

## LETTER TO THE EDITOR

**COULD THE NEW RABBIT HAEMORRHAGIC DISEASE VIRUS VARIANT (RHDVB) BE FULLY REPLACING CLASSICAL RHD STRAINS IN THE IBERIAN PENINSULA?**

Until recently, since the arrival of rabbit haemorrhagic disease (RHD) virus (RHDV) in the Iberian Peninsula in 1988, all the identified Iberian strains had belonged to the classic RHDV subtype (Alda *et al.*, 2010). In 2011, however, a new isolate type (RHDVb) that is phylogenetically divergent from classic RHDV was first described in the Iberian Peninsula in Spain. This variant affects both domestic (Dalton *et al.*, 2012) and wild rabbits (Calvete *et al.*, 2013), causing disease and even death in kits <30 d of age. This new variant differs antigenically from classic strains, so the protection conferred by existing vaccines has markedly decreased, forcing an increased frequency of vaccination up to every four months to prevent disease in rabbitries (Dalton *et al.*, 2012; Grasa and Malo, 2012).

Given that wild rabbits are the main reservoir of RHDV in the farmed rabbit industry in the Iberian Peninsula, we report the evolution of the prevalence of classic and RHDVb variants in cases of mortality by RHD occurring in 4 experimental wild rabbit populations in Zaragoza province in northern Spain. The populations, which are 2 km apart, were founded in 2009 by the translocation of wild rabbits as an R&D collaboration project (between CITA and the Animal Health Department of TRAGSA Group) that aimed to study RHD epidemiology. To obtain samples of rabbits that had died from the disease before scavengers ate them, populations were monitored daily from 2009 to 2011 and twice per week from January 2012 to May 2013.

During 2009 and 2010, the classic RHDV variant was the only isolate identified in all rabbits found dead from the disease (n=3 and n=24, respectively). In 2011, the year of the first detection of the RHDVb variant, this new variant was found in 22 samples, whereas the classic variant was only identified in nine. In three other samples, both variants were found simultaneously, suggesting co-infection. During 2012 and from January 2013 until May 2013, however, only RHDVb was identified (n=8 and n=15, respectively), showing the evident predominance of the new variant over time. These results suggest that RHDVb could be the main, if not the only, aetiological agent involved in RHD outbreaks in rabbitries in the near future. Therefore, it seems necessary and urgent to include the RHDVb valency in commercial vaccines against RHD. Agencies and programmes devoted to the conservation of wild rabbits and endangered predator species are concerned, because these results suggest a competitive advantage of the new variant over the classic strains in wild populations, implying still-unknown changes in the epidemiology of RHD in the field.

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