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DETECTION OF FIELD NEWCASTLE DISEASE VIRUS GENOTYPE VII AND INFECTIOUS BURSAL DISEASE VIRUS IN A COMMERCIAL LAYING FLOCK IN THE AKMOLA REGION

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ABSTRACT

Infectious bursal disease virus (IBDV) and Newcastle disease virus (NDV) remain important pathogens in commercial poultry production. In vaccinated flocks, molecular detection requires careful interpretation because viral genetic material may originate from either field infection or vaccine-associated signals. We investigated a mortality episode in a vaccinated commercial laying flock in the Akmola Region using reverse transcription polymerase chain reaction (RT-PCR) and Sanger sequencing of selected viral genomic fragments. Five deceased laying hens were examined. NDV RNA was detected in all five birds by targeting the L gene, and sequencing supported its assignment to genotype VII and a field-associated rather than vaccine-lineage sequence. IBDV RNA was detected in two of the five birds by targeting VP2; sequencing identified a field-associated sequence most closely related to GenBank accession D00869.2.2 within the analyzed fragment. The findings demonstrate concurrent detection of genetically distinct field-associated NDV and IBDV sequences within the investigated mortality episode. Given the very small sample size and the absence of quantitative virological, serological, and detailed pathological data, the study does not establish the causal contribution of either virus to the observed production losses or mortality, nor does it demonstrate flock-level co-circulation. The results nevertheless illustrate the value of sequence-based verification when interpreting molecular detections in vaccinated poultry.

Keywords: IBDV, NDV, co-infection, infectious bursal disease, Newcastle disease, genotype VII, molecular diagnostics, commercial egg production.

INTRODUCTION

Infectious bursal disease (IBD, Gumboro disease) and Newcastle disease (ND) continue to determine the structure of infectious risk in commercial poultry production, as they affect the flock not only through clinical morbidity and mortality but also through long-term immunological and production consequences. The infectious bursal disease virus (IBDV) belongs to the *Birnaviridae* family and is a bisegmented RNA virus. Its pronounced tropism for lymphoid tissue, primarily the bursa of Fabricius, underlies its immunosuppressive effect and the subsequent reduction in the efficacy of post-vaccination responses. The Newcastle disease virus (NDV) belongs to the genus *Orthoavulavirus* of the *Paramyxoviridae* family and is a single-stranded, negative-sense RNA virus. It is characterized by high contagiousness and significant genetic variability, which is reflected in a diversity of genetic lineages and a range of clinical manifestations—from subclinical and respiratory forms to systemic disease with high mortality. For NDV, an important molecular marker of pathogenicity is the cleavage profile of the F protein, which dictates the virus's capacity for systemic replication and the overall severity of the disease.

IBDV is considered one of the key immunosuppressive factors in chickens: damage to lymphoid tissue, diminished functional capacity of the B-cell compartment, and the secondary weakening of vaccine responses create conditions under which even moderate infectious loads manifest more severely and are accompanied by pronounced production losses. Conversely, NDV is a pathogen with high epizootic potential. Its ability to spread rapidly within a farm determines its economic significance, particularly in laying flocks, where drops in egg production, deteriorated feed conversion, and protracted recovery of productivity serve as primary indicators of herd distress.

In recent years, accumulated data in Kazakhstan have confirmed that the risks associated with IBDV and NDV remain highly relevant in practice. At the national level, unfavorable epizootic situations among poultry are routinely described, accompanied by laboratory confirmations of the circulation of genetically significant variants of these viruses, most notably NDV genotype VII. For commercial production, this is of fundamental importance, as genotype VII is regarded as the most unfavorable in terms of both epizootic potential and the scale of its consequences. In environments where this genotype is present, preventive programs must be evaluated not merely by the fact that vaccination was performed, but by the flock's actual capacity to withstand field pressure, reduce viral shedding, and limit intra-farm spread. Otherwise, even with a formally correct vaccination scheme, episodes of clinically significant disease can occur, and farms will continue to face recurrent production shortfalls.

