

Avian leukosis and reticuloendotheliosis viruses: biology, epidemiological risks, and the need for molecular surveillance in Kazakhstan

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Abstract

Background and Aim. Avian leukosis virus (ALV) and reticuloendotheliosis virus (REV) induce severe immunosuppression and neoplastic processes, increasing susceptibility to concurrent infections and causing substantial hidden economic losses. Despite active viral circulation in neighboring countries (e.g., China, Russia), epidemiological data for Kazakhstan remain scarce. This review aims to synthesize current knowledge on retroviral biology, raise awareness of this hidden threat among veterinary professionals, and justify the need for systematic control at poultry facilities.

Material and Methods. A comprehensive analysis of current scientific literature addressing the biology, classification, life cycle, and molecular mechanisms of retrovirus-host cell interactions was conducted. The role of exogenous and endogenous retroviruses in the development of infectious and oncological diseases was examined. Additionally, available information on the epizootiological situation in countries bordering Kazakhstan was reviewed, alongside contemporary approaches to the diagnosis, therapy, and prevention of retroviral infections.

Results. ALV and REV exhibit high genetic variability and establish persistent infections via host genome integration. These infections often progress subclinically: virus-induced lesions remain undetected, and secondary outbreaks are frequently misattributed to vaccine failure. The broad host range and active pathogen circulation in border regions pose a high risk of introduction into Kazakhstan, exacerbated by the current lack of systematic molecular epidemiology monitoring.

Conclusion. Implementing continuous molecular-genetic monitoring of avian retroviruses in Kazakhstan is critical to ensure poultry biosecurity, mitigate economic losses, and develop effective disease control strategies.

Keywords: Avian retroviruses; epidemiology; immune response; pathogenesis.

Introduction

Avian species, with a particular emphasis on the domestic chicken (*Gallus gallus domesticus*), have served as indispensable and historically monumental models in the realm of biomedical and oncological research for over a century. The unique developmental biology of the avian embryo, which develops in ovo and offers unparalleled accessibility for experimental manipulation, combined with the groundbreaking early discoveries of avian viral agents, positioned poultry at the very epicenter of virological science. Avian retroviruses were first identified as filterable, carcinogenic agents capable of inducing solid tumors in chickens at the dawn of the 20th century, largely stemming from the seminal work of Peyton Rous in 1911. However, avian retroviruses have persisted to evolve continuously since their initial discovery, adapting to modern intensive poultry farming practices and making them a crucial focus for continuous, highly prioritized global research. Studying these viruses has not only protected agricultural interests but has also led to a profoundly better understanding of the

fundamental molecular mechanisms of viral replication, reverse transcription, oncogene capture, and carcinogenesis [1].

Retroviruses constitute a highly complex family of enveloped, single-stranded positivesense RNA viruses (*Retroviridae*). Structurally, the viral particle encompasses a lipid bilayer envelope derived from the host cell membrane, embedded with viral glycoproteins that mediate receptor recognition and entry. Upon entering a susceptible host cell, these viruses utilize the virally encoded, multifunctional enzyme reverse transcriptase which possesses both RNA-dependent DNA polymerase and RNase H activities to synthesize a doublestranded DNA provirus from their RNA template. Subsequently, the viral integrase enzyme facilitates the irreversible insertion of this synthesized DNA into the host cell's chromatin (a mechanism universally known as reverse transcription and integration). This specific type of infection establishes a permanent, persistent state, as the integrated provirus behaves essentially as a host gene and is transmitted vertically along with the host cell's genetic material during cellular division [2, 3]. In the avian virosphere, there are both exogenous retroviruses (which are actively transcribed, assembled into infectious virions, and transmitted horizontally between living organisms, or vertically to offspring via the egg albumen) and endogenous retroviruses (which represent ancient viral infections that have integrated into the germline genome over the course of millennia of evolution, currently existing as stable DNA sequences that are inherited in a strict Mendelian fashion) [4].

From a taxonomic and clinical perspective, birds are predominantly susceptible to two main groups of retroviruses, classified under the subfamily *Orthoretrovirinae*: alpharetroviruses (genus *Alpharetrovirus*) and gammaretroviruses (genus *Gammaretrovirus*). Both genera belong to the *Retroviridae* family and are fundamentally characterized by their shared ability to irreversibly integrate viral DNA into the host genome via the reverse transcription of the viral RNA blueprint [5].

