



Genome Sequence of a Circovirus Strain from a Pigeon in the Lymphocyte-Depleted Bursa of Fabricius of a Common Raven

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Abstract

Fabricius in a Common Raven. The findings underscore the potential pathogenicity of this virus and its ability to induce immunosuppression in avian species, particularly in those that are already compromised.

The close genetic relationship of this strain to other avian Circoviruses highlights the risk of interspecies transmission, which poses significant implications for avian health management and biodiversity conservation. As circoviruses can impact the immune systems of affected birds, ongoing surveillance and research are essential to better understand the epidemiology and pathogenic mechanisms associated with these viruses. Ultimately, this research contributes to the broader understanding of Circovirus dynamics in avian populations, emphasizing the need for targeted management strategies to protect both wild and domestic birds from the potential impacts of circoviral infections.

None

None

References

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