Current approaches to ND prevention are based on the dual objective of vaccination: preventing clinically manifest disease and mortality, while limiting replication and viral shedding to reduce the probability of silent NDV circulation. Live vaccines provide clinical protection, but sterilizing immunity is not always achieved and heavily depends on flock coverage, the quality of vaccine administration, technical discipline, maternally-derived antibodies (MDAs), and stress factors. For sustained long-term productivity, inadequate flock protection can ultimately maintain viral circulation. Consequently, increased attention is being directed toward the antigenic matching of vaccines with circulating field strains, including genotype VII, as a primary strategy for mitigating epidemiological pressure.

IBD prevention requires a somewhat different systemic approach, as IBDV-induced immunosuppression exacerbates concurrent infectious issues and frequently manifests as a sub-

clinical background characterized by reduced predictability of vaccine responses and an increase in respiratory and enteric complications. Due to the evolution of IBDV, prevention strategies must incorporate the careful selection of a vaccine platform and the evaluation of protective potential, taking into account MDAs and the intensity of field pressure. Sanitary protocols are equally critical, as the virus is highly resilient in the external environment. It is also essential to utilize live, immune-complex, and recombinant vector vaccines to minimize the risk of vaccine-induced damage to lymphoid tissues. Efficacy is typically evaluated based on the uniformity of responses to concurrent vaccines, the incidence rate of secondary infections, and the overall stability of production metrics.

In commercial poultry farming, interpreting molecular diagnostics in vaccinated flocks presents a particular challenge. The overlapping of vaccine and field signals, especially when using live vaccines, must be considered a realistic scenario; therefore, PCR positivity alone is often insufficient. It is necessary to determine whether the detected signal reflects vaccine-associated replication or the circulation of a field virus capable of sustaining transmission and triggering an outbreak. For this reason, genetic verification is increasingly utilized in outbreak investigations. Sequencing allows for the assignment of the virus to a specific lineage and confirms its field origin, providing actionable data for risk management. For NDV, the detection of genotype VII alters the alert level and dictates the scope of required biosecurity measures. For IBDV, the analysis of variable regions, including VP2 markers, helps assess alignment with field variants and potential correlations with the flock's immunological instability.

In Kazakhstan, the importance of investigating such co-infections is amplified by the heterogeneity of the epizootic environment, where commercial farms coexist with private backyard holdings and the migratory routes of wild birds. This dynamic creates multiple channels for the introduction and maintenance of infections, necessitating a combination of vaccination, stringent monitoring, and preparedness for the rapid identification of field strains. A scientifically rigorous description of these episodes expands the regional database regarding IBDV and NDV circulation and establishes benchmarks

for auditing prevention strategies and enhancing control measures at the farm level.

MATERIALS AND METHODS

Study design and collection of biological samples. This study was designed as a descriptive diagnostic investigation of a mortality episode that occurred in 2021 at a commercial laying facility in the Akmola region. Biological material was obtained from five deceased laying hens. According to the available farm records, the episode was associated with growth retardation, loss of body weight, and a decrease in egg production. The available documentation did not provide the exact dates of individual mortality events; therefore, this parameter was not incorporated into the analysis. The carcasses had been subjected to pathological examination by specialists at the poultry facility before the biological material was submitted to our laboratory. The laboratory team did not perform the necropsy. The macroscopic findings reported by the facility included darkening of the liver and spleen. Because a standardized necropsy protocol, histopathological examination, and photographic documentation were not available to the laboratory, these observations were considered non-specific and were not used to infer the etiology or severity of disease. Tracheal and cloacal swabs were collected from each bird, together with tissue samples from the brain, trachea, liver, lungs, proventriculus, kidney, and spleen. Swabs and tissue samples were placed in sterile tubes containing transport media and delivered to the laboratory under controlled temperature conditions. Upon arrival, the samples underwent primary processing; aliquots were frozen and stored at -70°C until RNA extraction and subsequent molecular testing. According to farm records, the examined birds had previously been vaccinated against Marek's disease, infectious bursal disease, avian infectious bronchitis (strain H120), avian pneumovirus infection, Newcastle disease (strain La-Sota), avian infectious encephalomyelitis, and infectious laryngotracheitis.