Avian alpharetroviruses include an extensive group of pathogens historically referred to as the leukosis and sarcoma group. Prominent members include the avian leukosis virus (ALV), Rous sarcoma virus (RSV), avian myeloblastosis virus (AMV), and turkey lymphoproliferative disease virus (LPDV). The genomic architecture of a standard, replication-competent alpharetrovirus typically consists of three primary open reading frames: *gag* (encoding group-specific internal structural proteins such as the matrix, capsid, and nucleocapsid), *pol* (encoding reverse transcriptase and integrase), and *env* (encoding the envelope glycoproteins). These coding sequences are flanked by Long Terminal Repeats (LTRs) containing vital enhancer and promoter elements. These viruses are fundamentally characterized by high oncogenic activity and are capable of inducing various types of devastating neoplastic processes in infected birds, primarily through insertional mutagenesis where the viral LTR abnormally activates cellular proto-oncogenes.

Avian gammaretroviruses include the highly significant reticuloendotheliosis virus (REV), which exists in two distinct virological forms: a defective, acute transforming strain (REV-T) and a replicationcompetent helper virus (REV-A). Unlike ALV, REV-T carries a specialized viral oncogene (*v-rel*), which allows it to induce rapid and aggressive cellular transformation. Additionally, avian gammaretroviruses encompass the spleen necrosis virus (SNV), chick syncytial virus (CSV), and duck infectious anaemia virus (DIAV). These viruses are distinguished by a remarkably broad spectrum of pathogenic effects that extend far beyond simple tumor formation, critically including profound cellular immunosuppression and severe disruption of the normal developmental pathways of hematopoietic tissues [6].

Consequently, both taxonomic groups of these avian retroviruses play a highly significant and detrimental role in the overall epidemiology and pathogenesis of concurrent avian diseases, representing substantial scientific interest for veterinary virology, global food security, and strict infectious disease control protocols within the modern, high-density poultry industry.

Materials and Methods

To systematically prepare this comprehensive literature review, critically evaluate the epizootiological significance of avian retroviruses, and scientifically substantiate the urgent need for their systematic control and monitoring within the Republic of Kazakhstan, we analyzed a wide array of scientific publications indexed in primary biological databases, prominently including Medline (PubMed), Scopus, Web of Science, and Google Scholar. The systematic literature search

was meticulously conducted using the following specialized Boolean keyword combinations: (“avian retroviruses” or “avian retroviral infections”) and/or (“avian leukosis virus” or “ALV”) and/or (“reticuloendotheliosis virus” or “REV”) and/or (“retrovirus prevalence” or “molecular epidemiology” or “immunosuppression” or “phylogenetic analysis”).

The initial search yielded hundreds of preliminary results, which were subjected to rigorous inclusion and exclusion criteria. Articles were included if they were published in peer-reviewed journals, written in English, and provided high-quality genomic, diagnostic, or epidemiological data. In total, 40 distinct data sources were selected for the final, intensive analysis following a comprehensive thematic screening and the strict exclusion of duplicate, outdated, or non-relevant records. Based on the careful categorization of the retrieved literature, the final review incorporated 38 peer-reviewed journal articles consisting of foundational veterinary virology textbooks, viral encyclopedias, and official taxonomic reports from the International Committee on Taxonomy of Viruses (ICTV).

Geographically and thematically, the thoroughly analyzed literature encompasses 1 specific local study confirming the active circulation of avian leukosis virus within the borders of Kazakhstan, multiple high-resolution epidemiological reports from immediate neighboring countries (specifically the Russian Federation and the People's Republic of China) alongside other globally significant poultry-producing regions. Furthermore, the dataset includes foundational molecular studies detailing the genomic structure, receptor-binding mechanisms, and deep pathogenesis of alpharetroviruses and gammaretroviruses, as well as the latest advances in molecular diagnostic assays, explicitly focusing on multiplexing technologies and novel gene editing prevention strategies.

Results

Avian retroviruses, predominantly and persistently affecting various domesticated and wild bird species, are established and thoroughly documented etiological agents for a wide array of severe, life-threatening pathologies. These encompass diverse neoplastic formations (ranging from lymphomas to sarcomas and hemangiomas), pronounced and debilitating immunosuppression, and other systemic morbidities that severely degrade flock health [7]. Among naturally occurring avian retroviruses, ALV, REV, LPDV are historically and contemporarily the most prevalent. ALV and REV, classified molecularly as simple retroviruses (lacking complex accessory genes like *tat* or *rev* found in lentiviruses), represent highly significant oncogenic agents. Their epidemiology is highly dynamic, intricately dependent on the geographical region, biosecurity levels, and the specific genetic characteristics of the affected avian populations. These resilient pathogens are persistently detected across both wild, migratory avian reservoirs and highly concentrated commercial poultry production ecosystems [8, 9, 10].

