Review of: "Bagaza virus in wild birds, Portugal, 2021"

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The article “Bagaza virus in wild birds, Portugal, 2021” reports the detection of this virus in red-legged partridges and a corn bunting collected from a site in southern Portugal. The authors used RT-PCR and histopathology to demonstrate infection with virus in organ samples from the birds. The article is well written, and the conclusions are supported by the data. The phylogeny, despite being based on short sequences (218 & 171 base pairs) clearly demonstrates that the amplicons generated from RNA samples belong to Bagaza virus and that the sequences share high identity (99-100%) with virus isolates from Spain, originally detected in 2010. As the authors state, further sequence, and ideally a complete genome is needed to make further deductions on the origin and relationship to other Bagaza virus isolates. The weakest component of the article is the histopathology. The quality of the images could be improved, and non-infected tissue sections are needed to highlight the pathological changes observed in the infected tissue. Also, annotation in the form of arrows, should be included to identify the lesions.