RNA extraction and reverse transcription. RNA was extracted from tracheal and cloacal swabs, as well as from chicken tissue samples, using TRIzol (Sigma) in accordance with the manufacturer's protocol. Spectrophotometric analy-

Table 1. Primers used in the study

№	Infectious agent	Genome type	Target	Matrices	Ref.
1	Avian Influenza virus A (AIV)	RNA	<i>PB1</i>	Cloacal and tracheal swab	[11]
2	Astroviruses (AstroV)	RNA	<i>L</i>	Cloacal swab	[12]
3	Infectious bursal disease virus (IBDV)	RNA	<i>VP2</i>	Cloacal swab	[13]
4	Avian Infectious Bronchitis Virus (IBV)	RNA	<i>S1</i>	Trachea, cloacal swab	[14]
5	Newcastle Disease Virus (NDV)	RNA	<i>L</i>	Swabs	[5]
6	Infectious laryngotracheitis virus (ILTV)	DNA	<i>TK</i>	Trachea	[15]
7	Reticuloendotheliosis virus (REV)	DNA	<i>LTR</i>	Liver	[16]
8	Marek disease virus (MDV)	DNA	<i>VP16</i>	Liver	[16]
9	Chicken circovirus (CCV)	DNA	<i>VP1/VP2</i>	Proventriculus	[16]
10	Avipoxvirus (AviPoxV)	DNA	<i>4b</i>	Tracheal swab, spleen	[17]
11	Fowl adenovirus (FAdV)	DNA	<i>Hexon</i>	Liver, spleen	[18]
12	<i>Chlamydia</i> spp. и <i>Ch. psittaci</i>	DNA	<i>OmpA</i>	Trachea	[19]
13	<i>Mycoplasma synoviae</i> (MS)	DNA	<i>16S</i>	Lung	[20]
14	<i>Salmonella enterica</i>	DNA	<i>iroB</i>	Cloacal swab	[21]

sis was performed using a NanoDrop 2000 spectrophotometer (Thermo Fisher Sci.). Complementary DNA (cDNA) was synthesized utilizing M-MLV reverse transcriptase (NEB). Each reaction mixture contained 10 µl of the RNA sample, 1 µl of random hexamer primers (Thermo Fisher Sci.), and 9 µl of reverse transcription buffer, strictly following the manufacturer's protocol. The reaction mixture was incubated at 25°C for 10 minutes, then at 37°C for 60 minutes, and subsequently heated at 70°C for 10 minutes.

Molecular RT-PCR/PCR diagnostics. Screening diagnostics were carried out using RT-PCR/PCR methods. Published protocols and primer systems were utilized for each targeted pathogen (Table 1). Amplification was performed using Hot-Start Taq DNA polymerase (NEB) according to the manufacturer's instructions. The amplification conditions were as follows: 95°C for 5 minutes, followed by 40 cycles of 94°C for 30 seconds, 54°C for 30 seconds, and 72°C for 1 minute, with a final elongation step at 72°C for 5 minutes. PCR products were analyzed via electrophoresis in a 1.5% agarose gel and visualized under UV light.

Target fragment amplification and Sanger DNA sequencing. To confirm the etiology and facilitate subsequent genetic interpretation, fragments of the VP2 (IBDV) and L (NDV) genes were amplified according to published protocols. The lengths of the analyzed fragments were 365 and 611 bp, respectively. Conventional PCR was performed using the primers listed in Table 2. Amplification was carried out using Hot-Start Taq DNA polymerase (New England Biolabs, NEB) according to the manufacturer's instructions. The PCR temperature profile included initial denaturation at 95°C for 5 min, followed by 40 cycles of: 94°C for 30 s, 54°C for 30 s, 72°C for 1 min, with a final elongation step at 72°C for 5 min. The resulting PCR products were purified using a PCR product purification kit (QIAGEN). For verification of the nucleotide sequences, the purified amplicons were sequenced via the Sanger method using the BigDye® Terminator v3.1 cycle sequencing kit (Applied Biosystems), followed by analysis on an ABI 3500XL Genetic Analyzer (Applied Biosystems).