ALV is an exceptionally widespread group of oncogenic alpharetroviruses within the *Retroviridae* family and serves as a primary, persistent cause of neoplastic diseases in poultry, especially in commercial meat and egg-laying chickens. Active infection is robustly associated with lymphoid leukosis, diffuse internal organ neoplasms, severe physiological growth retardation, drastically decreased reproductive capacity, and catastrophic drops in overall egg production metrics [11, 12, 13, 14]. Furthermore, ALV induces severe, generalized immunosuppression that fundamentally compromises the host's ability to resist secondary environmental pathogens. ALV is divided into several distinct subgroups determined precisely by genomic nucleotide sequences, which absolutely dictate host cell range, strain pathogenicity, and primary transmission routes. The specific pathogenicity and cellular tropism of ALV are intimately associated with its *env* gene, which encodes the vital viral envelope glycoprotein complex (comprising the surface gp85 and transmembrane gp37 subunits). The highly variable gp85 surface protein strictly dictates host cell receptor binding and ultimately determines subgroup specificity [15, 16].

ALV subgroups (A, B, C, D, J, and K) are classified as exogenous; they are highly capable of rapid horizontal transmission via direct contact or fomites, as well as vertical transmission, and typically exhibit pronounced pathogenicity. Conversely, subgroups E and F are strictly endogenous, existing purely as dormant or defective proviruses within the host genome, transmitting exclusively vertically through Mendelian inheritance, and generally demonstrating minimal to no direct pathogenicity. Subgroup ALV-J has emerged globally as the most virulent, economically devastating, and epidemiologically significant exogenous variant since its discovery in the late 1980s. Genetically

linked to earlier subgroups A, B, and C, ALV-J exhibits extraordinarily high adaptability, aggressively affecting *Galliformes*, *Anseriformes*, and *Passeriformes* [5, 17, 18]. It is widely suggested by molecular phylogenists that ALV subgroups J and K originally emerged through complex genetic recombination events between different exogenous and endogenous ALV variants within a single coinfecting host. This high propensity for rapid genomic recombination significantly complicates infection control, confounds differential diagnosis, and continuously generates novel variants.

The molecular entry mechanism of ALV-J specifically relies on the chicken sodium-hydrogen exchanger type 1 (chNHE1) serving as its obligate cellular receptor. Recent investigations have demonstrated that the N123I mutation within the receptor-binding domain (RBD) of the ALV-J gp85 protein significantly enhances the binding affinity to the chNHE1 receptor, thereby profoundly intensifying viral replication capabilities and increasing *in vivo* viral shedding among infected commercial flocks [19]. Furthermore, the absolute necessity of the chNHE1 receptor for viral entry has spurred highly advanced genomic engineering efforts. Recent advancements utilizing the CRISPR/Cas9 system to precisely delete the critical tryptophan residue at position 38 (W38) of the chNHE1 gene in chicken primordial germ cells have successfully generated edited cell lines exhibiting complete and highly stable resistance to ALV-J infection, presenting a groundbreaking, futureproof strategy for breeding disease-resistant poultry lines [20].

While both are classified as retroviruses, the tumors induced by REV differ mechanistically and substantially from ALV-induced neoplasms. ALV typically induces B-cell lymphomas through slow insertional mutagenesis near the *c-myc* proto-oncogene [21], whereas REV-associated B-cell lymphomas are considerably rarer, exhibit a highly prolonged latent period, and are triggered by insertional mutagenesis affecting different regulatory pathways [22]. REV, a gammaretrovirus, successfully affects a remarkably broad spectrum of avian species, including commercial chickens, turkeys, ducks, geese, pigeons, and numerous wild migratory birds [9, 11]. One uniquely aggressive representative is the T-strain (REV-T), an acute transforming virus capable of rapidly transforming primary avian hematopoietic cells in a matter of days due to its evolutionary acquisition of the potent viral oncogene *v-rel* [23]. The complete genome of the replication-competent REV-A helper strain is a single-stranded positive-sense RNA (approximately 9,000 nucleotides in length) canonically structured as 5'-LTR-*gag-pol-env*-LTR-3'. The Long Terminal Repeats (LTRs) essentially regulate robust transcription and facilitate proviral integration into the host DNA [24].

