Not-So-Novel Michigan Rabbit Calicivirus

To the Editor: A disease outbreak in a Michigan rabbitry led Bergin et al. (*1*) to identify a new rabbit calicivirus distinct from rabbit hemorrhagic disease virus, which they designated as Michigan rabbit calicivirus (MRCV). They found that in domestic rabbits from the United States, 2 different forms of rabbit calicivirus with differences in pathogenicity are circulating. Bergin et al. showed that, phylogenetically, MRCV was more closely related to the nonpathogenic rabbit calicivirus (RCV) than to pathogenic strains and used this observation as an argument for its classification as a novel calicivirus. However, they did not include the publicly available sequences of other nonpathogenic strains, such as Ashington (97% of the capsid viral protein [VP] 60) and the newly identified *Lagovirus* spp. RCV-A1 (complete genome) (*2*).

Using the same dataset as Bergin et al. and including these sequences, we performed genetic analyses focusing mainly on the capsid VP60. The lack of information for open reading frame 1 for the nonpathogenic strains led to this option. Independently of the sequences' length, RCV-A1 was more closely related to the *Lagovirus* spp. European brown hare syndrome virus, here used as an outgroup, and clearly apart from a highly supported primary group that was further subdivided into 2 also highly supported subgroups, 1 composed of pathogenic rabbit hemorrhagic disease virus strains and another encompassing the RCV-like group (RCV, Ashington and Lambay [*2*], and MRCV). Here, only the phylogenetic tree that corresponds to the more complete VP60 sequences is shown (Figure).

We conclude that MRCV is not a novel calicivirus but a new variant of the nonpathogenic RCV-like group. However, the low pathogenicity presented by MRCV and the presence of viral RNA in the liver rather than in the intestine are clearly new features among the nonpathogenic RCV-like group (*5*).

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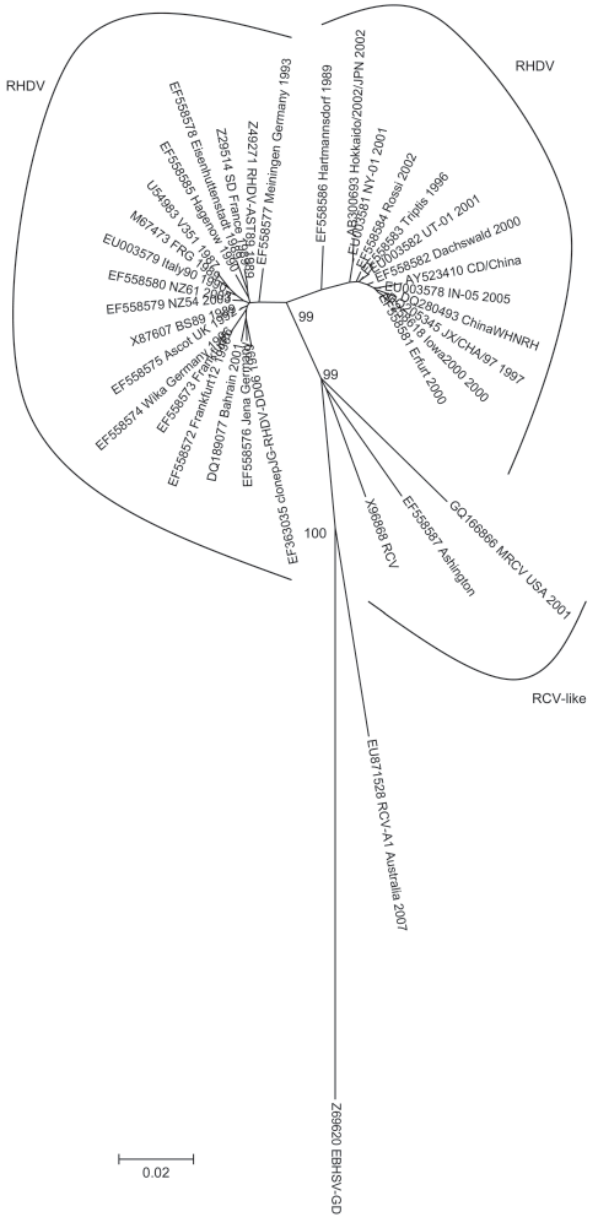

Figure. Evolutionary relationships of *Lagovirus* strains. The evolutionary history was inferred by using the neighbor-joining method (*3*) with the pairwise deletion option. The tree is drawn to scale. There were a total of 563 positions (97% of the capsid viral protein (VP [60 aa sequence]). Phylogenetic analyses were conducted in MEGA 4 (*4*). Reliability of the tree was assessed by bootstrap with 1,000 replicates and is indicated in the nodes (only relevant values are shown). Several genetic distance methods were used, and similar results were obtained, but only p-distance is shown. GenBank accession numbers of the sequences used are indicated. Scale bars indicates nucleotides substitutions per site. RHDV, rabbit hemorrhagic disease virus; RCV, rabbit calicivirus; EBHSV, European brown hare syndrome virus.

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In Response: We thank Abrantes and Esteves for their interest in our article (*1*). We demonstrated that a disease outbreak among rabbits in the United States was associated with a calicivirus distinct from members of the species *Rabbit hemorrhagic disease virus* (RHDV) (*1*). Rabbit hemorrhagic disease is classified as a disease of foreign animals in the United States and is caused by the only calicivirus in the genus *Lagovirus* previously associated with disease in rabbits. Our phylogenetic analysis established that Michigan rabbit calicivirus (MRCV) is distinct from RHDV and more closely related to a nonpathogenic rabbit calicivirus (RCV). We are pleased that Abrantes and Esteves agree with us on this point.

In regard to phylogeny, the additional analysis performed by Abrantes and Esteves is an extension to, not an omission of, the original disease-focused paper. It is difficult to understand their objection to the term novel, a point that seems semantic. This term has more than just a phylogenetic connotation, and our use of it is consistent with other reports in this journal (*3*,*4*).

In Abrantes and Esteves' analysis, although RCV, Ashington, MRCV, and RCV-A1 appear to share common ancestry, MRCV branches separately from Ashington and RCV. The limited sequence availability for RCV and Ashington hampers detailed analysis of the interrelatedness of these viruses.

In conclusion, we describe MRCV as a novel calicivirus on the basis of its identification as the first non-RHDV *Lagovirus* sp. detected in the United States, its unique pathogenic potential to rabbits among the currently described non-RHDV lagoviruses, and its genetic distinction from RHDV. The phylogenetic relationships of the non-RHDV caliciviruses will no doubt be further refined as more members with complete or near-complete sequences, like MRCV, become available. Perhaps this will shed further light on the apparent pathogenicity of MRCV under certain circumstances.

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Note to Readers: The authority for formal recognition of any new viral species resides with the International Committee on Taxonomy of Viruses (ICTV; www.ictvonline.org). ICTV currently recognizes 2 species, *Rabbit hemorrhagic disease virus* and *European brown hare syndrome virus*, in the genus *Lagovirus*, family *Caliciviridae*. ICTV does not make policies for designation or recognition of strains or variants of viruses within a species. A proposal for formal recognition of any new virus species should be made through the appropriate ICTV study group.