Bioinformatics analysis. Sanger sequencing chromatograms underwent initial quality control, including visual assessment of peak quality and trimming of low-quality regions at the ends of the reads. When bidirectional reads were available, a consensus sequence was generated from aligned positions. The obtained nucleotide sequences were compared with reference sequences in the GenBank database using the Nucleotide BLAST (BLASTn) tool. The closest matching records were documented and used for etiological verification and preliminary genetic characterization, including assessment of NDV genotype assignment and distinction from vaccine-associated lineages within the analyzed fragment.

Phylogenetic analysis. Phylogenetic trees were constructed using the Maximum Likelihood (ML) method based Table 2. Primers for NDV and IBDV amplification and sequencing

on the nucleotide sequences of the analyzed NDV L and IBDV VP2 fragments. The Tamura-Nei model was used as the nucleotide substitution model, and branch support was assessed by bootstrap analysis with 1000 replicates.

Statistical analysis. Given the descriptive nature of the investigation and the very small sample size ($n=5$), the data were summarized using absolute counts only. No percentages, confidence intervals, prevalence estimates, or inferential statistical tests were calculated. This approach was selected to avoid overinterpretation of proportions derived from a very small number of examined birds.

RESULTS

Characterization of the studied material and initial molecular screening. The biological material comprised samples from five deceased laying hens from a commercial facility in the Akmola region. According to the available farm records, the mortality episode was accompanied by growth retardation, reduced body weight, and a decrease in egg production. The carcasses had been examined pathologically at the poultry facility before submission of the biological material to the laboratory. The reported macroscopic findings included darkening of the liver and spleen. These observations were considered non-specific and were not used to assign an etiology. Initial molecular screening was performed using RT-PCR/PCR with an extended panel of viral and bacterial agents relevant to respiratory disease, enteric disease, immunosuppression, and systemic infections. Sequence-confirmed positive findings were obtained for two pathogens. NDV RNA was detected in all five examined birds based on the L-gene target. IBDV RNA was detected in two of the five birds based on the VP2 target. Thus, both viruses were detected within the investigated mortality episode; however, the small sample size and non-random sampling do not permit estimation of flock-level prevalence or inference of co-circulation throughout the farm.

Genetic verification of NDV. To genetically verify the NDV detection, L-gene amplicons from all five birds were subjected to Sanger sequencing followed by BLASTn analysis. The obtained NDV sequences showed the highest similarity to a genotype VII field reference from Russia (GenBank PP766718), supporting assignment of the detected virus to genotype VII within the analyzed fragment. In the context of the farm vaccination history, this finding supported interpretation of the detected signal as field-associated rather than representative of the reported La-Sota vaccine lineage. For further phylogenetic analysis, the sequence NDV/KZ/Akmola/2021-1, obtained from the sample with the clearest and most stable chromatogram, was selected as the representative sequence. The remaining reads supported reproducibility of target amplification and consistency of the genotype interpretation across the examined series. Because only a partial L-gene fragment was analyzed, the assignment is restricted to the resolution provided by this genomic region.

№	Наименование праймера	Последовательность	Источник
1	NDV-L-2173-nF3	5'- TGGACKATGATCTCRATTGCWGC	[5]
2	NDV-L-2783-nR3	5'- GTRTAGAGCCTTGAGTATTGRAG	[5]
3	IBDV-VP2-49-F	5'- AGCCTTCTGATGCCAACAAAC	[13]
4	IBDV-VP2-414-R	5'- ATCTGTCAAGTCACTCAGGC	[13]