REV infections in chickens present a remarkably broad clinical spectrum that varies drastically depending on the specific viral genotype, the age of the host at exposure, and the baseline immune status of the flock. Clinical presentations range from severe neurological disorders closely mimicking Marek's disease to chronic, utterly silent subclinical infections. Stunting syndrome conditions characterized by severe weight loss, physiological paleness, and specific feathering abnormalities frequently referred to as Nakanuke disease – is also routinely observed in the field, though REV's precise, direct pathogenic role in the multi-factorial etiology of this syndrome requires further advanced elucidation [25, 26]. Similar to the pathogenic mechanisms of ALV, REV severely disrupts both cellular (T-cell mediated) and humoral (B-cell mediated) immunity, leading to lymphoid depletion in the bursa of Fabricius and the thymus [27].

Pathogenesis, Immunosuppression, and Viral Co-Infections

The most insidious and biologically destructive characteristic of both ALV and REV is their profound capacity to induce long-lasting immunosuppression. The pathogenesis of this immunodeficiency is driven by virus-induced apoptosis of premature lymphocytes, severe disruption of cytokine signaling pathways, and the functional impairment of macrophages. This biological state of immunosuppression acts as an incredibly potent catalyst for secondary pathogens. When commercial flocks are afflicted with subclinical retroviral infections, they lose their ability to mount robust neutralizing antibody responses following routine vaccinations [28]. Consequently, this state paves the way for catastrophic coinfections. For instance, the pathogenesis and clinical severity of highly contagious respiratory pathogens, such as the Avian Infectious Bronchitis Virus (IBV) or Newcastle Disease Virus (NDV), are drastically exacerbated in retrovirus-compromised birds. Coinfection with IBV and ALV leads to significantly heightened respiratory distress, accelerated renal tissue damage (nephropathogenicity), and a much steeper drop in flock survivability compared to an IBV infection in a retrovirus-free, immunocompetent flock [29].

Advancements in Molecular Diagnostics

Traditional diagnostic protocols, such as standard Enzyme-Linked Immunosorbent Assays (ELISA) targeting the p27 group-specific antigen, possess a critical limitation: they are entirely incapable of differentiating between highly pathogenic exogenous subgroups and harmless endogenous retroviral proteins naturally expressed by the chicken genome. To overcome these critical diagnostic limitations and address the rapid emergence of complex recombinant strains, novel multiplex realtime quantitative PCR (qPCR) assays have been recently developed, enabling the highly sensitive, rapid, and simultaneous differential detection of the most epidemiologically significant subgroups: ALV-A, ALV-B, ALV-J, and ALV-K [30]. The implementation of such high-throughput, multiplexed molecular tools is strictly necessary for accurate epidemiological surveillance and the successful execution of rigorous eradication programs.

Prevalence and Epidemiological Distribution in Central Asia

Molecular genetic investigations and rigorous phylogenetic surveillance in countries immediately neighboring Kazakhstan, most notably the People's Republic of China [31–33] and the Russian Federation [34], reveal a widespread, deeply entrenched distribution and a highly concerning level of significant genetic diversity among ALV strains. Subtypes including ALV-A, ALV-B, ALV-J, and various novel recombinant forms are actively circulating, rapidly mutating, and relentlessly adapting to commercial poultry lines. Extensive epidemiological monitoring of native chicken lineages in China between 2022 and 2025 has revealed the concurrent circulation of highly adaptable ALV-J isolates, which predominantly cluster within Clades 1.2 and 1.3 and possess multiple specific functional point mutations and deletions in the 3' untranslated region, indicative of enhanced pathogenicity and rapid genetic evolution [35].

Preliminary and foundational data [36] definitively confirm the active circulation of ALV in at least the high-density agricultural regions of the Almaty region in Kazakhstan. Additionally, acute REV-induced outbreaks have been thoroughly documented in the border regions of China [37]. The broad, multi-species susceptibility to REV-A, combined seamlessly with its extremely high potential for interspecies transmission among migrating wild birds, actively maintains a robust, uncontrollable natural reservoir [38]. Despite this imminent and well-documented biological threat, comprehensive, systematic molecular epidemiological data regarding the true prevalence of gammaretroviruses and alpharetroviruses within the entirety of Kazakhstan remain critically and dangerously scarce.

