SHORT COMMUNICATION



Worldwide rapid spread of the novel rabbit haemorrhagic disease virus (GI.2/RHDV2/b)

Joana Abrantes³ Joana Abrantes³ Joana Abrantes³

Carlos Rouco¹ | Juan Antonio Aguayo-Adán¹ | Simone Santoro²

¹Departamento de Zoología, Universidad de Córdoba, Córdoba, Spain

²Department of Molecular Biology and **Biochemical Engineering, University Pablo** de Olavide, Seville, Spain

³CIBIO-InBIO/UP, Centro de Investigação em Biodiversidade e Recursos Genéticos/ Universidade do Porto, Vairão, Portugal

⁴Instituto de Estudios Sociales Avanzados, IESA-CSIC, Córdoba, Spain

Correspondence

Carlos Rouco, Departamento de Zoología, Universidad de Córdoba, Campus de Rabanales, Córdoba, Spain, Emails: c.rouco@gmail.com; crouco@uco.es

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Abstract

We describe the extremely rapid worldwide spread of the Lagovirus europaeus/GI.2/ RHDV2/b (henceforth GI.2), the causative infectious agent of the so-called 'novel' rabbit haemorrhagic disease of the European rabbit (Oryctolagus cuniculus). We tracked down all novel confirmed detections of GI.2 between May 2010 and November 2018 by carrying out a two-step in-depth review. We suggest that such spread would not have been possible without anthropogenic involvement. Our results also point out the importance of reviewing and adapting the protocols of virus detection and management in order to control, mitigate and contain properly, not only GI.2, but also new viruses that may emerge in the future.

KEYWORDS

European rabbit, globalization, oryctolagus cuniculus, RHDV2, RHDVb

1 | INTRODUCTION

Lagovirus europaeus/GI.2/RHDV2/b, also known as RHDV2 and RHDVb (henceforth GI.2), is the causative infectious agent of the 'novel variant' of rabbit haemorrhagic disease (RHD). It was identified in 2010 in France, causing a crash in domestic and wild rabbit populations (Le Gall-Reculé et al., 2011). GI.2 shows a distinct antigenic profile to the former virus (L. europaeus/Gl.1a-d, henceforth GI.1), as well as different susceptibility in the different age classes (i.e., kittens, sub-adults and adults). Indeed, while GI.1 exclusively kills adults, GI.2 also lethally affects sub-adults and kittens as young as 11 days (Dalton et al., 2012). This new lagovirus has been detected in hares (Hall et al., 2017; Velarde et al., 2016) and has an increased diversity due to recombination with pathogenic and non-pathogenic viruses (Lopes et al., 2015; Silvério et al., 2018). It appears to have replaced the former GI.1 variants in the wild (Rouco et al., 2018; Silvério et al., 2018).

| MATERIAL AND METHODS 2

In order to assess the scale of this epidemic, we tracked down all novel confirmed detections of GI.2 by carrying out a two-step in-depth review. First, we identified scientific articles conducting a search in 'Scopus' and 'Web of Science' for terms that stemmed from the following words: "new/novel RHD" or "RHDV2" or "RHDVb" or "GI.2". Second, we reviewed any GI.2 outbreak reported in all the immediate notifications and follow-up reports of the World Organisation for Animal Health and the website of the Federal Research Institute for Animal Health, FLI (for detections in Germany).

3 **RESULTS AND DISCUSSION**

A total of 133 GI.2 detections (68% on mainland continents and 32% on islands; Figure 1) were reported between May 2010 and



FIGURE 1 Worldwide spread of the Lagovirus europaeus/GI.2/RHDV2/b since its first detection in April 2010 in France until November 2018. Black dots represent outbreak detections

November 2018 in 18 scientific articles, 19 immediate notifications and follow-up reports and in the FLI website.

After the first detection in the Norwest of France in May 2010, the virus spread in less than 1 year to southern Europe (i.e., Portugal, Italy and Spain), followed by northern European countries (i.e., United Kingdom and Norway) and some islands, such as Azores (Portugal). In 2015, it reached Australia and Africa and was detected in other European countries, such as Sweden and the Canary Islands (Spain). One year later, GI.2 was detected in Canada and continued spreading within Europe. Only 6 years after its first detection in Europe, GI.2 occurred in America and Oceania (Figure 1). According to our records, the latest sites where GI.2 was detected were Morocco in 2017 and west Canada, New Zealand, United States and Israel in 2018 (Figure 1; see the full list of detections in Appendix S1).

GI.2 has caused important economic losses in rabbitries and impacted the livelihood of rural areas in southern Europe where rabbit hunting is one of the main economic resources. Moreover, it has caused a considerable decrease in wild rabbit populations worldwide, leading to ecological disruptions and negatively affecting the dynamics of endangered rabbit-specialist predators (Monterroso et al., 2016).

Traditionally, the spread of rabbit lagoviruses, which are highly resistant and stable when exposed to harsh environmental conditions, has been associated with wildlife vectors, such as arthropods, mammalian carnivores or raptor species (Abrantes, van der Loo, Le Pendu, & Esteves, 2012). Yet, the participation of these vectors would hardly explain the worldwide dissemination of GI.2, including into distant islands, in the short timeframe documented in this letter. We argue that the most plausible explanation for the observed rapid spread pattern of the virus is that human intervention played a major role.

Globalization has contributed to the increasing human-mediated introduction of non-native animal and plant species and pathogens (Kueffer, 2017), including the rapid dispersion across the world of viruses that cause human infectious diseases (Findlater & Bogoch, 2018). In addition, it is known that the current efficient global network of human transports facilitates the rapid dispersion of viruses that cause human infectious diseases (Findlater & Bogoch, 2018) and could be expected similarly for viruses affecting wildlife species, such as GI.2. At the time being, there is no evidence of any intentional releases of GI.2, yet, its spread occurred more rapidly than former intentionally released lagomorph viruses. This suggests that the extremely rapid spread of GI.2 was likely caused

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by human-mediated movement of farmed rabbits and/or by people displacements.

Timely detection of RHD virus outbreaks and RHD management would greatly benefit from the existence of standardized protocols of disease surveillance, prevention and control. Indeed, no protocols have been formerly defined nor agreed between different local laboratories, frequently leading to incomplete, inconsistent and patchy information regarding RHD virus epidemiology, particularly in some regions. For example, in Africa, RHD virus has been known to be circulating since the late 1980s (Morisse, Gall, & Boilletot, 1991), but it was not until more recently that the first complete genome sequences were obtained and made publicly available (Lopes, Rouco, Esteves, & Abrantes, 2019). This has had consequences in disease containment, as seen for the recent GI.2 outbreaks.

In conclusion, we suggest that it is increasingly important to review and adapt the current adopted protocols of virus detection and management in order to control, mitigate and contain properly, not only GI.2, but also new viruses that may emerge in the future. This is not only critical because of the impact that these viruses can have on human society, but also on many natural ecosystems.

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ORCID

Carlos Rouco D https://orcid.org/0000-0003-1026-3253 Simone Santoro D https://orcid.org/0000-0003-0986-3278 Joana Abrantes D https://orcid.org/0000-0002-8391-7134 Miguel Delibes-Mateos D https://orcid.org/0000-0002-3823-5935

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of the article.

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