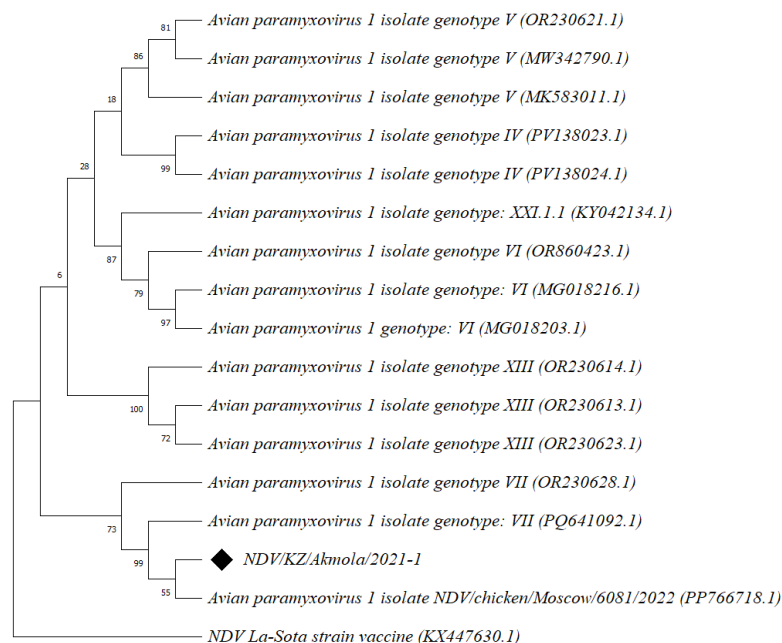


Figure 1. Maximum likelihood phylogenetic tree of NDV based on the sequenced fragment of the L gene. The tree illustrates the position of the representative sequence *NDV/KZ/Akmola/2021-1* (indicated by ♦) relative to reference sequences of various genotypes; the closest sequence according to BLASTn (PP766718.1) is included for comparison. Branch support was evaluated using bootstrap analysis (1000 replicates).

Genetic verification of IBDV. IBDV amplicons targeting the *VP2* gene from the two positive samples were sequenced by the Sanger method and analyzed using the same BLASTn approach. The obtained *VP2* sequence was most closely related to GenBank accession D00869.2 within the analyzed region and was consistent with a field-associated, non-vaccine sequence profile. The sequence IBDV/KZ/Akmola/2021-1 was selected as the representative sequence for the present study. The second sequence provided additional confirmation of IBDV detection and consistency of the BLASTn interpretation. These molecular findings demonstrate the presence of an IBDV field-associated sequence in two sampled birds but do not, by themselves, demonstrate active flock-wide transmission or establish immunosuppression in the affected birds.

Phylogenetic analysis of NDV (L locus). To refine the genetic position of the detected NDV and to independently corroborate the BLASTn results, a phylogenetic analysis was performed utilizing the sequenced fragment of the L gene. The analysis incorporated the representative sequence NDV/KZ/Akmola/2021-1 alongside a set of reference NDV sequences from the NCBI GenBank database. These references represented the major genetic lineages of class II paramyxoviruses, including genotype VII, as well as sequences characteristic of vaccine lineages (genotype II) to provide a clear differentiation between the field variant and the vaccine strain within the analyzed fragment. All sequences were trimmed to a uniform range corresponding to the overlapping region of the sequenced locus, after which multiple alignment and maximum likelihood tree construction were performed, with branching robustness evaluated via bootstrap analysis (1000 replicates). Tree rooting was conducted using an outgroup selected from a more distantly related NDV lineage within the available reference set to ensure correct topological orientation. The resulting tree revealed that NDV/KZ/Akmola/2021-1 clus-

tered within the clade corresponding to genotype VII and was positioned on the same branch as the reference sequences identified as most closely related via BLASTn (including PP766718). Thus, the phylogenetic analysis corroborated the direction of the BLASTn interpretation and supported the assignment of the detected sequence to NDV genotype VII within the analyzed fragment. The phylogenetic tree for NDV is presented in Figure 1.

The phylogenetic analysis was based on a partial fragment of the L gene and, for the representative sequence, on unidirectional Sanger data; therefore, the phylogenetic interpretation is constrained by the limited length of the sequenced region and by the composition of the reference set. Nevertheless, the concordance between BLASTn and ML phylogenetic placement supports the assignment of *NDV/KZ/Akmola/2021-1* to genotype VII within the limits of the analyzed fragment. This genetic result supports a field-associated interpretation and differentiates the sequence from the La-Sota vaccine lineage, but it does not establish the clinical contribution of NDV to the mortality episode.