Discussion

The diverse findings synthesized and meticulously detailed in this literature review highlight a critical, yet frequently underestimated and severely underfunded, threat to the modern global poultry industry. Although ALV and REV may not consistently induce direct, acute flock mortality as frequently or visibly as more aggressive retroviruses like the historically notorious RSV, their insidious capacity to induce delayed lymphoblastomas and subtle neoplastic lesions of various internal organs often remains completely undetected during standard, routine veterinary post-mortem examinations on the farm level.

The absolute most profound consequence of these persistent retroviral infections is the systemic induction of severe, generalized immunodeficiency. This long-term immunosuppression acts as a biological catalyst, heavily predisposing affected flocks to devastating, rapidly spreading concurrent infections and significantly undermining the calculated efficacy of standard, expensive immunoprophylaxis programs. Consequently, otherwise properly vaccinated flocks that are silently infected with ALV or REV become highly vulnerable, biologically defenseless targets for lethal endemic pathogens, such as various strains of the avian influenza virus, Newcastle disease virus, and infectious bronchitis virus.

From a strict industrial and macroeconomic perspective, this complex viral dynamic translates into profound, multi-layered, and largely hidden economic losses. Massive financial capital and labor resources heavily allocated for comprehensive vaccination programs completely fail to yield the expected protective flock immunity. The ensuing, highly destructive secondary infection outbreaks are frequently, yet entirely erroneously, attributed to compromised vaccine batch quality, broken coldchain logistics, or poor administration techniques, rather than accurately pointing to the true

underlying culprit: the subclinical, silent circulation of immunosuppressive retroviruses. Furthermore, REV poses an exceptional, highly specific virological hazard due to its highly unusual capacity to physically integrate its genetic material directly into the larger genomes of other unrelated avian DNA viruses (such as the Fowlpox virus or Marek's disease virus), a phenomenon which heavily complicates standard diagnostic procedures and severely limits traditional infection control strategies.

An additional, highly critical dimension to the economic and epidemiological impact of avian retroviruses is the severe risk of iatrogenic transmission through contaminated biological products. The global poultry industry relies heavily on live-attenuated viral vaccines (e.g., vaccines against Marek's Disease, Infectious Bursal Disease, and Infectious Bronchitis) which are traditionally cultivated in Specific Pathogen Free (SPF) chicken embryos or primary avian cell cultures. If the breeding flocks producing these SPF eggs experience an undetected breach in biosecurity and become subclinically infected with exogenous ALV or REV, the resulting vaccine batches can become contaminated with live retroviruses. Administering these compromised biological products directly into day-old chicks essentially inoculates entire commercial flocks with immunosuppressive retroviruses, leading to catastrophic, widespread dissemination. This reality necessitates the implementation of ultrasensitive, multiplex molecular screening of all master seed viruses and final vaccine batches.

Currently, the Republic of Kazakhstan critically lacks a systematic, continuous, and statefunded molecular monitoring framework for retroviral infections in both domestic agricultural operations and wild, migrating avian populations; epidemiological surveillance remains strictly episodic and highly localized. The complete, systemic absence of robust, continuous national data regarding the true prevalence, exact subgroup distribution, and high-resolution genomic characterization of circulating ALV and REV strains represents a massive, glaring vulnerability in regional veterinary biosecurity and national food safety protocols.

This highly precarious epidemiological situation is further exacerbated by the inherent, everpresent risk of accidental retroviral transmission through imported live-attenuated vaccines manufactured for other severe avian diseases, as detailed above. Such undeniable biological risks dictate an absolute, urgent need for the rapid implementation of stringent, state-mandated quality control measures. These measures must demand the rigorous, mandatory retroviral molecular screening (utilizing advanced qPCR technologies) of both domestically produced and internationally imported biological products, strictly enforced alongside continuous, uncompromising biosecurity oversight of all commercial poultry breeding facilities operating within the nation.

The uncontrolled, silent circulation of immunosuppressive retroviruses is not merely a localized agricultural or economic issue; it is, fundamentally, a transnational biosecurity concern of the highest order. Poultry flocks suffering from severe retrovirus-induced immunodeficiency provide an optimal, highly unrestrictive biological environment for the prolonged replication, unchecked amplification, and rapid genetic adaptation of secondary viral and bacterial pathogens. In absolute essence, these immunocompromised birds function as massive, unregulated biological "bioreactors," actively facilitating accelerated viral mutation rates, dangerous antigenic drift, and the eventual, inevitable generation of novel, highly virulent pathogenic strains capable of crossing regional borders.

