

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

This study presents the complete genome sequence of a Circovirus strain isolated from a pigeon found in the lymphocyte-depleted bursa of Fabricius of a Common Raven. The isolation occurred in a wildlife rehabilitation setting, where the raven exhibited signs of immunosuppression. Using next-generation sequencing, we characterized the Circovirus genome, revealing a total length of approximately 2,000 base pairs. Bioinformatic analysis indicated the presence of typical circoviral features, including two major open reading frames (ORFs) that encode for the replicase and capsid proteins. Phylogenetic analysis positioned this strain within the Circovirus genus, showing close genetic relatedness to previously identified pigeon and avian circoviruses. The findings suggest potential interspecies transmission of Circovirus between pigeons and ravens, raising concerns about the implications for avian health and biodiversity. This research contributes to the understanding of Circovirus epidemiology and the potential impact on immunocompromised avian species. Further studies are warranted to explore the pathogenicity and transmission dynamics of this Circovirus strain in wild and domestic birds.

Keywords: Circovirus; Pigeon strain; Bursa of fabricius; Common Raven; Genome sequence; Immunosuppression

Introduction

Circoviruses are small, circular single-stranded DNA viruses that primarily infect birds and mammals, with a significant impact on avian health [1]. These viruses have been associated with various diseases in poultry and wild bird populations, often leading to immunosuppression, increased susceptibility to secondary infections, and overall poor health outcomes. The bursa of Fabricius, a critical organ for the development of the immune system in birds, plays a vital role in the maturation of B lymphocytes. Infections or pathological changes in this organ can severely compromise avian immunity [2]. The present study focuses on a Circovirus strain isolated from a pigeon discovered in the lymphocyte-depleted bursa of Fabricius of a Common Raven. This unique setting highlights the potential for interspecies transmission and the impact of Circovirus on immunocompromised birds [3]. Despite previous research on circoviruses in domestic poultry and wild birds, there is limited information regarding the genetic diversity and pathogenic potential of Circovirus strains in less commonly studied species. By sequencing and analyzing the complete genome of this Circovirus strain, we aim to enhance our understanding of its phylogenetic relationships and epidemiological implications [4-6]. This research may provide valuable insights into the role of Circoviruses in avian health, particularly in immunocompromised populations, and underscore the need for ongoing surveillance and management strategies in wildlife rehabilitation and conservation efforts.

Results and Discussion

The complete genome sequence of the Circovirus strain isolated from the lymphocyte-depleted bursa of Fabricius in a Common Raven was determined to be approximately 2,000 base pairs in length [7]. Bioinformatic analyses identified two major open reading frames (ORFs): ORF1, which encodes the replicase protein, and ORF2, responsible for the capsid protein. Phylogenetic analysis indicated that this strain is closely related to previously identified Circovirus strains from pigeons and other avian species, forming a distinct clade within the Circovirus genus [8]. Notably, the genomic features observed are consistent with those reported in other avian circoviruses, including

conserved motifs that are critical for viral replication and assembly.

The findings of this study provide significant insights into the genetic characteristics of a Circovirus strain affecting both pigeons and a Common Raven. The isolation of this virus in the lymphocyte-depleted bursa of Fabricius highlights its potential pathogenicity and ability to induce immunosuppression in affected birds. Given that the bursa is crucial for B cell maturation; its depletion could lead to increased vulnerability to other infections, potentially exacerbating health issues in both domestic and wild bird populations [9]. The close genetic relationship between the identified strain and other avian Circovirus strains suggests potential routes of interspecies transmission, raising concerns about the implications for avian biodiversity and health management. The potential for circoviruses to spread among different bird species underscores the necessity for ongoing surveillance, particularly in wildlife rehabilitation settings where birds of different species are in close proximity [10]. Further research is warranted to investigate the pathogenic mechanisms of this Circovirus strain and its impact on the health of immunocompromised birds. Understanding the dynamics of Circovirus transmission and its effects on avian immune systems will be critical for developing effective management strategies and improving the health outcomes of affected populations.

Conclusion

This study successfully characterized the complete genome sequence of a Circovirus strain isolated from the lymphocyte-depleted bursa of

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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.

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Conflict of Interest

None

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