Phylogenetic analysis of IBDV (VP2 locus). To further assess the genetic relationship of the detected IBDV, a phylogenetic analysis was conducted using the sequenced VP2 fragment. The analysis included the representative sequence IBDV/KZ/Akmola/2021-1 and a set of reference VP2 sequences representing major IBDV groups. All sequences were trimmed to the overlapping region of the available fragment, followed by multiple sequence alignment and construction of a Maximum Likelihood tree with 1000 bootstrap replicates. The representative sequence clustered with the reference sequence most closely related by BLASTn (D00869.2.2). This topology supports the interpretation of the detected VP2 sequence as field-associated within the analyzed region. However, because the analysis was based on a partial VP2 frag-

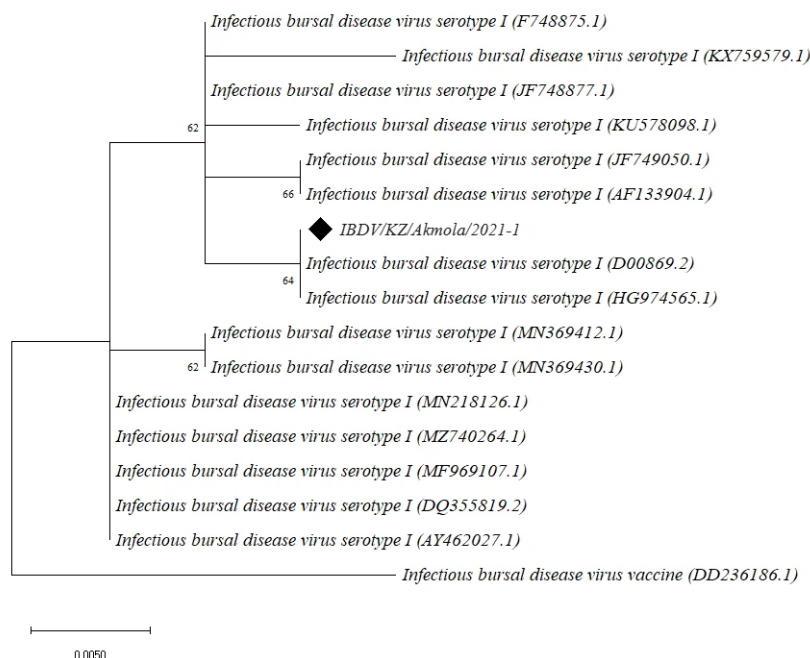


Figure 2. Maximum likelihood phylogenetic tree of IBDV based on the sequenced VP2 fragment, constructed using MEGA X software. The position of the representative sequence IBDV/KZ/Akmola/2021-1 (indicated by) relative to reference sequences is shown; the closest sequence according to BLASTn (D00869.2.2) is included for comparison. Branch support was evaluated using bootstrap analysis (1000 replicates). Interpretation is limited by the informativeness of the partial VP2 fragment and does not establish virulence or transmission.

ment, it should not be used to infer detailed intra-group classification, virulence, or epidemiological transmission. More extensive VP2 sequencing, additional segment A markers, or whole-genome sequencing would be required for high-resolution characterization.

The BLASTn and phylogenetic results were concordant for both detected viruses. For NDV, the closest BLASTn reference (PP766718) belonged to genotype VII, and the representative sequence *NDV/KZ/Akmola/2021-1* clustered within the corresponding genotype VII group in the ML tree. For IBDV, the representative sequence *IBDV/KZ/Akmola/2021-1* clustered with the reference sequence *D00869.2* identified by BLASTn as its closest match. Together, these analyses support the genetic characterization of the detected sequences as field-associated NDV genotype VII and field-associated IBDV within the limits of the sequenced fragments. They do not, however, establish the direction of transmission, flock-level circulation, or a causal relationship between either virus and the observed mortality or production losses.

DISCUSSION

This study describes the concurrent detection of field-associated NDV genotype VII and IBDV in samples collected from a vaccinated commercial laying flock in the Akmola region during a mortality episode accompanied by reduced body weight and egg production. NDV RNA was detected in all five examined birds, whereas IBDV RNA was detected in two birds. Sequencing supported assignment of the NDV sequence to genotype VII and the IBDV sequence to a field-associated profile within the analyzed VP2 fragment. These findings establish the presence of both viral agents in the investigated materials but do not establish that either virus alone,

or their combination, caused the observed clinical or production outcomes.

