreaks. While no temporal clusters were observed among RHDV-2, a temporal divergence was evident between available sequences and the ones in this study (data not shown).

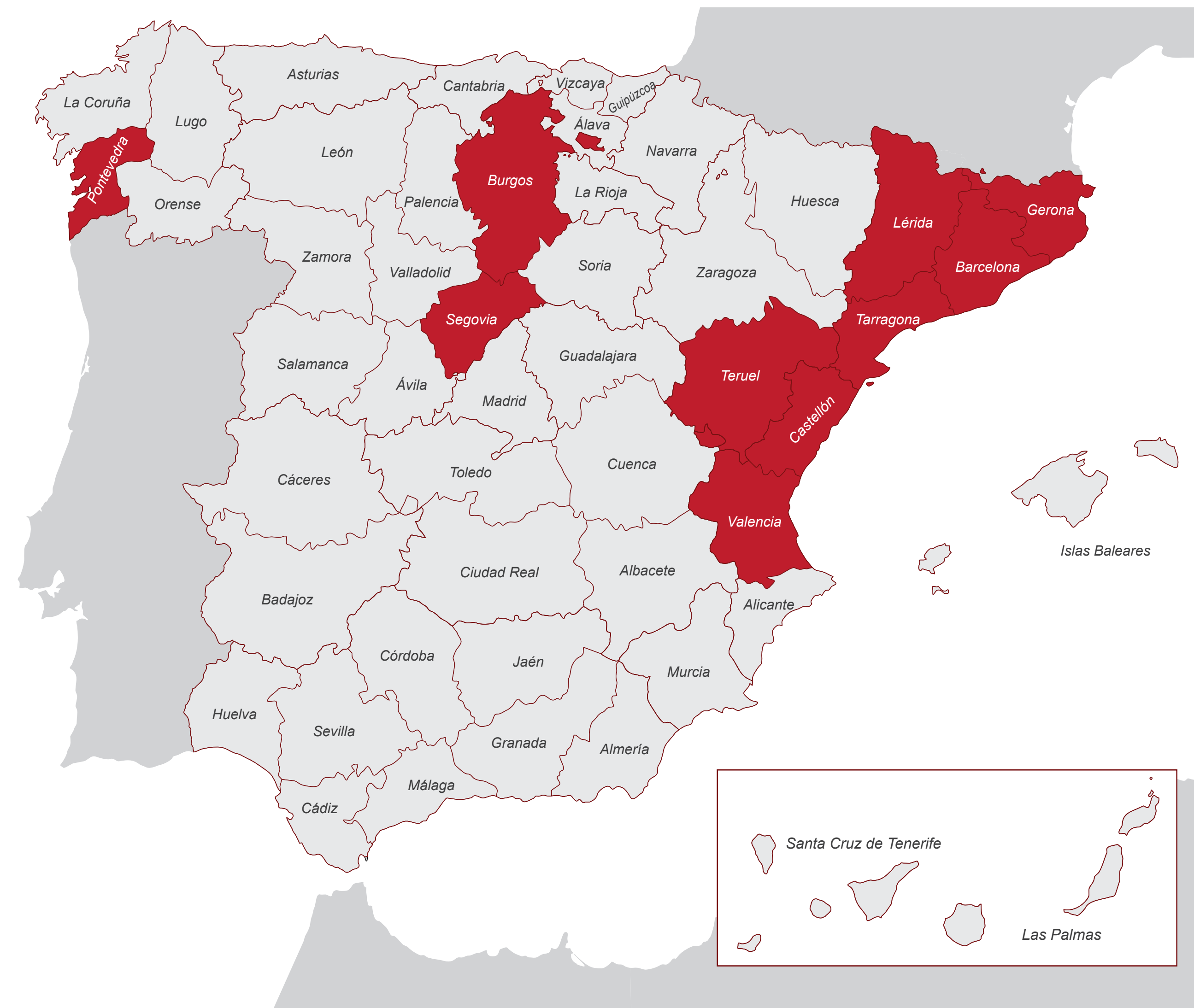


Fig 1. Spanish provinces with confirmed RHDV-2 outbreaks (shaded red).

A positive relationship between the reduction of suspected cases and the implementation of prevention programs, including RHDV-2 vaccination, was observed (Table 1).

Table 1. RHD suspected outbreaks recorded per month and percentage of positive samples per studied period.

|                               | All period | Pre-vaccine authorisation | Post-vaccine authorisation |
|-------------------------------|------------|---------------------------|----------------------------|
| Suspected outbreaks per month | 5.15       | 8.3                       | 3.5                        |
| Positive samples              | 48.51%     | 52.00%                    | 44.07%                     |



Fig 2. Phylogenetic tree based on the partial VP60 gene sequence from 2 classical RHDV (Genbank), 17 RHDV-2 (Genbank) and 65 RHDV (this study). Samples are identified by ID (accession or individual number), location (country/province) and date of sample collection (month/year).

## CONCLUSIONS

The results of this study, in agreement with other recent publications, support the fast spread of RHDV-2, and the displacement of classical RHDV in Spain. It also provides new insights on the role of vaccination in the virus spread during the RHD epidemic. A geographical and temporal association was observed regardless of the vaccination program that was established. It is necessary to continue implementing surveillance and vaccination programs in order to control the epidemiological evolution and reduce the economic consequences of this disease.

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