Finally, the undeniable transboundary dissemination of both ALV and REV via wild, migratory avian species constitutes a paramount, highly complex ecological threat. Geographically situated precisely in the very heart of the Eurasian continent, the vast territory of Kazakhstan is directly intersected by four of the eight major global migratory flyways, most notably the Central Asian and the East Asian-Australasian flyways. The extensive, highly biologically diverse network of freshwater lakes, wetlands, and river systems in Eastern and Northern Kazakhstan serves as crucial, densely populated staging, resting, and nesting grounds for hundreds of numerous migratory waterfowl species. This unique, undeniable geographical reality positions the country as a highly critical, high-risk hub for the potential intercontinental spread of avian retroviruses, rendering the immediate funding and execution of comprehensive, long-term molecular-epidemiological monitoring programs not just an academic pursuit, but an urgent scientific, economic, and practical imperative.

Conclusion

In summation, avian retroviral infections, particularly the highly adaptable ALV and the aggressive REV, remain a severe, critical, and continuously evolving issue at the very forefront of modern veterinary

virology, directly threatening the sustainability of the global poultry industry. The extraordinarily high genetic variability and rapid recombination rates of these viruses, combined with their fundamental, biological ability to irreversibly integrate directly into the host cell's chromatin and establish lifelong persistent infections, underscores the extreme complexity of attempting epizootiological control, rendering traditional disease prevention methods highly inadequate.

Numerous high-resolution genomic studies unequivocally indicate that various, highly mutated genetic variants of ALV (particularly Clades 1.2 and 1.3 of ALV-J, which boast mutations like N123I that heavily augment receptor binding) actively circulate and dominate widely in countries immediately neighboring Kazakhstan, most notably including China and Russia. This firmly confirms the active, relentless processes of viral evolution and the steady, cross-border dissemination of retro-viruses within regional domestic poultry populations. Of equal, distinct significance is REV, which is uniquely characterized by an exceptionally broad spectrum of devastating clinical manifestations, ranging from aggressive neoplastic processes and severe neurological disorders to profound, generalized cellular immunosuppression in infected birds of multiple species. The profound immunosuppressive effects dictated by both ALV and REV critically result in massively reduced avian resistance to other endemic infectious agents (such as IBV and AIV), severely deteriorated agricultural productivity, ruined vaccine efficacy, and exponentially increased, largely hidden economic losses throughout the poultry industry. Furthermore, the unusually wide range of susceptible natural hosts, comprehensively encompassing both highly concentrated commercial flocks and highly mobile wild migratory birds, massively contributes to the secure maintenance of natural, unreachable viral reservoirs and guarantees their further, unhindered dissemination across the continent.

Despite the existence of isolated, separate molecular data regarding the limited circulation of ALV specifically in Kazakhstan, cohesive, national-level information on the true prevalence, phylogenetic origins, and distribution density of avian retroviral infections within the broader country remains extremely, dangerously limited. The glaring lack of a systematic, statesponsored molecular epidemiological monitoring framework completely prevents a full, accurate assessment of the true scale of distribution and the complex genetic diversity of these stealthy pathogens. Concurrently, the official, documented registration of acute REV outbreaks in the immediate border regions of China firmly indicates an immediate, highly probable potential threat of the rapid introduction and silent spread of these highly pathogenic viruses deep into the sovereign territory of Kazakhstan via both trade routes and migratory flyways.

Consequently, initiating and consistently conducting highly comprehensive, state-of-the-art research aimed directly at the rapid identification, deep molecular-genetic characterization (including next-generation sequencing), and continuous geographic monitoring of avian retroviruses is of paramount scientific and practical importance. The highly actionable data gathered through such rigorous molecular surveillance can heavily facilitate a significantly better, clearer understanding of the regional epizootiological situation. Ultimately, this will directly drive the development of highly effective, targeted biosecurity protocols, the implementation of advanced diagnostic screening measures (such as multiplex qPCR), the exploration of novel prophylactic strategies (like CRISPR-mediated receptor editing), and the successful, permanent mitigation of the devastating economic damage inherently associated with retroviral infections in the modern poultry industry.

Authors' contributions

LM: original draft; KI: investigation, original draft; YO, YS: reviewing and editing.

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Conflicts of Interest

The authors declare that they have no conflicts of interest related to this study. No financial or non-financial competing interests exist that could have influenced the results or interpretation of the data presented in this manuscript.

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