In vaccinated flocks, PCR positivity alone may be insufficient to distinguish vaccine-associated signals from field infection. In the present study, Sanger sequencing provided genetic evidence supporting a field-associated origin of the detected NDV and IBDV sequences. This strengthens the etiological interpretation of the laboratory findings but should not be equated with proof of pathogenic causation.

The detection of IBDV in two of five birds warrants attention because IBDV is a recognized immunomodulatory pathogen; however, the present molecular data do not demonstrate immunosuppression in the examined birds. No bursal tissue, quantitative viral load data, serological measurements, or immunological parameters were available. Therefore, it would be inappropriate to conclude that IBDV reduced vaccine-induced immunity or increased susceptibility to NDV in this flock. At most, the findings indicate that an IBDV field-associated sequence was present concurrently with NDV in the investigated episode.

The study has several important limitations. First, only five deceased hens were examined, and the sampling was not designed to estimate prevalence or assess flock-level circulation. Second, the exact dates of individual mortality events were not available in the submitted documentation. Third, the pathological information was limited to non-specific macroscopic observations reported by the poultry facility; the necropsy was not performed by the laboratory team, and histopathology and photographic documentation were not available. Fourth, genetic characterization relied on partial L and VP2 fragments and therefore has limited phylogenetic resolution. Finally, the study did not include quantitative PCR, serol-

ogy, virus isolation, or other measures of infectivity and immune status. These limitations should be considered when interpreting the epidemiological and pathogenic significance of the findings.

Within these limitations, the practical value of the investigation lies in the demonstration that sequence-based verification can distinguish field-associated viral genetic signals from vaccine-related interpretations in a vaccinated flock. The detection of NDV genotype VII justifies review of biosecurity and vaccination practices, but it does not by itself identify the virus as the primary cause of mortality. Similarly, detection of IBDV supports inclusion of IBDV in the diagnostic differential but cannot establish a role for immunosuppression without additional pathological and immunological evidence.

CONCLUSION

This investigation identified NDV genotype VII and a field-associated IBDV sequence in biological samples collected from five deceased laying hens during a mortality episode in a vaccinated commercial flock in the Akmola region. NDV RNA was detected in all five birds, while IBDV RNA was detected in two. Sanger sequencing and phylogenetic analysis supported the genetic characterization of the detected sequences within the analyzed L and VP2 fragments.

Because of the very small sample size, limited pathological documentation, and absence of quantitative virological and immunological data, the findings should be interpreted as evidence of concurrent viral detection rather than proof of flock-level co-circulation, coinfection at the individual-bird level, or a causal relationship between the viruses and the observed mortality or production losses. The study nevertheless demonstrates the diagnostic usefulness of sequence-based verification in vaccinated poultry and supports its incorporation into outbreak investigations when PCR-positive results require discrimination between field-associated and vaccine-related signals.

A practical diagnostic strategy for commercial poultry enterprises should consider sequence-based verification after initial PCR detection when vaccine-derived and field-associated viral signals cannot otherwise be distinguished. Such an approach can improve genetic characterization and risk assessment while avoiding overinterpretation of molecular detection as evidence of pathogenic causation.

AUTHOR CONTRIBUTIONS

Conceptualization, Zh.A.V.; Methodology, K.M.A., N.D.A.; Investigation, I.K.R., K.M.A., N.D.A.; Data curation, I.K.R.; Resources, N.D.A.; Formal analysis: I.K.R., N.D.A.; Visualization, I.K.R.; Writing – original draft, I.K.R.; Writing – review and editing, I.K.R., Zh.A.V.; Supervision, Zh.A.V.; Project administration, I.K.R., Zh.A.V.; Funding acquisition, Zh.A.V. All authors have read and agreed to the published version of the manuscript.

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АҚМОЛА ОБЛЫСЫНДАҒЫ ЖҰМЫРТҚАЛАУШЫ КОММЕРЦИЯЛЫҚ ТАБЫНДА VII ГЕНОТИПТІ ДАЛАЛЫҚ НЬЮКАСЛ АУРУЫ ВИРУСЫ МЕН ИНФЕКЦИЯЛЫҚ БУРСАЛЫҚ АУРУ ВИРУСЫНЫҢ АНЫҚТАЛУЫ

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ТҮЙІН

Инфекциялық бурсалық ауру вирусы (IBDV) мен Ньюкасл ауруы вирусы (NDV) өнеркәсіптік құс шаруашылығында маңызды патогендер болып табылады. Вакцинацияланған табындарда молекулалық диагностиканы түсіндіру сақтықты талап етеді, өйткені вирустың генетикалық материалы далалық инфекцияны да, вакцинамен байланысты сигналды да көрсетуі мүмкін. Зерттеуде Ақмола облысындағы вакцинацияланған коммерциялық жұмыртқалаушы табындағы 2021 жылғы падеж эпизоды сипаттамалық диагностикалық тәсілмен зерттелді. Бес өлген жұмыртқалаушы тауықтан алынған материал ОТ-ПТР және кейінгі Сэнгер секвенирлеуі арқылы зерттелді. NDV РНҚ-сы барлық бес құстан L гені бойынша анықталды, ал секвенирлеу анықталған тізбекті VII генотипке жатқызуды және оның вакциналық линиядан айырмашылығын қолдады. IBDV РНҚ-сы бес құстың екеуінен VP2 гені бойынша анықталды; алынған тізбек зерттелген фрагмент шегінде GenBank D00869.2 тізбегіне ең жақын болды және далалық вирус профиліне сәйкес келді. Деректер зерттелген падеж эпизоды шеңберінде NDV мен IBDV-дің далалық сигналдарының қатар анықталғанын көрсетеді. Алайда үлгінің өте аз болуы және сандық вирусологиялық, серологиялық және толық патологиялық деректердің болмауы бұл вирустардың өлім-жітім мен өнімділіктің төмендеуіндегі себептік рөлін немесе табын деңгейіндегі коциркуляцияны дәлелдеуге мүмкіндік бермейді.

Түйінді сөздер: IBDV, NDV, коинфекция, инфекциялық бурса ауру, Ньюкасл ауруы, VII генотип, молекулалық диагностика, өнеркәсіптік жұмыртқа өндірісі.

УДК 619:578.82/.83:636.5

ОБНАРУЖЕНИЕ ПОЛЕВОГО ВИРУСА БОЛЕЗНИ НЬЮКАСЛА ГЕНОТИПА VII И ВИРУСА ИНФЕКЦИОННОЙ БУРСАЛЬНОЙ БОЛЕЗНИ У КУР В АҚМОЛИНСКОЙ ОБЛАСТИ

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АННОТАЦИЯ

Вирус инфекционной бурсальной болезни (IBDV) и вирус болезни Ньюкасла (NDV) остаются значимыми патогенами промышленного птицеводства. В вакцинированных стадах результаты молекулярной диагностики требуют осторожной интерпретации, поскольку выявление генетического материала может быть связано как с полевой инфекцией, так и с поствакцинальными сигналами. В работе исследован эпизод падежа в вакцинированном коммерческом стаде кур-несушек Акмолинской области с использованием ОТ-ПЦР и последующего секвенирования по Сэнгеру отдельных участков генома. Исследованы пять павших кур-несушек. РНҚ NDV выявлена у всех пяти птиц по мишени в гене L; секвенирование позволило отнести выявленную последовательность к генотипу VII и подтвердить ее отличие от вакцинных линий. РНҚ IBDV выявлена у двух из пяти птиц по гену VP2; полученная последовательность имела наибольшую близость к референсной последовательности GenBank D00869.2 в пределах исследованного фрагмента и соответствовала полевому профилю. Полученные данные свидетельствуют о совместном выявлении генетически различающихся полевых вариантов NDV и IBDV в рамках исследованного эпизода. Однако с учетом малого объема выборки и отсутствия количественных вирусологических, серологических и детальных патологоанатомических данных результаты не позволяют установить причинный вклад каждого вируса в падеж и снижение продуктивности или подтвердить коциркуляцию на уровне стада. Работа демонстрирует диагностическую ценность генетической верификации при интерпретации молекулярных результатов в вакцинированных стадах.

Ключевые слова: IBDV, NDV, коинфекция, инфекционная бурсальная болезнь, болезнь Ньюкасла, генотип VII, молекулярная диагностика, яичное промышленное производство.